From: Menachery, Vineet
Sent: Friday, April 17, 2020 10:27 AM
To: Shi, Pei yong;Tseng, Chien-Te K.;LeDuc, James W.;Weaver, Scott;McNees, Andrew G.
Subject: Re: NIH funded collaborations with Zheng-Li Shi?

None for me.

VDM

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Friday, April 17, 2020 9:53 AM
To: Tseng, Chien-Te K. <sktseng@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: RE: NIH funded collaborations with Zheng-Li Shi?

Not at this moment.

- Pei-Yong

From: Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Sent: Friday, April 17, 2020 9:03 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: RE: NIH funded collaborations with Zheng-Li Shi?

Not from my end, Jim.

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Friday, April 17, 2020 8:57 AM
To: Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: NIH funded collaborations with Zheng-Li Shi?

Do we have any NIH funded collaborations with Dr Shi from Wuhan? Replies would be appreciated. Responding to an inquiry

Thanks, Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Yuan Zhiming [yzm@wh.iov.cn]
Sent: 1/18/2020 7:33:47 PM
To: LeDuc, James W. [jwleduc@UTMB.EDU]; Shi, Pei yong [peshi@UTMB.EDU]
Subject: 回复: FW: WIRED interview: new coronavirus in Wuhan

Dear Jim,

Thanks for your information and we are working hard now on the related works. Hopefully some results could be relaesed soon.

The lab is under operation during the holiday and I will let you know the situation at the convenient time.

Regards

Zhiming

==========
Yuan Zhiming, Ph. D.
Professor of Wuhan Institute of Virology
President of Wuhan Branch
Chinese Academy of Sciences
Wuhan 430071, China
Tel: 86-27-87198195(O)
86-27-87197242(L)
Fax: 86-27-87199480
==========

From: LeDuc, James W.
Date: 2020-01-14 03:44
To: Shi, Pei yong; Yuan Zhiming
Subject: FW: WIRED interview: new coronavirus in Wuhan
See link below on a story just released this morning in Wired Magazine. I tried to stress the dramatic improvements in PH and technology between 2003 and now—note title.

Too bad she misspelled my name...

Nice work, Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch

Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Molteni, Megan <megan_molteni@wired.com>
Sent: Monday, January 13, 2020 1:07 PM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Cc: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: WIRED interview: new coronavirus in Wuhan

Here's a link to the story, which published this morning. Thanks again for sharing your story with me, very cool to see how much has changed in 20 years. If you've ever got any interesting infectious pathogen story tips going forward, don't hesitate to reach out.

Best regards,
Megan

On Fri, Jan 10, 2020 at 8:35 AM Molteni, Megan <megan_molteni@wired.com> wrote:

> Got it. Thanks again, Jim.
>
> On Fri, Jan 10, 2020 at 7:54 AM LeDuc, James W. <jwleduc@utmb.edu> wrote:
>
> > Megan, I have not spoken to anyone in China about the techniques they used, but I suspect that they used the same traditional methods to isolate the virus—inoculation of cell cultures. To determine the sequence, I suspect that they did next generation sequencing (see Armstrong, GL et al. Pathogen genomics in public health. NEJM, 26 Dec 2019, 381;26:2569-2580 for an overview of genomics applications in public health. Greg is at CDC).
> >
> > Thanks, Jim
> >
> > **From:** Molteni, Megan <megan_molteni@wired.com>
> > **Sent:** Friday, January 10, 2020 9:27 AM
> > **To:** LeDuc, James W. <jwleduc@UTMB.EDU>
> > **Cc:** Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
> > **Subject:** Re: WIRED interview: new coronavirus in Wuhan
> >
> >
> >
> > Jim, thank you so much for this. And Tom, thank you for helping to reconstruct these events. I know it was a long time ago!
> >
> > My only question is based on the news reporting you've seen out of Wuhan (or correspondence you've had with folks over there), is it fair to assume they used similar set of steps to isolate the virus and get a sequence? If not, where do you think they diverged, from a methods standpoint?

Thanks again,
Megan

On Fri, Jan 10, 2020 at 7:03 AM LeDuc, James W. <jwleduc@utmb.edu> wrote:

> Megan, I spoke to Tom Ksiazek who conducted the original SARS isolation. As mentioned below, he was able to isolate the virus from a throat swab taken from Dr Urban on his arrival into Thailand where he was hospitalized and later died. The specimens were immediately sent to CDC and arrived the evening of 13 Mar and were inoculated into cell cultures that same evening. Evidence of virus growth was first seen on day 5 post-inoculation and a sample of the replicating virus was sent that same day to the electron microscopy laboratory where a coronavirus-like particle was visualized by Cynthia Goldsmith. Based on this preliminary information, Dr Dean Erdman and his team designed consensus primers for coronavirus and were able to amplify a product by RT-PCR, which was then sequenced, further supporting that the isolate as a coronavirus. Virus RNA was sent to the DeRisi lab in California where he confirmed coronavirus identity using his then state-of-the-art array.
>
> Tom Ksiazek is copied here and can correct any errors and provide additional details if needed.
>
> Thanks, Jim
>
> **From:** Molteni, Megan <megan_molteni@wired.com>
> **Sent:** Thursday, January 09, 2020 8:57 PM
> **To:** LeDuc, James W. <jwleduc@UTMB.EDU>
> **Subject:** Re: WIRED interview: new coronavirus in Wuhan
>
>
>
> Thanks Jim, super helpful. Great to chat with you today. Much appreciated!
>
> On Thu, Jan 9, 2020 at 6:19 PM LeDuc, James W. <jwleduc@utmb.edu> wrote:
>
> > Time from receipt of clinical samples to isolation of virus was 5 days; EM identification was done that same day, Inoculated cells on 13 Mar 2003 and had isolate on 18 Mar. More tomorrow.
> >
> > Thanks, Jim
> >
> > **From:** Molteni, Megan <megan_molteni@wired.com>
> > **Sent:** Thursday, January 09, 2020 1:56 PM
> > **To:** LeDuc, James W. <jwleduc@UTMB.EDU>
> > **Subject:** Re: WIRED interview: new coronavirus in Wuhan
> >
> >
> >
> > Great, talk soon. Thanks!
> > M

On Thu, Jan 9, 2020 at 11:54 AM LeDuc, James W. <jwleduc@utmb.edu> wrote:

> Perfect—I'll be in my office at 3 CT. Call to 409-266-6516. If by chance I don't/can't answer, the office number is 409-266-6500 and someone should answer.
>
> Thanks, Jim
>
> ---
>
> **From:** Molteni, Megan <megan_molteni@wired.com>
> **Sent:** Thursday, January 09, 2020 1:50 PM
> **To:** LeDuc, James W. <jwleduc@UTMB.EDU>
> **Subject:** Re: WIRED interview: new coronavirus in Wuhan
>
>
>
> Hi Jim,
>
> I do appreciate that this kind of science is a massively collaborative effort. But hard to talk to everyone on a daily deadline so I very much appreciate your willingness to describe the work of the team. Can I give you call around 3pm CT today? Which number is better for you?
>
> Many thanks,
> Megan
>
> On Thu, Jan 9, 2020 at 11:32 AM LeDuc, James W. <jwleduc@utmb.edu> wrote:
>
> > Hi Megan,
> >
> > I'm happy to chat with you later today or tomorrow. Julie's kind words reflect the combined work of many, many people as I'm sure you appreciate, and all done under her able leadership during a very stressful time. I was coordinating the lab efforts of several talented folks on the front lines actually doing the work.
> >
> > I have a meeting today from 2:00-2:30 CT and again at 4:00-5:00 CT. Tomorrow is generally open from about 10:00 am to 4:00 pm CT. My direct line is 409-266-6516.
> >
> > Thanks, Jim
> >
> > James W. Le Duc, Ph.D.
> > Director
> > Galveston National Laboratory
> > University of Texas Medical Branch
> > Galveston, TX 77555-0610
> > (t) 409-266-6500
> > (f) 409-266-6810
> > (m) 409-789-2012

From: Molteni, Megan <megan_molteni@wired.com>
Sent: Thursday, January 09, 2020 1:13 PM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: Re: WIRED interview: new coronavirus in Wuhan

Hi Jim,

You probably saw Julie's email a little while ago. Any chance you're free today or tomorrow to reminisce about your work identifying SARS and talk about the current situation in Wuhan?

Many thanks,
Megan

On Thu, Jan 9, 2020 at 11:12 AM Molteni, Megan <megan_molteni@wired.com> wrote:

> Thanks Julie, this is hugely helpful. And I appreciate you providing the context in the midst of a retreat. Will follow up with Jim off-thread.
>
> All the best,
> Megan
>
> On Thu, Jan 9, 2020 at 11:01 AM Gerberding, Julie <julie.gerberding@merck.com> wrote:
>
> > Thanks for tracking this story Megan. I am tied up in a retreat unfortunately. The person who led this work is a brilliant global expert, Dr. James (Jim) LeDuc (copied above) who is now a Professor in charge of emerging pathogens at the University of Texas in Galveston. If you recall, with SARS Canadian scientists initially claimed that the infections were caused by a metapneumovirus but that proved to be a false positive. CDC took a more conservative approach. Though we strongly suspected we had isolated the causative coronavirus very early by observing its corona-like structure under an electron microscope, Dr. LeDuc made sure we first essentially satisfied Koch's postulates of disease causality and proved that we could isolate the virus from infected people, inoculate it into a non-human host and recapitulate the disease, and then isolate it from sites of infection in that host. Our approach involved collaborators in Europe who I believe did the actual animal work at the same time we were doing the genetic sequencing. (One lesson learned from the Canadian experience is that virus are ubiquitous

and that isolating and sequencing one does not necessarily mean it is causing the disease.). Hope this background helps. Dr. LeDuc can correct any lapses in my memory.
Best,
jlg
Sent from my iPhone

On Jan 9, 2020, at 12:30 PM, Molteni, Megan <megan_molteni@wired.com> wrote:

> **EXTERNAL EMAIL** – Use caution with any links or file attachments.
> Dr. Gerberding,
>
> I'm a reporter at WIRED and today I'm writing a quick-turn story about how scientists in China have been able to quickly sequence the infectious agent causing pneumonia-like symptoms in about a dozen patients in Wuhan. Specifically, I'm interested in how those methods compare to the search for the pathogen behind SARS in 2003. I reached out to the CDC to speak to someone on the agency's task force at the time and they recommended I get in touch with you. Do you have any time today for a quick phone interview?
>
> Many thanks,
> Megan
>
> --
> Megan Molteni
> Staff Writer | **WIRED**
> o: 415-276-4924
> c: 332-205-1724
> @MeganMolteni

> > > > > > > > delete it from
> > > > > > > > your system.
> > > > > > >
> > > > > > > --
> > > > > > > Megan Molteni
> > > > > > > Staff Writer | **WIRED**
> > > > > > > o: 415-276-4924
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> > > > > > Megan Molteni
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> > > > >
> > > > > --
> > > > > Megan Molteni
> > > > > Staff Writer | **WIRED**
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Megan Molteni
Staff Writer | **WIRED**
o: 415-276-4924
c: 332-205-1724
@MeganMolteni

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: LeDuc, James W.[jwleduc@UTMB.EDU]; Hu, Haitao[haihu@UTMB.EDU]
From: 侯炜[houwei@whu.edu.cn]
Sent: Mon 4/1/2019 8:29:11 AM (UTC-05:00)
Subject: Re: RE: RE: Hi

Hi Prof. Shi,

I will go to the campus tomorrow morning and visit the Lab of Dr. Hu. So when is it convenient for you to meet with each other?

Wei

> -----原始邮件-----
> 发件人: "Shi, Pei yong" <peshi@UTMB.EDU>
> 发送时间: 2019-04-01 20:11:35 (星期一)
> 收件人: "侯炜" <houwei@whu.edu.cn>
> 抄送: "LeDuc, James W." <jwleduc@UTMB.EDU>, "Hu, Haitao" <haihu@UTMB.EDU>
> 主题: RE: RE: Hi
>
> Hi Wei,
>
> When will you be on campus? I will work with your schedule.
>
> Sere you soon.
>
> Pei-Yong
>
> -----Original Message-----
> From: 侯炜 [mailto:houwei@whu.edu.cn]
> Sent: Sunday, March 31, 2019 10:23 PM
> To: Shi, Pei yong <peshi@UTMB.EDU>
> Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; Hu, Haitao <haihu@UTMB.EDU>
> Subject: Re: RE: Hi
>
> WARNING: This email originated from outside of UTMB's email system. Do not click links or open attachments unless you recognize the sender and know the content is safe.
>
>
> Hi Prof. Shi,
> This time I have no talk at UTMB for short time. Wish you to meet in your office.
>
> Wei
>
>
> > -----原始邮件-----
> > 发件人: "Shi, Pei yong" <peshi@UTMB.EDU>
> > 发送时间: 2019-04-01 02:47:22 (星期一)
> > 收件人: "LeDuc, James W." <jwleduc@UTMB.EDU>, "侯炜" <houwei@whu.edu.cn>
> > 抄送: "Hu, Haitao" <haihu@UTMB.EDU>
> > 主题: RE: Hi
> >

552.117

> > Thanks, Jim
> > Hope your [redacted]s recovering well.
> >
> > Hi Dr. Hou,
> > I will be happy to meet with you. Are you interested in giving a seminar at UTMB? If so, Haitao (cc'd) and I could arrange it. In addition, we could show you around and meet with faculty here.
> >
> > I look forward to meeting you.
> >
> > Best,
> > Pei-Yong
> >
> >
> >
> >
> > -----Original Message-----
> > From: LeDuc, James W.
> > Sent: Sunday, March 31, 2019 1:30 PM
> > To: 侯炜 <houwei@whu.edu.cn>
> > Cc: Shi, Pei yong <peshi@UTMB.EDU>
> > Subject: Re: Hi
> >
> > Hi Dr Hou
> >
> > Thanks for your note. Unfortunately [redacted] has been seriously ill and I have taken some time off to help her recuperate and will not be in next week. I am copying Dr Shinto see if he might have time to meet with you.
> >
> > With best regards
> >
> > Jim
> >
> > Sent from my iPhone
> >
> > > On Mar 31, 2019, at 10:39 AM, 侯炜 <houwei@whu.edu.cn> wrote:
> > >
> > > WARNING: This email originated from outside of UTMB's email system. Do not click links or open attachments unless you recognize the sender and know the content is safe.
> > >
> > >
> > > Dear Prof.Leduc,
> > >
> > > Very long time not to connect with you. Here I 'm in Galveston and will visit Dr. Haitao Hu's Lab next week. We have collaborated on multiple projects that investigate HIV and the associated opportunistic co-infections,and has been published on impactful scientific journals such as Plos Pathogens and Journal of Immunology. So this time I wish to have the opportunities to meet with other colleagues here at UTMB that share common research interests with my research groups in the aera of virology besides Dr. Hu. Could you have time to meet with me before I will leave here next Thursday morning?
> > >
> > >
> > > ----------
> > > Wei Hou, M.D.,Ph.D.
> > > Professor/Vice Dean
> > > State Key Laboratory of Virology/Institute of Medical Virology,
> > > School of Basic Medical Sciences Wuhan University, P.R.China Dong-hu

> > > Road 185, Wuhan 430071
> > > Tel:86-27-68789310(office)
> > > E-mail: houwei@whu.edu.cn
> > >
> > >
> > > 侯炜 医学博士
> > > 教授/副院长
> > > 病毒学国家重点实验室/医学病毒学研究所
> > > 武汉大学基础医学院
> > > 中国武汉
> > > 武汉市东湖路185号，邮编430071
> > > 联系电话：86-27-68789310
> > > E-mail:houwei@whu.edu.cn
> > >
> > >
> > >
> > > 积极思考造就积极人生，消极思考造就消极人生。
> >
>
>
> ---
> Wei Hou, M.D.,Ph.D.
> Professor/Vice Dean
> State Key Laboratory of Virology/Institute of Medical Virology, School of Basic Medical Sciences
Wuhan University, P.R.China Dong-hu Road 185, Wuhan 430071
> Tel:86-27-68789310(office)
> E-mail: houwei@whu.edu.cn
>
>
> 侯炜 医学博士
> 教授/副院长
> 病毒学国家重点实验室/医学病毒学研究所
> 武汉大学基础医学院
> 中国武汉
> 武汉市东湖路185号，邮编430071
> 联系电话：86-27-68789310
> E-mail:houwei@whu.edu.cn
>
>
>
> 积极思考造就积极人生，消极思考造就消极人生。

Wei Hou, M.D.,Ph.D.
Professor/Vice Dean
State Key Laboratory of Virology/Institute of Medical Virology, School of Basic Medical Sciences
Wuhan University, P.R.China
Dong-hu Road 185, Wuhan 430071
Tel:86-27-68789310(office)
E-mail: houwei@whu.edu.cn

侯炜 医学博士
教授/副院长
病毒学国家重点实验室/医学病毒学研究所

武汉大学基础医学院
中国武汉
武汉市东湖路185号，邮编430071
联系电话：86-27-68789310
E-mail:houwei@whu.edu.cn

积极思考造就积极人生，消极思考造就消极人生。

To: LeDuc, James W.[jwleduc@UTMB.EDU]
Cc: Reyes, Raul[rareyes@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 4/16/2020 10:28:31 AM (UTC-05:00)
Subject: Re: WIV questions

A few of the questions are about the WIV facility. Since I have never been there, I didn't want to comment. I know you interacted with them in the planning stages.

I'll forward those requests to Raul and Connie.

Thanks

VDM

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Thursday, April 16, 2020 10:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Reyes, Raul <rareyes@UTMB.EDU>; Holubar, Connie J. <cjholuba@UTMB.EDU>
Subject: RE: WIV questions

Me too…Probably best to refer to Raul and Connie who are managing responses unless there are specific questions that you feel we should/can address.

Thanks, Jim

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, April 16, 2020 10:22 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: WIV questions

Hey Jim,

I have been getting more questions about the Wuhan Institute of Virology and my interactions with them. I am not particularly interested in talking about them and have only had limited interactions. I have been sending a few to you. I just wanted to make sure you are ok with me deflecting those questions to you.

Thanks

VDM

To: 'David A Relman'[relman@stanford.edu]; 'Baric, Ralph S'[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; 'Peter Daszak'[daszak@ecohealthalliance.org]; 'Harvey V. Fineberg'[harvey.fineberg@moore.org]; 'Diane Griffin'[dgriffi6@jhmi.edu]; 'Peggy Hamburg'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Rusek, Benjamin[BRusek@nas.edu]
From: Saif, Linda[saif.2@osu.edu]
Sent: Tue 5/12/2020 4:28:58 PM (UTC-05:00)
Subject: Re: Virtual U.S. China dialogue meeting on COVID-19: final docs

---

From: Linda Saif <saif.2@osu.edu>
Date: Tuesday, May 12, 2020 12:44 PM
To: 'David A Relman' <relman@stanford.edu>, "rbaric@email.unc.edu" <rbaric@email.unc.edu>, "Stanley-Perlman@uiowa.edu" <Stanley-Perlman@uiowa.edu>, 'Peter Daszak' <daszak@ecohealthalliance.org>, "'Harvey V. Fineberg'" <harvey.fineberg@moore.org>, 'Diane Griffin' <dgriffi6@jhmi.edu>, 'Peggy Hamburg' <peggy@hbfam.net>, "'jwleduc@UTMB.EDU'" <jwleduc@UTMB.EDU>, "'Dave Franz (davidrfranz@gmail.com)'" <davidrfranz@gmail.com>, "'Shi, Pei yong (peshi@UTMB.EDU)'" <peshi@UTMB.EDU>
Cc: "Rusek, Benjamin" <BRusek@nas.edu>
Subject: Re: Virtual U.S. China dialogue meeting on COVID-19: final docs

Hi All,
Attached is a link to a document from Zhejiang University that was shared with me by a Chinese colleague.
_Handbook+of+COVID-19+Prevention+and+Treatment+F...
This may be what was referred to during our talks on Mon with our Chinese colleagues.
Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, January 3, 2019 5:32 PM
To: 'Kanabrocki, Joseph [MIC]';'David A Relman';'Dave Franz (davidrfranz@gmail.com)';LeDuc, James W.;Shi, Pei yong;'Stephen Higgs';'Diane Griffin';'Saif, Linda';'Baric, Ralph S'
Cc: ''Baric, Toni C' (antoinette_baric@med.unc.edu)';Hare, Hope;Bowman, Katherine;Cervenka, Nicole;'Swayne, David';'Gladue, Douglas';Lowenthal, Micah;'Doris R. Merrill'
Subject: RE: NASEM bio meetings in Harbin, China in Jan 2019 - travel memo and final agenda
Attachments: NAS SOS International_PrintCard.pdf; From -hvrizj- AGENDA_CAAS_NAS_JAN 2019 (20190103) from NAS clean.docx; Harbin Meeting Travel Memo for Jan 2019.docx

Greetings,

Happy new year! The (hopefully) final version of the Harbin meeting agenda (2019-1-03) is attached for your information, sorry for the delay. The agenda includes a visit to the 731 museum and a group tour of the Harbin International Ice and Snow Sculpture Festival on the last day of the meeting.

Due to the ongoing U.S. Government shutdown it is unlikely that Doug Gladue and David Swayne will be able to travel to the meeting. This is unfortunate and we will miss them. However they have provided their slides and other members of the delegation have volunteered to give their presentations on their behalf.

I have attached the latest version of the travel memo for your information. When you arrive in Harbin you will be met at the airport and driven to the Aoluguya Hotel (I do not have hotel room confirmation numbers yet, if I get those before Saturday I will send them in a second email.) **Please print out the memo and bring it with you.** It includes additional information that you may need before you leave.

FYI All travelers funded by NAS have been placed in the International SOS Global Assistance Program http://www.internationalsos.com/en/, (member number 11BMMS000238) while in Harbin (see attached card). Please also enroll in the U.S. Department of State Smart Traveler Enrollment Program (STEP) https://step.state.gov/step/ before you travel.

I will be in the office all day tomorrow if you have any final questions. Thanks again for agreeing to patriciate and I look forward to seeing you in China!

PS Some early photos of the festival:
https://www.theguardian.com/world/gallery/2019/jan/01/preparations-for-the-harbin-ice-and-snow-festival-in-pictures
https://www.cnn.com/travel/article/harbin-ice-and-snow-festival-2019-china/index.html
https://www.washingtonpost.com/lifestyle/kidspost/ice-becomes-works-of-art-at-annual-festival-in-harbin-china/2018/12/31/d53b2c18-0326-11e9-9122-82e98f91ee6f_story.html?utm_term=.f5f170cf1c21

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975
Cell 1-202-839-0075

From: Rusek, Benjamin
Sent: Monday, December 17, 2018 9:04 PM
To: 'Kanabrocki, Joseph [MIC]' <jkanabro@bsd.uchicago.edu>; 'David A Relman' <relman@stanford.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>; jwleduc@UTMB.EDU; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>; 'Stephen Higgs' <shiggs@bri.ksu.edu>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Swayne, David' <David.Swayne@ARS.USDA.GOV>; 'Gladue, Douglas' <Douglas.Gladue@ARS.USDA.GOV>; 'Saif, Linda' <saif.2@osu.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>
Cc: 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Hare, Hope <HHare@nas.edu>; Bowman, Katherine <KBowman@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>
Subject: RE: NASEM bio meetings in Harbin, China in Jan 2019 - conference call on 12/18 at 2 PM ET docs
Importance: High

Greetings,

Just a reminder that we are having a conference call to discuss the Harbin trip tomorrow **Tuesday, December 18th at 2:00 PM ET.**

At 2:00 PM ET please call 1-888-537-7715 and when prompted, enter passcode 552.136

Conference call agenda:
-Introduction
-Discussion of meeting and workshop goals (see attached one pager)
-Discussion of 12-11-18 agenda (attached)
-Discussion of DRAFT travel memo and logistics questions (attached)
-Other issues

We have attached a DRAFT travel memo for your initial review. We are missing a bit of information /detail so plan to send you the final memo (with more information about evening activities) the week before the meeting.

We look forward to talking to you tomorrow.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Cervenka, Nicole
Sent: Friday, December 14, 2018 5:04 PM
To: 'Kanabrocki, Joseph [MIC]' <jkanabro@bsd.uchicago.edu>; 'David A Relman' <relman@stanford.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>; jwleduc@UTMB.EDU; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>; 'Stephen Higgs' <shiggs@bri.ksu.edu>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Swayne, David' <David.Swayne@ARS.USDA.GOV>; 'Gladue, Douglas' <Douglas.Gladue@ARS.USDA.GOV>; 'Saif, Linda' <saif.2@osu.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>
Cc: 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Hare, Hope <HHare@nas.edu>;

Bowman, Katherine <KBowman@nas.edu>; Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: NASEM bio meetings in Harbin, China in Jan 2019 - conference call on 12/18 at 2 PM ET

Good Afternoon,

We will hold a 1-hour conference call for the Harbin trip on **Tuesday, December 18th at 2 PM ET.**

At 2:00 PM ET please call **1-888-537-7715** and when prompted, enter passcode **552.136**

We will also be sending out a conference call agenda and draft travel memo before the conference call.

Best regards,

Nicole

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Tuesday, December 11, 2018 5:41 PM
To: 'Kanabrocki, Joseph [MIC]' <jkanabro@bsd.uchicago.edu>; 'David A Relman' <relman@stanford.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>; jwleduc@UTMB.EDU; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>; 'Stephen Higgs' <shiggs@bri.ksu.edu>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Swayne, David' <David.Swayne@ARS.USDA.GOV>; 'Gladue, Douglas' <Douglas.Gladue@ARS.USDA.GOV>; 'Saif, Linda' <saif.2@osu.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>
Cc: 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Bowman, Katherine <KBowman@nas.edu>
Subject: NASEM bio meetings in Harbin, China in Jan 2019 - update and conference call
Importance: High

Greetings,

Thank you for agreeing to participate in the U.S. National Academy of Sciences, Engineering and Medicine (NASEM) and the Chinese Academy of Agricultural Sciences (CAAS) U*.S. China Dialogue and Workshop on the Challenges of Emerging Infections, Laboratory Safety, Global Health Security and Responsible Conduct in the Use of Gene Editing in Viral Infectious Disease Research*.

As you know the meetings will take place on January 8-9-10, 2019 on the campus of CAAS's Harbin Veterinary Research Institute in Harbin, China. The U.S. group will stay at the **Aoluguya Hotel** (No. 800, the 3rd Road of Chuangxin, Harbin) during the meeting.

I have attached the latest DRAFT of the agenda for your review and information. It includes the names of confirmed Chinese speakers and possible session goals and discussion questions. Please review (and propose modifications to) the talk titles we proposed.

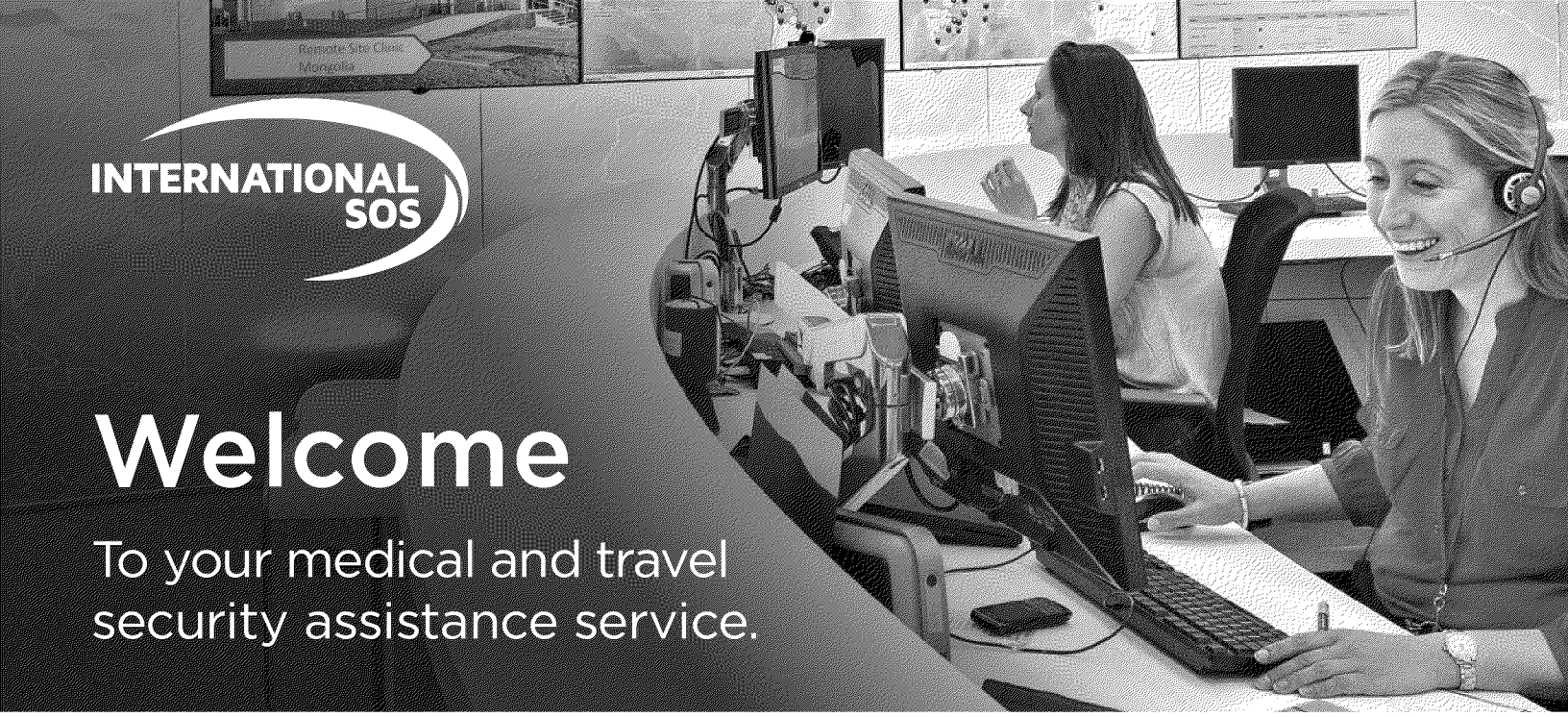
We would like to hold a conference call next week to discuss the agenda and other issues associated with the meeting. **Please send Nicole Cervenka (cced) your availability to participate in a one hour call from 9 AM to 6 PM ET, Monday Dec 17 to Thursday December 20th.** We will provide conference call in information when we send you the time for the call.

Thank you for working with Hope Hare (also cced) to make your flight arrangements and submit your visa application. We are working on the applications and will get passports back to you as soon as possible. We will also send you a travel memo with full logistical details before the conference call.

Kind regards,

Ben

Benjamin J. Rusek
Senior Program Officer
Policy and Global Affairs
The U.S. National Academy of Sciences, Engineering and Medicine
Room 526
500 5th Street, NW
Washington, DC 20001
Phone 1.202.334.3975
Fax 1.202.334.1730
Cell 1.202.839.0075



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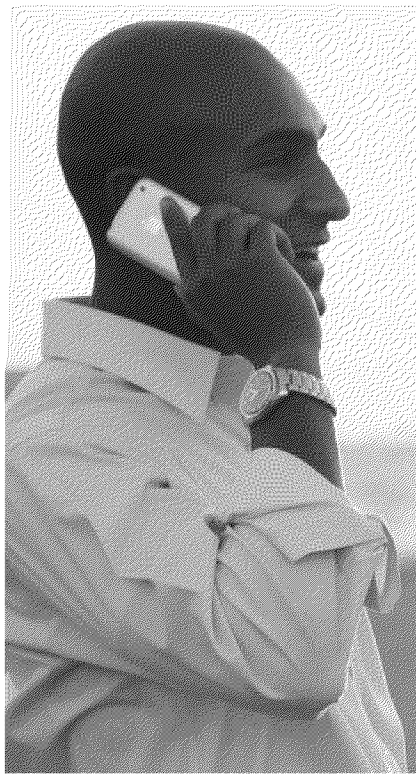

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- Sign up for health and security email alerts
- Inform friends and family that you are with International SOS, so they can get in touch with us should they have any concerns for your welfare while you are away.

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- Travel advice on loss of travel documents or legal assistance
- Assistance paying your medical fees

In an emergency, we provide all necessary emergency services, including:

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U.S.-China Dialogue and Workshop on the Challenges of Emerging Infections, Laboratory Safety, Global Health Security and Responsible Conduct in the Use of Gene Editing in Viral Infectious Disease Research

Harbin Veterinary Research Institute
Chinese Academy of Agricultural Sciences
Harbin, China

8-10 January 2019

Monday, 7 January

Some participants arrive at the Aoluguya Hotel (No. 800, the 3rd Road of Chuangxin, Harbin)

Evening activity for those that have arrived: group tour of the Harbin Ice Festival (proposed)

Tuesday, 8 January

7:50 Shuttle bus from Aoluguya Hotel to Harbin Veterinary Research Institute (HVRI)
(No 678 Haping Road, Xiangfang Qu, Haerbin, Heilongjiang Province, China 150060)

WELCOME AND OPENING REMARKS

9:00 **Welcome, Introductions, and Opening Remarks**
Chairs: Zhigao Bu

1. Welcome on behalf of Chinese Academy of Agricultural Sciences (CAAS): , **Kongming Wu**, Vice-President of CAAS
2. Remarks on Behalf of U.S. National Academies of Sciences, Engineering, and Medicine: **Benjamin Rusek**, Policy and Global Affairs, U.S. National Academy of Sciences (NAS) and **Diane Griffin**, Johns Hopkins Bloomberg School of Public Health and Vice-President of NAS

9:15 **Session 1. Keynote Addresses** *[20 min each]*
Chairs: Benjamin Rusek

1. **Prof. George F. Gao**, Director-General, Chinese Center for Disease Control and Prevention
   Oversight for Research on Viral Pathogens with Pandemic Potential – the Perspective from China
2. **Prof. Linda Saif**, Ohio State University
   Emerging swine coronaviruses and their interspecies transmission

Q&A/Discussion *[15-20 min]*

10:15 Coffee and Tea Break

EMERGING INFECTIOUS DISEASES

Goal for Sessions 2 and 3: Consider progress in understanding two diseases of concern to China and the U.S., including the health and economic implications and what advances in understanding may be enabled by recent scientific and technical developments such as gene editing.

10:30 Session 2. Swine Fever *[15 min each]*

Chairs: Linda Saif and **Hualan Chen**

1. **Prof. Xiaodong Wu**, China Animal Health and Epidemiology Center)
   Current Situation and Control Strategy of African Swine Fever in China
2. **Prof. Zhigao Bu,** Harbin Veterinary Research Institute, CAAS *Characterization of African Swine Fever Virus Isolated from China*
3. **Dr. Douglas Gladue**, U.S. Department of Agriculture
   Editing African swine fever virus field isolates for live attenuated vaccines: Current live attenuated vaccine status
4. **Prof. Hengsheng Ouyang,** Jilin University
   Genome-edited pigs protected from classical swine fever virus
   Q&A/Discussion *[10-15 min]*

Proposed discussion questions

- What is known about the epidemiology, health, and economic impacts of Africa Swine Fever?
- What is the latest progress on developing effective countermeasures and limiting the spread of this disease?
- What critical areas remain unknown or what are key challenges to preventing and responding to Africa Swine Fever outbreaks? How can new scientific and technical advances contribute to research and development?

11:45 Session 3. Influenza

Chairs: Linda Saif and **Hualan Chen**

1. **Overview: Perspectives on international collaborations for influenza research** *[10 min each]*
   Prof. Hualan Chen Harbin Veterinary Research Institute, CAAS
   Influenza Vaccine Research in China and Globally
   Prof. David Swayne, U.S. Department of Agriculture
   Collaborating on Influenza Research from the U.S. perspective
2. **Panel Discussion**
   Speakers provide 5 minutes opening remarks on the topics identified below, followed by discussion facilitated by the session Chairs
   Prof. Dayan Wang, National Institute for Viral Disease Control and Prevention, China CDC
   Human Infection with Zoonotic Influenza
   Prof. Chengjun Li, Harbin Veterinary Research Institute, CAAS
   Interactions between Influenza Viral RNP Complex Proteins and Host Cellular Factors

Proposed discussion questions

- What is known about the epidemiology, health, and economic impacts of Influenza?
- What is the latest progress on developing effective countermeasures?
- What critical areas remain unknown or what are key challenges to preventing and responding to influenza outbreaks? How can new scientific and technical advances contribute to research and development?

12:45 **Group Photo**

13:00 **Lunch**

VIRAL PATHOGENS: SCIENCE AND RESPONSIBILITY

Goal for Sessions 4, 5, and 6: Discuss relevant pathogen properties that researchers may seek to alter, and why, as part of studying viral pathogens with pandemic potential. Illustrate challenges and opportunities posed by new strategies such as use of gene editing, rational design approaches, other strategies enable by advancing biotechnology. Discuss the associated issues in the ethical planning and conduct of such research so that it can be conducted safety and securely.

14:30 **Session 4. Understanding and Engineering Viral Pathogens with Pandemic Potential** *[20 min each]*

Chairs: Diane Griffin and **George F. Gao**

1. **Ralph Baric**, University of North Carolina
   Advances in Understanding and Altering Pathogen Properties
2. **Prof. Weiwen Zhang**, Tianjin University
   Cutting Edging New Biotechnology: Strategies and Tools for Engineering

15:10 Coffee and Tea break

15:45 **Session 5. Bioethics and Responsible Planning for Pathogen Research** *[15 min each]*

Chairs: Diane Griffin and **George F. Gao**

1. **Prof. Zhiming Yuan**, Wuhan Institute of Virology, CAS
   Biosafey and Bioethics in Medical Research
2. **David Relman**, Stanford University
   Tradeoffs between benefits and risks in pathogen research
3. **Prof. Jianwei Wang,** Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College
   Biosafety Management of Synthetic Biology: Challenges and Progress
4. **Associate Prof. Yang Xue**, Tianjin University
   Biosafety and Bioethis Considerations in Dual-Use Risks Management – China's Efforts and Future Works

16:45 **Session 6. Panel on Science and Ethics in Research with Pathogens with Pandemic Potential**

Chairs: **Diane Griffin** and **George F. Gao**

Chairs facilitate a discussion between **Ralph Baric, Weiwen Zhang, Zhiming Yuan, David Relman, Jianwei Wang, Yang Xue** and the audience. *[45 min]*

Proposed discussion questions

- *What do recent advances in biotechnology, such as genome editing, enable researchers to achieve in improved characterization and alteration of the properties of pathogenic viruses?*
- *What do you see coming in the near term? What still remains very challenging and why?*
- *Because research on viral pathogens can raise security concerns, how do you think about making decisions on whether or not to conduct such research or about modifying research proposals? What are the responsibilities and best practices of the PI to ensure that pathogen research is conducted safely and securely over the course of the project?*
- *What ethical and policy challenges remain and what actions do you think are needed to help overcome these challenges?*

17:30 Transportation from HVRI

18:30 Dinner at Restaurant

Wednesday, 9 January

07:50 Transportation to HVRI

VECTOR AND HOST ENGINEERING

Goal for Session 7: Research to understand and prepare for viral pathogens may also involve work conducted on the hosts or vectors of such pathogens, for example to better understand host-pathogen responses and vector transmission. Discuss how advances in areas such as gene editing are affecting such research and best practices for safely and responsibly conducting such studies

9:00 **Session 7. Vector and Host Engineering: Safety and Security** *[15-20 min each]*
Chair: Jim Le Duc and **Zhiming Yuan**

1. **Prof. Qian Han**, Hainan University
   Biochemical Pathway of a Mosquito Innate Immunity, Melanization
2. **Stephen Higgs**, Kansas State University
   Best practices in safety and security for working with arthropods that serve as pathogen vectors, including responsible research with gene drive modified vectors

Q&A/ Discussion *[20 min]*

10:00 Coffee and tea break

10:30 **Session 7 resumes**

3. **Highlights of Recent Research:**
   Prof. Tongyan Zhao, Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences
   Vector Competence of Emerging Mosquito Borne Virus in China
4. **Prof. Gong Cheng**, Tsinghua University
   A Gut Commensal Bacterium Promotes Arbovirus Infection in Mosquitoes

Q&A/ Discussion *[30 min]*

Proposed discussion questions

- *What do recent advances in biotechnology, such as genome editing, enable researchers to achieve in studying and manipulating hosts and vectors of viral pathogens*
- *What do you see coming in the near term? What still remains very challenging and why?*
- *What are the responsibilities and best practices of the PI to ensure that pathogen research is conducted safely and securely over the course of the project?*
- *What ethical and policy challenges remain and what actions do you think are needed to help overcome these challenges?*

12:00 Lunch

EFFECTIVE OVERSIGHT SYSTEMS

Goal for Session 8: Discuss the systems of institutional review and oversight in China and in the US for safe and secure conduct of laboratory research on viral pathogens with pandeminc potential. Focus on the institutional systems including the important role of leadership in promoting institutional cultures that support responsible research practices.

13:30 Session 8. Best Practices in Laboratory Safety and Security for Pathogen Research

Chairs: Mifang Liang and **Joe Kanabrocki**

1. **Joseph Kanabrocki**, ***University of Chicago*** *[20 min]*
   Institutional review and oversight for research on viral pathogens with pandemic potential – a U.S. perspective
2. **David Franz** and **Zhiming Yuan** *[20 min together]*
   The Role of Leaders in Laboratory Safety: Culture and governance to steer toward behavior changes

Facilitated Discussion

Chair facilitates a discussion with the speakers and audience [25 min]

Proposed discussion questions

If assessment of anticipated risks and benefits results in the decision to undertake an experiment that involves characterizing or manipulating a pathogen with pandemic potential:

1. *How should the research-conducting institution oversee this research to ensure that it is conducted safely and securely over the course of the project? Does this oversight happen at one point or at multiple points over the course of the project?*
2. *What are the responsibilities of institutional leadership in promoting the culture of responsible conduct of science?*
3. *Are there particular scientific or experimental practices that should be incorporated into research design and conduct that can maximize safety and security for studies carried out to understand or alter the properties of pathogens with pandemic potential?*

14:40 Special Topic: One Health in China *[20 min]*

Chairs: Mifang Liang and **Joe Kanabrocki**

Understand how a One Health approach is shaping research to understand and address viral pathogens in China
Prof. Jiahai Lu, Sun Yat-sen University
Q&A/Discussion *[10 min]*

15:10 Coffee and Tea Break

RECENT RESEARCH AND PERSPECTIVES

Goal for Sessions 9 and 10: Gain further shared insights into how research communities are addressing issues in biosafety, biosecurity, and bioethics, particularly as applied to research on emerging infectious diseases caused by viral pathogens

15:30 **Session 9. Chinese Biosafety, Biosecurity, and Bioethics** *[15 min each]*
Chair: Mifang Liang and **Joe Kanabrocki** (give some opening comments)

1. **Dr. Peijun Zhai**, CNAS
   Overview of Laboratory Biosafety Management System in China
2. **Prof. Jiancheng Qi**, National Biological Protection Engineering Center, China
   Development and Application of Laboratory Biosafety Equipment in China
3. **Prof. Yunzhang Hu**, Institute of Medical Biology, Chinese Academy of Medical Sciences
   Kunming National Primate Research Center of High-Level Biosafety
4. **Prof. Ruifu Yang**, Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences
   Microbial Forensics: Building Capability for Source Tracing of Bioterrorism Pathogen.

Q&A/Discussion *[30 min]*

17:00 Transportation from HVRI to Restaurant

18:30 Dinner and optional group outing

Thursday, 10 January

7:50 Hotel shuttle bus transport to HVRI

9:00 **Special Topic: Update on Acute Flaccid Myelitis**
Diane Griffin, Johns Hopkins Bloomberg School of Public Health [20 min]
Review of what is currently known about the cause of Acute Flaccid Myelitis
Q&A/Discussion [*10 min]*

9:30 **Session 10: Chinese Perspectives on Emerging Infectious Diseases** *[15 min each]*
Chair: Pei-yong Shi and **Zhengli Shi**

1. **Prof. Changjiang Weng,** Harbin Veterinary Research Institute, CAAS
   DDX19, A novel Viral RNA Sensor, Regulates IFN Signaling upon Viral Infection
2. **Prof. Zhengli Shi,** Wuhan Institute of Virology, CAS
   Risks of MERS-cluster coronaviruses in China

3. **Prof. Haixue Zheng**, Lanzhou Veterinary Research Institute, CAAS,
   Rational Design of Master Seed Virus to Improve the Safety and Effectiveness of Foot and Mouth Disease Vaccine

10:15 Coffee and Tea Break

10:45 Session 10, cont'd

4. **Prof. Rui Gong**, Wuhan Institute of Virology, CAS
   Development of Neutralizing Antibodies Domains as Therapeutic Candidates Against Infectious Diseases
5. **Prof. Longding Liu**, Institute of Medical Biology, Chinese Academy of Medical Sciences
   Development of inactivated EV71 Vaccine (Human diploid cell) and Pathogenic Study of EV71 Infection in Rhesus Macaque
6. **Prof. Chengfeng Qin**, Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences
   Zika Virus Neurotropism the Bad and the Good

Q&A/Discussion *[30 min]*

12:00 Special Session 11

Chair: Pei-yong Shi and **Zhengli Shi**

1. **Prof. Chunbo Lou,** Institute of Microbiology, CAS
   Large Gene Cluster and Regulatory Manipulation for Activating the Cryptic Natural Product Clusters in Streptomyces
2. **Prof. Xiaoli Xue,** Key Laboratory of Synthetic Biology, Shanghai Institute of Plant Physiology, CAS
   Creating a Functional Single-chromosome Yeast

12:30 Lunch

13:00 Visit the Unit 731 Museum

LOOKING FORWARD (CLOSED SESSION, BY INVITATION ONLY)

Goal for Sessions 12: Identify shared priorities and potential opportunities for future discussions to advance safety and security

14:30 Session 12: China-U.S. Collaboration: Opportunities to Prevent Future Pandemics

Chairs: James Le Duc, Zhiming Yuan, Diane Griffin, and Zhigao Bu

Cooperating to combat emerging infectious diseases that affect China and the U.S. - Cooperation on laboratory safety: biocontainment research and collaboration across borders (including discussion on building a network of BSL-4 laboratories concept http://science.sciencemag.org/content/362/6412/267 and other collaborations between Chinese and American scientists)

16:00 Visit Harbin International Ice and Snow Festival

18:30 Transport to Restaurant

Friday, 11 January

AM and PM: transportation provided to airport

U.S.-China Dialogue and Workshop on the Challenges of Emerging Infections, Laboratory Safety, Global Health Security and Responsible Conduct in the Use of Gene Editing in Viral Infectious Disease Research

TRAVEL MEMORANDUM

TO: Harbin Travelers
FROM: Nicole Cervenka
SUBJECT: Travel Information for Harbin, January 2019

ARRIVALS

Traveler	Flight Number	Arrival	Time	Ticket Number	Cell Number
Gladue, Douglas*	MU 5197	January 6	9:25 PM		
Bowman, Katherine	CA 1639	January 6	10:15 PM	999 7270588053	001-443-415-5281
Rusek, Ben	CA 1639	January 6	10:15 PM	999 7270588052	001-202-839-0075
Higgs, Stephen	CA 1639	January 6	10:15 PM	999 7270588051	001-785-341-9004
Baric, Ralph	MU 5619	January 7	12:10 AM	006 726776464647	001-336-266-5433
Swayne, David*	MU 5619	January 7	12:10 AM		
Franz, David	CA 1623	January 7	2:50 PM	890 0745539926	001-240-674-0797
Shi, Pei-yong	G1205 (Train)	January 7	4:56 PM	(Train)	
Griffin, Diane	MU 5197	January 7	9:40 PM	781 7267764604	001-410-491-6059
Kanabrocki, Joseph	CA 1639	January 7	10:15 PM	999 7270587808	001- 773-612-6804
LeDuc, James +1	CA 1639	January 7	10:15 PM	999 7267764578	001-409-789-2012
Relman, David	CA 1639	January 7	10:15 PM	999 7267764580	001-650-407-0172
Saif, Linda	CA 1639	January 7	10:15 PM	890 0745523287	001-330-466-3444

*May not be able to attend (due to USG shut down) If for some reason you are delayed or rerouted onto another flight, please e-mail or text Ben Rusek (brusek@nas.edu 001-202-839-0075) and let him know your new flight information.

IMMIGRATION AND CUSTOMS PROCEDURES

While on the plane to your first destination in China, you will receive a landing card to complete. You will need some of the information in this memo to fill out the card so please print it and take it with you. After departing the plane, you will pass through immigration, following the signs for foreign citizens. China has now started requiring fingerprinting of travelers at immigration checkpoints so you may need to go to a machine to do this before entering the immigration line. The immigration officer will check your passport and visa. After you clear immigration if you checked a bag you will then collect your luggage. After you have your bags, you will go through customs. You should select the "GREEN" channel if you have nothing to declare. If you go through the Green channel, you will not be asked to complete a Baggage Declaration Form. From there, you will enter the transfer hall, recheck your baggage, go through security for domestic flights, and go to your gate. When you arrive in Harbin, you can pick up your rechecked bag at baggage claim.

GROUND TRANSPORTATION TO HOTEL

Upon arrival in Harbin, you will be met at the airport by a driver and an English-speaking volunteer from the Harbin Veterinary Research Institute (HVRI). They will be holding a sign with HVRI, your name written in English or "NAS," and will take you to the **Aoluguya Hotel** (see address in hotel section) where you will stay while in Harbin. The area immediately outside of baggage claim may be crowded, you may have to take a second look, but the driver will be there. Should your flight be delayed, a driver will wait for you. Some people arrive on the same flights (see arrivals table) or at the same time so you may wish to communicate before arriving in Harbin and meet up on the plane or at the airport.

If you cannot find the driver after having thoroughly looked for the sign with your name, please take an OFFICIAL TAXI ONLY (do not take a taxi van) to the Aoluguya Hotel (see address below). The airport taxi stand is well marked after you leave the customs and immigration part of the airport. The cost of a taxi ride to the hotel from HRB is RMB 120 ¥ (approximately $18). The Chinese currency is the Renminbi, abbreviated RMB, and the unit is the Yuan, abbreviated as ¥ or CNY; currently 1 USD = 6.88 CNY/RMB. You can use the currency exchange offices at the airports. Please ask for a receipt from the driver as you will need it for reimbursement. It is not customary to tip the drivers. Please pay by the meter in the taxi. DO NOT ACCEPT offers from unofficial drivers under any circumstances.

EMERGENCY CONTACT NUMBERS

Ben Rusek, traveling to Harbin	**U.S. Cell Phone (phone and data): +1-202-839-0075**
Katie Bowman, traveling to Harbin	**U.S. Cell Phone +1-443-415-5281**
Micah Lowenthal, in Washington, D.C.	**U.S. Cell Phone: +1-202-527-4467**
Rita Guenther, in Washington, D.C.	**U.S. Cell Phone: +1-202-430-2828**
Nicole Cervenka, in Washington, D.C.	**U.S. Office Phone: +1-202-334-2615**

Kentlands Travel
1-800-552-6425, after hours: **1-888-565-9174, 1-301-948-2448** (NAS Travel Code PGA190018)

U.S. Embassy in China	**(86-10) 8531-3300** (in Beijing, China)
No. 55 An Jia Lou Lu	**(86-10) 8531-4000** (Emergency Contact Number)
Beijing, China, 100600	BeijingACS@state.gov
U.S. Consulate General in Shenyang	**(86-24) 2322-1198**
U.S. Consulate General in Shanghai	**(86-21) 8011-2200**
1469 Huai Hai Zhong Road	ShanghaiACS@state.gov
Shanghai, China, 200031	

YOUR HOTEL IN HARBIN

Aoluguya Hotel
Address: No. 800 Chuangxin 3rd Road
Harbin, China, 150001

敖麓谷雅
黑龍江省哈爾濱市創新三路 800 號
Telephone: +86 451 85932358

SEE MAP AT THE END OF THIS MEMO

Aoluguya Hotel Information				
Traveler	**Arrive**	**Depart**	**Confirmation #**	**# of nights**
Gladue, Douglas*	January 6	January 11		5
Bowman, Katherine	January 6	January 11		5
Higgs, Stephen	January 6	January 11		5
Rusek, Ben	January 6	January 12		6
Baric, Ralph	January 7	January 11		5 (early AM arrival)
Swayne, David*	January 7	January 11		5 (early AM arrival)
Relman, David	January 7	January 10		3
Shi, Pei Yong	January 7	January 10		3
Griffin, Diane	January 7	January 11		4
Franz, David	January 7	January 11		4
Kanabrocki, Joseph	January 7	January 11		4
LeDuc, James +1	January 7	January 11		4
Saif, Linda	January 7	January 11		4

*May not be able to attend. Again if for some reason you are delayed or rerouted please e-mail or text Ben Rusek (brusek@nas.edu 001-202-839-0075) and let him know.

MEETING LOCATION

The workshop will be held at the Harbin Veterinary Research Institute (HVRI), a ~45-minute drive from the hotel. A shuttle bus will take you from the hotel to HVRI each morning and return you to the hotel every evening. **The shuttle bus will leave the hotel for the HVRI at 7:50 AM on the first day of the meeting.** The HVRI campus is located at:

Harbin Veterinary Research Institute

Weihai N Rd, Xiangfang Qu, Haerbin Shi, Heilongjiang Sheng, China, 150060

中国农业科学院哈尔滨兽医研究所

中国黑龙江省哈尔滨市香坊区威海北路 邮政编码: 150060

SEE MAP AT THE END OF THIS MEMO

MEALS

The Aoluguya Hotel has restaurants on the premises. Breakfast each morning is included with your room. Most lunches and dinners will be provided. We will reimburse reasonable expenses for other meals up to $101 per full day and $75 for the first and last days (travel days).

TRAVEL ISSUES

If you have any issues during travel (e.g., weather delays), inform Ben and to rebook contact:
Kentlands Travel, 1-800-552-6425, **after hours:** 1-888-565-9174
nas@uniglobekentlands.com
Reference number: PGA190018

DEPARTURE INFORMATION

HVRI has arranged drivers to take you from the hotel to the airport to leave Harbin. **Specific departure information will be provided by HVRI staff or Ben during the meeting.** Please confirm your departure details with Ben at least one day prior to your departure.

DEPARTURES

Traveler	Flight Number	Departure	Time	Ticket number
Relman, David	CA 1644	January 10	11:50 AM	999 7267764580
Shi, Pei Yong	CZ 6318	January 10	3:30 PM	784 7270588034
Swayne, David*	MU 5620	January 11	7:15 AM	
Baric, Ralph	CZ 6219	January 11	8:25 AM	006 726776464647
Gladue, Douglas*	CZ 6219	January 11	8:25 AM	
Kanabrocki, Joseph	CA 1640	January 11	8:30 AM	999 7270587808
Saif, Linda	CA 1640	January 11	8:30 AM	890 0745523287
Franz, David	CA1644	January 11	11:50 AM	890 0745539926
Griffin, Diane	CA 1644	January 11	11:50 AM	999 7267764606
Bowman, Katherine	CA 1644	January 11	11:50 AM	999 7270588053
LeDuc, James +1	CA 1644	January 11	11:50 AM	999 7267764578
Higgs, Stephen	HU 7786	January 11	5:25 PM	
Rusek, Ben	CA 1644	January 12	11:50 AM	999 7270588052

*May not be able to attend

TRAVEL TIPS

Getting Around

Taxis are inexpensive and convenient to use. To make communication easier, have the hotel write your destination in Chinese. Be aware that some drivers will attempt to negotiate the price of a ride and that asking them to run the meter will help avoid potential conflicts.

You can also use the app **DiDi,** which is similar to Uber of Lyft in the U.S. If you plan on using the app, download it from your smart phone's app store and set it up on your phone before you leave.

The bus system in Harbin is the most convenient public transportation option. Signage is in Chinese, but the stops should be announced in both Chinese and English. Passengers can pay by touching on with an "IC" card or by putting ¥1 or ¥2 into the fare box as they board the bus.

If for some reason you need a car and driver while in Harbin, you may request a car at the hotel front desk. Please arrange for payment directly with the hotel or with the car and driver service. Taxis can also be called by the concierge. It is helpful to have the hotel concierge write your destination in Chinese for the driver. Likewise, have the hotel address in Chinese for your return.

What to Pack

The weather will likely be cold at around 15°F. Therefore, it is a good idea to bring plenty of warm clothes, a hat, gloves, etc. The meeting will begin with business attire (coat and tie) and hope that it becomes less formal as the meeting proceeds.

Be sure to bring any medications or other items you will need, preferably in a carry-on just in case your luggage is delayed. **Many common over the counter medications are not available in China.**

A list of useful items includes: plenty of business cards, a travel alarm clock, warm layers, a hat, gloves, a small flashlight, pocket-packs of tissues and wet wipes, cold medication, Imodium, a camera and chapstick. It is best not to bring anything that would be an attractive target for thieves, such as expensive camera equipment. You will have to decide whether to bring a laptop computer. If you do bring one, it is generally a good idea to keep it with you at all times.

Money

You may want to obtain some Chinese money of your own for souvenir shopping, drinks, entertainment, and sightseeing. The exchange rate on December 12, 2018 was 6.88 Yuan per dollar. For purchases or exchanges, please bring cash, debit cards, or credit cards. Traveler's checks are much less useful and very inconvenient – only a few banks in China will change them – so we do not recommend that you bring them. Some ATM machines will accept international cards, including Bank of China and China Merchants Bank, and provide instructions in English. If an ATM requires a six-digit PIN, try adding two zeros to the front of your number. There are also Western Union locations in almost every China Post 中国邮政 and Agricultural Bank 农业银行; look for the yellow western union sign.

Some shops and restaurants will accept international credit cards. However some only accept Union Pay branded cards. It's always good to have one with you in case of emergency, but you should **not** rely on being able to use credit cards for all your purchases. Even some businesses that say that they take credit cards only take Chinese network credit cards (not Visa, MasterCard, or Amex). If you bring cash, please make sure that the bills are clean. Worn, stained, marked, or old bills are often rejected in China. When carrying Chinese currency an assortment of denominations is useful, as you might not always be able to change large bills. (Many people use their phone and the Chinese app WeChat to pay for purchases.)

Health Concerns

Drinking tap water in China is **not** recommended. Please drink bottled water whenever possible. The air quality in Harbin averaged around 100AQI (moderate) in December and January 2018, but has recently reached the 300s (hazardous). The U.S. Department of State recommends sensitive individuals should consider limiting prolonged outdoor activities, and that everyone should avoid outdoor exertion when the air quality is at hazardous levels.

Global Assistance for Travelers

Before you travel please enroll in the U.S. Department of State Smart Traveler Enrollment Program (STEP) https://step.state.gov/step/. All travelers funded by NAS have been placed on the International **SOS Global Assistance Program** http://www.internationalsos.com/en/, **(member number 11BMMS000238)** while in Harbin. As a traveler for NAS, you can utilize this resource by calling an International SOS Assistance center, which has physicians, multilingual coordinators, operations managers, logistics support personnel and medical and security professionals on hand to speak with you 24/7. SOS can give medical advice, arrange for you to be seen at a nearby medical center (pre-evaluated for quality), arrange for prescription medications, or even arrange for evacuation, if needed. Note that this is assistance, not insurance, but SOS

and NAS can arrange payment for services and work out reimbursement from your insurance later. The NAS membership number is 11BMMS000238. Your closest assistance center in China will be the Beijing office (+86-10-6462-9100). SOS International Alarm Centers can also be contacted in Hong Kong at (852) 2528 9900 and in the United States at (215) 942 8226. See the International SOS card or download the SOS App before you travel, which is the fastest way to access help in case of an emergency. NAS staff has experience working with International SOS and can provide assistance if requested; please ask for our assistance should you have medical concerns. Ben will have hard copies of SOS cards.

International SOS Recommended Hospital in Harbin

HEILONGJIANG PROVINCIAL HOSPITAL HARBIN, CHINA
No.82 Zhongshan Road
Xiangfang District,
Harbin
P.R. China 150036
Tel: + 86 0451 8802 5770

International SOS Affiliated Medical Joint Venture Clinics & Assistance Center

BEIJING OFFICE
Suite 105, Wing 1
Kunsha Building, No 16 Xinyuanli
Chaoyang District
Beijing
P.R China 100027
Tel: +86 (0) 10 6462 9199
Fax: +86 (0) 10 6462 9117

Additional information on medical providers specializing in treating foreigners for general medical, dental and orthodontic problems are available at https://china.usembassy-china.org.cn/

Information on vaccinations and other health precautions, such as safe food and water precautions and insect bite protection, may be obtained from the Centers for Disease Control and Prevention's hotline for international travelers at 1-877-FYI-TRIP (1-877-394-8747) or via the CDC's Internet site at: https://wwwnc.cdc.gov/travel/destinations/traveler/none/china

For information about outbreaks of infectious diseases abroad consult the World Health Organization's (WHO) website at http://www.who.int/en. Further health information for travelers is available at: http://www.who.int/countries/chn/en/

REIMBURSEMENT INFORMATION

For travel being funded by NAS, after you return to the United States, you will use an electronic Travel Expense Report (eTER) to request reimbursement for reasonable travel expenses, including:

- **Taxi cabs, shuttles, and public transportation expenses for meeting related trips are reimbursable.** *Sedan services are only reimbursable if the cost is comparable to a taxi fare.*
- **Meal costs** (based on actual expenses not paid by NAS; NAS does not reimburse for alcohol).
- **Incidental expenses**

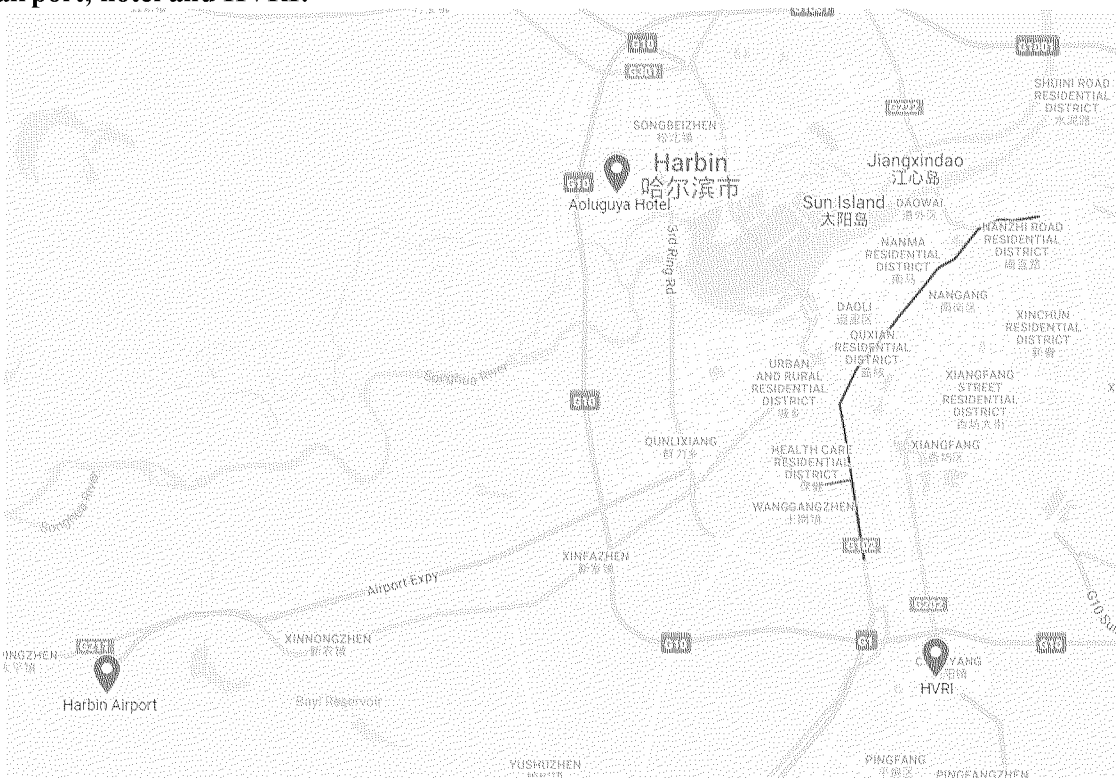
Please retain all receipts for any expenses over $75 incurred during travel on Academy business, including original airline receipts, even if they were direct billed to NAS. No charges over $75 can be reimbursed without an accompanying receipt. This includes items such as airfare, taxi charges, and meals as described above. It is Academies policy that all travel expense reports (TER) are completed within 25 days of travel. Sponsors may reject expenses not submitted on time. If you have questions, or trouble completing your TER, please contact your travel coordinator for assistance.

Please complete your Travel Expense Reimbursement (TER) via Concur, our online reimbursement tool (https://www.concursolutions.com) or download the mobile app (https://www.concur.com/en-us/mobile). Your Concur sign-in information, password, and detailed instructions for completing your TER will be sent in a separate email from your travel coordinator.
*If you are having trouble logging in to Concur, please contact the Travel Office traveloffice@nas.edu.

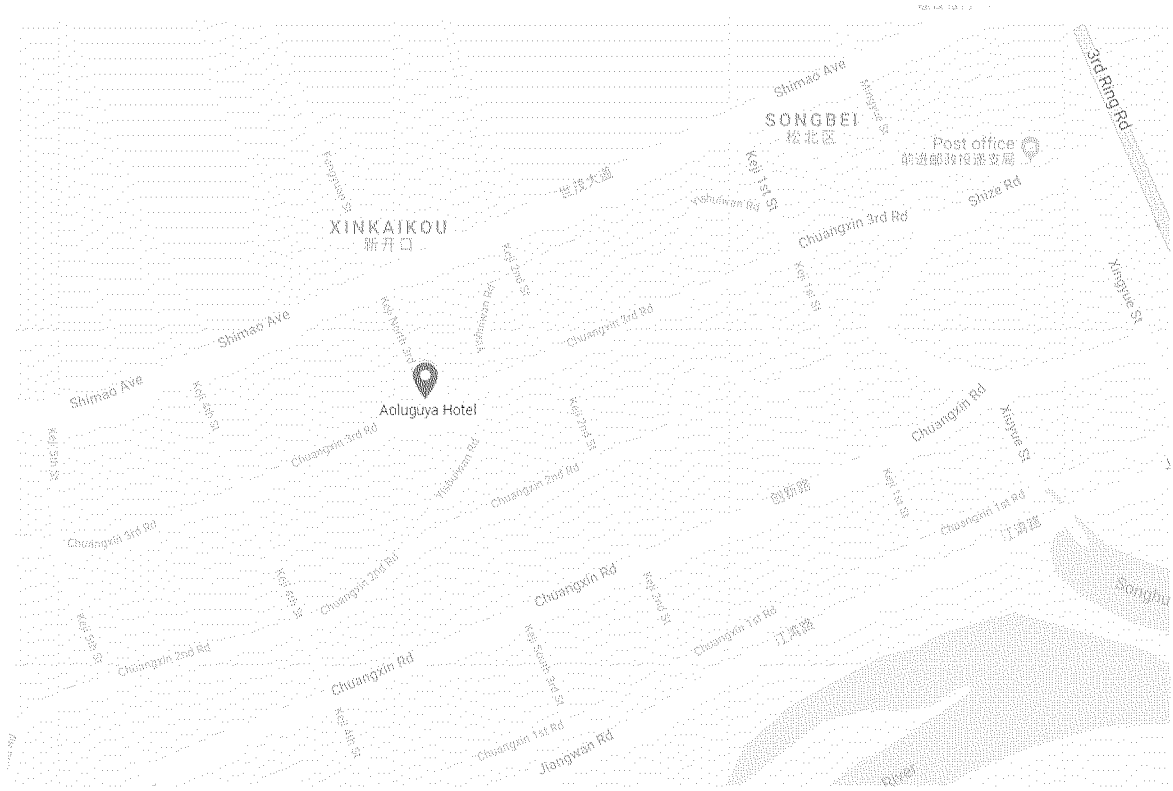
Your pre-populated TER will contain your itinerary and all items billed directly to the Academies. Please enter all out-of-pocket expenses and upload a PDF (when using the Concur website) or a picture (when using the Concur app) of receipts for all transportation costs and all other expenses over $75. When you have entered your reimbursable expenses, please notify your travel coordinator. Please DO NOT CLICK "Submit Report".

The Travel code for this trip is PGA190018.

Map of the airport, hotel and HVRI:



Hotel location, zoomed in:



From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Wednesday, May 6, 2020 4:42 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

Information on how to join the planning call **at 8:00 PM ET tomorrow, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd=552.136
Meeting ID: 934 1863 7725
Password: 552.136

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd=552.136
Password: 552.136

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :

US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Friday, May 8, 2020 1:31 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>

Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

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Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

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Password: **552.136**

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Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

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From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Yuan Zhiming <yzm@wh.iov.cn>
Sent: Thursday, January 23, 2020 8:03 PM
To: Shi, Pei yong;LeDuc, James W.
Cc: brusek;David Franz;George F GAO;mifangl
Subject: 回复: RE: Op Ed in Houston Chronicle

Dear all,
Thanks for your suggestion and I do agree with you. I will try my best to promote the sharing of strain and experience betweet us and let you know later.

Regards

Zhiming

==========
Yuan Zhiming, Ph. D.
Professor of Wuhan Institute of Virology
President of Wuhan Branch
Chinese Academy of Sciences
Wuhan 430071, China
Tel: 86-27-87198195(O)
86-27-87197242(L)
Fax: 86-27-87199480
==========

From: Shi, Pei yong
Date: 2020-01-22 23:56
To: LeDuc, James W.; 袁志明
CC: Benjamin Rusek (BRusek@nas.edu); Dave Franz (davidrfranz@gmail.com); George F GAO; Mifang Liang
Subject: RE: Op Ed in Houston Chronicle
I totally agree with Jim. The timing is critical here.

- Pei-Yong

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Wednesday, January 22, 2020 9:29 AM
To: 袁志明 <yzm@wh.iov.cn>
Cc: Benjamin Rusek (BRusek@nas.edu) <BRusek@nas.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>; George F GAO <gaof@im.ac.cn>; Mifang Liang <mifangl@hotmail.com>; Shi,

Pei yong <peshi@UTMB.EDU>
Subject: Re: Op Ed in Houston Chronicle

Thanks Zhiming. You are in a very challenging position and doing a great job. I would however recommend that you organize and quickly implement a way to share reference isolates. With cases occurring outside China, others will soon have their own isolates and China will have lost the opportunity for leadership. And if scientific publications start appearing from Chinese investigators without the world having independent access to a strain, China will likely be heavily criticized.

Keep up the good work

Jim
Sent from my iPhone

On Jan 22, 2020, at 6:30 AM, 袁志明 <yzm@wh.iov.cn> wrote:

Dear Jim,
Thanks for your information and your positive attitute to Chinese public health response system and the practice. We are still work hard the on the novel coronovirus and hope to get the help from your team.

Regards

Zhiming

-----原始邮件-----

发件人:"LeDuc, James W." <jwleduc@UTMB.EDU>

发送时间:2020-01-22 06:33:54 (星期三)

收件人: "Benjamin Rusek (BRusek@nas.edu)" <BRusek@nas.edu>, "Dave Franz (davidrfranz@gmail.com)" <davidrfranz@gmail.com>, "Yuan Zhiming" <yzm@wh.iov.cn>, "George F GAO" <gaof@im.ac.cn>, "Mifang Liang" <mifangl@hotmail.com>, "Shi, Pei yong" <peshi@UTMB.EDU>

抄送:

主题: Op Ed in Houston Chronicle

Ben, Dave, Zhiming, George, Mifang and Pei-Yong

The attached, slightly modified to include mention of the new case in Washington State, is scheduled to appear in Wednesday 22 Jan's Houston Chronicle. Note mention of the NASEM/CAS collaborations.

Just FYI,

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, May 11, 2020 12:00 AM
To: Rusek, Benjamin;'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';Alison Andre;'Jennifer Ryan';Bowman, Katherine
Subject: Re. List of Chinese participants - Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Well done on getting confirmation of this meeting from CAS, and a very impressive list of senior people who will attend. Having so many senior academicians, including Chen Zhu - a former VP of CAS and essentially former Minister for Health is particularly important and shows that they are taking this meeting extremely seriously.

I look forward to seeing some familiar faces on the calls and to two great sessions!

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>;

'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
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Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

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Ben

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The U.S. National Academy of Sciences
1-202-334-3975

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Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd=
Password: **552.136**

552.136

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
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Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and

2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Sunday, May 10, 2020 11:06 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

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Sent: Sunday, May 10, 2020 12:15 PM
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Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
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Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)

5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Monday, May 18, 2020 10:35 AM
To: Hare, Hope;'relman@stanford.edu';'rbaric@email.unc.edu';'saif.2@osu.edu';'stanley-perlman@uiowa.edu';'daszak@ecohealthalliance.org';'harvey.fineberg@moore.org';'dgriffi6@jhmi.edu';'peggy@hbfam.net';LeDuc, James W.;'davidrfranz@gmail.com';Shi, Pei yong;Dzau, Victor J.;'fsharples_3@hotmail.com';Lowenthal, Micah;'antoinette_baric@med.unc.edu';'andre@ecohealthalliance.org';'jennifer.ryan@moore.org';Bowman, Katherine;Kanarek, Morgan;'Raymond JEANLOZ'
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Attachments: News draft.docx

Here is the copy of the CAS draft website posting.

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 18, 2020 10:18 AM
To: Hare, Hope <HHare@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
3) Ideas for topics (and additional American experts) for future virtual dialogue sessions
4) Discussion of George Gao's joint statement idea
5) CAS idea to post a blurb about the meetings on the CAS website
6) Other issues, concerns

I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: [redacted] **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 4:26 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Cc: Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
Here is the Zoom link for this meeting: [redacted] **552.136**
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001

Phone: 202-334-3435

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

Scientists from China and US Share Experience in COVID-19 Prevention and Control

About 30 scientists from China and the United States held an online dialogue to share their experience in COVID-19 prevention and control and opinions on the prevention of future pandemic on May 12th and 14th (Beijing time).

The virtual dialogue was jointly organized by the Chinese Academy of Sciences (CAS), the National Academy of Sciences (NAS) and the National Academy of Medicine (NAM).

Participants shared their experience in fighting against COVID-19 and exchanged views on such topics as clinical issues related to treatment and management of patients, and limiting the spread of COVID-19 and steps towards restarting society.

COVID-19, an infectious disease caused by the most recently discovered coronavirus, has so far spread to 216 countries, areas and territories, with over 4.5 million confirmed cases and claiming 300 thousand deaths globally, according to the World Health Organization.

"The pandemic will not really be controlled in any country, until it is ultimately controlled in every country. So it's in our mutual interest to do our best to learn as rapidly and as effectively as we can from one another," said Dr. Harvey Fineberg, President of the Gordon and Betty Moore Foundation, one participant of the dialogue.

Experts taking part in the dialogue agreed that it is of great importance to have a discussion to promote exchanges between the scientific communities of the two countries.

"It's an extension of a dialogue that's been going between scientists in China and the U.S.. We are very happy to be able to continue this dialogue in this time when actually all the work we are doing becomes very important," said Diane Griffin, Vice President of NAS, in the dialogue.

Dr. George F. Gao, convener from the Chinese side, Director-General of the Chinese Center for Disease Prevention and Control, said, "This is a great dialogue. We hope that both sides could continue to organize dialogues like this, and contribute to the global efforts in fighting against the COVID-19 pandemic from the scientific perspective."

From: Diane Griffin <dgriffi6@jhmi.edu>
Sent: Monday, May 18, 2020 10:13 AM
To: Rusek, Benjamin;Hare, Hope;'relman@stanford.edu';'rbaric@email.unc.edu';'saif.2@osu.edu';'stanley-perlman@uiowa.edu';'daszak@ecohealthalliance.org';'harvey.fineberg@moore.org';'peggy@hbfam.net';LeDuc, James W.;'davidrfranz@gmail.com';Shi, Pei yong;Dzau, Victor J.;'fsharples_3@hotmail.com';Lowenthal, Micah;'antoinette_baric@med.unc.edu';'andre@ecohealthalliance.org';'jennifer.ryan@moore.org';Bowman, Katherine;Kanarek, Morgan;'Raymond JEANLOZ'
Subject: Re: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben et al - They changed the time of my student's presentation, now ends at 11:45, so I will be late. Start without me and i'll join as soon as I can.

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Monday, May 18, 2020 10:18 AM
To: Hare, Hope <HHare@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; Diane Griffin <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
3) Ideas for topics (and additional American experts) for future virtual dialogue sessions
4) Discussion of George Gao's joint statement idea
5) CAS idea to post a blurb about the meetings on the CAS website
6) Other issues, concerns

I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: https://nasem.zoom.us/j/97552421870?pwd= **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 4:26 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
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It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
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https://nasem.zoom.us/j/97552421870?pwd= **552.136**
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

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From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Monday, May 18, 2020 9:18 AM
To: Hare, Hope;'relman@stanford.edu';'rbaric@email.unc.edu';'saif.2@osu.edu';'stanley-perlman@uiowa.edu';'daszak@ecohealthalliance.org';'harvey.fineberg@moore.org';'dgriffi6@jhmi.edu';'peggy@hbfam.net';LeDuc, James W.;'davidrfranz@gmail.com';Shi, Pei yong;Dzau, Victor J.;'fsharples_3@hotmail.com';Lowenthal, Micah;'antoinette_baric@med.unc.edu';'andre@ecohealthalliance.org';'jennifer.ryan@moore.org';Bowman, Katherine;Kanarek, Morgan;'Raymond JEANLOZ'
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Attachments: Draft Covid-19 US-China dialogue agenda v4.docx; Topics for future collaborations between the NAS and CAS on COVID-draft 1 Day 1 and 2.docx

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
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I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: https://nasem.zoom.us/j/[redacted] **552.136**

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Ben

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The U.S. National Academy of Sciences
1-202-334-3975

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Cc: Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

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Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

The National Academies of
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Day 1

Introductory remarks and group introductions: **George Gao** and **Diane Griffin**

China situational overview: **George Gao** (5 mins)

U.S. situational overview: **Harvey Fineberg** (5 mins)

Clinical Issues Related to Treatment and Management of Patients

- **Clinical manifestations of COVID-19 disease:** What range of clinical, end-organ, organ, and other body system manifestations of disease has been documented in China? (Relman or Dzau)
- **Influence of Patient Characteristics:** How did patient age, gender, general health condition, or other characteristics influence the efficacy of drugs, NPIs, or best practices? How was this determined? (Relman or Dzau or Perlman)
- **Protection of Medical Personnel**: What measures have proven most effective in preventing infection of medical personnel? (Le Duc)
- **Drug Treatments:** What has been the Chinese experience with developing drug treatments or using existing drugs in treatment of patients, from prophylaxis to pre-symptomatic patients to patients with severe symptoms? (Hamburg)
- **Non-pharmaceutical Interventions**: Were effective non-pharmaceutical interventions (NPIs) for patient care identified? Were there other best practices for management of COVID-19 patients that emerged from the pandemic experience? (Hamburg)
- **Immune plasma:** What is China's experience in using immune plasma or other antibody-based therapies in the treatment of COVID-19 patients or prevention of further spread of disease? (Hamburg)
- **Lessons Learned:** Were other lessons learned from China's pandemic experience that should be applied to future staffing and equipping of hospitals or other patient care facilities? (Dzau or Griffin)
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area? (Le Duc)

Day 2

Limiting the Spread of COVID-19 and Steps Toward Restarting Society

- **Incubation period:** Has the incubation period of the virus in humans been determined? What variability may exist and can factors be identified that may influence such variability? (Baric)
- **Viral Load**: What is known about magnitude of viral load required to initiate infection? Has it been determined at what point a patient is most infectious? (Baric)

- **Viral shedding**: What is the degree of shedding among pre-symptomatic/asymptomatic individuals? Do "recovered" patients continue to shed infectious virus? If yes, for how long? Has post-infection viral shedding been demonstrated to result in new infections? Has an explanation regarding pathogenesis leading to apparent recrudescence of disease in previously positive, then negative patients been arrived at? (Shi)
- **Immune response**: How is immune response being measured? Is it via binding assays versus neutralization tests; use of antibody assays in diagnosis of acute disease and as an indicator of protection? Was there standardization of your testing tools? (Saif)
- **Immunity**: After recovery, do patients have immunity? How protective is this immunity? Is there indication of persistence of such immunity? (Saif)
- **Vaccines:** Has the Chinese research community made progress in the development of COVID-19 vaccines? (Perlman or Baric)
- **Exposure routes:** Has progress been made in understanding the routes of exposure to COVID-19—air, water, and surfaces, both indoors and outdoors? (Fineberg)
- **Contact with Animals:** Would increased surveillance of or interventions to reduce contact with pets, wild, or livestock animal species help limit the future spread of COVID-19 or other coronaviruses? (Daszak)
- **Halting Spread:** What measures have proven most effective in halting viral spread in China? (Fineberg)
- **Preventing a Fall Resurgence:** What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)
- **Reestablishing Normality:** What lessons has China learned about returning society and the economy to a "normal" state? (Fineberg)
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area? (Franz)

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, May 7, 2020 3:58 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Attachments: Draft Covid-19 US-China dialogue agenda.docx

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg'

<harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

Clinical Issues Related to Treatment and Management of Patients

- **Clinical manifestations of COVID-19 disease:** What range of clinical, end-organ, organ, and other body system manifestations of disease has been documented in China?
- **Drug Treatments:** What has been the Chinese experience with developing drug treatments or using existing drugs in treatment of patients, from prophylaxis to presymptomatic patients to patients with severe symptoms?
- **Non-pharmaceutical Interventions**: Were effective non-pharmaceutical interventions (NPIs) for patient care identified? Were there other best practices for management of COVID-19 patients that emerged from the pandemic experience?
- **Protection of Medical Personnel**: What measures have proven most effective in preventing infection of medical personnel?
- **Lessons Learned:** Were there any other lessons learned from China's pandemic experience that should be applied to future staffing and equipping of hospitals or other patient care facilities?
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area?
- **Influence of Patient Characteristics:** How did patient age, gender, general health condition, or other characteristics influence the efficacy of drugs, NPIs, or best practices? How was this determined?
- **Immune plasma:** What is China's experience in using immune plasma or other antibody-based therapies in the treatment of COVID-19 patients or prevention of further spread of disease?
- **Vaccines:** Has the Chinese research community made progress in the development of COVID-19 vaccines?
-

Limiting the Spread of COVID-19 and Steps Toward Restarting Society

- **Incubation period:** Has the incubation period of the virus in humans been determined? What variability may exist and can factors be identified that may influence such variability?
- **Viral Load**: What is known about magnitude of viral load required to initiate infection? Has it been determined at what point a patient is most infectious?
- **Viral shedding**: What is the degree of shedding among pre-symptomatic/asymptomatic individuals? Do "recovered" patients continue to shed infectious virus? If yes, for how long? Has post-infection viral shedding been demonstrated to result in new infections? Has an explanation regarding pathogenesis leading to apparent recrudescence of disease in previously positive, then negative patients been arrived at?
- **Immunity**: After recovery, do patients have immunity? How protective is this immunity? Is there indication of persistence of such immunity?

- **Halting Spread:** What measures have proven most effective in halting viral spread in China?
- **Preventing a Fall Resurgence:** What steps should be taken in anticipation of a fall resurgence in transmission?
- **Reestablishing Normality:** What lessons has China learned about returning society and the economy to a "normal" state?
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area?
- **Exposure routes:** Has progress been made in understanding the routes of exposure to COVID-19—air, water, and surfaces, both indoors and outdoors?
- **Immune response**: How is immune response being measured? Is it via binding assays versus neutralization tests; use of antibody assays in diagnosis of acute disease and as an indicator of protection? Was there standardization of your testing tools?
- **Contact with Animals:** Would increased surveillance of or interventions to reduce contact with pets, wild, or livestock animal species help limit the future spread of COVID-19 or other coronaviruses?

From:	Rusek, Benjamin [BRusek@nas.edu]
Sent:	5/12/2020 3:10:07 PM
To:	'David A Relman' [relman@stanford.edu]; 'Baric, Ralph S' [rbaric@email.unc.edu]; 'Saif, Linda' [saif.2@osu.edu]; 'Perlman, Stanley' [stanley-perlman@uiowa.edu]; 'Peter Daszak' [daszak@ecohealthalliance.org]; 'Harvey V. Fineberg' [harvey.fineberg@moore.org]; 'Diane Griffin' [dgriffi6@jhmi.edu]; 'Peggy Hamburg' [peggy@hbfam.net]; LeDuc, James W. [jwleduc@UTMB.EDU]; 'Dave Franz (davidrfranz@gmail.com)' [davidrfranz@gmail.com]; Shi, Pei yong [peshi@UTMB.EDU]; Dzau, Victor J. [VDzau@nas.edu]
CC:	'Frances Sharples' [fsharples_3@hotmail.com]; Lowenthal, Micah [mlowenth@nas.edu]; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' [antoinette_baric@med.unc.edu]; 'Alison Andre' [andre@ecohealthalliance.org]; 'Jennifer Ryan' [jennifer.ryan@moore.org]; Bowman, Katherine [KBowman@nas.edu]; Hare, Hope [HHare@nas.edu]; Kanarek, Morgan [MKanarek@nas.edu]; Clark, David [DClark@nas.edu]
Subject:	RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Attachments:	Topics for future collaborations between the NAS and CAS on COVID-draft 1.docx

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: https://nasem.zoom.us/j/98730322332?pwd **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C'

(antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd **552.136**
(Password **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C'

(antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>;

'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

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I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

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Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
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International numbers available: https://nasem.zoom.us/u/a5XnNJEND

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Topics for future collaborations between the NAS and CAS on COVID-19, Day 1.

1. Natural experiment underway in the USA as states implement various strategies of public health response to address COVID-19 and resume normal activities
2. Clinical Disease—Acute and Convalescence
    a. Early predictors of severe disease/cytokine storm
    b. Long-term sequela seen in survivors
    c. Better understanding/recognition of Pediatric Inflammatory Syndrome of COVID
3. Pathogenesis and Treatment options
    a. Antiviral drug targets and development (not really discussed but important for future dialogue)
    b. Monoclonal antibody therapies (anti-IL-6 monoclonal antibody treatment; "balance" with coagulation dysfunction)
    c. Clinical trial of chloroquine treatment (preliminary results shared)
4. Prophylactics and Preventatives
    a. Passive antibody therapy (raised question but not really discussed)
    b. Vaccine development
        i. Various techniques under development (not discussed)
        ii. Animal models (mentioned but details not shared)
        iii. Clinical testing (not discussed)
        iv. Production capacity (not discussed)
        v. Ethics considerations (not discussed)
    c. Isolation of contacts (Wuhan lock-down)
    d. Educational tools for communications with populations at risk

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Sunday, May 10, 2020 11:15 AM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Attachments: Chinese Participants-0510.docx

The list of Chinese participants is attached.

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Chinese Participants

Bin Cao: Dr. Bin Cao is a physician and professor at the China-Japan Friendship Hospital.

Zhu Chen: Dr. Zhu Chen is president of the Red Cross Society of China, CAS member. He was previously minister of the National Health Commission of China. (Only available on the 14th)

George F. Gao: Dr. George F. Gao is Director-General of CCDC, a professor at the CAS Institute of Microbiology, CAS member.

Dongfeng Gu: Dr. Dongfeng Gu is Vice President of Southern University of Science and Technology, CAS member.

Hualiang Jiang: Dr. Hualiang Jiang is a professor at the CAS Shanghai Institute of Materia Medica, CAS member.

Lanjuan Li: Dr. Lanjuan Li is a physician and professor in infectious diseases, a member of the Chinese Academy of Engineering, and she is currently director of the State Key Laboratory for Diagnosis and Treatment of Infectious Diseases. (Only available on the 12th)

Zhengli Shi: Dr. Zhengli Shi is a professor at CAS Wuhan Institute of Virology.

Wenjie Tan: Dr. Wenjie Tan is a professor at the National Institute of Viral Disease Control and Prevention, CCDC.

Chen Wang: Dr. Chen Wang is Vice President and a member of the Chinese Academy of Engineering, and President of the Chinese Academy of Medical Sciences. (To be confirmed)

Haiming Wei: Dr. Haiming Wei is a professor at the University of Science and Technology of China.

Zhiming Yuan: Dr. Zhiming Yuan is a professor at CAS Wuhan Institute of Virology, Director of Wuhan P4 lab.

Yongqing Zhang: Dr. Yongqing Zhang is Deputy Director General of CAS Bureau of Frontier sciences and Education, a Professor at CAS Institute of Genetics and Developmental Biology.

Guoping Zhao: Dr. Guoping Zhao is a professor at CAS Shanghai Institutes for Biological Sciences, CAS member.

Qi Zhou: Dr. Qi Zhou is Deputy Secretary-General of CAS, Director of CAS Institute of Zoology, CAS member.

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Attachments: Draft Covid-19 US-China dialogue agenda v3.docx

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From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)

5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

Day 1

Introductory remarks and group introductions: **George Gao** and **Diane Griffin**

China situational overview: **George Gao** (5 mins)

U.S. situational overview: **Harvey Fineberg** (5 mins)

Clinical Issues Related to Treatment and Management of Patients

- **Clinical manifestations of COVID-19 disease:** What range of clinical, end-organ, organ, and other body system manifestations of disease has been documented in China? (Relman or Dzau)
- **Influence of Patient Characteristics:** How did patient age, gender, general health condition, or other characteristics influence the efficacy of drugs, NPIs, or best practices? How was this determined? (Relman or Dzau or Perlman)
- **Protection of Medical Personnel**: What measures have proven most effective in preventing infection of medical personnel? (Le Duc)
- **Drug Treatments:** What has been the Chinese experience with developing drug treatments or using existing drugs in treatment of patients, from prophylaxis to pre-symptomatic patients to patients with severe symptoms? (Hamburg)
- **Non-pharmaceutical Interventions**: Were effective non-pharmaceutical interventions (NPIs) for patient care identified? Were there other best practices for management of COVID-19 patients that emerged from the pandemic experience? (Hamburg)
- **Immune plasma:** What is China's experience in using immune plasma or other antibody-based therapies in the treatment of COVID-19 patients or prevention of further spread of disease? (Hamburg)
- **Lessons Learned:** Were other lessons learned from China's pandemic experience that should be applied to future staffing and equipping of hospitals or other patient care facilities? (Dzau or Griffin)
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area? (Le Duc)

Day 2

Limiting the Spread of COVID-19 and Steps Toward Restarting Society

- **Incubation period:** Has the incubation period of the virus in humans been determined? What variability may exist and can factors be identified that may influence such variability? (Baric)
- **Viral Load**: What is known about magnitude of viral load required to initiate infection? Has it been determined at what point a patient is most infectious? (Baric)

- **Viral shedding**: What is the degree of shedding among pre-symptomatic/asymptomatic individuals? Do "recovered" patients continue to shed infectious virus? If yes, for how long? Has post-infection viral shedding been demonstrated to result in new infections? Has an explanation regarding pathogenesis leading to apparent recrudescence of disease in previously positive, then negative patients been arrived at? (Shi)
- **Immune response**: How is immune response being measured? Is it via binding assays versus neutralization tests; use of antibody assays in diagnosis of acute disease and as an indicator of protection? Was there standardization of your testing tools? **(Saif)**
- **Immunity**: After recovery, do patients have immunity? How protective is this immunity? Is there indication of persistence of such immunity? **(Saif)**
- **Vaccines:** Has the Chinese research community made progress in the development of COVID-19 vaccines? **(Saif)**
- **Exposure routes:** Has progress been made in understanding the routes of exposure to COVID-19—air, water, and surfaces, both indoors and outdoors? (Fineberg)
- **Contact with Animals:** Would increased surveillance of or interventions to reduce contact with pets, wild, or livestock animal species help limit the future spread of COVID-19 or other coronaviruses? (Daszak)
- **Halting Spread:** What measures have proven most effective in halting viral spread in China? (Fineberg)
- **Preventing a Fall Resurgence:** What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)
- **Reestablishing Normality:** What lessons has China learned about returning society and the economy to a "normal" state? (Fineberg)
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area? (Franz)

From: Saif, Linda <saif.2@osu.edu>
Sent: Thursday, May 14, 2020 7:28 AM
To: Rusek, Benjamin;'David A Relman';'Baric, Ralph S';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong;Dzau, Victor J.
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope;Kanarek, Morgan;Clark, David
Subject: Re: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Only available 3-4 pm on Fri
Linda
Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

From: "Rusek, Benjamin" <BRusek@nas.edu>
Date: Thursday, May 14, 2020 1:33 AM
To: 'David A Relman' <relman@stanford.edu>, "rbaric@email.unc.edu" <rbaric@email.unc.edu>, Linda Saif <saif.2@osu.edu>, "Stanley-Perlman@uiowa.edu" <Stanley-Perlman@uiowa.edu>, 'Peter Daszak' <daszak@ecohealthalliance.org>, "'Harvey V. Fineberg'" <harvey.fineberg@moore.org>, 'Diane Griffin' <dgriffi6@jhmi.edu>, 'Peggy Hamburg' <peggy@hbfam.net>, "'jwleduc@UTMB.EDU'" <jwleduc@UTMB.EDU>, "'Dave Franz (davidrfranz@gmail.com)'" <davidrfranz@gmail.com>, "'Shi, Pei yong (peshi@UTMB.EDU)'" <peshi@UTMB.EDU>, "Dzau, Victor J." <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>, "Lowenthal, Micah" <mlowenth@nas.edu>, "'Baric, Toni C' (antoinette_baric@med.unc.edu)'" <antoinette_baric@med.unc.edu>, 'Alison Andre' <andre@ecohealthalliance.org>, 'Jennifer Ryan' <jennifer.ryan@moore.org>, "Bowman, Katherine" <KBowman@nas.edu>, "Hare, Hope" <HHare@nas.edu>, "Kanarek, Morgan" <MKanarek@nas.edu>, "Clark, David" <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

Thank you for participating in the call tonight. We thought it would be useful to have an American group conversation about the calls and discuss potential next steps.

Please let me know what times you are available between 2:00 PM - 6:00 PM ET today (Thursday, May 14) and on Friday, May 15 between 11:00 AM - 3:00 PM ET for a 30-45 min discussion.

Once we find the least worst time for folks I will send out a Zoom link.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 13, 2020 4:00 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

I have attached two ppts from the Monday evening Zoom call and an updated Chinese participant list for the Zoom call tonight. I look forward to seeing and speaking with you all again tonight.

Here is the Zoom link for the session tonight:
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, May 12, 2020 4:10 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>

Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Importance: High

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: [redacted] **552.136**
(Password: **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those

listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>;

'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>;

'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Thursday, May 14, 2020 7:25 AM
To: Rusek, Benjamin;'David A Relman';Baric, Ralph S;'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong;Dzau, Victor J.
Cc: 'Frances Sharples';Lowenthal, Micah;'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope;Kanarek, Morgan;Clark, David
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

HI Ben,
Ralph has availability only between 11-12 on Friday.
Toni

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, May 14, 2020 1:33 AM
To: 'David A Relman' <relman@stanford.edu>; Baric, Ralph S <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

Thank you for participating in the call tonight. We thought it would be useful to have an American group conversation about the calls and discuss potential next steps.

Please let me know what times you are available between 2:00 PM - 6:00 PM ET today (Thursday, May 14) and on Friday, May 15 between 11:00 AM - 3:00 PM ET for a 30-45 min discussion.

Once we find the least worst time for folks I will send out a Zoom link.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 13, 2020 4:00 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

I have attached two ppts from the Monday evening Zoom call and an updated Chinese participant list for the Zoom call tonight. I look forward to seeing and speaking with you all again tonight.

Here is the Zoom link for the session tonight:
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, May 12, 2020 4:10 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Importance: High

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and

to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
(Password: **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences

1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>

Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>

Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Diane Griffin <dgriffi6@jhmi.edu>
Sent: Thursday, May 14, 2020 7:01 AM
To: Rusek, Benjamin;'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong;Dzau, Victor J.
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope;Kanarek, Morgan;Clark, David
Subject: Re: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Ben - busy time right now so only:
5-6 today
1:30-2:30 tomorrow

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, May 14, 2020 1:33 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; Diane Griffin <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

Thank you for participating in the call tonight. We thought it would be useful to have an American group conversation about the calls and discuss potential next steps.

Please let me know what times you are available between 2:00 PM - 6:00 PM ET today (Thursday, May 14) and on Friday, May 15 between 11:00 AM - 3:00 PM ET for a 30-45 min discussion.

Once we find the least worst time for folks I will send out a Zoom link.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 13, 2020 4:00 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

I have attached two ppts from the Monday evening Zoom call and an updated Chinese participant list for the Zoom call tonight. I look forward to seeing and speaking with you all again tonight.

Here is the Zoom link for the session tonight:
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: https://nasem.zoom.us/j/98730322332?pwd= **552.136**
Meeting ID: 987 3032 2332
Meeting Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, May 12, 2020 4:10 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg'

<harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Importance: High

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: https://nasem.zoom.us/j/98730322332?pwd= **552.136**
Meeting ID: 987 3032 2332
Meeting Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: [redacted] **552.136**
(Password: **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM

To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Wednesday, May 13, 2020 3:00 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong;Dzau, Victor J.
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope;Kanarek, Morgan;Clark, David
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Attachments: NAS-CAS+meeting-Dr. Gao.pptx; Wang Gui-Qiang+in+COVID-19.pptx; Chinese Participants-0513.docx

Greetings,

I have attached two ppts from the Monday evening Zoom call and an updated Chinese participant list for the Zoom call tonight. I look forward to seeing and speaking with you all again tonight.

Here is the Zoom link for the session tonight:
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, May 12, 2020 4:10 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>

Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Importance: High

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: https://nasem.zoom.us/j/98730322332?pwd= **552.136**
Meeting ID: 987 3032 2332
Meeting Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
(Password: **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd= **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those

listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>;

'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

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Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>;

'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
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Kind regards,

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1-202-334-3975

China Situational Overview

Where are we now in China after a successful lock-down

George F Gao
China CDC

What we did between the end of Dec 2019 and early Jan 2020

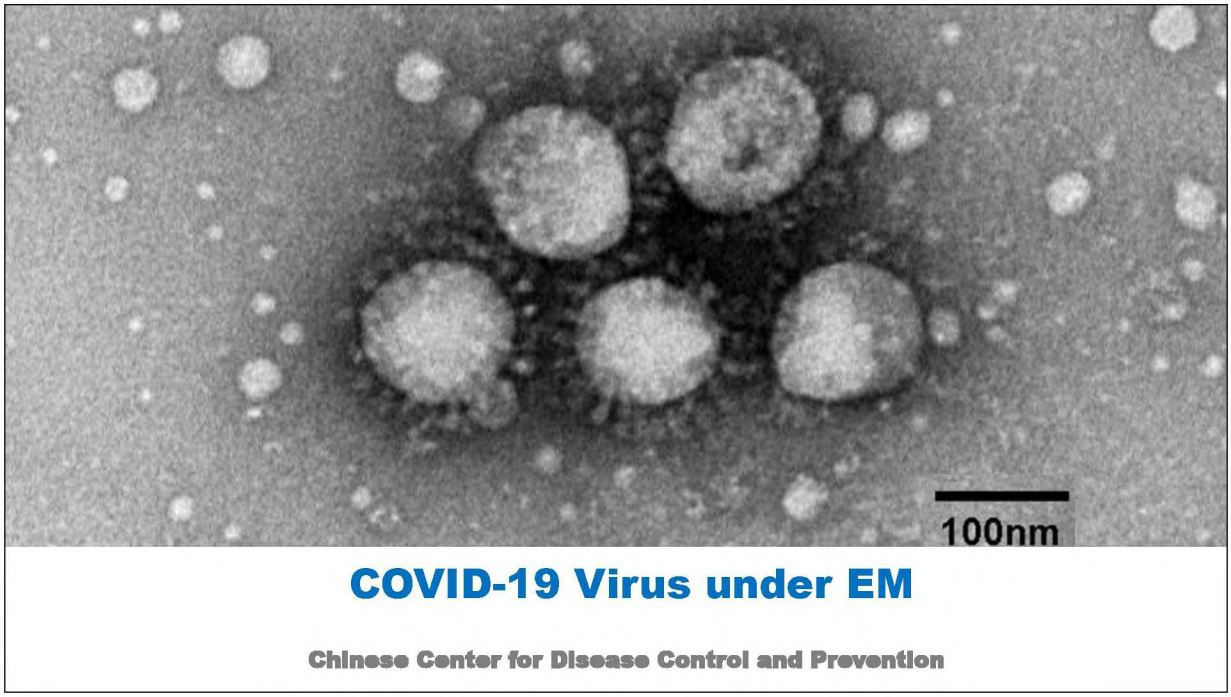
Distinguished the PUE from common cold

Seq the viral genome

Isolated the virus

Shared the data

…

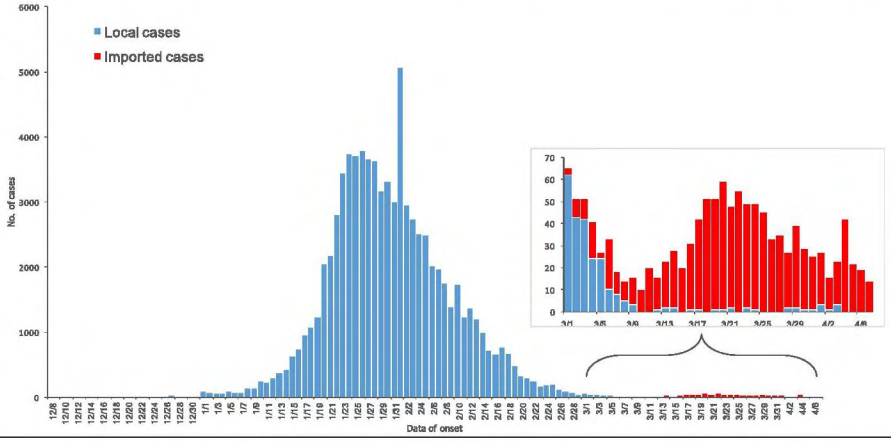


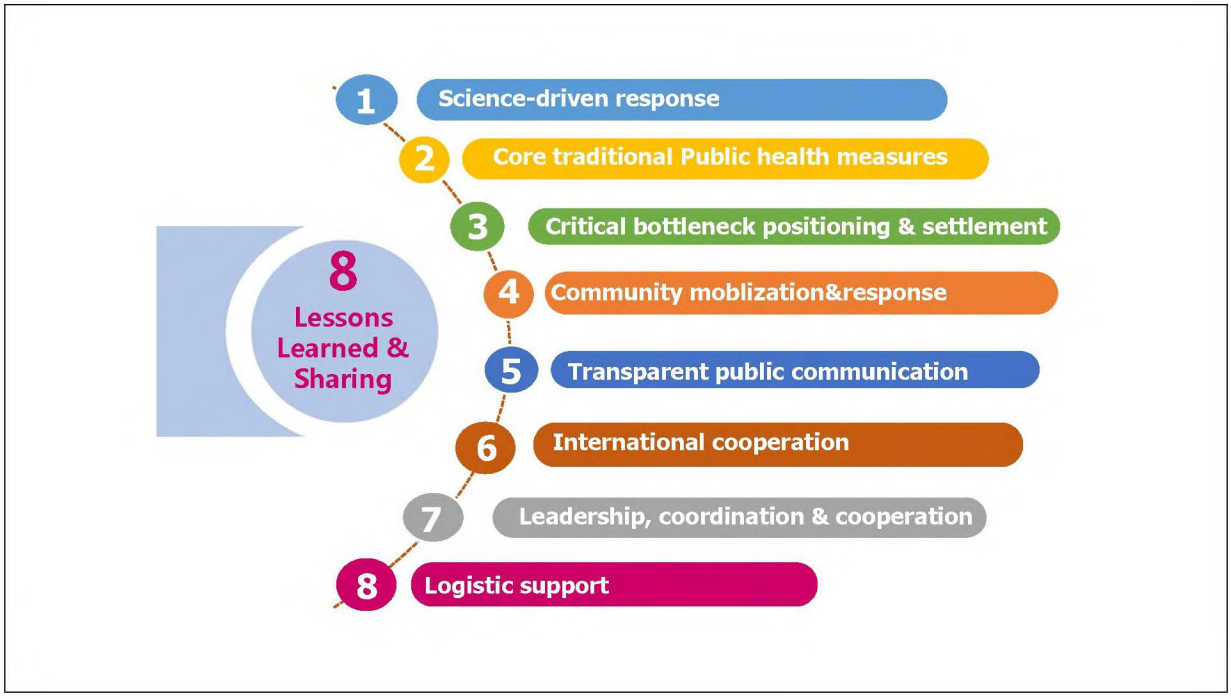
Electron micrograph of SARS-CoV-2


Key Experiences
FOUR Defense Lines
• 1st Line-Wuhan and Hubei
• 2nd Line-Beijing
• 3rd Line-Hubei's surrounding regions
• 4th Line-nationwide
FOUR Earlys
• Early Detection
• Early Reporting
• Early Isolation
• Early Treatment
For the People, By the People
• Community engagement
• Community health education
• Communities hygiene & Disinfection
Coordination
Cooperation
Communicati
• Resources allocation (HCW, PPE, etc)
• Logistic support
• Public understanding & Infodemic response

Epidemic of COVID-19 in China

Lab confirmed (as of April 18)	*Imported cases*	*"Asymptomatic infections"*
● *Cumulative cases: 82735* ● *Cumulative recovered: 77062* ● *Cumulative deaths: 4632* ● *Crude CFR: 5.60%*	● *Jan 31, the 1st imported case* ● *By April 18, 1575 confirmed, 44 possible*	● *By April 18, 1105 individuals, including 44 newly report, 999 under medical observation*




1
Science-driven response
2
Core traditional Public health measures
3
Critical bottleneck positioning & settlement
4
Community moblization&response
5
Transparent public communication
6
International cooperation
7
Leadership, coordination & cooperation
8
Logistic support
8
Lessons Learned & Sharing

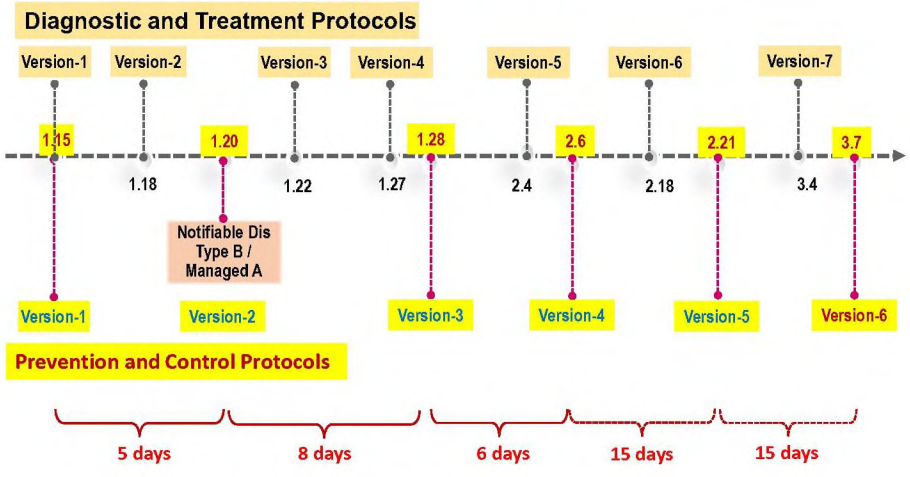
Timely Risk-based Precise Strategy

Science-driven timely adjustment

- **Low-risk areas -- strictly prevent importation**
  - No confirmed cases were reported, or no new confirmed cases were reported for 14 consecutive days.
- **Middle-risk areas -- prevent importation, stop local transmission**
  - Cumulative number of confirmed cases does not exceed 50, and there are new confirmed cases reported within 14 days; Or
  - Cumulative number of confirmed cases exceeds 50, and there are new confirmed cases reported within 14 days but without clustering outbreaks.
- **High-risk areas -- stop local transmission, prevent exportation, implement strict measures**
  - There are more than 50 confirmed cases with a clustered outbreak within 14 days.

Development and Revisions of Technical Documents

Science-driven timely adjustment



Traditional Containment Measures (Non-pharmaceutical intervention)

Mask Wearing

Protect yourself, Protect others

Wearing a mask based on risk assessment

- For general public
  - No need in general, e.g., at home, in open areas.
  - Wearing a surgical mask when gathering, in an elevator or public vehicle, face-to-face interact, high risk area (hospital, clinics)
- For Occupational exposure
  - Settings: Health care settings; airplane, public vehicle (e.g., train, bus), supermarket, restaurant, etc.
  - KN95/N95 for health professionals, surgical mask for others

Proactive Defense Strategy
"Dance" with the virus

Strictly prevent importation and community resurgence

- Control strategy for imported cases
- Tailored control measures at varied risk levels
- Four early measures in new situation
  - Strengthen case reporting and surveillance
  - Enhance laboratory test capability in county level
  - Maintain gridded community prevention and control measures
- Resuming production and work
- Prevention and control protocols at varied risk levels

Control Strategy for Imported Cases

- Whole chain management from border to community to home
- Entry Screening
  - 14-day history and health status reporting
  - Temperature screening
  - Four categories of persons: confirmed case, suspicious case, person with fever, close contacts
  - Medical examination for suspected symptoms
  - Transfer
    - Suspected cases to designated hospitals
    - Close contacts to designated hotels for quarantine
- Quarantine policy for travelers
  - 2 weeks' quarantine in the designated hotels
  - Depending on the risk evaluation and local policy
  - Regardless of domestic or foreigners

Resuming Measures

- **Health code and travel cards**
  - Jointly promote travel card service; provide different colors of "health codes" for the accurate management of people with different risk score results to provide support for the orderly flow of personnel
- **"point-to-point" labor cooperation**
  - Organize migrant workers to return to work in an orderly manner through cross-regional **"point-to-point" labor cooperation**; implement "point-to-point" one-stop direct chartered car (railway and highway) transportation services;
  - Carry out the mode of “delivering labor to the door” in the labor export place and “returning to the factory” in the labor input place
- **Prevention & control guidance for work resumption in enterprises**
  - Health monitoring & reporting; workplace and individual precautions

国务院应对新型冠状病毒感染肺炎疫情联防联控机制关于印发企事业单位复工复产疫情防控措施指南的通知
国发明电〔2020〕4号 http://www.gov.cn/zhengce/content/2020-02/22/content_5482025.htm

Learned from Transition Stage

- **Risk-based adjustment of strategies and measures adapted to local context by local government**
- **Adhere to Four Early Measures:**
  - Control importation (cross boarder and province), esp. in key and big cities
  - Prevent local spread (epidemiological investigation, close contact tracking and management)
- **Fine-tune approaches to balance the reponses and economic development**
  - strengthen the surveillance to and response measures by employers/workplaces while resuming work
- **Utilize hi-tech such as big data and AI technologies to carry out targeted measures** (e.g. tracing of travel history, close contacts, transmission chain, etc.)

Has the second round epidemic been begun?

On 10th-11th May, 5~10 new local cases were reported from Jilin Province and Wuhan City.

Thank You

王贵强简介

手机和微信：
13911405123
Email:
john131212@sina.com

教授，主任医师，博士生导师，中央保健会诊专家
北京大学第一医院感染疾病科主任，兼任肝病中心主任
中华医学会感染病学分会主任委员
中国医院协会抗菌药物合理应用工作委员会主任委员
中国医师协会感染病医师分会副会长
中华医学会全科医师教育学院副院长
国家免疫规划专家咨询委员会委员
国家卫健委传染病标准委员会委员
国家卫健委新冠病毒肺炎医疗救治专家组成员
国家卫健委新冠病毒肺炎恢复期血浆治疗专家组成员
境外抗疫医疗专家组国家顾问团成员
国务院应对新冠病毒肺炎联防联控机制科研攻关专家组成员
科技部新冠肺炎国际合作专家组成员
美国《临床感染病》杂志编委，《中华传染病杂志》和《中华临床感染病杂志》副总编辑，《临床肝胆病学》共同主编等。

Email:
john131212@sina.com
Mobile: +86 13911405123

Gui-Qiang Wang, MD

Professor, Chief physician

Chairman, Department of infectious diseases,

Director, Center for liver disease, Peking University first hospital;

President, Society of Infectious Diseases, Chinese Medical Association;

Chairman, Antimicrobial Stewardship Working Committee, Chinese hospital association;

Vice President, Infectious Disease Physicians Branch, Chinese Medical Doctor Association;

Vice President, General Practitioner Education College, Chinese Medical Association;

Member, National Immunization Program Expert Advisory Committee;

Member, National Health Commission Infectious Diseases Standards Committee;

Member, National Health Commission COVID-19 Medical Treatment Expert Group;

Member, National Health Commission COVID-19 Convalescent Plasma Therapy Expert Group;

Member, National Advisory Board of Overseas Anti-epidemic Medical Expert Group;

Member, The State Council Expert Group on Joint prevention and control mechanism of COVID-19;

Member, COVID-19 International Cooperation Expert Group, Ministry of Science and Technology

Email:
john131212@sina.com
Mobile: +86 13911405123

- **王**贵强教授自**COVID-19疫情爆**发后，作为国家卫生健康委员会医疗救**治**专家组成员，到安徽蚌埠和阜阳等地指导重症和危重症患者救治。参**加中国COVID-19**诊断和治疗方案第五版、第六版和第七版的编写和更**新工作；参加恢复期血**浆治疗**COVID-19治**疗方案的编写工作。
- **受国家**卫生健康委员会和外交部委托，向世界各国（**160余国家**）**介**绍**中国**诊断和治疗方案。多次参加国务院联防联控新闻发布会，介绍新冠**肺炎**诊疗方案更新，解答公众和媒体的提问，进行科普宣教等。
- **主持国家科技部**应急项目"**法匹拉**韦联合托珠单抗治疗新冠肺炎的多中**心**临床研究"，**主持**"**COVID-19恢复期患者核酸**"**复阳**"发生机制、转归及**治**疗干预的研究"**等**。

Email:
john131212@sina.com
Mobile: +86 13911405123

- Since the outbreak of COVID 19, professor wang guiqiang, as a member of the medical treatment expert group of the national health commission, has guided clinical diagnosis and treatment, and participated in the compilation and update of the fifth, sixth and seventh version of the Chinese COVID 19 diagnosis and treatment protocol. Participated in the preparation of the convalescent plasma therapy protocol for COVID-19;
- On behalf of the National Health Commission, he introduced China's diagnosis and treatment protocol to more than 160 countries in the world. On behalf of the National Health Commission, he participated in the press conferences of the state council on joint prevention and control for many times, presented the Protocol, answered questions from the public and the media, and explained COVID-19 prevention and control knowledge to the public.
- Leading the emergency project of the ministry of science and technology "Favipiravir Combined Tocilizumab in the Treatment of Corona Virus Disease 2019-A Multicenter, Randomized and Controlled Clinical Trial Study", and leading "The study on the mechanism, outcome and therapeutic intervention of COVID -19 convalescent patients that the nucleic acid reversion"

Chinese Participants

Ling Chen: Dr. Ling Chen is a professor and founding director of CAS Guangzhou Institute of Biomedicine and Health, former deputy director of State Key Lab of Respiratory Disease.

Zhu Chen: Dr. Zhu Chen is president of the Red Cross Society of China, CAS member. He was previously minister of the National Health Commission of China.

George F. Gao: Dr. George F. Gao is Director-General of CCDC, a professor at the CAS Institute of Microbiology, CAS member.

Dongfeng Gu: Dr. Dongfeng Gu is vice president of Southern University of Science and Technology, CAS member.

Zhengli Shi: Dr. Zhengli Shi is a professor at CAS Wuhan Institute of Virology.

Chen Wang: Dr. Chen Wang is vice president and a member of the Chinese Academy of Engineering, and president of the Chinese Academy of Medical Sciences.

Haiming Wei: Dr. Haiming Wei is Vice President of College of Life Sciences, the University of Science and Technology of China.

Guoping Zhao: Dr. Guoping Zhao is a professor at CAS Shanghai Institutes for Biological Sciences, CAS member.

Xi Zhou: Dr. Xi Zhou is a professor at CAS Wuhan Institute of Virology ， Deputy Director of State Key Laboratory of Virology

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, May 4, 2020 7:59 PM
To: Rusek, Benjamin;'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';Harvey V. Fineberg;'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
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Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

That time works for me and I look forward to the discussion.

A great initiative and great timing!

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Attachments: Draft Covid-19 US-China dialogue agenda.docx

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Clinical Issues Related to Treatment and Management of Patients

- **Clinical manifestations of COVID-19 disease:** What range of clinical, end-organ, organ, and other body system manifestations of disease has been documented in China?
- **Drug Treatments:** What has been the Chinese experience with developing drug treatments or using existing drugs in treatment of patients, from prophylaxis to presymptomatic patients to patients with severe symptoms?
- **Non-pharmaceutical Interventions**: Were effective non-pharmaceutical interventions (NPIs) for patient care identified? Were there other best practices for management of COVID-19 patients that emerged from the pandemic experience?
- **Protection of Medical Personnel**: What measures have proven most effective in preventing infection of medical personnel?
- **Lessons Learned:** Were there any other lessons learned from China's pandemic experience that should be applied to future staffing and equipping of hospitals or other patient care facilities?
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area?
- **Influence of Patient Characteristics:** How did patient age, gender, general health condition, or other characteristics influence the efficacy of drugs, NPIs, or best practices? How was this determined?
- **Immune plasma:** What is China's experience in using immune plasma or other antibody-based therapies in the treatment of COVID-19 patients or prevention of further spread of disease?
- **Vaccines:** Has the Chinese research community made progress in the development of COVID-19 vaccines?
-

Limiting the Spread of COVID-19 and Steps Toward Restarting Society

- **Incubation period:** Has the incubation period of the virus in humans been determined? What variability may exist and can factors be identified that may influence such variability?
- **Viral Load**: What is known about magnitude of viral load required to initiate infection? Has it been determined at what point a patient is most infectious?
- **Viral shedding**: What is the degree of shedding among pre-symptomatic/asymptomatic individuals? Do "recovered" patients continue to shed infectious virus? If yes, for how long? Has post-infection viral shedding been demonstrated to result in new infections? Has an explanation regarding pathogenesis leading to apparent recrudescence of disease in previously positive, then negative patients been arrived at?
- **Immunity**: After recovery, do patients have immunity? How protective is this immunity? Is there indication of persistence of such immunity?

- **Halting Spread:** What measures have proven most effective in halting viral spread in China?
- **Preventing a Fall Resurgence:** What steps should be taken in anticipation of a fall resurgence in transmission?
- **Reestablishing Normality:** What lessons has China learned about returning society and the economy to a "normal" state?
- **Future Collaboration**: What are the most fruitful areas of future scientific collaborations between our countries in this area?
- **Exposure routes:** Has progress been made in understanding the routes of exposure to COVID-19—air, water, and surfaces, both indoors and outdoors?
- **Immune response**: How is immune response being measured? Is it via binding assays versus neutralization tests; use of antibody assays in diagnosis of acute disease and as an indicator of protection? Was there standardization of your testing tools?
- **Contact with Animals:** Would increased surveillance of or interventions to reduce contact with pets, wild, or livestock animal species help limit the future spread of COVID-19 or other coronaviruses?

From: David A Relman <relman@stanford.edu>
Sent: Thursday, May 14, 2020 9:18 AM
To: Rusek, Benjamin;'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong;Dzau, Victor J.
Cc: 'Frances Sharples';Lowenthal, Micah;'Alison Andre';'Jennifer Ryan';Bowman, Katherine;Hare, Hope;Kanarek, Morgan;Clark, David;David A Relman
Subject: Re: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Hi Ben-
Today and tomorrow are tight for me. Monday and Tues are much better for me.
My availability:
Today 4-5 pm ET
Tomorrow 2:30-3:00 pm ET
Best, David

From: "Rusek, Benjamin" <BRusek@nas.edu>
Date: Wednesday, May 13, 2020 at 10:33 PM
To: David A Relman <relman@stanford.edu>, "'Baric, Ralph S'" <rbaric@email.unc.edu>, "'Saif, Linda'" <saif.2@osu.edu>, "'Perlman, Stanley'" <stanley-perlman@uiowa.edu>, 'Peter Daszak' <daszak@ecohealthalliance.org>, "'Harvey V. Fineberg'" <harvey.fineberg@moore.org>, 'Diane Griffin' <dgriffi6@jhmi.edu>, 'Peggy Hamburg' <peggy@hbfam.net>, "'jwleduc@UTMB.EDU'" <jwleduc@UTMB.EDU>, "'Dave Franz (davidrfranz@gmail.com)'" <davidrfranz@gmail.com>, "'Shi, Pei yong (peshi@UTMB.EDU)'" <peshi@UTMB.EDU>, "Dzau, Victor J." <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>, "Lowenthal, Micah" <mlowenth@nas.edu>, "'Baric, Toni C' (antoinette_baric@med.unc.edu)'" <antoinette_baric@med.unc.edu>, 'Alison Andre' <andre@ecohealthalliance.org>, 'Jennifer Ryan' <jennifer.ryan@moore.org>, "Bowman, Katherine" <KBowman@nas.edu>, "Hare, Hope" <HHare@nas.edu>, "Kanarek, Morgan" <MKanarek@nas.edu>, "Clark, David" <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

Thank you for participating in the call tonight. We thought it would be useful to have an American group conversation about the calls and discuss potential next steps.

Please let me know what times you are available between 2:00 PM - 6:00 PM ET today (Thursday, May 14) and on Friday, May 15 between 11:00 AM - 3:00 PM ET for a 30-45 min discussion.

Once we find the least worst time for folks I will send out a Zoom link.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 13, 2020 4:00 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et

Greetings,

I have attached two ppts from the Monday evening Zoom call and an updated Chinese participant list for the Zoom call tonight. I look forward to seeing and speaking with you all again tonight.

Here is the Zoom link for the session tonight:
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, May 12, 2020 4:10 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et
Importance: High

Greetings,

Thank you for participating in and asking thoughtful questions during the Zoom call last night. Thanks especially to Diane Griffin for outstanding moderating, to Harvey Fineberg for giving a clear and concise overview of the U.S. situation and to Jim Le Duc for drafting a list (see attachment) of possible future areas of collaboration that came up during the discussion.

Although Zoom seemed to work well for most of the participants I asked CAS staff to help the group move on quickly if a Chinese speaker's audio is malfunctioning. I let CAS know that during the next session we want to start discussing the agenda / remaining list of questions right away. I reiterated that we find a discussion format to be the most useful and asked that they send any slide presentations to me in advance of the call (so I can send them to you). I also asked CAS for copies of the PPT slides that were shared with the group last night. Please let me know if you have any thoughts on how to make the Zoom session tomorrow night more productive.

Here is the Zoom link for the next session
Meeting Time: **Wednesday, May 13, 2020 9:00 -11:00 PM (ET)**
Meeting link: [redacted] **552.136**
Meeting ID: 987 3032 2332
Meeting Password: 552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 6:13 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; Clark, David <DClark@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)
Importance: High

Greetings,

I have attached all the documents that you need for **the first U.S. China dialogue Zoom call tonight [Monday, May 11 from 9:00 PM – 11:00 PM (ET)]** so you have them all in one place. They are 1) the slightly updated Chinese participant list (availability is Beijing time) 2) the American participant list and 3) the American version of the agenda. Please remember that because we want the Chinese participants to lead the discussion their version of the agenda does not include your names after the questions.

At the beginning of the call Diane Griffin will ask each person to introduce themselves briefly (just say your name and affiliations). **Please do this in the order that you appear on the American participant list.** (FYI Peter Daszak and Victor Dzau will join the call later.) George Gao and then Harvey Fineberg will give the brief overviews and then we will discuss the Day 1 questions. Re this discussion, please try and prompt the Chinese participants to answer and address the questions and issues on the agenda, we will also need to mind the time closely if we are going to get through the entire Day 1 question list.

The Zoom link is here again:
Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: [redacted] **552.136**
(Password: **552.136** Meeting ID: 948 6152 5373, but you should not need it, it's in the link)

Re logistics, CAS agreed to allow us to use the Zoom record feature to produce a transcript of the call. I will have host access to Zoom and there will be an NAS IT professional (David Clark) in the Zoom call in case there is a problem. If for some reason we need to abandon the Zoom call and reconvene over the phone we have set up an alternative conference call in line (with Conference America). That number is 1-888-537-7715 (and then enter 12223052#), CAS will also be able to access the line via a toll free Chinese phone number. We will only activate this line if we decide to abandon the Zoom call.

If you have any final questions or concerns please feel free to email or call me (at the number below) before the meeting. Thank you again for agreeing to participate in the virtual dialogue, I looks forward to seeing and hearing you all later this evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 11, 2020 12:06 AM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Hare, Hope <HHare@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call

And here is the Zoom link for the call on Monday night.

Time: Monday, May 11, 2020 9:00 PM (ET)
Meeting Link: https://nasem.zoom.us/j/94861525373?pwd **552.136**
Password: **552.136**

PS I tested Zoom with CAS and many of the Chinese group members earlier tonight, the video was clear and I could hear everyone well. Hopefully it will work well when we are all connected.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Sunday, May 10, 2020 12:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

The list of Chinese participants is attached.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Saturday, May 9, 2020 11:24 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

We have created a proposed draft agenda (with topics slightly rearranged) that, as we discussed during the call on Thursday, starts with a brief introduction of the situation in China and the U.S. We hope that Harvey Fineberg can give a (very) brief overview of the situation in the U.S.

To ensure that each question is addressed during the discussion, we have listed the names of American delegation member after each question. We have asked and expect the Chinese group to take the lead but we hope that those listed can ensure that each question is covered. (FYI this version is for your information only, we will send an agenda

without the names listed after the questions to the Chinese.) Please let me know if you have thoughts or concerns about this plan.

FYI I plan to send a new version of the agenda to CAS and George Gao on Sunday evening (before I test the Zoom connection with CAS at 9:00 PM ET).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 8, 2020 2:31 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; ''Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thanks for joining the call last night. We received good news from CAS this morning. They agreed to hold the two sessions as we requested. However because George Gao is not available on the second day they want to push the second session back by one day. That's not bad because as I noted on the call, Jim Le Duc and Harvey Fineberg were not available at that time anyway.

So for the Americans we will keep the time on Monday, May 11 (from 9-11:00 PM ET) as planned but move the second session back one day to Wednesday, May 13th (from 9-11:00 PM ET). I hope the new time for the second session works for most of you.

In addition they said that the topical agenda (topic list we sent) looks fine and that there would about a dozen Chinese experts (said no more than 13) on the call on their side.

I will send you more info later today.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, May 7, 2020 4:58 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>; 'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Below you will find an agenda for tonight's **(8:00 PM ET)** call. Diane is the U.S. chair so will lead the call (with input from others).

1) Introductions (Diane, Ben, group)
2) The China bio dialogue: brief background, previous meetings and key Chinese participants (Jim, Dave, Diane, Peggy, Pei-yong, Ben, others)
3) Recent work (2020) to set up the virtual dialogue sessions, purpose of the call and issues we should probably avoid (Diane, Ben, others)
4) Discussion topics/questions (see attachment), assign discussion leaders for each question (Diane, others)
5) Call logistics (best way to interact on the Zoom call, recording the sessions, plan between calls, etc.) (Ben, Micah, Diane)
6) Other questions or concerns (group)

I have re attached the "agenda" (list of topics/questions) for the dialogue meetings next week for your information. Also the Zoom call in information is below:

https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 6, 2020 5:42 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; 'Harvey V. Fineberg' <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; 'Shi, Pei yong (peshi@UTMB.EDU)' <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; "Baric, Toni C' (antoinette_baric@med.unc.edu)' <antoinette_baric@med.unc.edu>; 'Alison Andre' <andre@ecohealthalliance.org>;

'Jennifer Ryan' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Information on how to join the planning call **at 8:00 PM ET, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>;

'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: LeDuc, James W.
Sent: Friday, April 3, 2020 12:48 PM
To: Shi, Pei yong;Yuan Zhiming;zlshi
Subject: How did covid-19 begin? Its initial origin story is shaky. from The Washington Post

https://www.washingtonpost.com/opinions/global-opinions/how-did-covid-19-begin-its-initial-origin-story-is-shaky/2020/04/02/1475d488-7521-11ea-87da-77a8136c1a6d_story.html

Please see link to article that appeared today in the Washington Post. I've has inquiries already. Any information you might have to address the work done in the Wuhan CDC would be helpful. BSL2 work there on coronaviruses? True?

Thanks, and I hope you are all well. Things are heating up here but so far everyone is well.

Best wishes, Jim

From: LeDuc, James W. [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: 2/12/2020 8:41:52 AM
To: Shi, Pei yong [peshi@UTMB.EDU]; df@wh.iov.cn; zlshi [zlshi@wh.iov.cn]
CC: yzm [yzm@wh.iov.cn]; wangyy [wangyy@wh.iov.cn]; Ksiazek, Thomas G. [tgksiaze@UTMB.EDU]
Subject: RE: RE: sharing of isolates of 2019nCoV

I strongly agree. We need to show international scientific collaborations at this time of potentially global crisis.

Thank you Fei for your continued efforts.

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, February 12, 2020 7:10 AM
To: df@wh.iov.cn; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: RE: RE: sharing of isolates of 2019nCoV

Thanks, Fei
Although US CDC has already shared the virus isolate with a number of US institutions (including UTMB) last week, it is still important to successfully transfer and share the isolate(s) from China.
Best,
- Pei-Yong

From: df@wh.iov.cn <df@wh.iov.cn>
Sent: Wednesday, February 12, 2020 3:34 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: RE: sharing of isolates of 2019nCoV

No prompt reply from the Custom until today. President Bai is trying to push it in Beijing. Please wait for a while.

With best

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong
Date: 2020-02-05 20:41
To: df@wh.iov.cn; zlshi
CC: LeDuc, James W.; yzm; wangyy; Ksiazek, Thomas G.
Subject: RE: FW: sharing of isolates of 2019nCoV
Hi Fei,
Thanks for the update. We look forward to further progress.
Best,
- Pei-Yong

From: df@wh.iov.cn <df@wh.iov.cn>
Sent: Wednesday, February 5, 2020 5:57 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: FW: sharing of isolates of 2019nCoV

Thanks for your information.
We are trying to discuss this with the General Administration of Customs in Beijing directly.
I will keep on contacting with you.

Best wishes,
Fei

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong
Date: 2020-02-04 22:52
To: df@wh.iov.cn; zlshi
CC: LeDuc, James W.; Yuan Zhiming; wangyy@wh.iov.cn; Ksiazek, Thomas G.
Subject: FW: sharing of isolates of 2019nCoV
Dear Fei and Zhengli,

Please see the response from President Bai. Zhiming and Yanyi were copied on the original email. Let us know anything we could help to facilitate the isolate transfer.

Best regards,

- Pei-Yong

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Tuesday, February 4, 2020 8:39 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: FW: sharing of isolates of 2019nCoV

From: "president-office@cas.cn" <president-office@cas.cn>
Date: February 3, 2020 at 11:20:56 PM EST
To: dgriffi6 <dgriffi6@jhmi.edu>, MHamburg <MHamburg@nas.edu>
Cc: mlowenth <mlowenth@nas.edu>, Peggy Hamburg <peggy@hbfam.net>, jwleduc <jwleduc@nas.edu>, jhilderbr <jhilderbr@arizona.edu>, BRsek <BRsek@nas.edu>, jboright <jboright@nas.edu>, clbai <clbai@cas.cn>, zhangyp <zhangyp@cashq.ac.cn>, gaof <gaof@im.ac.cn>, jh-cao <jh-cao@cashq.ac.cn>, liyin <liyin@cashq.ac.cn>, sunhui <sunhui@cashq.ac.cn>, wangyy <wangyy@wh.iov.cn>, yzm <yzm@wh.iov.cn>
Subject: sharing of isolates of 2019nCoV

Diane E. Griffin, Vice President, NAS,
Margaret Hamburg, Foreign Secretary, NAM

Dear Prof. Griffin and Prof. Hamburg,

Thank you for your concerns on the recent outbreak of the 2019 novo-coronavirus epidemic. Upon receiving your letter dated January 28, my colleagues have discussed with Dr. George Fu Gao and other experts and we are willing to share isolates of the 2019 nCoV with the international community. We believe this is critical to engaging joint international efforts to contain the spread of the virus.

The National Biosafety Laboratory Wuhan of the Chinese Academy of Sciences is prepared and willing to work with The University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. We are in the process of getting it ready.

I look forward to hearing your further advice on this matter.

With best regards,

Chunli Bai
President
Chinese Academy of Sciences
The Alliance of International Science Organizations (ANSO)

Subject: NAS-CAS dialogue organizing meeting
Location: Zoom or Skype

Start: Thu 5/7/2020 7:00 PM
End: Thu 5/7/2020 8:00 PM

Recurrence: (none)

Organizer: LeDuc, James W.

Zoom link: https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Meeting ID: 934 1863 7725
Password: **552.136**

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd= **552.136**
Password: **552.136**

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :
US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Wednesday, May 6, 2020 4:42 PM
To: 'David A Relman';'Baric, Ralph S';'Saif, Linda';'Perlman, Stanley';'Peter Daszak';'Harvey V. Fineberg';'Diane Griffin';'Peggy Hamburg';LeDuc, James W.;'Dave Franz (davidrfranz@gmail.com)';Shi, Pei yong
Cc: 'Frances Sharples';Lowenthal, Micah;''Baric, Toni C' (antoinette_baric@med.unc.edu)';'Alison Andre';'Jennifer Ryan';Bowman, Katherine
Subject: RE: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7

Greetings,

Information on how to join the planning call **at 8:00 PM ET tomorrow, Thursday, May 7 is below:**

Zoom link: https://nasem.zoom.us/j/93418637725?pwd=552.136
Meeting ID: 934 1863 7725
Password: 552.136

Please join by Zoom (but the call in phone number is below my email signature if you need it). Thank you again for agreeing to participate in the planned virtual dialogue meeting next week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Benjamin Rusek is inviting you to a scheduled Zoom meeting.

Topic: Zoom meeting to discuss U.S. China dialogue
Time: May 7, 2020 08:00 PM Eastern Time (US and Canada)

Join from PC, Mac, Linux, iOS or Android:
https://nasem.zoom.us/j/93418637725?pwd=552.136
Password: 552.136

Or iPhone one-tap :
US: +16513728299,,93418637725# or +13017158592,,93418637725#
Or Telephone:
Dial(for higher quality, dial a number based on your current location) :

US: +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 213 338 8477 or +1 253 215 8782 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or 888 475 4499 (Toll Free) or 877 853 5257 (Toll Free)
Meeting ID: 934 1863 7725
Password: **552.136**
International numbers available: https://nasem.zoom.us/u/a5XnNJEND

Would you like to test your Zoom connection? Please click on the link below.
https://nasem.zoom.us/test

From: Rusek, Benjamin
Sent: Monday, May 4, 2020 6:15 PM
To: 'David A Relman' <relman@stanford.edu>; 'Baric, Ralph S' <rbaric@email.unc.edu>; 'Saif, Linda' <saif.2@osu.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; 'Peter Daszak' <daszak@ecohealthalliance.org>; Harvey V. Fineberg <harvey.fineberg@moore.org>; 'Diane Griffin' <dgriffi6@jhmi.edu>; 'Peggy Hamburg' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>; Shi, Pei yong (peshi@UTMB.EDU) <peshi@UTMB.EDU>
Cc: 'Frances Sharples' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'Baric, Toni C' (antoinette_baric@med.unc.edu) <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; Jennifer Ryan <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>
Subject: Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7
Importance: High

Greetings,

Thank you for agreeing to participate in a virtual bilateral dialogue meeting between Chinese and American experts studying and fighting the COVID-19 pandemic. I am reaching out to you now so 1) the group is connected by email and 2) to organize the planning teleconference for the American participants on May 7. The purpose of the May 7 discussion is to fill you in on the dialogue background, discuss the topics/questions (list in your invitation letter and attached) and issues we should probably avoid (origin questions, politics), logistics, and address any other questions or concerns you may have.

We are proposing that this ~1 hour discussion take place over Zoom at 8:00 PM ET on Thursday, May 7. If this time does not work for someone we could push the time up or back slightly. Please let me know. Also if Thursday evening is impossible I can brief you on the discussion over the phone sometime on Friday.

Re the actually dialogue meeting with the Chinese group, as your invitation letter notes we have proposed that the dialogue meeting take place on the evenings of Monday, May 11th (to address the first set of bullet points) and Tuesday, May 12th (to ask/answer follow-up questions and address the second set of bullet points), at 9:00 PM ET for the Americans. George Gao has not yet let us know if these exact times work but we should hear back from him soon (the Chinese May day holidays end on the 5th).

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

To: 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; 'dgriffi6@jhu.edu'[dgriffi6@jhu.edu]; 'shiggs@k-state.edu'[shiggs@k-state.edu]; 'kanabrocki@uchicago.edu'[kanabrocki@uchicago.edu]; LeDuc, James W.[jwleduc@UTMB.EDU]; 'relman@stanford.edu'[relman@stanford.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Bowman, Katherine[KBowman@nas.edu]; Hare, Hope[HHare@nas.edu]; 'Baric, Toni C' (antoinette_baric@med.unc.edu)[antoinette_baric@med.unc.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Thur 1/17/2019 4:51:14 PM (UTC-06:00)
Subject: RE: National Academies Travel Reimbursement: Harbin 2019 meeting - docs and photos

Greetings,

I trust that everyone made it back to the U.S. safely. Please do send Hope any expenses that you might have incurred during your travel.

Please also send me the final version of your presentation as delivered. We will not post your slides publically but will create and send you a PDF document that contains the final agenda, participant list and the presentations. I have about half of the Chinese presentations right now and am working to get as many of the rest as HVRI will release. Katie and I are working on meeting reports and summary documents.

I put the photos I took during the trip in a Google Photo album (Friday trip to the snow festival and my indoor ski slope adventure is at the end): https://photos.app.goo.gl/rayKqR4X46ZLND7g7

Feel free to add your pictures to the album or email pictures and I will add them.

Thank again for making the trip.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, January 11, 2019 2:02 PM
To: 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'dgriffi6@jhu.edu' <dgriffi6@jhu.edu>; 'shiggs@k-state.edu' <shiggs@k-state.edu>; 'kanabrocki@uchicago.edu' <kanabrocki@uchicago.edu>; 'jwleduc@utmb.edu' <jwleduc@utmb.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'peshi@utmb.edu' <peshi@utmb.edu>
Cc: Rusek, Benjamin <BRusek@nas.edu>; Bowman, Katherine <KBowman@nas.edu>
Subject: National Academies Travel Reimbursement: Harbin 2019 meeting

Thank you for participating in our meeting! Please let me know if you incurred any expenses during this trip that you would like reimbursed. If so, please send me a list so that I can enter them onto your travel report.
I will need the following details for each expense:

- Date incurred
- Type of expense
- Amount of expense

If the expense is over $75, please include a receipt. If it is not over $75, I only need the details.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine

500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

The National Academies of
SCIENCES · ENGINEERING · MEDICINE

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 3:26 PM
To: 'relman@stanford.edu';'rbaric@email.unc.edu';'saif.2@osu.edu';'stanley-perlman@uiowa.edu';'daszak@ecohealthalliance.org';'harvey.fineberg@moore.org';'dgriffi6@jhmi.edu';'peggy@hbfam.net';LeDuc, James W.;'davidrfranz@gmail.com';Shi, Pei yong;Dzau, Victor J.;'fsharples_3@hotmail.com';Lowenthal, Micah;'antoinette_baric@med.unc.edu';'andre@ecohealthalliance.org';'jennifer.ryan@moore.org';Bowman, Katherine;Kanarek, Morgan;'Raymond JEANLOZ'
Cc: Rusek, Benjamin
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
Here is the Zoom link for this meeting:
https://nasem.zoom.us/j/99353621870?pwd **552.136**
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

The National Academies of
SCIENCES · ENGINEERING · MEDICINE

From: Shan, Chao [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=3306114A447E496CB9EBA019AE29AE6E-SHAN, CHAO]
Sent: 4/11/2019 9:20:11 AM
To: Bente, Dennis A. [dabente@UTMB.EDU]; 夏菡 [hanxia@wh.iov.cn]; Shi, Pei yong [peshi@UTMB.EDU]; LeDuc, James W. [jwleduc@UTMB.EDU]
CC: 袁院长 [yzm@wh.iov.cn]
Subject: RE: Application for collaboration funding

Hi Han,

We can talk over the phone to discuss how to write the proposal. Looking forward to talking with you.

Best,
Chao

From: Bente, Dennis A. <dabente@UTMB.EDU>
Sent: Thursday, April 11, 2019 12:09 AM
To: 夏菡 <hanxia@wh.iov.cn>; Shi, Pei yong <peshi@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Shan, Chao <chshan@UTMB.EDU>
Cc: 袁院长 <yzm@wh.iov.cn>
Subject: RE: Application for collaboration funding

Dear Han,

Thank you very much for sending the CAS funding opportunity. We discussed this amongst us today, and we believe that the production for horse anti-CCHFV serum based on VSV-CCHFV-GP is a good idea. However, we think it should be a part of a larger applications which will include Chao's vaccine platform as well. We believe that this will make it more competitive. Chao will reach out to you in the next days.
Dr. LeDuc will also try to find a US based funding mechanism to see if we can match the Chinese funds with US funds (if the project gets funded).

Best wishes,

Dennis

From: 夏菡 <hanxia@wh.iov.cn>
Sent: Monday, April 8, 2019 9:48 PM
To: Bente, Dennis A. <dabente@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>
Cc: 袁院长 <yzm@wh.iov.cn>
Subject: Application for collaboration funding

Hi Dennis, Dr.Peiyong Shi and Dr. Leduc

Hope you are doing well!

We missed the funding application support by CAS for the collaboration study of BSL-4 agent last year. The new round application for 2019 is opening and the deadline is May 5 (http://english.whiov.cas.cn/Notice2016/201904/t20190404_207607.html). The application information attached (English).

Based on Dennis and I discussed previously, I am thinking about if we can try to put the "Production for horse anti-CCHFV serum based on VSV-CCHFV-GP" as a proposal if Dr. Tom Geisbert agreed. The VSV-CCHFV-GP has constructed in the UTMB and the horse immunizing will conducted in Wuhan. The neutralization work for the horse serum in cells of Chinese strains will be done in Wuhan and other strains in UTMB. If it worked in vitro, then we can test it in the mice.

Please let me know what's your thought.

Thanks,
Han

552.136

From: Xie, Xuping [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=CB93AD14389748EFB3D9D65FB328203D-XIE, XUPING]
Sent: 10/16/2019 8:36:28 PM
To: Shi, Pei yong [peshi@UTMB.EDU]
CC: 周缘 [zhouyuan@wh.iov.cn]; Zhang, Xianwen [zhxianwe@UTMB.EDU]; 陈新文 [chenxw@wh.iov.cn]
Subject: Re: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

Please let us know whether it woks. If not, I can help renew it tomorrow.

Best,

Xuping

Sent from my iPhone

On Oct 16, 2019, at 7:16 PM, Shi, Pei yong <peshi@utmb.edu> wrote:

Hi Yuan,

Please try the following information and see if it works. If my ASV membership has expired, we can renew it easily.

ASM membership and author billing
Username: [redacted]
Password: [redacted]
Membership number: [redacted]

We could talk over WeChat if it is easier.

Thanks!

Pei-Yong

From: Xie, Xuping <xuxie@UTMB.EDU>
Sent: Wednesday, October 16, 2019 12:07 PM
To: 周缘 <zhouyuan@wh.iov.cn>; Shi, Pei yong <peshi@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Cc: 陈新文 <chenxw@wh.iov.cn>
Subject: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

We are not the member of the ASM. Based on the linker for the payment, it appears Pei-Yong is also not the member of ASM. I would like to wait for Pei-Yong's confirmation.

Best,

Xuping

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Tuesday, October 15, 2019 10:01 PM
To: Xie, Xuping <xuxie@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Cc: 陈新文 <chenxw@wh.iov.cn>
Subject: Re: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear all ,How are you?

I need a writer's member name (should be a email) and password on ASM, because members can discount the page fee. I'm not one of the authors,so I can't get a discount even if I pay the membership fee. It's a little expensive(3300 dollars),Please see the picture below.

<image001.jpg>

Yuan

--
周缘
中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

-----原始邮件-----
发件人:"Xie, Xuping" <xuxie@UTMB.EDU>
发送时间:2019-10-15 22:04:06 (星期二)

收件人: "周缘" <zhouyuan@wh.iov.cn>

抄送: "Zhang, Xianwen" <zhxianwe@UTMB.EDU>, "Shi, Pei yong" <peshi@UTMB.EDU>

主题: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Yuan,

Thanks. Please let us know if we can assist.

Best,

Xuping

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, October 15, 2019 8:59 AM
To: 周缘 <zhouyuan@wh.iov.cn>
Cc: Xie, Xuping <xuxie@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Subject: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Thanks, Yuan

Pei-Yong

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Tuesday, October 15, 2019 1:52 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Prof.Pei-yong,

I'll deal with it as soon as possible!

Yuan

--
周缘
中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2019-10-14 20:00:19 (星期一)
收件人: "周缘" <zhouyuan@wh.iov.cn>
抄送:
主题: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Yuan,

Please see the forwarded the email. Thanks so much for taking care of it.

Best regards,

Pei-Yong

From: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Sent: Monday, October 14, 2019 4:00 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: asm.authorservicessupport@cenveo.com
Subject: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Dr. Pei-Yong Shi,

Your article, Zika virus NS2A-mediated virion assembly (Manuscript # mBio02375-19), is scheduled to be published in issue 6 of mBio.

To facilitate prompt publication of your article, please use this link to the Author Services system to do any of the following:

- Pay publication fees
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From: Shan, Chao [/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=3306114a447e496cb9eba019ae29ae6e-Shan, Chao]
Sent: 5/3/2019 11:04:38 AM
To: LeDuc, James W. [jwleduc@UTMB.EDU]; Shi, Pei yong [peshi@UTMB.EDU]; Bente, Dennis A. [dabente@UTMB.EDU]; yzm@wh.iov.cn; hanxia@wh.iov.cn
Subject: Wuhan CCHFV application
Attachments: Application Form Wuhan-UTMB May 3 2019.doc

Dear All,

Here is the application I wrote with help from Han for Wuhan collaboration. Please take a look and let me know if anything needs to be changed.

Thanks very much for all the supports from you.

Best,
Chao

No.	
Grant No.	
Confidentiality Level	Open

Wuhan National Biosafety Laboratory, Chinese Academy of Sciences

Advanced Customer Cultivation Project

Application Form

Project name: Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus

Project leader (Signature): _____

Organization: University of Texas Medical Branch, Texas, USA

Phone number: +1(409) 266-6500

E-mail: jwleduc@utmb.edu

Made by Research Planning Office of Wuhan Institute of Virology, CAS

Filled in on 30/4/2019

Instruction for Form Filling

1. Each item of the application form must be true, complete, accurate and clarified.
2. The "Confidentiality Level" on the cover shall be filled in with "Open".
3. All the application materials shall be submitted in duplicate in A4 book size in print (double page).
4. After the form is filled in completely, the applicant's organization shall review the truthfulness, completeness and effectiveness of the information filled in.
5. The application form shall only be considered effective with the signature of the principal of the applicant's organization.

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Basic Information

<table>
<tr><td colspan="2">Project name</td><td colspan="8">Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus</td></tr>
<tr><td colspan="2">Type of project</td><td colspan="8">☐Frontline of the fundamental ☐Major common key technology √Application demonstration research ☐Others</td></tr>
<tr><td colspan="2">Funding Category</td><td colspan="8">√Key Project ☐General Project</td></tr>
<tr><td colspan="2">Budget</td><td colspan="8">Total estimate: 50 (RMB 10,000 yuan) (Note: please calculate for one year only)</td></tr>
<tr><td colspan="2">Implementation period (one year)</td><td colspan="8">From (01/07/2019) to (31/12/2019)</td></tr>
<tr><td colspan="2">Assessment period</td><td colspan="8">From (01/07/2019) to (31/12/2021)</td></tr>
<tr><td rowspan="3">Project leader</td><td>Name</td><td colspan="2">James Le Duc</td><td>Sex</td><td colspan="2">M</td><td>Birthday</td><td>11/23/1945</td></tr>
<tr><td>Title</td><td colspan="2">Professor</td><td>Duty</td><td colspan="2">Director</td><td>Highest degree</td><td>Ph.D.</td></tr>
<tr><td>Organization</td><td colspan="7">University of Texas Medical Branch, Texas, USA</td></tr>
<tr><td>Research group in WIV, CAS</td><td>Principal Investigator (Signature)</td><td colspan="3">Zhiming Yuan</td><td>Person to contact (Signature)</td><td colspan="2">Chao Shan</td></tr>
<tr><td>Project Implementation</td><td colspan="8">☐Authorization √Cooperation ☐Independent Completion</td></tr>
<tr><td rowspan="2">Project team</td><td>Total number</td><td>Senior</td><td>Intermediate</td><td>Junior</td><td>Assistant personnel</td><td>Post-doctor</td><td>Doctor candidate</td><td>Master candidate</td></tr>
<tr><td>6</td><td>6</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td rowspan="4">Main participants of the project implementation</td><td>Name</td><td>Age</td><td>Title</td><td>Organization</td><td>Time Commitment (Months)</td><td colspan="2">Task Assignment</td><td>Signature</td></tr>
<tr><td>James Le Duc</td><td>73</td><td>Professor</td><td>UTMB</td><td>3</td><td colspan="2">Project leader</td><td></td></tr>
<tr><td>Pei-Yong Shi</td><td>53</td><td>Professor</td><td>UTMB</td><td>3</td><td colspan="2">Co-Project leader</td><td></td></tr>
<tr><td>Dennis Bente</td><td>43</td><td>Associate professor</td><td>UTMB</td><td>3</td><td colspan="2">Co-Project leader</td><td></td></tr>
</table>

	Zhiming Yuan	56	Professor	WHIOV	3	Project Leader in WHIOV	
	Chao Shan	34	Professor	WHIOV	6	Vaccine development and efficacy test	
	Han Xia	36	Associate professor	WHIOV	6	Anti-CCHFV polyclonal antibody generation	

Text

[= 1 * ROMAN]. Research Background

1. Research purpose

The purposes of the project (1) Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV). (2) Generation horse source polyclonal antibody for anti-CCHFV therapy.

2. Foreign and domestic research background, trend of development

Crimean-Congo hemorrhagic fever (also known as Xinjiang hemorrhagic fever) is caused by CCHFV in humans. CCHFV is a tick-borne virus with a wide geographical distribution, including Africa, the Balkans, the Middle East, Russia, western Asia and eastern Asia and needs high containment laboratory to conduct research. There are currently no licensed vaccines to prevent CCHFV-associated disease. CCHFV causes severe disease in human beings with a reported mortality rate of 3%–30% [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2013</Year><RecNum>110</RecNum><DisplayText>(1)</DisplayText><record><rec-number>110</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="a4688135-8d5c-4363-a3ef-afb1028964bb">110</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Forrester, N. L.</author><author>Watts, D. M.</author><author>McAuley, A. J.</author><author>Whitehouse, C. A.</author><author>Bray, M.</author></authors></contributors><titles><title>Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity</title><secondary-title>Antiviral Res</secondary-title></titles><periodical><full-title>Antiviral Res</full-title></periodical><pages>159-89</pages><volume>100</volume><number>1</number><edition>2013/07/29</edition><keywords><keyword>Animals</keyword><keyword>Genetic Variation</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>History, 20th Century</keyword><keyword>History, 21st Century</keyword><keyword>Humans</keyword><keyword>Phylogeny</keyword><keyword>Arbovirus</keyword><keyword>Bunyavirus</keyword><keyword>Crimean–Congo hemorrhagic fever virus</keyword><keyword>Nairovirus</keyword><keyword>Tick-borne virus</keyword><keyword>Viral hemorrhagic fever</keyword></keywords><dates><year>2013</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>23906741</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/23906741</url></related-urls></urls><electronic-resource-num>1

0.1016/j.antiviral.2013.07.006</electronic-resource-num><language>eng</language></record></Cite></EndNote>].

Currently, mainly two forms of the vaccine of CCFHV. Inactivated CCHFV vaccine: the vaccine is made on suckling mouse brain and used only in Bulgaria and is not approved for use in other countries [ADDIN EN.CITE <EndNote><Cite><Author>Mousavi-Jazi</Author><Year>2012</Year><RecNum>106</RecNum><DisplayText>(2)</DisplayText><record><rec-number>106</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="9eda4adb-313b-4322-9da6-36fce16d1a95">106</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Mousavi-Jazi, M.</author><author>Karlberg, H.</author><author>Papa, A.</author><author>Christova, I.</author><author>Mirazimi, A.</author></authors></contributors><titles><title>Healthy individuals' immune response to the Bulgarian Crimean-Congo hemorrhagic fever virus vaccine</title><secondary-title>Vaccine</secondary-title></titles><periodical><full-title>Vaccine</full-title></periodical><pages>6225-9</pages><volume>30</volume><number>44</number><edition>2012/08/14</edition><keywords><keyword>Adult</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Enzyme-Linked Immunospot Assay</keyword><keyword>Female</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Humans</keyword><keyword>Interferon-gamma</keyword><keyword>Male</keyword><keyword>Middle Aged</keyword><keyword>Neutralization Tests</keyword><keyword>T-Lymphocytes</keyword><keyword>Vaccines, Inactivated</keyword><keyword>Viral Vaccines</keyword></keywords><dates><year>2012</year><pub-dates><date>Sep</date></pub-dates></dates><isbn>1873-2518</isbn><accession-num>22902680</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/22902680</url></related-urls></urls><electronic-resource-num>10.1016/j.vaccine.2012.08.003</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. A formalin-inactivated preparation of CCHFV was also found to be protective against CCHFV infection in mice[ADDIN EN.CITE <EndNote><Cite><Author>Canakoglu</Author><Year>2015</Year><RecNum>121</RecNum><DisplayText>(3)</DisplayText><record><rec-number>121</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812016" guid="2fe103ce-96a5-46c6-9f76-59e484a881cd">121</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Canakoglu, N.</author><author>Berber, E.</author><author>Tonbak, S.</author><author>Ertek, M.</author><author>Sozdutmaz, I.</author><author>Aktas, M.</author><author>Kalkan, A.</author><author>Ozdarendeli, A.</author></authors></contributors><titles><title>Immunization of knock-out α/β interferon receptor mice against high lethal dose of Crimean-Congo hemorrhagic fever virus with a cell culture based

vaccine</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0003579</pages><volume>9</volume><number>3</number><edition>2015/03/11</edition><keywords><keyword>Animals</keyword><keyword>Cell Culture Techniques</keyword><keyword>Female</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Humans</keyword><keyword>Immunization</keyword><keyword>Mice</keyword><keyword>Mice, Knockout</keyword><keyword>Receptor, Interferon alpha-beta</keyword><keyword>Viral Vaccines</keyword></keywords><dates><year>2015</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>25760444</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25760444</url></related-urls></urls><custom2>PMC4356576</custom2><electronic-resource-num>10.1371/journal.pntd.0003579</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. Subunit CCHFV vaccine. Since CCHFV glycoproteins are displayed on the surface of the virion, it was used as the target to develop vaccine. Using vaccinia virus as vehicle to deliver the glycoproteins of CCHFV was shown to provide 100% protection to lethally challenged mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. DNA vaccine expressing nucleoprotein (NP) and ubiquitin-linked versions of GPC-derived Gn and Gc or virus-like particle vaccination has been shown to confer protection against lethal CCHFV challenge [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Mice fed transgenic plants expressing the CCHFV glycoproteins and immunized with purified glycoprotein from *Drosophila* insect cell developed antibodies against the glycoproteins, while the latter did not confer the protection[ADDIN EN.CITE ADDIN EN.CITE.DATA].

Polyclonal antibody was widely used for antiviral treatment. The FDA has approved the production of anti-rabies virus polyclonal antibodies for commercial use. The polyclonal anti-Ebola antibody from horse can effectively protect mice from lethal Ebola virus infection. During the 2014 Ebola outbreak, the antibody was used to treat Ebola virus infection and rescued patient life. Those cases indicate that antibody therapy plays an important role in prevention and control outbreaks of emerging diseases[ADDIN EN.CITE ADDIN EN.CITE.DATA].

3. References

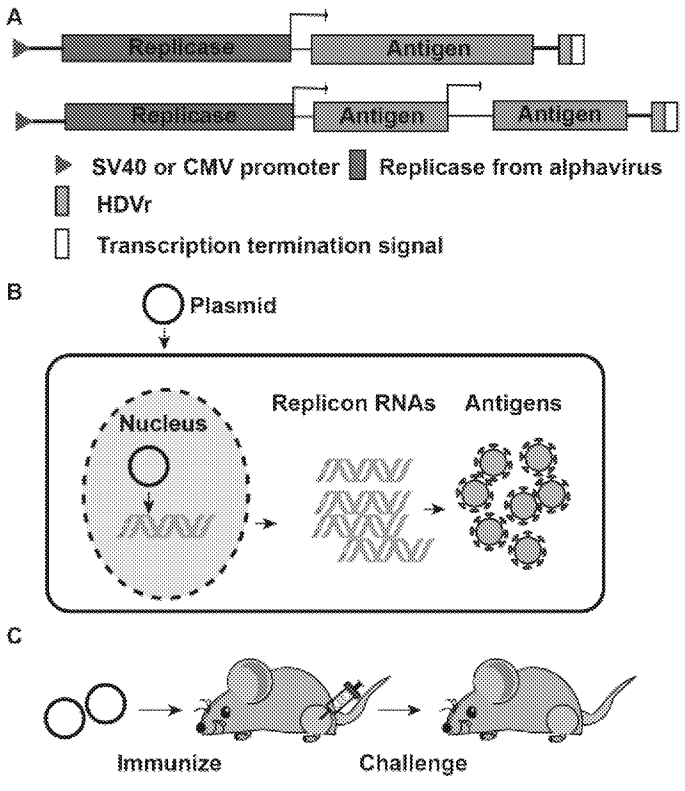
[ADDIN EN.REFLIST]

[= 2 * ROMAN]. Research Contents

1. Research contents

Aim 1 Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV). We will first develop the DNA-launched replicon of alphavirus due to its rapid replication capacity in mammalian cells to deliver foreign genes (Figure 1A). The replicon will be launched by eukaryotic cytomegalovirus (CMV) promoter or SV40 promoter. After the replicon built, we will engineer the CCHFV glycoproteins G_N and G_C (e.g., GPC open-reading frame) into the replicon DNA plasmids and characterize the immunogenicity and vaccine efficacy in a mouse model (Figure 1 B&C). We choose CCHFV as a target vaccine because (i) CCHFV represents the second most widespread of all medically important arboviruses (after dengue virus) and (ii) WHO and NIAID have classified it as an R&D Blueprint priority disease and Category A priority pathogen, respectively.

Aim 2 Generation horse source polyclonal antibody for anti-CCHFV therapy. VSV-CCHFV-GPC recombinant virus will be generated and used to immunized the horse. Multiple doses may be used to boost horse and facilitate the immune response. The polyclonal antibody from horse will be analyzed. Once positive antibody was confirmed, the antibody will be purified from horse and used for mice efficacy study.



2. Research methods and experimental program

Figure 1 Experimental scheme. (A) A CHIKV (alphavirus) replicon-based antigen deliver system. CHIKV replicon RNA containing one or two

antigen-expressing subgenomes is launched through DNA plasmid using eukaryotic promoter (red triangle) to transcribe CHIKV replicon RNA inside mammalian cells. An HDVr (hepatitis delta ribozyme; orange box) and a transcription termination signal sequence (white box) are engineered at the 3' end of viral RNA. (B) DNA plasmid is delivered into cells to launch CHIKV replicon. The replication of replicon RNAs results in robust expression of antigens. (C) Immunization of mice with CHIKV replicon DNA. The plasmid DNA is delivered to animals. The vaccinated animals are analyzed for immunogenicity and challenged for efficacy testing.

Aim 1 Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV).

(1) **Construct alphavirus replicon as delivery system.** Alphavirus replicons are genomes with one or more of the structural protein genes deleted, but with all nonstructural genes and cis-acting sequences retained such that they replicate once introduced or produced in the cytoplasm (Fig. 1A). However, because the compatible alphavirus structural proteins are missing, infectious virus cannot be produced. The alphavirus replicon subgenomic promoter can be left intact such that subgenomic RNA is produced, which for alphaviruses is in high molar excess compared to the genomic RNA. Thus, if a foreign gene is used to replace the alphavirus structural polyprotein encoded by the subgenomic RNA, large amounts are expressed but viral spread cannot occur. Here we choose chikungunya virus (CHIKV) replicon among other alphaviruses in this proposal.

(2) **Antigen selection of CCHFV vaccine.** Like other Bunyaviruses, CCHFV contains a tri-segmented, negative sense RNA genome: small (S), medium (M), and large (L) segments. Among the six genetically distinct clades of CCHFV, there are 20, 31, and 22% sequence divergence for S, M, and L segment, respectively [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2013</Year><RecNum>110</RecNum><DisplayText>(1)</DisplayText><record><rec-number>110</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="a4688135-8d5c-4363-a3ef-afb1028964bb">110</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Forrester, N. L.</author><author>Watts, D. M.</author><author>McAuley, A. J.</author><author>Whitehouse, C. A.</author><author>Bray,

M.</author></authors></contributors><titles><title>Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity</title><secondary-title>Antiviral Res</secondary-title></titles><periodical><full-title>Antiviral Res</full-title></periodical><pages>159-89</pages><volume>100</volume><number>1</number><edition>2013/07/29</edition><keywords><keyword>Animals</keyword><keyword>Genetic Variation</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>History, 20th Century</keyword><keyword>History, 21st Century</keyword><keyword>Humans</keyword><keyword>Phylogeny</keyword><keyword>Arbovirus</keyword><keyword>Bunyavirus</keyword><keyword>Crimean–Congo hemorrhagic fever virus</keyword><keyword>Nairovirus</keyword><keyword>Tick-borne virus</keyword><keyword>Viral hemorrhagic fever</keyword></keywords><dates><year>2013</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>23906741</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/23906741</url></related-urls></urls><electronic-resource-num>10.1016/j.antiviral.2013.07.006</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. The M segment encodes the glycoprotein precursor (GPC) that is processed to two structural glycoproteins G_N and G_C, along with several non-structural glycoproteins. G_N and G_C are the major antigenic proteins that elicit protective immune response in humans, as observed with other Bunyaviruses [ADDIN EN.CITE <EndNote><Cite><Author>Faburay</Author><Year>2016</Year><RecNum>131</RecNum><DisplayText>(12)</DisplayText><record><rec-number>131</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556820677" guid="3638de14-24e8-4407-8efe-5a76314e8107">131</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Faburay, B.</author><author>Wilson, W. C.</author><author>Gaudreault, N. N.</author><author>Davis, A. S.</author><author>Shivanna, V.</author><author>Bawa, B.</author><author>Sunwoo, S. Y.</author><author>Ma, W.</author><author>Drolet, B. S.</author><author>Morozov, I.</author><author>McVey, D. S.</author><author>Richt, J.

A.</author></authors></contributors><titles><title>A Recombinant Rift Valley Fever Virus Glycoprotein Subunit Vaccine Confers Full Protection against Rift Valley Fever Challenge in Sheep</title><secondary-title>Sci Rep</secondary-title></titles><periodical><full-title>Sci Rep</full-title></periodical><pages>27719</pages><volume>6</volume><edition>2016/06/14</edition><keywords><keyword>Animals</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibody Formation</keyword><keyword>Glycoproteins</keyword><keyword>Immunoglobulin G</keyword><keyword>Liver</keyword><keyword>Lymph Nodes</keyword><keyword>Recombinant Proteins</keyword><keyword>Rift Valley Fever</keyword><keyword>Rift Valley fever virus</keyword><keyword>Sheep</keyword><keyword>Sheep Diseases</keyword><keyword>Temperature</keyword><keyword>Vaccines, Subunit</keyword><keyword>Viremia</keyword><keyword>Virulence</keyword></keywords><dates><year>2016</year><pub-dates><date>06</date></pub-dates></dates><isbn>2045-2322</isbn><accession-num>27296136</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/27296136</url></related-urls></urls><custom2>PMC4906348</custom2><electronic-resource-num>10.1038/srep27719</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. Monoclonal antibodies against CCHFV G_N and G_C potently neutralize diverse CCHFV strains *in vitro* [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2017</Year><RecNum>132</RecNum><DisplayText>(13)</DisplayText><record><rec-number>132</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556820738" guid="1092b9f5-fd56-4d1e-ab08-64c4c801ea82">132</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Guerrero, L. I. W.</author><author>Albariño, C. G.</author><author>Bergeron, É</author><author>Nichol, S. T.</author><author>Spiropoulou, C. F.</author></authors></contributors><titles><title>Identification of broadly neutralizing monoclonal antibodies against Crimean-Congo hemorrhagic fever virus</title><secondary-title>Antiviral Res</secondary-title></titles><periodical><full-title>Antiviral

Res</full-title></periodical><pages>112-120</pages><volume>146</volume><edition>2017/08/24</edition><keywords><keyword>Animals</keyword><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Epitopes</keyword><keyword>Glycoproteins</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>Humans</keyword><keyword>Mutation</keyword><keyword>Neutralization Tests</keyword><keyword>Phylogeny</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Crimean-Congo hemorrhagic fever virus</keyword><keyword>Monoclonal antibodies</keyword><keyword>Neutralization assay</keyword><keyword>Virus-like particles</keyword></keywords><dates><year>2017</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>28842265</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/28842265</url></related-urls></urls><electronic-resource-num>10.1016/j.antiviral.2017.08.014</electronic-resource-num><language>eng</language></record></Cite></EndNote>], and adoptive transfer of these antibodies confer *in vivo* protection in suckling mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These results support the possibility of cross-protection against all strains from the six CCHFV clades. The results also justify expression of the complete GPC polyprotein for vaccine development.

(3) **Construction of CCFHV vaccine candidates.** We will engineer the full open-reading frame of CCHFV GPC into the CHIKV replicon plasmid. The complete GPC is selected to ensure the correct processing and conformation of the individual G_N and G_C proteins. The GPC sequence from clinical CCHFV strain FK16116 (China) [ADDIN EN.CITE ADDIN EN.CITE.DATA] and Turkey200406546 (UTMB), rather than laboratory strain IbAr10200, will be used for human codon optimization and inserted into the replicon plasmids. The resulting GPC-replicon plasmids will be evaluated in cell culture for the expression and processing of GN and GC proteins using Western blot. Once the protein expression has been confirmed, we will test the GPC-replicon plasmid in a CCHFV mouse model.

(4) **Testing CCHFV vaccine candidates *in vivo*.** We will test the GPC-replicon plasmids for immunogenicity, safety, and efficacy in a mouse model. Over the last seven decades, attempts have

been made to establish an animal model for CCHF in adult mice, rats, guinea pigs, hamsters, rabbits, and other laboratory animals. They met with very limited success showing little or no signs of infection or disease when infected with CCHFV. Until 2010, the only animal that manifested disease after CCHFV infection was the newborn suckling mouse. In recent years, small animal models have been developed using STAT-1$^{-/-}$ [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2010</Year><RecNum>115</RecNum><DisplayText>(16)</DisplayText><record><rec-number>115</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812015" guid="3f1f6230-804e-46e3-8483-dac0c54cf730">115</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Alimonti, J. B.</author><author>Shieh, W. J.</author><author>Camus, G.</author><author>Ströher, U.</author><author>Zaki, S.</author><author>Jones, S. M.</author></authors></contributors><titles><title>Pathogenesis and immune response of Crimean-Congo hemorrhagic fever virus in a STAT-1 knockout mouse model</title><secondary-title>J Virol</secondary-title></titles><periodical><full-title>J Virol</full-title></periodical><pages>11089-100</pages><volume>84</volume><number>21</number><edition>2010/08/25</edition><keywords><keyword>Animals</keyword><keyword>Disease Models, Animal</keyword><keyword>Disease Susceptibility</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>Humans</keyword><keyword>Mice</keyword><keyword>Mice, Knockout</keyword><keyword>STAT1 Transcription Factor</keyword></keywords><dates><year>2010</year><pub-dates><date>Nov</date></pub-dates></dates><isbn>1098-5514</isbn><accession-num>20739514</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/20739514</url></related-urls></urls><custom2>PMC2953203</custom2><electronic-resource-num>10.1128/JVI.01383-10</electronic-resource-num><language>eng</language></record></Cite></EndNote>] or IFNAR$^{-/-}$ (type-I interferon receptor) knockout mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Since these mice succumb to CCHFV infection, we will test our vaccine candidates in the IFNAR$^{-/-}$ mice. More recently, transient depletion of interferon receptors through intraperitoneal injection with a monoclonal antibody (Mab MAR1-5A3, Leinco Technologies) immediately prior to challenge has been shown to allow efficient

viral replication [ADDIN EN.CITE ADDIN EN.CITE.DATA]. We will also use the wild-type C57BL/6 mice to evaluate the vaccine efficacy since this model allows a full immune response to immunization while allowing the virus replicate after challenge. The mouse efficacy experiments with CCHFV will be performed by Dr. Chao Shan and Dr. Han Xia at the BSL-4 facility at Wuhan Institute of Virology, Chinese Academy of Sciences.

Using the IFNAR$^{-/-}$ mice, we will intramuscularly immunize different doses of replicon-GPC plasmid (1, 5, 10, and 20 μg; n=12 per group, male and female) or PBS (as sham control) using the TriGrid Delivery System. On day 28 post-immunization, the immunized mice will be bled and measured for antibody titers using CCHFV VLP ELISA [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2015</Year><RecNum>136</RecNum><DisplayText>(20)</DisplayText><record><rec-number>136</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556821443" guid="951bec17-5bed-4e75-80a1-9f1b854ce673">136</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Metcalfe, M. G.</author><author>Albariño, C. G.</author><author>Guerrero, L. W.</author><author>Pegan, S. D.</author><author>Spiropoulou, C. F.</author><author>Bergeron, É</author></authors></contributors><titles><title>Assessment of Inhibitors of Pathogenic Crimean-Congo Hemorrhagic Fever Virus Strains Using Virus-Like Particles</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0004259</pages><volume>9</volume><number>12</number><edition>2015/12/01</edition><keywords><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Drug Evaluation, Preclinical</keyword><keyword>Genes, Reporter</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Molecular Sequence Data</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Transcription, Genetic</keyword><keyword>Virion</keyword><keyword>Virus Internalization</keyword><keyword>Virus

Replication</keyword></keywords><dates><year>2015</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>26625182</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/26625182</url></related-urls></urls><custom2>PMC4666410</custom2><electronic-resource-num>10.1371/journal.pntd.0004259</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. On the same day, the animals will be challenged with 100 PFU of clinical CCHFV strain FK16116 (China). The challenged animals will be measured for the following parameters for efficacy: (i) Viremia and viral loads in different organs using qRT-PCR and plaque assays, (ii) weight loss, (iii) survival (Deaths are expected on days 2-6 post-challenge in the sham group), (iv) antibody titers on 28 days after challenge, and (v) T cell activation. Comparison of the antibody titers before and after challenge will indicate if the vaccine elicits sterilizing immunity (i.e., no detectable viremia and no increase in antibody titers after challenge). Using the wild-type mice, we will immunize C57BL/6 mice with the GPC-replicon plasmid and measure the five parameters described above. The immunized mice will be challenged with 100 PFU of clinical CCHFV strain FK16116 (China) by the intraperitoneal route; however, to facilitate viral infection and replication, the animals will be pretreated with 2 mg of interferon receptor-blocking antibodies one day before the CCHFV challenge, and further treated with 0.5 mg of antibody at 24 h after challenge [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These *in vivo* studies will reveal the immunogenicity, safety, and efficacy of the vaccine candidates. Comparison of the results from different dosage groups (1, 5, 10, and 20 μg DNA) will also allow us estimate the correlates of protections against CCHFV infection in the mouse model.

Aim 2 Generation horse source polyclonal antibody for anti-CCHFV therapy.

(1) Production of VSV-CCHFV-GPC recombinant virus.

(2) Immunization horse for polyclonal antibody. VSV-CCHFV-GPC recombinant virus (1×10^6 PFU) will be used to immunized horse by intramuscularly (multi-point injection) route. On day 28 post-immunization, the immunized mice will be bled and measured for antibody titers using CCHFV VLP ELISA [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2015</Year><RecNum>136</RecNum><DisplayText>(20)</DisplayText><record><rec-number>136</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556821443"

guid="951bec17-5bed-4e75-80a1-9f1b854ce673">136</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Metcalfe, M. G.</author><author>Albariño, C. G.</author><author>Guerrero, L. W.</author><author>Pegan, S. D.</author><author>Spiropoulou, C. F.</author><author>Bergeron, É</author></authors></contributors><titles><title>Assessment of Inhibitors of Pathogenic Crimean-Congo Hemorrhagic Fever Virus Strains Using Virus-Like Particles</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0004259</pages><volume>9</volume><number>12</number><edition>2015/12/01</edition><keywords><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Drug Evaluation, Preclinical</keyword><keyword>Genes, Reporter</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Molecular Sequence Data</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Transcription, Genetic</keyword><keyword>Virion</keyword><keyword>Virus Internalization</keyword><keyword>Virus Replication</keyword></keywords><dates><year>2015</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>26625182</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/26625182</url></related-urls></urls><custom2>PMC4666410</custom2><electronic-resource-num>10.1371/journal.pntd.0004259</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. If the antibody titer reaches desired point, the blood will be bled for antibody purification. If not, the boost will be happened to facilitate immune response and wait another 28 days.

(3) Polyclonal antibody purification from horse blood. Once desired anti-CCHFV antibody titer reached, the horse blood will be bled. Protein G Agarose will be used to purify the horse polyclonal antibody based on the manufacture manual. The eluted polyclonal antibody will be

dialyed in PBS and aliquoted. Purified polyclonal antibody will be measured by CCHFV VLP ELISA to confirm antibody titer.

(4) Mice efficacy study.

Using the IFNAR$^{-/-}$ mice, we will intraperitoneal inject different doses of purified antibody (or PBS (as sham control) one day before CCHFV FK16116 infection. On the day of infection, the blood will be collected and 100 PFU CCHFV will be injected subcutaneously. The challenged animals will be measured for the following parameters for efficacy: (i) Viremia and viral loads in different organs using qRT-PCR and plaque assays, (ii) weight loss, (iii) survival (Deaths are expected on days 2-6 post-challenge in the sham group).

3. Expected outcome

The proposed experiments will generate CCHFV vaccine candidate built upon the FK16116 and Turkey200406546 strain. The cross-protection against different stain will be evaluated after challenge. Comparison of the immunogenicity and efficacy from the mouse experiments will allow us down select the final candidate. In an unlikely situation that a single-shot immunization of the replicon-GPC plasmid is not sufficient to elicit protective antibody titers or full protection against CCHFV infection, we will boost the animals with a second dose of replicon-GPC plasmid. The mouse efficacy results will allow us strategize further preclinical development, including efficacy test in a non-human primate model. In addition, by selecting the polyclonal antibody from horse will allow us have the potential candidate for anti-CCHFV treatment.

4. Key problems and technical difficulties to be solved

Vaccine development. The proposed study will establish a DNA replicon platform for CHIKV. And the platform will be served as the vehicle to deliver the CCHFV-GPC for vaccine candidate. The cell culture and mouse study will define the expression pattern. This information will be critical to guide vaccine and therapeutics development. We will also explore the cross-protection when use two different antigens to immunize mice. The polyclonal antibody will provide potential treatment option for CCHFV infection.

5. Innovations of the research proposal

The innovation of this project derives from the research plan that integrates three powerful components into a translational product: (i) the robust self-amplifying ability of alphavirus replicon,

(ii) the ease of DNA plasmid as a vector to launch the replicative RNAs (using the mammalian transcription machinery), and (iii) the cutting-edge device for DNA delivery in clinical use. Although alphavirus replicon has been used for protein expression and vaccine development for almost three decades, previous efforts have mainly focused on the virus-like particle-RNA packaging (VLP) approach [ADDIN EN.CITE <EndNote><Cite><Author>Lundstrom</Author><Year>2017</Year><RecNum>137</RecNum><DisplayText>(21)</DisplayText><record><rec-number>137</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556823011" guid="45f9f958-084b-4a4f-a13b-67585a1d3c8d">137</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Lundstrom, K.</author></authors></contributors><titles><title>Oncolytic Alphaviruses in Cancer Immunotherapy</title><secondary-title>Vaccines (Basel)</secondary-title></titles><periodical><full-title>Vaccines (Basel)</full-title></periodical><volume>5</volume><number>2</number><edition>2017/04/12</edition><keywords><keyword>cancer immunotherapy</keyword><keyword>oncolytic alphaviruses</keyword><keyword>tumor eradication</keyword></keywords><dates><year>2017</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>2076-393X</isbn><accession-num>28417936</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/28417936</url></related-urls></urls><custom2>PMC5492006</custom2><electronic-resource-num>10.3390/vaccines5020009</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. For the VLP approach, viral structural proteins are supplied in trans to package the viral replicon RNA (carrying an antigen of interest) into VLPs; such VLPs are used to immunize animals. The drawbacks of the VLP approach include the requirement of eukaryotic cell culture electroporation for VLP production, moderate yield of VLP manufacture (when compared with the doses required for vaccination and treatment), pre-immune inhibition when multiple rounds of VLP infection are needed, and the "cold chain" transportation from manufactures to clinics. All the above drawbacks of the VLP approach could be mitigated by the proposed DNA-launched replicon in this project.

Despite the potential concern of integration of exogenous DNA into the cellular chromosome, the DNA plasmid approach has been actively pursued for vaccine development and cancer therapy. For example, the current frontrunner ZIKV vaccine in the phase II clinical trial is built upon a DNA plasmid (expressing two viral structure proteins prM and E). This type of traditional DNA vaccine requires multiple high doses to achieve protective immunity. For the ZIKV DNA vaccines, each human volunteer requires three shots, with 1 to 5 mg of DNA per shot, to achieve short-term neutralizing antibody titers [ADDIN EN.CITE ADDIN EN.CITE.DATA]. It should be noted that the adverse potential of DNA integration into the cellular genome remains to be determined in clinics. Compared with the traditional non-amplifying DNA vaccine, our DNA-launched replicon is self-replicative, and requires a much lower dose to achieve efficacy. The significantly reduced dose will minimize the risk of potential DNA integration. In addition, due to the self-amplifying nature of the proposed replicon DNA platform, protective immunity and efficacy could potentially be achieved with a single dose to control explosive outbreaks, which is particularly important when responding to public health emergency. Therefore, the replicon DNA platform has the potential to overcome the most critical weakness of the traditional DNA vaccine, and could be developed into a transformative new DNA delivery technology.

Collectively, we hypothesize that, in combination with the cutting-edge device for delivery, the DNA-launched replicon platform will transform into robust translational products for vaccine and therapeutics development. Since the goal of the Advanced Customer Cultivation Project to develop solutions to prevent and control human diseases, the combination of the well-proven alphaviral replicon system with the ease of DNA engineering and the state-of-the-art DNA delivery represents a practical innovation for vaccine platform development.

Passive immunotherapy with sera of animal origin has been used for over 120 years to treat bacterial and viral infections, envenomations and drug intoxications. The lower manufacturing costs of hyperimmune equine antisera therefore represents an attractive alternate avenue of treatment, especially to developing and third-world countries, compared to the more costly production process of viral specific mAbs. However, currently the study of anti-CCHFV antisera via the immunization of horses and the safety and efficiency has not been reported. Since the highly replication efficiency

and the safety of the VSV vector, in this study the VSV-CCHFV-GP will be chose as the antigen for horse.

[= 3 * ROMAN]. Research Plan

1. Research schedule

Aim	Tasks and milestones	2019											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter							X	X	X	X	X	X
	Characterize SEAP replicons in cell culture												
	Characterize SEAP replicon in mice												
	Clone GPC CHIKV replicon												
	Test GPC replicon in cell culture												
	Test efficacy in mouse model												
2	Generation VSV-CCHFV-GP recombinant virus							X	X	X	X	X	X
	Immunization horse and characterization antibody response												
	Purify antibody from horse												
	Test efficacy in mouse model												

Aim	Tasks and milestones	2020											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter												
	Characterize SEAP replicons in cell culture	X	X	X									
	Characterize SEAP replicon in mice				X	X	X	X					
	Clone GPC CHIKV replicon								X	X	X	X	
	Test GPC replicon in cell culture												X
	Test efficacy in mouse model												
2	Generation VSV-CCHFV-GP recombinant virus												
	Immunization horse and characterization antibody response	X	X	X	X	X	X	X	X				
	Purify antibody from horse									X	X	X	X
	Test efficacy in mouse model												

Aim	Tasks and milestones	2021											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter												
	Characterize SEAP replicons in cell culture												
	Characterize SEAP replicon in mice												
	Clone GPC CHIKV replicon												
	Test GPC replicon in cell culture	X	X	X									
	Test efficacy in mouse model				X	X	X	X	X	X	X	X	
2	Generation VSV-CCHFV-GP recombinant virus												
	Immunization horse and characterization antibody response												
	Purify antibody from horse												
	Test efficacy in mouse model				X	X	X	X	X	X	X	X	

2. Conditions necessary to conduct the research (including lab equipments, instruments and etc.)

Biosafety cabinet

PCR thermal cycler

Real-Time PCR thermal cycler

Table top centrifuge

Water bath

DNA gel electrophoresis system

Protein gel electrophoresis system

TriGrid Delivery System (Ichor, for DNA vaccine delivery)

ChemiDoc System

Pipettes

CO2 incubators

Microscopy

Refrigerator

-80 freezer

-30 freezer

Liquid nitrogen tank

IV. Introduction of Leader and Participants

James Le Duc, PhD, is the director of the Galveston National Laboratory, one of the largest active biocontainment facilities on a U.S. academic campus. Dr. Le Duc joined UTMB in late 2006 from the Centers for Disease Control and Prevention in Atlanta, where he was the influenza coordinator and director of the Division of Viral and Rickettsial Diseases. With more than four decades of experience working in the fields of biodefense and public health, his work has taken him around the world, from West Africa, where he began his professional career as a field biologist working for the Smithsonian Institution, to Brazil and Panama during a 23-year career as a U.S. Army officer in the medical research and development command.

Pei-Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas, USA. He is an elected Fellow of American Academy of Microbiology, adjunct Professor of Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore, and Honorary Professor at the Wuhan Institute of Virology, Chinese Academy of Sciences. He received his Ph.D. in virology in 1996 from Georgia State University. After postdoctoral training at Yale University, he joined Bristol-Myers Squibb as a Principal Scientist to develop HIV and HCV therapeutics from 1998 to 2000. He then moved to the Wadsworth Center, New York State Department of Health, to study West Nile virus. From 2008 to 2015, he served as Dengue Unit Head and Executive Director to lead drug discovery at Novartis Institute for Tropical Diseases. His group developed the first infectious clones of the epidemic strain of West Nile virus and Zika virus, discovered two RNA cap methylation activities of flavivirus NS5 protein, identified essential RNA elements for flavivirus replication, established various platforms for flavivirus vaccine and drug discovery, and pioneered therapeutics development for dengue virus. He is internationally recognized for his scholar and administrative accomplishments at leading research institution, public health sector, and pharmaceutical industry. Dr. Shi has more than 20 years experiences in handling BSL2 and ABSL2 agent.

Dennis A. Bente, DVM, Ph.D., is an associate professor from University of Texas Medical Branch, Galveston Texas, USA. Dr. Bente received his DVM in 2000 and Ph.D. in 2003 from University of Veterinary Medicine at Germany. The goal of Dr. Bente's research is to better understand the

transmission and pathogenesis of tick - borne hemorrhagic fever viruses and to develop countermeasures to combat the disease. The intersection between arbovirology and hemorrhagic fever research requires an interdisciplinary approach, involving virology (classical techniques as well as molecular techniques such as reverse genetics), immunology (human and animal models), and tick physiology. Dr. Bente's is the first laboratory in the world to establish a tick - host transmission model in a BSL-4 setting. A number of collaborations have been established with other virologists at UTMB, including Drs. Alan Barrett, Thomas Ksiazek, David Beasley, Alexander Freiberg and Thomas Geisbert, that include studies on Crimean - Congo hemorrhagic fever virus, Kyasanur forest disease virus, Alkhurma hemorrhagic fever virus, and West - Nile virus. Dr. Bente has more than 10 years experiences in handling BSL2, BSL3, BSL4, ABSL2, ABSL3 and ABSL4 agent.

Zhiming Yuan, Ph.D., professor from Wuhan Institute of Virology, the director of the Wuhan National biosafety laboratory (BSL-4), and the President of Wuhan Branch, Chinese Academy of Sciences. His research interest including: (1) Diagnosis, evolution, and pathogenesis of aborviruses, (2) Tropical Disease vector control with microbial agents, and (3) Laboratory biorisk management and applied biosafety research.

Chao Shan, Ph.D., professor from Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China. Dr. Shan Received his Ph.D. in Biochemistry and Molecular Biology in Wuhan Institute of Virology, Chinese Academy of Sciences in China in 2014. And he joined Novartis Institute for Tropical Diseases (NITD) from 2013 to 2015. He served as postdoctoral fellow in University of Texas Medical Branch from 2015 to 2019. During his training at Wuhan Institute of Virology and NITD, he worked with Dengue virus, Japanese encephalitis virus and EV71 virus *in vitro*. After joining in UTMB in December 2015, Dr. Shan has completed BSL3, BSL4, ABSL2, ABSL3 and ABSL4 training in University of Texas Medical Branch. He built the first reverse genetic system for Zika virus and developed the first live-attenuated Zika vaccine in the world.

Han Xia, Ph.D., is associate professor from Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China. Dr. Xia received his Ph.D. in Biochemistry and Molecular Biology in Wuhan Institute of Virology, Chinese Academy of Sciences in China in 2014. And she served as postdoctoral fellow and the

complete the BSL-4 training in University of Texas Medical Branch from 2013 to 2016, working with the reverse genetic system developing of CCHFV and CCHFV-vector-host interaction through NGS strategy. Currently, her research interest is the epidemiology, diagnoses, and evolution of arbovirus.

[= 7 * ROMAN]. Budget

Unit: RMB 10,000 yuan

Budget Form of Project Expenditure		
Item	Amount	Detailed calculation
1. Equipment		
(1) Equipment purchase	0	
(2) Trial-manufacture purchase	0	
(3) Equipment modification and rent	0	
2. Reagents and consumables	15	Cloning and related reagent, kit, sequencing, cell culture reagent and consumables
3. Analysis	15	Horse purchase, immunization, antibody purification, DNA synthesis
4. Fuel and power	3	Transport
5. Travel/meeting/international cooperation and exchanges	5	Project meeting for WHIOV and UTMB, hotel etc.
6. Publication/literature/information dissemination/intellectual property	3	Publication and patent
7. Labor costs	5	Subsidy
8. Expert consultation	1	Project consultation
9. Other expenditure	3	Shipping fee about reagent and material
Total	50	

Note: Budget preparation and expenditure execution are conducted according to *Measures of Academy-Level Scientific Research Projects of Chinese Academy of Sciences*.

[= 8 * ROMAN]. Review opinions of applicant's organization

Our joint proposal, "Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus" represents the culmination of many years of collaboration between the Galveston National Laboratory, the U.S. National Academy of Sciences and the Wuhan Institute of Virology, Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences. We are very excited about the possibility of collaborating in the implementation of this important study and making use of the unique resources of both our biocontainment laboratories.

The study is non-confidential and we anticipate that our findings will be published in the peer reviewed scientific literature under shared co-authorship.

Organization (official seal) Principal (Signature)

03/05/2019

[= 9 * ROMAN]. Opinions of the Biosafety Committee in Project Implementation Organization

Chairman of Committee (Signature)

(d/m/y)

[= 10 * ROMAN]. Opinions of Science and Technology Steering Committee of Wuhan National Biosafety Laboratory, CAS

Chairman of Committee (official seal)

(d/m/y)

[ADDIN EN.REFLIST]

From: LeDuc, James W. [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: 5/3/2019 1:56:10 PM
To: Shan, Chao [chshan@UTMB.EDU]; Shi, Pei yong [peshi@UTMB.EDU]; Bente, Dennis A. [dabente@UTMB.EDU]; yzm@wh.iov.cn; hanxia@wh.iov.cn
Subject: RE: Wuhan CCHFV application
Attachments: Application Form Wuhan-UTMB May 3 2019-jwl.doc

Please see attached with some minor edits and questions in track change. Very nicely done! Good luck to us all!

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Shan, Chao <chshan@UTMB.EDU>
Sent: Friday, May 03, 2019 11:05 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; yzm@wh.iov.cn; hanxia@wh.iov.cn
Subject: Wuhan CCHFV application

Dear All,

Here is the application I wrote with help from Han for Wuhan collaboration. Please take a look and let me know if anything needs to be changed.

Thanks very much for all the supports from you.

Best,
Chao

No.	
Grant No.	
Confidentiality Level	Open

Wuhan National Biosafety Laboratory, Chinese Academy of Sciences

Advanced Customer Cultivation Project

Application Form

Project name: Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus

Project leader (Signature):

Organization: University of Texas Medical Branch, Texas, USA

Phone number: +1(409) 266-6500

E-mail: jwleduc@utmb.edu

Made by Research Planning Office of Wuhan Institute of Virology, CAS

Filled in on 30/4/2019

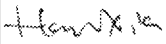
Instruction for Form Filling

1. Each item of the application form must be true, complete, accurate and clarified.
2. The "Confidentiality Level" on the cover shall be filled in with "Open".
3. All the application materials shall be submitted in duplicate in A4 book size in print (double page).
4. After the form is filled in completely, the applicant's organization shall review the truthfulness, completeness and effectiveness of the information filled in.
5. The application form shall only be considered effective with the signature of the principal of the applicant's organization.

.

Basic Information

<table>
<tr><td>Project name</td><td colspan="8">Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus</td></tr>
<tr><td>Type of project</td><td colspan="8">☐Frontline of the fundamental ☐Major common key technology √Application demonstration research ☐Others</td></tr>
<tr><td>Funding Category</td><td colspan="8">√Key Project ☐General Project</td></tr>
<tr><td>Budget</td><td colspan="8">Total estimate: 50 (RMB 10,000 yuan) (Note: please calculate for one year only)</td></tr>
<tr><td>Implementation period (one year)</td><td colspan="8">From (01/07/2019) to (31/12/2019)</td></tr>
<tr><td>Assessment period</td><td colspan="8">From (01/07/2019) to (31/12/2021)</td></tr>
<tr><td rowspan="3">Project leader</td><td>Name</td><td>James Le Duc</td><td>Sex</td><td>M</td><td>Birthday</td><td colspan="3">11/23/1945</td></tr>
<tr><td>Title</td><td>Professor</td><td>Duty</td><td>Director</td><td>Highest degree</td><td colspan="3">Ph.D.</td></tr>
<tr><td>Organization</td><td colspan="7">University of Texas Medical Branch, Texas, USA</td></tr>
<tr><td>Research group in WIV, CAS</td><td>Principal Investigator (Signature)</td><td colspan="3">Zhiming Yuan</td><td>Person to contact (Signature)</td><td colspan="2">Chao Shan</td></tr>
<tr><td>Project Implementation</td><td colspan="8">☐Authorization √Cooperation ☐Independent Completion</td></tr>
<tr><td rowspan="2">Project team</td><td>Total number</td><td>Senior</td><td>Intermediate</td><td>Junior</td><td>Assistant personnel</td><td>Post-doctor</td><td>Doctor candidate</td><td>Master candidate</td></tr>
<tr><td>6</td><td>6</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td rowspan="4">Main participants of the project implementation</td><td>Name</td><td>Age</td><td>Title</td><td>Organization</td><td>Time Commitment (Months)</td><td colspan="2">Task Assignment</td><td>Signature</td></tr>
<tr><td>James Le Duc</td><td>73</td><td>Professor</td><td>UTMB</td><td>3</td><td colspan="2">Project leader</td><td></td></tr>
<tr><td>Pei-Yong Shi</td><td>53</td><td>Professor</td><td>UTMB</td><td>3</td><td colspan="2">Co-Project leader</td><td></td></tr>
<tr><td>Dennis Bente</td><td>43</td><td>Associate professor</td><td>UTMB</td><td>3</td><td colspan="2">Co-Project leader</td><td></td></tr>
</table>

	Zhiming Yuan	56	Professor	WHIOV	3	Project Leader in WHIOV	
	Chao Shan	34	Professor	WHIOV	6	Vaccine development and efficacy test	
	Han Xia	36	Associate professor	WHIOV	6	Anti-CCHFV polyclonal antibody generation	

Text

[= 1 * ROMAN]. Research Background

1. Research purpose

The purposes of the project (1) Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV). (2) Generation horse source polyclonal antibody for anti-CCHFV therapy.

2. Foreign and domestic research background, trend of development

Crimean-Congo hemorrhagic fever (also known as Xinjiang hemorrhagic fever) is caused by CCHFV in humans. CCHFV is a tick-borne virus with a wide geographical distribution, including Africa, the Balkans, the Middle East, Russia, western Asia and eastern Asia and needs high containment laboratory to conduct research. There are currently no licensed vaccines to prevent CCHFV-associated disease. CCHFV causes severe disease in human beings with a reported mortality rate of 3%–30% [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2013</Year><RecNum>110</RecNum><DisplayText>(1)</DisplayText><record><rec-number>110</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="a4688135-8d5c-4363-a3ef-afb1028964bb">110</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Forrester, N. L.</author><author>Watts, D. M.</author><author>McAuley, A. J.</author><author>Whitehouse, C. A.</author><author>Bray, M.</author></authors></contributors><titles><title>Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity</title><secondary-title>Antiviral Res</secondary-title></titles><periodical><full-title>Antiviral Res</full-title></periodical><pages>159-89</pages><volume>100</volume><number>1</number><edition>2013/07/29</edition><keywords><keyword>Animals</keyword><keyword>Genetic Variation</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>History, 20th Century</keyword><keyword>History, 21st Century</keyword><keyword>Humans</keyword><keyword>Phylogeny</keyword><keyword>Arbovirus</keyword><keyword>Bunyavirus</keyword><keyword>Crimean–Congo hemorrhagic fever virus</keyword><keyword>Nairovirus</keyword><keyword>Tick-borne virus</keyword><keyword>Viral hemorrhagic fever</keyword></keywords><dates><year>2013</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>23906741</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/23906741</url></related-urls></urls><electronic-resource-num>1

0.1016/j.antiviral.2013.07.006</electronic-resource-num><language>eng</language></record></Cite></EndNote>].

Currently, there are mainly two forms of the vaccine of CCFHV. Inactivated CCHFV vaccine: the vaccine is made on suckling mouse brain and used only in Bulgaria and is not approved for use in other countries [ADDIN EN.CITE <EndNote><Cite><Author>Mousavi-Jazi</Author><Year>2012</Year><RecNum>106</RecNum><DisplayText>(2)</DisplayText><record><rec-number>106</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="9eda4adb-313b-4322-9da6-36fce16d1a95">106</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Mousavi-Jazi, M.</author><author>Karlberg, H.</author><author>Papa, A.</author><author>Christova, I.</author><author>Mirazimi, A.</author></authors></contributors><titles><title>Healthy individuals' immune response to the Bulgarian Crimean-Congo hemorrhagic fever virus vaccine</title><secondary-title>Vaccine</secondary-title></titles><periodical><full-title>Vaccine</full-title></periodical><pages>6225-9</pages><volume>30</volume><number>44</number><edition>2012/08/14</edition><keywords><keyword>Adult</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Enzyme-Linked Immunospot Assay</keyword><keyword>Female</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Humans</keyword><keyword>Interferon-gamma</keyword><keyword>Male</keyword><keyword>Middle Aged</keyword><keyword>Neutralization Tests</keyword><keyword>T-Lymphocytes</keyword><keyword>Vaccines, Inactivated</keyword><keyword>Viral Vaccines</keyword></keywords><dates><year>2012</year><pub-dates><date>Sep</date></pub-dates></dates><isbn>1873-2518</isbn><accession-num>22902680</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/22902680</url></related-urls></urls><electronic-resource-num>10.1016/j.vaccine.2012.08.003</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. A formalin-inactivated preparation of CCHFV was also found to be protective against CCHFV infection in mice[ADDIN EN.CITE <EndNote><Cite><Author>Canakoglu</Author><Year>2015</Year><RecNum>121</RecNum><DisplayText>(3)</DisplayText><record><rec-number>121</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812016" guid="2fe103ce-96a5-46c6-9f76-59e484a881cd">121</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Canakoglu, N.</author><author>Berber, E.</author><author>Tonbak, S.</author><author>Ertek, M.</author><author>Sozdutmaz, I.</author><author>Aktas, M.</author><author>Kalkan, A.</author><author>Ozdarendeli, A.</author></authors></contributors><titles><title>Immunization of knock-out α/β interferon receptor mice against high lethal dose of Crimean-Congo hemorrhagic fever virus with a cell culture based

vaccine</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0003579</pages><volume>9</volume><number>3</number><edition>2015/03/11</edition><keywords><keyword>Animals</keyword><keyword>Cell Culture Techniques</keyword><keyword>Female</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Humans</keyword><keyword>Immunization</keyword><keyword>Mice</keyword><keyword>Mice, Knockout</keyword><keyword>Receptor, Interferon alpha-beta</keyword><keyword>Viral Vaccines</keyword></keywords><dates><year>2015</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>25760444</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25760444</url></related-urls></urls><custom2>PMC4356576</custom2><electronic-resource-num>10.1371/journal.pntd.0003579</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. Subunit CCHFV vaccine. Since CCHFV glycoproteins are displayed on the surface of the virion, it was used as the target to develop vaccine. Using vaccinia virus as vehicle to deliver the glycoproteins of CCHFV was shown to provide 100% protection to lethally challenged mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. DNA vaccine expressing nucleoprotein (NP) and ubiquitin-linked versions of GPC-derived Gn and Gc or virus-like particle vaccination has been shown to confer protection against lethal CCHFV challenge [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Mice fed transgenic plants expressing the CCHFV glycoproteins and immunized with purified glycoprotein from *Drosophila* insect cell developed antibodies against the glycoproteins, while the latter did not confer the protection[ADDIN EN.CITE ADDIN EN.CITE.DATA].

Polyclonal antibody was widely used for antiviral treatment. The FDA has approved the production of anti-rabies virus polyclonal antibodies for commercial use. The polyclonal anti-Ebola antibody from horse can effectively protect mice from lethal Ebola virus infection. During the 2014 Ebola outbreak, the monoclonal anti-Ebola antibody was used to treat Ebola virus infection and rescued patient life. Those cases indicate that antibody therapy may plays an important role in prevention and control outbreaks of emerging diseases[ADDIN EN.CITE ADDIN EN.CITE.DATA].

Comment [LIW1]: this suggests that the horse anti-Ebola antibody was successfully used to treat humans during the West Africa Ebola outbreak. We need to be clear that it was monoclonal antibody used for treatment as referenced. See suggested changes

3. References

[ADDIN EN.REFLIST]

[= 2 * ROMAN]. Research Contents

1. Research contents

Aim 1 Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV). We will first develop the DNA-launched replicon of alphavirus due to its rapid replication capacity in mammalian cells to deliver foreign genes (Figure 1A). The replicon will be launched by eukaryotic cytomegalovirus (CMV) promoter or SV40 promoter. After the replicon is built, we will engineer the CCHFV glycoproteins G_N and G_C (e.g., GPC open-reading frame) into the replicon DNA plasmids and characterize the immunogenicity and vaccine efficacy in a mouse model (Figure 1 B&C). We choose CCHFV as a target vaccine because (i) CCHFV represents the second most widespread of all medically important arboviruses (after dengue virus) and (ii) WHO and NIAID have classified it as an R&D Blueprint priority disease and Category A priority pathogen, respectively.

Aim 2 Generation horse ~~source~~ polyclonal antibody for anti-CCHFV therapy. VSV-CCHFV-GPC recombinant virus will be generated and used to immunized the horse. Multiple booster doses may be used to ~~boost horse and facilitate~~enhance the horse immune response. The polyclonal antibody from the horse will be analyzed for specificity and titer. Once positive antibody ~~wa~~is confirmed, the horse antibody will be purified ~~from horse~~ and assayed for protective and therapeutic efficacy in ~~used for~~ mice. ~~efficacy study.~~

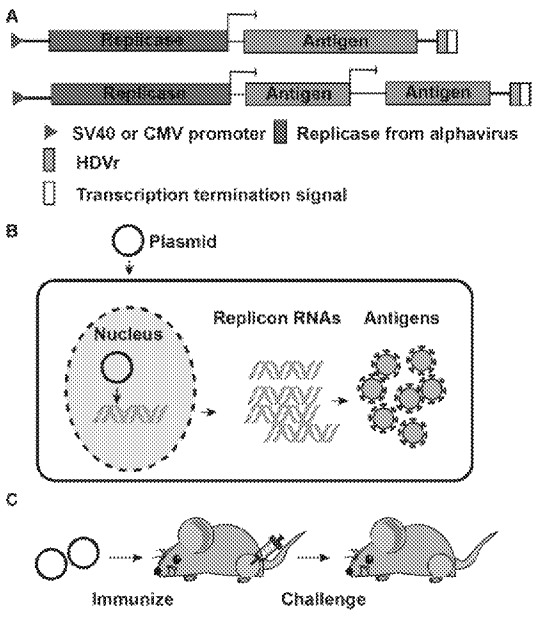


Figure 1 Experimental scheme. (A) A CHIKV (alphavirus) replicon-based

2. Research methods and experimental program

antigen deliver system. CHIKV replicon RNA containing one or two antigen-expressing subgenomes be ~~is~~ launched through DNA plasmid using eukaryotic promoter (red triangle) to transcribe CHIKV replicon RNA inside mammalian cells. An HDVr (hepatitis delta ribozyme; orange box) and a transcription termination signal sequence (white box) will be ~~are~~-engineered at the 3' end of viral RNA. (B) DNA plasmid will be~~is~~ delivered into cells to launch CHIKV replicon. The replication of replicon RNAs results in robust expression of antigens. (C) Immunization of mice with CHIKV replicon DNA. The plasmid DNA will be~~is~~ delivered to animals. The vaccinated animals will be~~are~~ analyzed for immunogenicity and challenged for efficacy testing.

Aim 1 Develop a replicon-based DNA vaccine for Crimean-Congo hemorrhagic fever virus (CCHFV).

(1) **Construct alphavirus replicon as delivery system.** Alphavirus replicons are genomes with one or more of the structural protein genes deleted, but with all nonstructural genes and cis-acting sequences retained such that they replicate once introduced or produced in the cytoplasm (Fig. 1A). However, because the compatible alphavirus structural proteins are missing, infectious virus cannot be produced. The alphavirus replicon subgenomic promoter can be left intact such that subgenomic RNA is produced, which for alphaviruses is in high molar excess compared to the genomic RNA. Thus, if a foreign gene is used to replace the alphavirus structural polyprotein encoded by the subgenomic RNA, large amounts are expressed but viral spread cannot occur. Here we choose chikungunya virus (CHIKV) replicon among other alphaviruses in this proposal.

Comment [LJW2]: not sure what is meant in this sentence. "We choose chik virus recplion as our delivery system in this proposal."?

(2) **Antigen selection of CCHFV vaccine.** Like other Bunyaviruses, CCHFV contains a tri-segmented, negative sense RNA genome: small (S), medium (M), and large (L) segments. Among the six genetically distinct clades of CCHFV, there are 20, 31, and 22% sequence divergence for S, M, and L segment, respectively [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2013</Year><RecNum>110</RecNum><DisplayText>(1)</DisplayText><record><rec-number>110</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812014" guid="a4688135-8d5c-4363-a3ef-afb1028964bb">110</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Forrester, N. L.</author><author>Watts, D. M.</author><author>McAuley, A.

J.</author><author>Whitehouse, C. A.</author><author>Bray, M.</author></authors></contributors><titles><title>Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity</title><secondary-title>Antiviral Res</secondary-title></titles><periodical><full-title>Antiviral Res</full-title></periodical><pages>159-89</pages><volume>100</volume><number>1</number><edition>2013/07/29</edition><keywords><keyword>Animals</keyword><keyword>Genetic Variation</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>History, 20th Century</keyword><keyword>History, 21st Century</keyword><keyword>Humans</keyword><keyword>Phylogeny</keyword><keyword>Arbovirus</keyword><keyword>Bunyavirus</keyword><keyword>Crimean–Congo hemorrhagic fever virus</keyword><keyword>Nairovirus</keyword><keyword>Tick-borne virus</keyword><keyword>Viral hemorrhagic fever</keyword></keywords><dates><year>2013</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>23906741</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/23906741</url></related-urls></urls><electronic-resource-num>10.1016/j.antiviral.2013.07.006</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. The M segment encodes the glycoprotein precursor (GPC) that is processed to two structural glycoproteins G_N and G_C, along with several non-structural G_N and G_C are the major antigenic proteins that elicit protective immune response in humans, as observed with other Bunyaviruses [ADDIN EN.CITE <EndNote><Cite><Author>Faburay</Author><Year>2016</Year><RecNum>131</RecNum><DisplayText>(12)</DisplayText><record><rec-number>131</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556820677" guid="3638de14-24e8-4407-8efe-5a76314e8107">131</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Faburay, B.</author><author>Wilson, W. C.</author><author>Gaudreault, N. N.</author><author>Davis, A. S.</author><author>Shivanna, V.</author><author>Bawa, B.</author><author>Sunwoo, S. Y.</author><author>Ma, W.</author><author>Drolet, B. S.</author><author>Morozov,

I.</author><author>McVey, D. S.</author><author>Richt, J. A.</author></authors></contributors><titles><title>A Recombinant Rift Valley Fever Virus Glycoprotein Subunit Vaccine Confers Full Protection against Rift Valley Fever Challenge in Sheep</title><secondary-title>Sci Rep</secondary-title></titles><periodical><full-title>Sci Rep</full-title></periodical><pages>27719</pages><volume>6</volume><edition>2016/06/14</edition><keywords><keyword>Animals</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibody Formation</keyword><keyword>Glycoproteins</keyword><keyword>Immunoglobulin G</keyword><keyword>Liver</keyword><keyword>Lymph Nodes</keyword><keyword>Recombinant Proteins</keyword><keyword>Rift Valley Fever</keyword><keyword>Rift Valley fever virus</keyword><keyword>Sheep</keyword><keyword>Sheep Diseases</keyword><keyword>Temperature</keyword><keyword>Vaccines, Subunit</keyword><keyword>Viremia</keyword><keyword>Virulence</keyword></keywords><dates><year>2016</year><pub-dates><date>06</date></pub-dates></dates><isbn>2045-2322</isbn><accession-num>27296136</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/27296136</url></related-urls></urls><custom2>PMC4906348</custom2><electronic-resource-num>10.1038/srep27719</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. Monoclonal antibodies against CCHFV G_N and G_C potently neutralize diverse CCHFV strains *in vitro* [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2017</Year><RecNum>132</RecNum><DisplayText>(13)</DisplayText><record><rec-number>132</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556820738" guid="1092b9f5-fd56-4d1e-ab08-64c4c801ea82">132</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Guerrero, L. I. W.</author><author>Albariño, C. G.</author><author>Bergeron, É</author><author>Nichol, S. T.</author><author>Spiropoulou, C. F.</author></authors></contributors><titles><title>Identification of broadly neutralizing monoclonal antibodies against Crimean-Congo hemorrhagic fever virus</title><secondary-title>Antiviral

Res</secondary-title></titles><periodical><full-title>Antiviral Res</full-title></periodical><pages>112-120</pages><volume>146</volume><edition>2017/08/24</edition><keywords><keyword>Animals</keyword><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Epitopes</keyword><keyword>Glycoproteins</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>Humans</keyword><keyword>Mutation</keyword><keyword>Neutralization Tests</keyword><keyword>Phylogeny</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Crimean-Congo hemorrhagic fever virus</keyword><keyword>Monoclonal antibodies</keyword><keyword>Neutralization assay</keyword><keyword>Virus-like particles</keyword></keywords><dates><year>2017</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1872-9096</isbn><accession-num>28842265</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/28842265</url></related-urls></urls><electronic-esource-num>10.1016/j.antiviral.2017.08.014</electronic-resource-num><language>eng</language></record></Cite></EndNote>], and adoptive transfer of these antibodies confer *in vivo* protection in suckling mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These results support the possibility of cross-protection against all strains from the six CCHFV clades. The results also justify expression of the complete GPC polyprotein for vaccine development.

(3) **Construction of CCFHV vaccine candidates.** We will engineer the full open-reading frame of CCHFV GPC into the CHIKV replicon plasmid. The complete GPC will be used~~is selected~~ to ensure the correct processing and conformation of the individual G_N and G_C proteins. The GPC sequence from clinical CCHFV strain FK16116 (China) [ADDIN EN.CITE ADDIN EN.CITE.DATA] and Turkey200406546 (UTMB), rather than laboratory strain IbAr10200, will be used for human codon optimization and inserted into the replicon plasmids. The resulting GPC-replicon plasmids will be evaluated in cell culture for the expression and processing of GN and GC proteins using Western blot. Once the protein expression has been confirmed, we will test the GPC-replicon plasmid in a CCHFV mouse model.

(4) **Testing CCHFV vaccine candidates *in vivo*.** We will test the GPC-replicon plasmids for immunogenicity, safety, and efficacy in a mouse model. Over the last seven decades, attempts have been made to establish an animal model for CCHF in adult mice, rats, guinea pigs, hamsters, rabbits, and other laboratory animals. They met with very limited success showing little or no signs of infection or disease when infected with CCHFV. Until 2010, the only animal that manifested disease after CCHFV infection was the newborn suckling mouse. In recent years, small animal models have been developed using STAT-1$^{-/-}$ [ADDIN EN.CITE <EndNote><Cite><Author>Bente</Author><Year>2010</Year><RecNum>115</RecNum><DisplayText>(16)</DisplayText><record><rec-number>115</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556812015" guid="3f1f6230-804e-46e3-8483-dac0c54cf730">115</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Bente, D. A.</author><author>Alimonti, J. B.</author><author>Shieh, W. J.</author><author>Camus, G.</author><author>Ströher, U.</author><author>Zaki, S.</author><author>Jones, S. M.</author></authors></contributors><titles><title>Pathogenesis and immune response of Crimean-Congo hemorrhagic fever virus in a STAT-1 knockout mouse model</title><secondary-title>J Virol</secondary-title></titles><periodical><full-title>J Virol</full-title></periodical><pages>11089-100</pages><volume>84</volume><number>21</number><edition>2010/08/25</edition><keywords><keyword>Animals</keyword><keyword>Disease Models, Animal</keyword><keyword>Disease Susceptibility</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Hemorrhagic Fever, Crimean</keyword><keyword>Humans</keyword><keyword>Mice</keyword><keyword>Mice, Knockout</keyword><keyword>STAT1 Transcription Factor</keyword></keywords><dates><year>2010</year><pub-dates><date>Nov</date></pub-dates></dates><isbn>1098-5514</isbn><accession-num>20739514</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/20739514</url></related-urls></urls><custom2>PMC2953203</custom2><electronic-resource-num>10.1128/JVI.01383-10</electronic-resource-num><language>eng</language></record></Cite></EndNote>] or IFNAR$^{-/-}$ (type-I interferon receptor) knockout mice [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Since these mice succumb to CCHFV infection, we will test our vaccine candidates in the IFNAR$^{-/-}$ mice. More recently, transient

depletion of interferon receptors through intraperitoneal injection with a monoclonal antibody (Mab MAR1-5A3, Leinco Technologies) immediately prior to challenge has been shown to allow efficient viral replication [ADDIN EN.CITE ADDIN EN.CITE.DATA]. We will also use the wild-type C57BL/6 mice to evaluate the vaccine efficacy since this model allows a full immune response to immunization while allowing the virus to replicate after challenge. The mouse efficacy experiments with CCHFV will be performed by Dr. Chao Shan and Dr. Han Xia at the BSL-4 facility at Wuhan Institute of Virology, Chinese Academy of Sciences.

Using the IFNAR$^{-/-}$ mice, we will intramuscularly immunize different doses of replicon-GPC plasmid (1, 5, 10, and 20 μg; n=12 per group, male and female) or PBS (as sham control) using the TriGrid Delivery System. On day 28 post-immunization, the immunized mice will be bled and measured for antibody titers using CCHFV VLP ELISA [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2015</Year><RecNum>136</RecNum><DisplayText>(20)</DisplayText><record><rec-number>136</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556821443" guid="951bec17-5bed-4e75-80a1-9f1b854ce673">136</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Metcalfe, M. G.</author><author>Albariño, C. G.</author><author>Guerrero, L. W.</author><author>Pegan, S. D.</author><author>Spiropoulou, C. F.</author><author>Bergeron, É</author></authors></contributors><titles><title>Assessment of Inhibitors of Pathogenic Crimean-Congo Hemorrhagic Fever Virus Strains Using Virus-Like Particles</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0004259</pages><volume>9</volume><number>12</number><edition>2015/12/01</edition><keywords><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Drug Evaluation, Preclinical</keyword><keyword>Genes, Reporter</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Molecular Sequence Data</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Transcription,

Genetic</keyword><keyword>Virion</keyword><keyword>Virus Internalization</keyword><keyword>Virus Replication</keyword></keywords><dates><year>2015</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>26625182</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/26625182</url></related-urls></urls><custom2>PMC4666410</custom2><electronic-resource-num>10.1371/journal.pntd.0004259</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. On the same day, the animals will be challenged with 100 PFU of clinical CCHFV strain FK16116 (China). The challenged animals will be measured for the following parameters for efficacy: (i) Viremia and viral loads in different organs using qRT-PCR and plaque assays, (ii) weight loss, (iii) survival (Deaths are expected on days 2-6 post-challenge in the sham group), (iv) antibody titers on 28 days after challenge, and (v) T cell activation. Comparison of the antibody titers before and after challenge will indicate if the vaccine elicits sterilizing immunity (i.e., no detectable viremia and no increase in antibody titers after challenge). Using the wild-type mice, we will immunize C57BL/6 mice with the GPC-replicon plasmid and measure the five parameters described above. The immunized mice will be challenged with 100 PFU of clinical CCHFV strain FK16116 (China) by the intraperitoneal route; however, to facilitate viral infection and replication, the animals will be pretreated with 2 mg of interferon receptor-blocking antibodies one day before the CCHFV challenge, and further treated with 0.5 mg of antibody at 24 h after challenge [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These *in vivo* studies will reveal the immunogenicity, safety, and efficacy of the vaccine candidates. Comparison of the results from different dosage groups (1, 5, 10, and 20 μg DNA) will also allow us to estimate the correlates of protections against CCHFV infection in the mouse model.

Aim 2 Generation horse ~~source~~ polyclonal antibody for anti-CCHFV therapy.

(1) Production of VSV-CCHFV-GPC recombinant virus.

(2) Immunization of the horse for polyclonal antibody production. VSV-CCHFV-GPC recombinant virus (1×10^6 PFU) will be used to immunized a horse by intramuscularly (multi-point injection) route. On day 28 post-immunization, the immunized ~~horse/mice~~ will be bled and measured for antibody titers using CCHFV VLP ELISA [ADDIN EN.CITE <EndNote><Cite><Author>Zivcec</Author><Year>2015</Year><RecNum>136</RecNum><

Comment [LJW3]: confirm that this is what you mean.

DisplayText>(20)</DisplayText><record><rec-number>136</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556821443" guid="951bec17-5bed-4e75-80a1-9f1b854ce673">136</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zivcec, M.</author><author>Metcalfe, M. G.</author><author>Albariño, C. G.</author><author>Guerrero, L. W.</author><author>Pegan, S. D.</author><author>Spiropoulou, C. F.</author><author>Bergeron, É</author></authors></contributors><titles><title>Assessment of Inhibitors of Pathogenic Crimean-Congo Hemorrhagic Fever Virus Strains Using Virus-Like Particles</title><secondary-title>PLoS Negl Trop Dis</secondary-title></titles><periodical><full-title>PLoS Negl Trop Dis</full-title></periodical><pages>e0004259</pages><volume>9</volume><number>12</number><edition>2015/12/01</edition><keywords><keyword>Antibodies, Monoclonal</keyword><keyword>Antibodies, Neutralizing</keyword><keyword>Antibodies, Viral</keyword><keyword>Drug Evaluation, Preclinical</keyword><keyword>Genes, Reporter</keyword><keyword>Hemorrhagic Fever Virus, Crimean-Congo</keyword><keyword>Molecular Sequence Data</keyword><keyword>Sequence Analysis, DNA</keyword><keyword>Transcription, Genetic</keyword><keyword>Virion</keyword><keyword>Virus Internalization</keyword><keyword>Virus Replication</keyword></keywords><dates><year>2015</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>26625182</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/26625182</url></related-urls></urls><custom2>PMC4666410</custom2><electronic-resource-num>10.1371/journal.pntd.0004259</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. If the antibody titer reaches desired point, the horse~~blood~~ will be bled for antibody purification. If not, ~~a~~the booster innoculation will be given~~happened~~ to facilitate the immune response and antibody titer will be assayed at ~~wait another~~ 28 days.

Comment [LJW4]: what's the target titer?

(3) Polyclonal antibody purification from horse blood. Once desired anti-CCHFV antibody titer is reached, the horse ~~blood~~ will be bled. Protein G Agarose will be used to purify the horse polyclonal antibody based on the manufacture manual. The eluted polyclonal antibody will be ~~dialyzed~~dialyzed in PBS and aliquoted. Purified polyclonal antibody will be measured by CCHFV VLP ELISA to confirm antibody titer.

Comment [LJW5]: identify titer desired someplace in the proposal

(4) Mice efficacy study.

Using the IFNAR$^{-/-}$ mice, we will intraperitoneally inject different doses of purified antibody (or PBS (as sham control) one day before CCHFV FK16116 infection. On the day of infection, the blood will be collected and 100 PFU CCHFV will be injected subcutaneously. The challenged animals will be measured for the following parameters for efficacy: (i) Viremia and viral loads in different organs using qRT-PCR and plaque assays, (ii) weight loss, (iii) survival (Deaths are expected on days 2-6 post-challenge in the sham group).

3. Expected outcome

The proposed experiments will generate a CCHFV vaccine candidate built upon the FK16116 and Turkey200406546 strain. The cross-protection against different stains will be evaluated after challenge. Comparison of the immunogenicity and efficacy from the mouse experiments will allow us to down select the final candidate. In an unlikely situation that a single-shot immunization of the replicon-GPC plasmid is not sufficient to elicit protective antibody titers or full protection against CCHFV infection, we will boost the animals with a second dose of replicon-GPC plasmid. The mouse efficacy results will allow us to strategize further regarding preclinical development, including efficacy test in a non-human primate model. In addition, by producing~~selecting~~ the horse polyclonal antibody, ~~from horse~~ we will ~~allow us~~ have ~~the~~ potential candidate for anti-CCHFV treatment.

Comment [LJW6]: please confirm that this is your intent

4. Key problems and technical difficulties to be solved.

Vaccine development. ~~The~~ proposed study will establish a DNA replicon platform for CHIKV. ~~And~~ ~~t~~This platform will ~~be~~ served as the vehicle to deliver the CCHFV-GPC for our vaccine candidate. The cell culture and mouse study will define the expression pattern. This information will be critical to guide vaccine and therapeutics development. We will also explore the cross-protection by

Comment [LJW7]: should these activities be listed as problems to be resolved over the course of the study?

using~~when use~~ two different antigens to immunize mice. The polyclonal antibody will provide potential treatment option for CCHFV infection.

5. Innovations of the research proposal

The innovation of this project derives from the research plan that integrates three powerful components into a translational product: (i) the robust self-amplifying ability of alphavirus replicon, (ii) the ease of DNA plasmid as a vector to launch the replicative RNAs (using the mammalian transcription machinery), and (iii) the cutting-edge device for DNA delivery in clinical use. Although alphavirus replicon has been used for protein expression and vaccine development for almost three decades, previous efforts have mainly focused on the virus-like particle-RNA packaging (VLP) approach [ADDIN EN.CITE <EndNote><Cite><Author>Lundstrom</Author><Year>2017</Year><RecNum>137</RecNum><DisplayText>(21)</DisplayText><record><rec-number>137</rec-number><foreign-keys><key app="EN" db-id="fw5a0favmxv0w2ex9wqvwxwnz9pat9z0szft" timestamp="1556823011" guid="45f9f958-084b-4a4f-al3b-67585ald3c8d">137</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Lundstrom, K.</author></authors></contributors><titles><title>Oncolytic Alphaviruses in Cancer Immunotherapy</title><secondary-title>Vaccines (Basel)</secondary-title></titles><periodical><full-title>Vaccines (Basel)</full-title></periodical><volume>5</volume><number>2</number><edition>2017/04/12</edition><keywords><keyword>cancer immunotherapy</keyword><keyword>oncolytic alphaviruses</keyword><keyword>tumor eradication</keyword></keywords><dates><year>2017</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>2076-393X</isbn><accession-num>28417936</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/28417936</url></related-urls></urls><custom2>PMC5492006</custom2><electronic-resource-num>10.3390/vaccines5020009</electronic-resource-num><language>eng</language></record></Cite></EndNote>]. For the VLP approach, viral structural proteins are supplied in trans to package the viral replicon RNA (carrying an antigen of interest) into VLPs; such VLPs are used to immunize animals. The drawbacks of the VLP approach include the requirement of eukaryotic cell culture electroporation for VLP production, moderate

yield of VLP manufacture (when compared with the doses required for vaccination and treatment), pre-immune inhibition when multiple rounds of VLP infection are needed, and the "cold chain" transportation from manufactures to clinics. All the above drawbacks of the VLP approach could be mitigated by the proposed DNA-launched replicon in this project.

Despite the potential concern of integration of exogenous DNA into the cellular chromosome, the DNA plasmid approach has been actively pursued for vaccine development and cancer therapy. For example, the current frontrunner ZIKV vaccine in the phase II clinical trial is built upon a DNA plasmid (expressing two viral structure proteins prM and E). This type of traditional DNA vaccine requires multiple high doses to achieve protective immunity. For the ZIKV DNA vaccines, each human volunteer requires three shots, with 1 to 5 mg of DNA per shot, to achieve short-term neutralizing antibody titers [ADDIN EN.CITE ADDIN EN.CITE.DATA]. It should be noted that the adverse potential of DNA integration into the cellular genome remains to be determined in clinics. Compared with the traditional non-amplifying DNA vaccine, our DNA-launched replicon is self-replicative, and requires a much lower dose to achieve efficacy. The significantly reduced dose will minimize the risk of potential DNA integration. In addition, due to the self-amplifying nature of the proposed replicon DNA platform, protective immunity and efficacy could potentially be achieved with a single dose to control explosive outbreaks, which is particularly important when responding to public health emergency. Therefore, the replicon DNA platform has the potential to overcome the most critical weakness of the traditional DNA vaccine, and could be developed into a transformative new DNA delivery technology.

Collectively, we hypothesize that, in combination with the cutting-edge device for delivery, the DNA-launched replicon platform will transform into robust translational products for vaccine and therapeutics development. Since the goal of the Advanced Customer Cultivation Project is to develop solutions to prevent and control human diseases, the combination of the well-proven alphaviral replicon system with the ease of DNA engineering and the state-of-the-art DNA delivery represents a practical innovation for vaccine platform development.

Passive immunotherapy with sera of animal origin has been used for over 120 years to treat bacterial and viral infections, envenomations and drug intoxications. The lower manufacturing costs of hyperimmune equine antisera therefore represents an attractive alternate avenue of treatment,

especially to developing and third-world countries, compared to the more costly production process of viral specific mAbs. However, currently the study of anti-CCHFV antisera via the immunization of horses and the safety and efficiency has not been reported. Since the highly replication efficiency and the safety of the VSV vector, in this study the VSV-CCHFV-GP will be used~~chose~~ as the antigen for horse.

[= 3 * ROMAN]. Research Plan

1. Research schedule

Aim	Tasks and milestones	2019											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter							X	X	X	X	X	X
	Characterize SEAP replicons in cell culture												
	Characterize SEAP replicon in mice												
	Clone GPC CHIKV replicon												
	Test GPC replicon in cell culture												
	Test efficacy in mouse model												
2	Generation VSV-CCHFV-GP recombinant virus							X	X	X	X	X	X
	Immunization horse and characterization antibody response												
	Purify antibody from horse												
	Test efficacy in mouse model												

Aim	Tasks and milestones	2020											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter												
	Characterize SEAP replicons in cell culture	X	X	X									
	Characterize SEAP replicon in mice				X	X	X	X					
	Clone GPC CHIKV replicon								X	X	X	X	
	Test GPC replicon in cell culture												X
	Test efficacy in mouse model												
2	Generation VSV-CCHFV-GP recombinant virus												
	Immunization horse and characterization antibody response	X	X	X	X	X	X	X	X				
	Purify antibody from horse									X	X	X	X
	Test efficacy in mouse model												

Aim	Tasks and milestones	2021											
		1	2	3	4	5	6	7	8	9	10	11	12
1	Clone CHIKV replicon and SEAP reporter												
	Characterize SEAP replicons in cell culture												
	Characterize SEAP replicon in mice												
	Clone GPC CHIKV replicon												
	Test GPC replicon in cell culture	X	X	X									
	Test efficacy in mouse model				X	X	X	X	X	X	X	X	
2	Generation VSV-CCHFV-GP recombinant virus												
	Immunization horse and characterization antibody response												
	Purify antibody from horse												
	Test efficacy in mouse model				X	X	X	X	X	X	X	X	

2. Conditions necessary to conduct the research (including lab equipments, instruments and etc.)

Biosafety cabinet

PCR thermal cycler

Real-Time PCR thermal cycler

Table top centrifuge

Water bath

DNA gel electrophoresis system

Protein gel electrophoresis system

TriGrid Delivery System (Ichor, for DNA vaccine delivery)

ChemiDoc System

Pipettes

CO2 incubators

Microscopy

Refrigerator

-80 freezer

-30 freezer

Liquid nitrogen tank

IV. Introduction of Leader and Participants

James Le Duc, PhD, is the director of the Galveston National Laboratory, one of the largest active biocontainment facilities on a U.S. academic campus. Dr. Le Duc joined UTMB in late 2006 from the Centers for Disease Control and Prevention in Atlanta, where he was the influenza coordinator and director of the Division of Viral and Rickettsial Diseases. With more than four decades of experience working in the fields of biodefense and public health, his work has taken him around the world, from West Africa, where he began his professional career as a field biologist working for the Smithsonian Institution, to Brazil and Panama during a 23-year career as a U.S. Army officer in the medical research and development command.

Pei-Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas, USA. He is an elected Fellow of American Academy of Microbiology, adjunct Professor of Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore, and Honorary Professor at the Wuhan Institute of Virology, Chinese Academy of Sciences. He received his Ph.D. in virology in 1996 from Georgia State University. After postdoctoral training at Yale University, he joined Bristol-Myers Squibb as a Principal Scientist to develop HIV and HCV therapeutics from 1998 to 2000. He then moved to the Wadsworth Center, New York State Department of Health, to study West Nile virus. From 2008 to 2015, he served as Dengue Unit Head and Executive Director to lead drug discovery at Novartis Institute for Tropical Diseases. His group developed the first infectious clones of the epidemic strain of West Nile virus and Zika virus, discovered two RNA cap methylation activities of flavivirus NS5 protein, identified essential RNA elements for flavivirus replication, established various platforms for flavivirus vaccine and drug discovery, and pioneered therapeutics development for dengue virus. He is internationally recognized for his scholar and administrative accomplishments at leading research institution, public health sector, and pharmaceutical industry. Dr. Shi has more than 20 years experiences in handling BSL2 and ABSL2 agent.

Dennis A. Bente, DVM, Ph.D., is an associate professor from University of Texas Medical Branch, Galveston Texas, USA. Dr. Bente received his DVM in 2000 and Ph.D. in 2003 from University of Veterinary Medicine at Germany. The goal of Dr. Bente's research is to better understand the

transmission and pathogenesis of tick - borne hemorrhagic fever viruses and to develop countermeasures to combat the disease. The intersection between arbovirology and hemorrhagic fever research requires an interdisciplinary approach, involving virology (classical techniques as well as molecular techniques such as reverse genetics), immunology (human and animal models), and tick physiology. Dr. Bente's is the first laboratory in the world to establish a tick - host transmission model in a BSL-4 setting. A number of collaborations have been established with other virologists at UTMB, including Drs. Alan Barrett, Thomas Ksiazek, David Beasley, Alexander Freiberg and Thomas Geisbert, that include studies on Crimean - Congo hemorrhagic fever virus, Kyasanur forest disease virus, Alkhurma hemorrhagic fever virus, and West - Nile virus. Dr. Bente has more than 10 years experiences in handling BSL2, BSL3, BSL4, ABSL2, ABSL3 and ABSL4 agent.

Zhiming Yuan, Ph.D., professor from Wuhan Institute of Virology, the director of the Wuhan National biosafety laboratory (BSL-4), and the President of Wuhan Branch, Chinese Academy of Sciences. His research interest including: (1) Diagnosis, evolution, and pathogenesis of aborviruses, (2) Tropical Disease vector control with microbial agents, and (3) Laboratory biorisk management and applied biosafety research.

Chao Shan, Ph.D., professor from Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China. Dr. Shan Received his Ph.D. in Biochemistry and Molecular Biology in Wuhan Institute of Virology, Chinese Academy of Sciences in China in 2014. And he joined Novartis Institute for Tropical Diseases (NITD) from 2013 to 2015. He served as postdoctoral fellow in University of Texas Medical Branch from 2015 to 2019. During his training at Wuhan Institute of Virology and NITD, he worked with Dengue virus, Japanese encephalitis virus and EV71 virus *in vitro*. After joining in UTMB in December 2015, Dr. Shan has completed BSL3, BSL4, ABSL2, ABSL3 and ABSL4 training in University of Texas Medical Branch. He built the first reverse genetic system for Zika virus and developed the first live-attenuated Zika vaccine in the world.

Han Xia, Ph.D., is associate professor from Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China. Dr. Xia received his Ph.D. in Biochemistry and Molecular Biology in Wuhan Institute of Virology, Chinese Academy of Sciences in China in 2014. And she served as postdoctoral fellow and the

complete the BSL-4 training in University of Texas Medical Branch from 2013 to 2016, working with reverse genetic system developing of CCHFV and CCHFV-vector-host interaction through NGS strategy. Currently, her research interest is the epidemiology, diagnoses, and evolution of arbovirus.

[= 7 * ROMAN]. Budget

Unit: RMB 10,000 yuan

Budget Form of Project Expenditure		
Item	Amount	Detailed calculation
1. Equipment		
(1) Equipment purchase	0	
(2) Trial-manufacture purchase	0	
(3) Equipment modification and rent	0	
2. Reagents and consumables	15	Cloning and related reagent, kit, sequencing, cell culture reagent and consumables
3. Analysis	15	Horse purchase, immunization, antibody purification, DNA synthesis
4. Fuel and power	3	Transport
5. Travel/meeting/international cooperation and exchanges	5	Project meeting for WHIOV and UTMB, hotel etc.
6. Publication/literature/information dissemination/intellectual property	3	Publication and patent
7. Labor costs	5	Subsidy
8. Expert consultation	1	Project consultation
9. Other expenditure	3	Shipping fee about reagent and material
Total	50	

Note: Budget preparation and expenditure execution are conducted according to *Measures of Academy-Level Scientific Research Projects of Chinese Academy of Sciences*.

[= 8 * ROMAN]. Review opinions of applicant's organization

Our joint proposal, "Vaccine Development and Polyclonal Antiserum for Crimean-Congo Hemorrhagic Fever Virus" represents the culmination of many years of collaboration between the Galveston National Laboratory, the U.S. National Academy of Sciences and the Wuhan Institute of Virology, Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences. We are very excited about the possibility of collaborating in the implementation of this important study and making use of the unique resources of both our biocontainment laboratories.

The study is non-confidential and we anticipate that our findings will be published in the peer reviewed scientific literature under shared co-authorship.

Organization (official seal) Principal (Signature)

03/05/2019

[= 9 * ROMAN]. Opinions of the Biosafety Committee in Project Implementation Organization

Chairman of Committee (Signature)

(d/m/y)

[= 10 * ROMAN]. Opinions of Science and Technology Steering Committee of Wuhan National Biosafety Laboratory, CAS

Chairman of Committee (official seal)

(d/m/y)

[ADDIN EN.REFLIST]

From: Menachery, Vineet
Sent: Friday, April 17, 2020 10:27 AM
To: Shi, Pei yong;Tseng, Chien-Te K.;LeDuc, James W.;Weaver, Scott;McNees, Andrew G.
Subject: Re: NIH funded collaborations with Zheng-Li Shi?

None for me.

VDM

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Friday, April 17, 2020 9:53 AM
To: Tseng, Chien-Te K. <sktseng@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: RE: NIH funded collaborations with Zheng-Li Shi?

Not at this moment.

- Pei-Yong

From: Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Sent: Friday, April 17, 2020 9:03 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: RE: NIH funded collaborations with Zheng-Li Shi?

Not from my end, Jim.

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Friday, April 17, 2020 8:57 AM
To: Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>
Subject: NIH funded collaborations with Zheng-Li Shi?

Do we have any NIH funded collaborations with Dr Shi from Wuhan? Replies would be appreciated. Responding to an inquiry

Thanks, Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: LeDuc, James W.
Sent: Tuesday, January 21, 2020 4:34 PM
To: Benjamin Rusek (BRusek@nas.edu);Dave Franz (davidrfranz@gmail.com);Yuan Zhiming;George F GAO;Mifang Liang;Shi, Pei yong
Subject: Op Ed in Houston Chronicle
Attachments: Chinese Response to New Virus_Le Duc 21Jan revised.docx

Ben, Dave, Zhiming, George, Mifang and Pei-Yong

The attached, slightly modified to include mention of the new case in Washington State, is scheduled to appear in Wednesday 22 Jan's Houston Chronicle. Note mention of the NASEM/CAS collaborations.

Just FYI,

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

Chinese Response to New Virus: Good News/Bad News

By James W. Le Duc

Fast action and open communications by China is helping the world prepare for another potentially devastating infectious disease outbreak. While the situation is rapidly evolving, there is good news that may not make the headlines. Many will recall the dark days in the spring of 2003 when Asia and the world were threatened by the appearance of a new virus disease, Severe Acute Respiratory Syndrome, or SARS, which first appeared in southern China and quickly spread to other countries around the world, ultimately causing over 8000 cases with nearly 10% of those ending in death. SARS was caused by a novel coronavirus then unknown to medical science. There was no known cure, no diagnostic tests and little understanding of where it came from or how it was spread, although person-to-person transmission was obvious as health care workers treating the first cases were themselves among the early victims. Initially, China was reluctant to share information or alert the international community of the magnitude of the epidemic, leading to international criticism and a dangerous global health situation. Fortunately, China reversed its position, opened to collaborations with the WHO, U.S. and others, and the epidemic was eventually controlled.

Today, with another novel coronavirus discovered in China, the start is very different. In quick measure, Chinese health officials recognized that a new disease had emerged, quickly isolated patients, and instituted an impressive set of interventions in attempts to limit disease spread and characterize the new pathogen. Importantly, they have been transparent in sharing their findings with the world, thus allowing other nations to take precautions and be on the lookout for the new disease. Already, the genome of the new virus was sequenced and posted for easy access by international experts, allowing rapid exploration of possible treatments, development of diagnostics and epidemiological investigations.

China's ability to respond quickly and efficiently to this new threat is the result of nearly two decades of investments and collaborations to improve public health in China. The Chinese Centers for Disease Control incorporates many of the strengths of our own CDC, but is designed to meet the needs of a 1.4 billion plus population. In addition, China has invested in building a robust scientific capacity and partnered with containment laboratories such as ours to incorporate best practices when studying dangerous pathogens.

The current outbreak demonstrates a welcome openness to health information sharing with the global community. To diagnose an outbreak early requires astute healthcare providers able to recognize when something new or unusual is occurring; however, clinical recognition alone is meaningless if there is no capacity to investigate cases or characterize the disease-causing agent.

For the last few years, our National Academy of Science, Engineering and Medicine has worked with the Chinese Academy of Sciences to build relationships and share information on emerging diseases and advancements in vaccines and treatments. In Galveston, we welcomed leading Chinese health officials to collaborate on biocontainment facility design, biosafety training and laboratory operations. This dialogue, along with U.S.-based educational opportunities for Chinese students, benefit us all.

China's response to the new coronavirus demonstrates their investments in physical laboratories and scientific collaborations over the past decade are paying dividends, not only to China, but the entire world. Control of a new disease efficiently transmitted person-to-person is nearly impossible as we witnessed during the 2009 novel influenza pandemic and much must still be done together during this quickly evolving situation.

The outbreak is still in the early stages, but it is now clear that the new virus may be transmitted person-to-person, although the efficiency of such transmission remains in question. A few hundred patients have been identified, deaths occurred and the disease has spread from the epicenter in Wuhan to major cities in China and other Asian countries. Our CDC is now screening travelers arriving from Wuhan at U.S. airports, and the WHO is set to consider a global emergency response. With millions about to travel for the Chinese New Year, avoiding a global catastrophe must be the current goal.

The good news is that, at a time when US-China relations are being tested on many fronts, relations within the public health and scientific research arenas remain open and positive, which lays a solid foundation for curtailing this latest threat.

James Le Duc, PhD, is the Director of the Galveston National Laboratory at the University of Texas Medical Branch and a professor in UTMB's Department of Microbiology and Immunology.

705 words in body

From: Lawal, Adeola
Sent: Monday, January 27, 2020 4:51 PM
To: df@wh.iov.cn;Shi, Pei yong;LeDuc, James W.
Subject: FW: MTA to receive New coronavirus 2019 isolate: nCoV-2019 (IVCAS 6.7512)
Attachments: Shi - RECEIVING materials.docx

Greetings,

Please see attached MTA in support of our request to receive the following materials: New coronavirus 2019 isolate: nCoV-2019 (IVCAS 6.7512), from your institute. We look forward to getting this MTA in place.

Best wishes,

Ade Lawal, JD
Associate Legal Officer
UTMB Office of Technology Transfer
409.772.0369

MATERIAL TRANSFER AGREEMENT

This Material Transfer Agreement ("**Agreement**") is made between The University of Texas Medical Branch at Galveston, d/b/a UTMB Health ("**UTMB**"), a health institution of The University of Texas System ("System"), an agency of the State of Texas, located at 301 University Blvd., Galveston, TX 77555-0926, and Wuhan Institute of Virology Chinese Academy of Sciences Wuhan, China ("**Provider**") located at [redacted].

From the laboratory of Professor Fei Deng, Ph.D., Professor Zhengli Shi, Ph.D., ("**Provider Scientists**"), Provider agrees to provide UTMB with certain materials for the purpose stated herein under the following conditions:

1. **Material and Research.** The Materials covered by this Agreement are as follows: New coronavirus 2019 isolate: nCoV-2019 (IVCAS 6.7512), ("**Material**"). The Material shall be used by UTMB in research ("**Research**"), as defined in **Attachment A**, and the Research will be conducted by UTMB under the supervision of, Pei-Yong Shi, Ph.D. and Dr. James LeDuc, ("**UTMB Scientists**").
2. **Use of Material.** This Material is made available for internal research use only in laboratory animals or in vitro experiments. The Material is considered proprietary to Provider and Provider shall be free, in its sole discretion, to distribute the Material to others and to use it for its own purposes. Except as provided for by this Agreement, UTMB shall not distribute, transfer, or release the Material to any person or entity other than laboratory personnel under UTMB Scientist's direct supervision, unless written permission is obtained from Provider. UTMB agrees that all of its UTMB Scientist(s) involved in the Research will have read the terms and conditions of this Agreement and abide by the terms and conditions of this Agreement.
3. **Rights.** The Material shall not be used by UTMB for any products or processes for any purpose other than performing the Research hereunder. .
4. **Confidentiality**. All Material and information relating to the Material that is disclosed by Provider to UTMB shall be considered to be confidential, subject to Section 5. Publication of this Agreement. UTMB will use reasonable efforts to prevent the disclosure of Provider's confidential information to third parties for a period of three (3) years from receipt, provided that UTMB's obligation shall not apply to information that:
   a) is already in the UTMB's possession at the time of disclosure;
   b) is or later becomes part of the public domain through no fault of the UTMB;

c) is received from a third party having no obligations of confidentiality to UTMB;
d) is independently developed by the UTMB; or
e) is required by law or regulation to be disclosed.

In the event that information is required to be disclosed pursuant to subsection (e), UTMB shall notify the UTMB, in order to allow UTMB to assert whatever exclusions or exemptions may be available to it under such law or regulation.

5. **Publication.** UTMB will inform Provider of results of Research, in confidence, related to the Material by providing Provider with a draft manuscript describing such results. If UTMB's Scientist desires to publish or present such Research results, then, not less than forty-five (45) days prior to submission to a third-party, UTMB will provide Provider with a copy of any manuscript or abstract disclosing such Research results for the purpose of protecting the Material and intellectual property of Provider that might be disclosed by such publication. In any such publication or presentation of Research results, UTMB agrees to acknowledge Provider scientist as provider of the Material.
6. **Intellectual Property.** Inventorship of any invention will be determined based on U.S. patent law. Ownership shall follow inventorship.
7. **Warranty.** The Material is experimental in nature and it is provided "AS IS" WITHOUT WARRANTY OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE OR SAFETY OR ANY OTHER WARRANTY, EXPRESS OR IMPLIED. UTMB MAKES NO REPRESENTATION OR WARRANTY THAT THE USE OF THE MATERIAL WILL NOT INFRINGE ANY PATENT OR OTHER PROPRIETARY RIGHT.
8. **Liability.** Provider shall indemnify and hold harmless UTMB, System, their Regents, officers, agents and employees, from any liability, loss or damage they may suffer as a result of claims, demands, costs or judgments against them arising out of the Provider's use of the results generated by UTMB's activities to be carried out pursuant to this Agreement excluding claims, loss, or damage that arise from the negligence or willful malfeasance of any Regent, officer, agent or employee of UTMB or System.
9. **Compliance.** UTMB will use the Material in compliance with all laws, governmental regulations and guidelines applicable to the Material. Moreover, if the Material is used in the United States, then UTMB will comply with current United States NIH guidelines.
10. **Export Control.** UTMB further agrees that if the U.S. export laws are or become applicable, it will not export any Materials received under this Agreement to any countries for which the United States government requires an export license or other supporting documentation at the time of export or transfer, unless UTMB

has obtained prior written authorization from the appropriate authority responsible for such matters.

11. **Assignment.** This Agreement is not assignable, whether by operation of law or otherwise, without the prior written consent of Provider.
12. **Publicity.** Except as stated herein, neither party shall use the name of the other without express written consent, subject to Section 5. Publication of this Agreement.
13. **Term and Termination.** This Agreement shall be effective as of the date of the last signature and terminate one (1) year from that date. Upon termination, UTMB will immediately destroy all the Material then in its possession.

UNIVERSITY OF TEXAS MEDICAL BRANCH	**WUHAN INSTITUTE OF VIROLOGY CHINESE ACADEMY OF SCIENCES**
_____	_____
Carolee A. King, JD Senior Vice President and General Counsel Date: _____	Name of Authorized Signatory Title: Date: _____
Read and understood:	Read and understood:
_____	_____
Signature of UTMB Scientist	Signature of Provider Scientist
Read and understood:	
_____	
Signature of UTMB Scientist	

Attachment A – Scope of Research

We are studying the new coronavirus through sharing the viral isolate (strain IVCAS 6.7512). Our goal is to use the viral isolate for testing vaccine, therapeutics, and viral pathogenesis. UTMB scientists will use the viral isolate to test vaccine, therapeutics, and viral pathogenesis.

`

To: 施一[shiyi@im.ac.cn]; Shi, Pei yong[peshi@UTMB.EDU]
From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: Sun 3/15/2020 10:53:16 AM (UTC-05:00)
Subject: RE: RE: Help

Hi Yi,

Thanks for the follow up. I asked our biosafety engineer to summarize how we provide oversight for the construction and validation of biocontainment labs in the USA and his response is pasted below. Some additional thoughts for your consideration include:

- Oversight of some especially dangerous pathogens is managed by the federal government under the select agent program. You can find the complete list if you google "select agents list." Human pathogens are managed by the Department of Health and Human Services/Centers for Disease Control and Prevention (CDC), agricultural pathogens are managed by the Department of Agriculture (USDA), and those pathogens affecting both humans and animals are jointly managed.
- CDC and USDA inspect laboratories prior to allowing them to handle select agents based on criteria outlined in the Biosafety in Microbiological and Biomedical Laboratories (BMBL). The latest edition is available on line.
- Pathogens not designated as select agents are managed by local oversight, usually provided by the institutional biosafety committee (IBC). Details are available on line. It is important to ensure the quality of the individuals involved in the IBC and the independence of the IBC from those attempting to conduct the studies.
- Some localities have established local laws/regulations that require prior notification of work with certain pathogens be approved by the city or other jurisdiction; however, this varies considerably from location to location and is not a requirement in our community. Nonetheless, we have found it quite valuable to actively engage with our community members to ensure that they understand the work that we are doing, have seen first-hand the safety and security measures that are in place to protect both our scientists and the local community, and that they take personal pride in the work we are doing.
- There are strict restrictions on certain experiments that could enhance virulence or transmissibility of a pathogen and oversight of these "gain of function studies" and "dual use research of concern" projects continues to evolve. Most funding for such research is provided by the US government and studies that may fall into this area of concern are very carefully reviewed prior to funding. Reports from the National Science Advisory Board for Biosecurity (NSABB) are available on line and provide very detailed consideration of this issue.

Here in the US we use the BMBL and even though it is guidance and non-prescriptive document, we need to comply with it. For International laboratories, I would recommend following the WHO Biosafety guidelines. Other good resources are the Canadian Biosafety Standards (https://www.canada.ca/en/public-health/services/canadian-biosafety-standards-guidelines.html) and the Australian/New Zealand Standard AS/NZS 2243.3:2010.

I hope this helps. Please feel free to contact me again should you have additional questions. With best wishes during these stressful times.

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: 施一 <shiyi@im.ac.cn>
Sent: Sunday, March 15, 2020 12:15 AM

To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: Re: RE: Help

Hi Jim,

First, thanks for introduction to you by Pei-Yong. I remembered that I have met you in the P4 meeting in Galveston.

Here, I just have several questions about the admission of pathogen manipulation in P3 lab and P4 lab. As you know, in China, the admission of pathogen manipulation has to be approved by the national and local governments. Usually, it will take a long time and many documents to get the approval. How about in USA?

If we want to manipulate one pathogen in P3 and P4 labs in USA, do we need the approval of the governments?
Shall we communicate with the residents near the P3 and P4 labs about the pathogen manipulation?
How the government administer these issues? Pei-Yong told me that the government will have a guidance about the pathogen manipulation and the affiliations can determine it by themselves.

We want to give some suggestions to the Chinese government.

Best,

Yi Shi

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-03-15 01:14:10 (星期日)
收件人: "LeDuc, James W." <jwleduc@UTMB.EDU>
抄送: "shiyi@im.ac.cn" <shiyi@im.ac.cn>
主题: RE: Help

552.117

Hi Yi,
I forgot to copy you on my original email (as I was picking up my [redacted] at Houston airport).
Please send a few key questions to Dr. LeDuc to initiate the call.
Thanks!

- Pei-Yong

From: Shi, Pei yong
Sent: Saturday, March 14, 2020 9:36 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: Help

Hi Jim,
I am introducing Dr. Yi Shi who has questions about BSL3 and BSL4 regulations in US. Thanks for helping him.
Best,
Pei-Yong

Get Outlook for Android

From: df@wh.iov.cn
Sent: Monday, January 27, 2020 9:46 AM
To: Shi, Pei yong;zlshi
Cc: LeDuc, James W.;Ksiazek, Thomas G.;Lawal, Adeola
Subject: Re: RE: Request for new coronavirus isolates

Request letter received.

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong
Date: 2020-01-27 21:54
To: df@wh.iov.cn; zlshi
CC: LeDuc, James W.; Ksiazek, Thomas G.; Lawal, Adeola
Subject: RE: Request for new coronavirus isolates

Dear Fei and Zhengli,

Thanks you for the rapid response to our request. Please see the attached request letter. As indicated in the letter, this collaboration will use the viral isolate to test vaccine, therapeutics, and viral pathogenesis.

I'm copying our Technology Transfer Office to send you the MAT for signatures.

Hi Ade,
Would you please email UTMB's MTA for this request to Professor Fei Deng (df@wh.iov.cn)?

Sender: Professor Fei Deng, Wuhan Institute of Virology, Chinese Academy of Sciences, China
Receiver: Pei-Yong Shi and James LeDuc, UTMB
Reagent: New coronavirus 2019 isolate: nCoV-2019 (IVCAS 6.7512)
Scope of work: UTMB scientists will use the viral isolate to test vaccine, therapeutics, and viral pathogenesis

Since this is an urgent matter, please help with the process as soon as possible.

Thanks!

Pei-Yong

Pei-Yong Shi, Ph.D.
I.H. Kempner Professor of Human Genetics
Vice Chair for Innovation and Commercialization
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555
Phone: 409-772-6370
Email: peshi@utmb.edu

From: df@wh.iov.cn <df@wh.iov.cn>
Sent: Monday, January 27, 2020 1:33 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: Request for new coronavirus isolates

Dear Prof.Peiyong,
Nice to hear from you.

Yes we glad to share the virus isolate with UTMB for research collaborate. I suggest you send a formal request letter to our institute. And a MTA is needed, you can use your UTMB MTA and fill the information, and I suggest you to discuss with Prof.Zhengli for the detail research content for collaboration. Our strain is nCoV-2019 (IVCAS 6.7512).
You can send your documents to me, I will try to get export permittion for this.

With best wishes,
Fei

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong
Date: 2020-01-27 02:58
To: df@wh.iov.cn; zlshi@wh.iov.cn
CC: LeDuc, James W.; Ksiazek, Thomas G.
Subject: Request for new coronavirus isolates
Dear Zhengli and Fei,

Happy Chinese New Year and congratulations for your amazing work on the new coronavirus!

We are writing to see if you are willing to collaborate with UTMB on studying the nCoV through sharing the viral isolates. We understand that, since many labs are currently isolating the viruses through imported cases, the window of leadership for Chinese scientists is closing rapidly. We greatly appreciate your rapid response to this request.

Best regards from Galveston,
Pei-Yong

Pei-Yong Shi, Ph.D.
I.H. Kempner Professor of Human Genetics
Vice Chair for Innovation and Commercialization
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555
Phone: 409-772-6370
Email: peshi@utmb.edu

Cc: Tao Peng[peng_tao@gibh.ac.cn]; Jenny Mckimm-Breschkin[jennifer.mckimm@unimelb.edu.au]; Subhash Vasudevan[subhash.vasudevan@duke-nus.edu.sg]; Jinhong Chang[jinhong.chang@bblumberg.org]; Jennifer Moffat[moffatj@upstate.edu]; David Durantel[david.durantel@inserm.fr]; Johan Neyts[johan.neyts@kuleuven.be]; Jose Este[jaeste@irsicaixa.es]; Nesya Goris[ngoris@virovet.com]; Mike Bray[mikebrayavr@gmail.com]
To: Miguel Angel Martinez[mmartinez@irsicaixa.es]; Luis Menéndez Arias[lmenendez@cbm.csic.es]; Carmen Mirabelli[camirabe@med.umich.edu]; Lieve Naesens[Lieve.Naesens@kuleuven.be]; panxiaoben[panxiaoben@pkuph.edu.cn]; Anna Papa[annap.med@gmail.com]; Eve-Isabelle Pecheur[eve-isabelle.pecheur@inserm.fr]; Dan Pevear[danpevear@yahoo.com]; Jocelyne Piret[jocelyne.piret@crchudequebec.ulaval.ca]; Oliver Planz[oliver.planz@uni-tuebingen.de]; Miguel Quinones-Mateu[meq@case.edu]; Růžek Daniel[ruzekd@paru.cas.cz]; Luis M. Schang[lms428@cornell.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Sujan Shresta[sujan@lji.org]; Jessica R. (CDC/OID/NCEZID) Spengler (CTR)[wsk7@cdc.gov]; Christina Spiropoulou (CDC/OID/NCEZID)[ccs8@cdc.gov]; Eike Steinmann[eike.steinmann@twincore.de]; Youichi Suzuki[californiacircle@gmail.com]; Bart Tarbet[bart.tarbet@usu.edu]; John Tavis[john.tavis@health.slu.edu]; Evelien Vanderlinden[evelien.vanderlinden@kuleuven.be]; Robert Vrancken[rvrancken@virovet.com]; Satoru Watanabe[satoru.watanabe@duke-nus.edu.sg]; Priscilla L. Yang[priscilla_yang@hms.harvard.edu]; Hui-Ling Yen[hyen@hku.hk]; yin zheng[yinzheng@yahoo.com]; whiov[zhangbo@wh.iov.cn]; larry[zhang_jiancun@gibh.ac.cn]; 钟劲[jzhong@ips.ac.cn]; Zou Gang[zougang588@163.com]
From: Mike Bray[mikebrayavr@gmail.com]
Sent: Thur 5/9/2019 9:23:09 AM (UTC-05:00)
Subject: Antiviral Research editorial board meeting at ICAR

Dear AVR editorial board members,

ICAR will begin on Sunday in Baltimore, and I'm looking forward to seeing many of you at the meeting. Els Frensdorff-Breuring at Elsevier sent you an invitation some time ago to attend the annual EB breakfast, which she said would be at 6:30 Tuesday morning. In fact, the AVR editors will meet at 6:30, and **you're invited to join us in the same room at 7:30**, so you'll get an extra hour of sleep! The breakfast will be held in the Columbia/Frederick room at the Hyatt.

[We have a confirmed attendance list for the EB breakfast, so if you won't be at ICAR, there's no need for you to let me know.]

As every year, the purpose of the EB meeting is threefold. First, it's an opportunity for we editors to thank you for the help you provide by reviewing manuscripts – we couldn't maintain the high qualify of the journal without you. Second, it gives you the chance to meet and chat with the AVR editors and your fellow EB members. And third, our publisher at Elsevier, Donna Wilson, will give an overview of the journal's performance during the past year.

In that regard, AVR continues to do very well. We're in our 38th year, and the number of papers we publish and their quality continue to increase. Our impact factor has consistently been above 4.0 in recent years, placing us in the top third of virology journals. As a sign of confidence, Elsevier has allowed us to increase the number of editors, so we now have 8 editors handling manuscripts, with Johan Neyts, our current ISAR president, in the role of advisory editor.

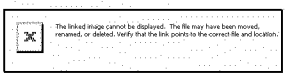
I'll end the EB meeting and this message by inviting you to contribute review articles or commentaries to the journal. AVR's scope is quite broad, and all of you are doing interesting work, so I'm sure that there are many different topics you could write about. Please feel free to discuss your ideas directly with me if you're at ICAR, or by email if you're not able to join us.

Best wishes,

Mike

Mike Bray, MD MPH
Editor-in-chief
Antiviral Research

From: Virologica Sinica <virosin@wh.iov.cn>
Sent: Monday, May 11, 2020 9:11 AM
To: Shi, Pei yong
Subject: To Dr.Shi - Virologica Sinica, Volume 35, Issue 2



Dear Dr. Shi,

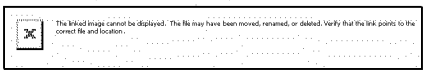
It is my pleasure to present you the review, research articles, and letters recently published in *Virologica Sinica*.

Your suggestions are welcome!

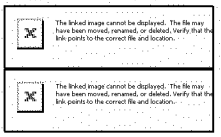
Zheng-Li Shi, Ph.D.
Editor-in-Chief, *Virologica Sinica*

Browse the website www.virosin.org for more information

Enjoy **rapid** & **free** publication in *Virologica Sinica*



Virologica Sinica is an academic journal which aims at presenting the cutting-edge research on viruses. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including research on animal, plant and microbe viruses. The journal welcomes articles on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related biotechniques. *Virologica Sinica*, the official journal of the Chinese Society for Microbiology, will serve as a platform for the communication and exchange of academic information and ideas in an international context.



The journal is indexed by: Science Citation Index (SCI), Journal Citation Reports (JCR), PubMed/Medline, Pubmed Central, Scopus, BIOSIS, Google Scholar.

About the cover: While host proteins incorporated into virions during viral budding from infected cell are known to play essential roles in multiple process of viral life cycle of progeny virus, these characteristics have been largely neglected in studies on rabies virus (RABV). In this issue, Zhang *et*

al. performed proteomics studies of the RABV virions with good purity and integrity to define 49 cellular proteins incorporated into mature virions, and 24 of them were likely involved in virus replication according to the functional annotation analysis. Furthermore, Zhang et al. used cryo-electron microscopy (Cryo-EM) to observe the purified RABV virions, generating high-resolution pictures of RABV particles with unprecedented structure details. The cover image clearly displays an intact bullet-shaped structure with four distinct electron-dense layers consisting of glycoprotein spike, viral envelope, matrix protein helix and RNP complex from outside to inside. Please see page 143–155 for details.

2020, Vol. 35, Issue 2

REVIEW

Bacteriophages and Lysins in Biofilm Control

Free Full Text (HTML) *Free* Full Text (PDF)

Marzanna Łusiak-Szelachowska, Beata Weber-Dąbrowska, Andrzej Górski

To formulate the optimal strategy of combatting bacterial biofilms, in this review we update current knowledge on the growing problem of biofilm formation and its resistance to antibiotics which has spurred the search for new strategies to deal with this complication. Based on recent findings, the role of bacteriophages in the prevention and elimination of biofilm-related infections has been emphasized. *In vitro*, *ex vivo* and *in vivo* biofilm treatment models with single bacteriophages or phage cocktails have been compared. A combined use of bacteriophages with antibiotics *in vitro* or *in vivo* confirms earlier reports of the synergistic effect of these agents in improving biofilm removal. Furthermore, studies on the application of phage-derived lysins *in vitro, ex vivo* or *in vivo* against biofilm-related infections are encouraging. The strategy of combined use of phage and antibiotics seems to be different from using lysins and antibiotics. These findings suggest that phages and lysins alone or in combination with antibiotics may be an efficient weapon against biofilm formation *in vivo* and *ex vivo*, which could be useful in formulating novel strategies to combat bacterial infections. Those findings proved to be relevant in the prevention and destruction of biofilms occurring during urinary tract infections, orthopedic implant-related infections, periodontal and peri-implant infections. In conclusion, it appears that most efficient strategy of eliminating biofilms involves phages or lysins in combination with antibiotics, but the optimal scheme of their administration requires further studies.

RESEARCH ARTICLE

Genome Analysis of Dasineura jujubifolia Toursvirus 2, A Novel Ascovirus

Free Full Text (HTML) *Free* Full Text (PDF)

Jun Wang, Minglu Yang, Haibing Xiao, Guo-Hua Huang, Fei Deng, Zhihong Hu

So far, ascoviruses have only been identified from Lepidoptera host insects and their transmission vectors—endoparasitic wasps. Here, we reported the first finding of a complete novel ascovirus genome

from a Diptera insect, *Dasineura jujubifolia.* Initially, sequence fragments with homology to ascoviruses were incidentally identified during metagenomic sequencing of the mitochondria of *D. jujubifolia* (Cecidomyiidae, Diptera) which is a major pest on *Ziziphus jujuba*. Then a full circular viral genome was assembled from the metagenomic data, which has an A+T percentage of 74% and contains 142,600 bp with 141 open reading frames (ORFs). Among the 141 ORFs, 37 were conserved in all sequenced ascoviruses (core genes) including proteins predicted to participate in DNA replication, gene transcription, protein modification, virus assembly, lipid metabolism and apoptosis. Multi-gene families including those encode for baculovirus repeated open reading frames (BROs), myristylated membrane proteins, RING/U-box E3 ubiquitin ligases, and ATP-binding cassette (ABC) transporters were found in the virus genome. Phylogenetic analysis showed that the newly identified virus belongs to genus *Toursvirus* of *Ascoviridae*, and is therefore named as *Dasineura jujubifolia toursvirus 2* (DjTV-2a). The virus becomes the second reported species of the genus after *Diadromus pulchellus toursvirus 1* (DpTV-1a). The genome arrangement of DjTV-2a is quite different from that of DpTV-1a, suggesting these two viruses separated in an early time of evolution. The results suggest that the ascoviruses may infect a much broader range of hosts than our previous knowledge, and shed lights on the evolution of ascoviruses and particularly on that of the toursviruses.

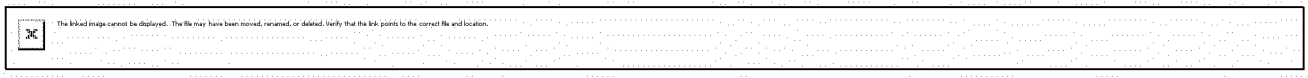
RESEARCH ARTICLE

Proteomic Profiling of Purified Rabies Virus Particles

Free Full Text (HTML) ***Free*** Full Text (PDF)

Yan Zhang, Yuyang Wang, Ye Feng, Zhongzhong Tu, Zhiyong Lou, Changchun Tu

While host proteins incorporated into virions during viral budding from infected cell are known to play essential roles in multiple process of the life cycle of progeny virus, these characteristics have been largely neglected in studies on rabies virus (RABV). Here, we purified the RABV virions with good purity and integrity, and analyzed their proteome by nano LC–MS/MS, followed by the confirmation with immunoblot and immuno-electronic microscopy. In addition to the 5 viral proteins, 49 cellular proteins were reproducibly identified to be incorporated into matured RABV virions. Function annotation suggested that 24 of them were likely involved in virus replication. Furthermore, cryo-EM was employed to observe the purified RABV virions, generating high-resolution pictures of the bullet-shaped virion structure of RABV. This study has provided new insights into the host proteins composition in RABV virion and shed the light for further investigation on molecular mechanisms of RABV infection, as well as the discovery of new anti-RABV therapeutics.



RESEARCH ARTICLE

Structural Basis of Glycan Recognition in Globally Predominant Human P[8] Rotavirus

Free Full Text (HTML) ***Free*** Full Text (PDF)

Xiaoman Sun, Lei Dang, Dandi Li, Jianxun Qi, Mengxuan Wang, Wengang Chai, Qing Zhang, Hong Wang, Ruixia Bai, Ming Tan, Zhaojun Duan

Rotavirus (RV) causes acute gastroenteritis in infants and children worldwide. Recent studies showed that glycans such as histo-blood group antigens (HBGAs) function as cell attachment factors affecting RV host susceptibility and prevalence. P[8] is the predominant RV genotype in humans, but the structural basis of how P[8] RVs interact with glycan ligands remains elusive. In this study, we characterized the interactions between P[8] VP8*s and glycans which showed that VP8*, the RV glycan binding domain, recognized both mucin core 2 and H type 1 antigens according to the ELISA-based oligosaccharide binding assays. Importantly, we determined the structural basis of P[8] RV-glycans interaction from the crystal structures of a Rotateq P[8] VP8* in complex with core 2 and H type 1 glycans at 1.8 Å and 2.3 Å,

respectively, revealing a common binding pocket and similar binding mode. Structural and sequence analysis demonstrated that the glycan binding site is conserved among RVs in the P[II] genogroup, while genotype-specific amino acid variations determined different glycan binding preference. Our data elucidated the detailed structural basis of the interactions between human P[8] RVs and different host glycan factors, shedding light on RV infection, epidemiology, and development of anti-viral agents.

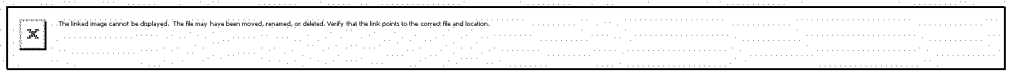
RESEARCH ARTICLE

Analysis of Expression Profiles of Long Noncoding RNAs and mRNAs in A549 Cells Infected with H3N2 Swine Influenza Virus by RNA Sequencing

Free Full Text (HTML) *Free* Full Text (PDF)

Yina Zhang, Tianqi Yu, Yingnan Ding, Yahui Li, Jing Lei, Boli Hu, Jiyong Zhou

Long noncoding RNAs (lncRNAs) participate in regulating many biological processes. However, their roles in influenza A virus (IAV) pathogenicity are largely unknown. Here, we analyzed the expression profiles of lncRNAs and mRNAs in H3N2-infected cells and mock-infected cells by high-throughput sequencing. The results showed that 6129 lncRNAs and 50,031 mRNA transcripts in A549 cells displayed differential expression after H3N2 infection compared with mock infection. Among the differentially expressed lncRNAs, 4963 were upregulated, and 1166 were downregulated. Functional annotation and enrichment analysis using gene ontology and Kyoto Encyclopedia of Genes and Genomes databases (KEGG) suggested that target genes of the differentially expressed lncRNAs were enriched in some biological processes, such as cellular metabolism and autophagy. The up- or downregulated lncRNAs were selected and further verified by quantitative real-time polymerase chain reaction (RT-qPCR) and reverse transcription PCR (RT-PCR). To the best of our knowledge, this is the first report of a comparative expression analysis of lncRNAs in A549 cells infected with H3N2. Our results support the need for further analyses of the functions of differentially expressed lncRNAs during H3N2 infection.



RESEARCH ARTICLE

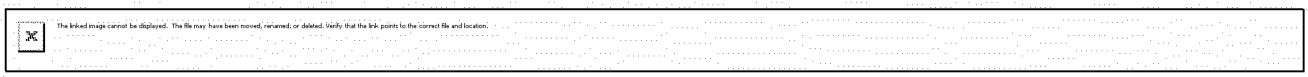
Premature Stop Codon at Residue 101 within HIV-1 Rev Does Not Influence Viral Replication of Clade BC but Severely Reduces Viral Fitness of Clade B

Free Full Text (HTML) *Free* Full Text (PDF)

Zheng Wang, Xiaolin Ji, Yanling Hao, Kunxue Hong, Liying Ma, Dan Li, Yiming Shao

HIV-1 Rev is an accessory protein that plays a key role in nuclear exportation, stabilization, and translation of the viral mRNAs. Rev of HIV-1 clade BC often shows a truncation of 16 AAs due to a premature stop codon at residue 101. This stop codon presents the highest frequency in clade BC and the lowest frequency in clade B. In order to discover the potential biological effect of this truncation on Rev activity and virus replication of clade BC, we constructed Rev expression vectors of clade BC with or without 16 AAs within C-terminal separately, and replaced the stop codon by Q in a CRF07_BC infectious clone. We found that 16 AAs truncation had no effect on expression and activity of Rev in clade BC. Also, the mutation from the stop codon to Q had no effect on virus replication of clade BC. Next, to investigate the effect of this truncation on Rev activity and replication capacity of clade B, Rev expression vectors of clade B carrying or lacking 16 AAs in C-terminal were constructed respectively, and residue Q at position 101 within Rev was substituted by the stop codon in a clade B infectious clone. It was found that 16 AAs truncation significantly down-regulated Rev expression and impaired clade B Rev activity. Furthermore, a Q-to-stop codon substitution within Rev significantly reduced viral replication

fitness of clade B. These results indicate that the premature stop codon at residue 101 within Rev exerts diverse impact on viral replication among different HIV-1 clades.



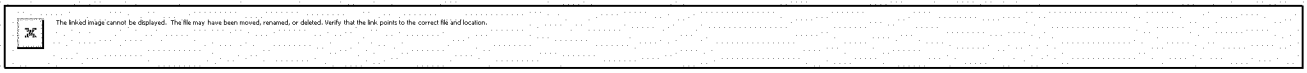
RESEARCH ARTICLE

Highly Efficient Base Editing in Viral Genome Based on Bacterial Artificial Chromosome Using a Cas9-Cytidine Deaminase Fused Protein

Free Full Text (HTML) ***Free*** Full Text (PDF)

Ke Zheng, Fang-Fang Jiang, Le Su, Xin Wang, Yu-Xin Chen, Huan-Chun Chen, Zheng-Fei Liu

Viruses evolve rapidly and continuously threaten animal health and economy, posing a great demand for rapid and efficient genome editing technologies to study virulence mechanism and develop effective vaccine. We present a highly efficient viral genome manipulation method using CRISPR-guided cytidine deaminase. We cloned pseudorabies virus genome into bacterial artificial chromosome, and used CRISPR-guided cytidine deaminase to directly convert cytidine (C) to uridine (U) to induce premature stop mutagenesis in viral genes. The editing efficiencies were 100%. Comprehensive bioinformatic analysis revealed that a large number of editable sites exist in pseudorabies virus (PRV) genomes. Notably, in our study viral genome exists as a plasmid in *E. coli*, suggesting that this method is virus species-independent. This application of base-editing provided an alternative approach to generate mutant virus and might accelerate study on virulence and vaccine development.



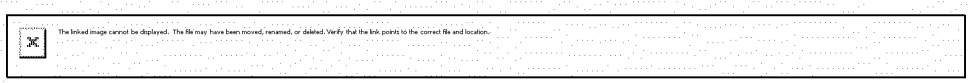
RESEARCH ARTICLE

Endosomes and Microtubles are Required for Productive Infection in Aquareovirus

Free Full Text (HTML) ***Free*** Full Text (PDF)

Fuxian Zhang, Hong Guo, Qingxiu Chen, Zheng Ruan, Qin Fang

Grass carp reovirus (GCRV), the genus *Aquareovirus* in family *Reoviridae*, is viewed as the most pathogenic aquareovirus. To understand the molecular mechanism of how aquareovirus initiates productive infection, the roles of endosome and microtubule in cell entry of GCRV are investigated by using quantum dots (QDs)-tracking in combination with biochemical approaches. We found that GCRV infection and viral protein synthesis were significantly inhibited by pretreating host cells with endosome acidification inhibitors NH_4Cl, chloroquine and bafilomycin A1 (Bafi). Confocal images indicated that GCRV particles could colocalize with Rab5, Rab7 and lysosomes in host cells. Further ultrastructural examination validated that viral particle was found in late endosomes. Moreover, disruption of microtubules with nocodazole clearly blocked GCRV entry, while no inhibitory effects were observed with cytochalasin D treated cells in viral infection, hinting that intracellular transportation of endocytic uptake in GCRV infected cells is via microtubules but not actin filament. Notably, viral particles were observed to transport along microtubules by using QD-labeled GCRV. Altogether, our results suggest that GCRV can use endosomes and microtubules to initiate productive infection.



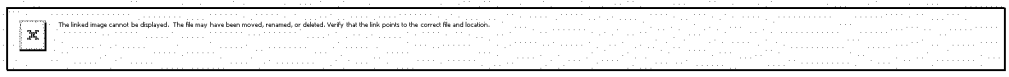
RESEARCH ARTICLE

A Deleted Deletion Site in a New Vector Strain and Exceptional Genomic Stability of Plaque-Purified Modified Vaccinia Ankara (MVA)

Free Full Text (HTML) ***Free*** Full Text (PDF)

Ingo Jordan, Deborah Horn, Kristin Thiele, Lars Haag, Katharina Fiddeke, Volker Sandig

Vectored vaccines based on highly attenuated modified vaccinia Ankara (MVA) are reported to be immunogenic, tolerant to pre-existing immunity, and able to accommodate and stably maintain very large transgenes. MVA is usually produced on primary chicken embryo fibroblasts, but production processes based on continuous cell lines emerge as increasingly robust and cost-effective alternatives. An isolate of a hitherto undescribed genotype was recovered by passage of a non-plaque-purified preparation of MVA in a continuous anatine suspension cell line (CR.pIX) in chemically defined medium. The novel isolate (MVA-CR19) replicated to higher infectious titers in the extracellular volume of suspension cultures and induced fewer syncytia in adherent cultures. We now extend previous studies with the investigation of the point mutations in structural genes of MVA-CR19 and describe an additional point mutation in a regulatory gene. We furthermore map and discuss an extensive rearrangement of the left telomer of MVA-CR19 that appears to have occurred by duplication of the right telomer. This event caused deletions and duplications of genes that may modulate immunologic properties of MVA-CR19 as a vaccine vector. Our characterizations also highlight the exceptional genetic stability of plaque-purified MVA: although the phenotype of MVA-CR19 appears to be advantageous for replication, we found that all genetic markers that differentiate wildtype and MVA-CR19 are stably maintained in passages of recombinant viruses based on either wildtype or MVA-CR.



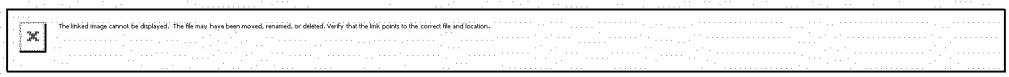
RESEARCH ARTICLE

Monoclonal Antibody-Based Serological Detection of Rice Stripe Mosaic Virus Infection in Rice Plants or Leafhoppers

Free Full Text (HTML) ***Free*** Full Text (PDF)

Liqian Guo, Jiayu Wu, Rui Chen, Jian Hong, Xueping Zhou, Jianxiang Wu

Rice stripe mosaic virus (RSMV) is a rhabdovirus recently found in southern part of China and can cause severe reduction in rice production. To establish serological methods for RSMV epidemiological studies and to establish a control strategy for this virus, we first purified RSMV virions from infected rice plants and then used them as an immunogen to produce four RSMV-specific monoclonal antibodies (MAbs) (i.e.,1D4, 4A8, 8E4 and 11F11). With these MAbs, we have developed a highly specific and sensitive antigen-coated plate enzyme-linked immunosorbent assay (ACP-ELISA), a Dot-ELISA and a Tissue print-ELISA for rapid detections of RSMV infection in rice plants or in leafhoppers. Our results showed that RSMV can be readily detected in RSMV-infected rice plant tissue crude extracts diluted at 1:20,971,520 (w/v, g/mL) through ACP-ELISA or diluted at 1:327,680 (w/v, g/mL) through Dot-ELISA. Both ACP-ELISA and Dot-ELISA can also be used to detect RSMV infection in individual RSMV viruliferous leafhopper (*Recilia dorsalis*) homogenate diluted at 1:307,200 and 1:163,840 (individual leafhopper/μL), respectively. Detection of RSMV infection in field-collected rice samples or in RSMV viruliferous leafhoppers indicated that the three serological methods can produce same results with that produced by RT-PCR (19 of the 33 rice samples and 5 of the 16 leafhoppers were RSMV-positive). We consider that the four MAbs produced in this study are very specific and sensitive, and the three new serological methods are very useful for detections of RSMV infection in rice plants or in leafhoppers and the establishment of the disease control strategies.



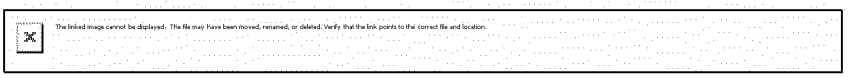
LETTER

Screening and Identification of Marburg Virus Entry Inhibitors Using Approved Drugs

Free Full Text (HTML) ***Free*** Full Text (PDF)

Li Zhang, Shan Lei, Hui Xie, Qianqian Li, Shuo Liu, Qiang Liu, Weijin Huang, Xinyue Xiao, Youchun Wang

Marburg virus (MARV), the causative agent of lethal hemorrhagic fever, causes similar clinical symptoms and mortality as the related Ebola virus. However, fewer studies have been conducted on MARV, and no drugs specific for this virus are currently available. Repurposing of clinically approved drugs is among the most efficient ways to identify novel drugs for existing viral diseases, offering the advantages of lower costs and faster clinical development. In this study, a high-throughput pseudovirus system expressing the MARV glycoprotein was used to screen 767 approved drugs in a compound library obtained from the National Institutes for Food and Drug Control, China (NIFDC). Thirty-three drugs with known activities (including antimalarial, antipsychotic, antihistamine, and anticholinergic) proved to be entry inhibitors against MARV *in vitro*. The anti-MARV activity of these drugs was further verified *in vivo* using a bioluminescent imaging mouse model, in which 10 drugs exhibited over 50% inhibitory activity. This study identifies multiple leads for the further development of drugs against MARV.



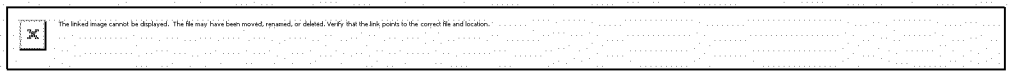
LETTER

Meta-Transcriptome Profiling of Novel Invasive Pest *Spodoptera frugiperda* in Yunnan, China

Free Full Text (HTML) ***Free*** Full Text (PDF)

Junming Shi, Weiwei Li, Yunyu Wang, Quanyan Chen, Fei Deng

Summarily, this work documented the bio-community of the novel invasive pest *S. frugiperda* in China via meta-transcriptome, which presents a high biodiversity, especially concerning bacterial community. And the presence of parasitoids and pathogens of the fall armyworm larvae in China suggests a great capacity to utilize them as biological control agents. Additionally, evidences of Corn strain and Rice strain were simultaneously detected via different molecular marker, suggesting a possible mixed species invasion or interstrain hybrids of *COI-RS Tpi-C* invasion.



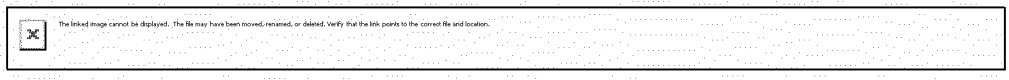
LETTER

Identification and Characterization of the First Equine Parainfluenza Virus 5

Free Full Text (HTML) ***Free*** Full Text (PDF)

Jinxin Xie, Panpan Tong, Aoyuntuya Zhang, Lei Zhang, Xiaozhen Song, Ling Kuang

Parainfluenza virus 5 (PIV5), known as canine parainfluenza virus in the veterinary field, is a negative-sense, nonsegmented, single-stranded RNA virus belonging to the *Paramyxoviridae* family (Chen 2018). The virus was first reported in primary monkey kidney cells in 1954 (Hsiung 1972), then it has been frequently discovered in various hosts, including humans, dogs, pigs, cats, rodents, calves, and lesser pandas (Chatziandreou *et al*. 2004; Lee and Lee 2013; Liu *et al*. 2015; Zhai *et al*. 2017; Jiang *et al*. 2018). So far, PIV5 has not been reported in horse. In this study, using metagenomics analysis we have identified a novel equine PIV5.



MEETING REPORT

WSV 2019: The First Committee Meeting of the World Society for Virology

Free Full Text (HTML) ***Free*** Full Text (PDF)

Ahmed S. Abdel-Moneim, Matthew D. Moore, Mahmoud M. Naguib, Jesus L. Romalde, Maria Söderlund-Venermo

To: Mike Bray[mikebrayavr@gmail.com]; Miguel Angel Martinez[mmartinez@irsicaixa.es]; Luis Menéndez Arias[lmenendez@cbm.csic.es]; Carmen Mirabelli[camirabe@med.umich.edu]; Lieve Naesens[Lieve.Naesens@kuleuven.be]; panxiaoben[panxiaoben@pkuph.edu.cn]; Anna Papa[annap.med@gmail.com]; Eve-Isabelle Pecheur[eve-isabelle.pecheur@inserm.fr]; Dan Pevear[danpevear@yahoo.com]; Jocelyne Piret[jocelyne.piret@crchudequebec.ulaval.ca]; Oliver Planz[oliver.planz@uni-tuebingen.de]; Miguel Quinones-Mateu[meq@case.edu]; Růžek Daniel[ruzekd@paru.cas.cz]; Luis M. Schang[lms428@cornell.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Sujan Shresta[sujan@lji.org]; Jessica R. (CDC/OID/NCEZID) Spengler (CTR)[wsk7@cdc.gov]; Christina Spiropoulou (CDC/OID/NCEZID)[ccs8@cdc.gov]; Eike Steinmann[eike.steinmann@twincore.de]; Youichi Suzuki[californiacircle@gmail.com]; Bart Tarbet[bart.tarbet@usu.edu]; John Tavis[john.tavis@health.slu.edu]; Evelien Vanderlinden[evelien.vanderlinden@kuleuven.be]; Robert Vrancken[rvrancken@virovet.com]; Satoru Watanabe[satoru.watanabe@duke-nus.edu.sg]; Priscilla L. Yang[priscilla_yang@hms.harvard.edu]; Hui-Ling Yen[hyen@hku.hk]; yin zheng[yinzheng@yahoo.com]; whiov[zhangbo@wh.iov.cn]; larry[zhang_jiancun@gibh.ac.cn]; 钟劲[jzhong@ips.ac.cn]; Zou Gang[zougang588@163.com]
Cc: Tao Peng[peng_tao@gibh.ac.cn]; Jinhong Chang[jinhong.chang@bblumberg.org]; Johan Neyts[johan.neyts@kuleuven.be]; Jose Este[jaeste@cienciatraducida.com]; Nesya Goris[ngoris@virovet.com]; Subhash Vasudevan[subhash.vasudevan@duke-nus.edu.sg]; Jennifer McKimm-Breschkin[jmbvirology@gmail.com]; Jenny Mckimm-Breschkin[jennifer.mckimm@unimelb.edu.au]; Jennifer Moffat[moffatj@upstate.edu]
From: David Durantel[david.durantel@inserm.fr]
Sent: Sat 2/8/2020 3:30:53 AM (UTC-06:00)
Subject: Re: Rapid review of coronavirus manuscripts by AVR
david_durantel.vcf

Dear all,

This is an excellent idea! I'll pass on the message locally...

"Bravo" to all

David

Le 08/02/2020 à 01:12, Mike Bray a écrit :

> Dear AVR editorial board members,
>
> As the coronavirus epidemic continues to expand, we at AVR will do our best to support the development of new antivirals and vaccines and to enhance understanding of the biology of the novel agent, responses to infection and the pathogenesis of severe disease. Our editor Tao Peng is handling research reports, and I'll be in charge of review articles, with assistance from Jinhong Chang and other editors.
>
> To permit quick publication of important new findings, we've put together a group of some 20 experts in coronavirus research and related areas, who have agreed to provide rapid reviews of research reports, with a turn-around time of no more than a few days. A number of you are members of that team (thanks!). Please let your colleagues know about this opportunity for rapid publication, and don't hesitate to contact me or other AVR editors with ideas about other ways our journal can respond to the epidemic.
>
> All the best,
>
> Mike
>
> Mike Bray, MD MPH
> Editor-in-chief
> Antiviral Research

--
David Durantel, PhD, HDR
Director of Research INSERM
Editor of Antiviral Research

Full Name: David Durantel
Last Name: Durantel
First Name: David
Company: Cancer Research Center of Lyon (CRCL) and University of Lyon

Business Address: 151 cours Albert Thomas 69003 Lyon France

Business Phone: +33 472 681 959
Mobile Phone: +33 682 509 187

E-mail: david.durantel@inserm.fr

From: TEMI-production@journals.tandf.co.uk
Sent: Thursday, April 4, 2019 1:56 AM
To: chenxw@wh.iov.cn;Xie, Xuping;Shi, Pei yong
Cc: chenxw@wh.iov.cn;Shi, Pei yong
Subject: RE: Emerging Microbes & Infections - Author Query (TEMI 1598291) #TrackingId:3386191

Thank you, Xuping and Xinwen.

Regards,

Malathi
Emerging Microbes & Infections

From:xuxie@UTMB.EDU
Sent:03-04-2019 07.29 PM
To:chenxw@wh.iov.cn,xuxie@UTMB.EDU,peshi@UTMB.EDU,malathi@novatechset.com
Cc:peshi@UTMB.EDU,chenxw@wh.iov.cn,TEMI-production@journals.tandf.co.uk
Subject:RE: Emerging Microbes & Infections - Author Query (TEMI 1598291)

Dear Malathi,

Please process as Dr. Chen suggested. I am sorry for confusing and any inconvenience it have caused.

Best,

Xuping

From: 陈新文 <chenxw@wh.iov.cn>
Sent: Wednesday, April 3, 2019 4:19 AM
To: TEMI-production@journals.tandf.co.uk
Cc: Xie, Xuping <xuxie@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: Emerging Microbes & Infections - Author Query (TEMI 1598291) #TrackingId:3386191

Dear Malathi,

Please retain the affiliation as is in the proof. I am the professor of [b]University of Chinese Academy of Sciences, Beijing, People's Republic of China.

All my best regards,

Xinwen

-----原始邮件-----

发件人:TEMI-production@journals.tandf.co.uk

发送时间:2019-04-03 17:10:54 (星期三)

收件人: chenxw@wh.iov.cn, xuxie@utmb.edu, peshi@utmb.edu

抄送:

主题: Emerging Microbes & Infections - Author Query (TEMI 1598291) #TrackingId:3386191

Dear Authors,

Could you please advise me on the query below at the earliest.

Regards,

Malathi
Emerging Microbes & Infections

From:malathi@novatechset.com
Sent:28-03-2019 01:21
To:xuxie@utmb.edu,malathi@novatechset.com
Cc:mastercopy_ti@novatechset.com,tandfteam@novatechset.com
Subject: Emerging Microbes & Infections - Author Query (TEMI 1598291)

Dear Xuping Xie,

I am writing to you on behalf of the journal, ***Emerging Microbes & Infections***. Thank you very much for sending in the corrections to your article, **Genetic and biochemical characterizations of Zika virus NS2A protein**. I have gone through your corrected proofs and request you to respond to the below queries at the earliest to avoid any delays in the publication process.

Queries:

Please note, you have removed the affiliation ([b]University of Chinese Academy of Sciences, Beijing, People's Republic of China) of author (Xinwen Chen), but according to T&F policy, the affiliation should not be removed once the manuscript has been submitted for publication. Can you please confirm if the author was not present in that affiliation when the research was conducted? If yes, then we can remove the affiliation, otherwise we will retain the affiliation as is in the proof.

Please advise how to proceed with affiliation.

Please reply to all recipients of this message.

Thanks in advance for your understanding in this regard.

Best wishes,

Malathi Boopalan
On behalf of Emerging Microbes & Infections
Taylor and Francis
4 Park Square
Milton Park
Abingdon
Oxfordshire
OX14 4RN
UNITED KINGDOM
Email : TEMI-production@journals.tandf.co.uk

From: TEMI-production@journals.tandf.co.uk
Sent: Wednesday, April 3, 2019 4:11 AM
To: chenxw@wh.iov.cn;Xie, Xuping;Shi, Pei yong
Subject: Emerging Microbes & Infections - Author Query (TEMI 1598291) #TrackingId:3386191

Dear Authors,

Could you please advise me on the query below at the earliest.

Regards,

Malathi
Emerging Microbes & Infections

From:malathi@novatechset.com
Sent:28-03-2019 01:21
To:xuxie@utmb.edu,malathi@novatechset.com
Cc:mastercopy_ti@novatechset.com,tandfteam@novatechset.com
Subject: Emerging Microbes & Infections - Author Query (TEMI 1598291)

Dear Xuping Xie,

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Please advise how to proceed with affiliation.

Please reply to all recipients of this message.

Thanks in advance for your understanding in this regard.

Best wishes,

Malathi Boopalan
On behalf of Emerging Microbes & Infections
Taylor and Francis
4 Park Square
Milton Park
Abingdon
Oxfordshire
OX14 4RN
UNITED KINGDOM
Email : TEMI-production@journals.tandf.co.uk

To: Menachery, Vineet[vimenach@UTMB.EDU]; Ralph Baric[rbaric@email.unc.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; Lisa Gralinski[lgralins@email.unc.edu]; Anne Beall[aebeall@email.unc.edu]; Martin Ferris[mtferris@email.unc.edu]; bottomly@ohsu.edu[bottomly@ohsu.edu]; Shannon McWeeney[mcweeney@ohsu.edu]; Mark Heise[mark_heisem@med.unc.edu]
From: Plante, Jessica A.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=23798AF99BC14D6E80C3FC0ADB52D51F-PLANTE, JES]
Sent: Sun 2/16/2020 6:26:02 PM (UTC-06:00)
Subject: Muc4 manuscript for final pre-submission review
Muc4 - mBio - 20200216.docx

Hello,

The Muc4 paper has been revamped with the very generous help Vineet and Ralph and formatted for mBio. Right now the intention is to upload it either Monday or Tuesday. I'm hopeful that you'll all be pleased with the finished product, but if you would like any changes made (especially to your name/initials and affiliation) please let me know.

Thank you, and enjoy the rest of your weekend.

-Jess

To: Shi, Pei yong[peshi@UTMB.EDU]
From: 吴莹[yingwu@whu.edu.cn]
Sent: Wed 8/14/2019 12:40:18 AM (UTC-05:00)
Subject: 向史佩勇老师请教Zika相关研究问题

佩勇老师您好！
　久闻大名！我是武汉大学基础医学院的吴莹，是秦成峰和周溪的师妹，以前在中科院微生物研究所工作了十年，是高福老师的助理和秘书，目前在武汉大学工作，自己有个独立的课题组，进行Zika病毒致病机制的研究。我拜读了很多您发表的文献，也在很多会上听过您的报告，受益匪浅。目前我们发现zika病毒2A蛋白很可能与雄性不育有关，我们自己表达的2A功能很明显，但是很难用western检测出来。我们精读了您和陈新文所长的Genetic and biochemical characterizations of Zika virus NS2A protein这篇文章，看到让我们崇拜的Zika-2A 蛋白的western 检测结果。 想求您馈赠Zika-2A 以及这些截短体的质粒（共10个，请见如下列表）来进一步做机制及筛选主要相关功能域的研究，冒昧了，不知可否？

具体10个质粒如下：
①pXJ-SPG-C16-ctNS2A-eGFP-Glyc plasmids：（9个）
1-226；
1-192；
1-147；
1-123；
1-103；
1-56；
1-26；
0（SPG-C16eGFP）；
eGFP-Glyc；
②pXJ-SPG-C16-NS2A-HA（1个）

期待您的回复，非常感谢！

祝好！
吴莹
Institute of Medical Virology,
School of Basic Medical Sciences,
Wuhan University,
185 Donghu Road Wuhan 430071,
P.R.China
Tel: 86-15901455682

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Tue 4/14/2020 5:50:14 PM (UTC-05:00)
Subject: Questions

Dr Menachery and Professor Baric

I've just read this article:

https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=02%7C01%7Cvimenach%40utmb.edu%7C8a0a1896f8b74dfc1bcd08d7e0c65347%7C7bef256d85db4526a72d31aea2546852%7C0%7C1%7C637225014744618770&sdata=5TaM5gL2PEAINggeBJstR6zFiN4n2A0V94lHs96cnfQ%3D&reserved=0

which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Sun 4/26/2020 4:27:20 PM (UTC-05:00)
Subject: Questions - reply requested

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April?

Look forward to hearing from you.

best wishes
Marcus Williamson

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

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which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

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best wishes
Marcus Williamson

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: vinu arumugham[vaccine.safety@aol.com]
Sent: Sat 4/25/2020 7:40:32 PM (UTC-05:00)
Subject: Sloppy Wuhan lab created SARS-CoV-2

Root cause of COVID-19? Biotechnology's dirty secret: Contamination. Bioinformatics evidence demonstrates that SARS-CoV-2 was created in a laboratory, unlikely to be a bioweapon but most likely a result of sloppy experiments

https://doi.org/10.5281/zenodo.3766462

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Fri 5/1/2020 5:20:36 AM (UTC-05:00)
Subject: Questions - reply requested

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April?

Look forward to hearing from you.

best wishes
Marcus Williamson

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=02%7C01%7Cvimenach%40utmb.edu%7Cea09aed4f29646d4984a08d7edb97859%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637239253156501192&sdata=1hdNEJkmZf8GvYwjR12GlT9ndcLGUqh5XO4WST022Po%3D&reserved=0

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Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Plante, Jessica A.[japlante@UTMB.EDU]; mtferris[mtferris@email.unc.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 1/17/2020 8:57:35 AM (UTC-06:00)
Muc4 Paper - Rewritten for Virology - To RSB 20191209-rsb.docx

Hi Vineet and Jess, Hope you are having a nice new year. Nice job on the paper. I have appended my comments on the paper. I think marty needs to discuss genotyping in the methods section. Be glad to chat. Ralph

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Halford, Bethany[B_Halford@acs.org]
Sent: Tue 4/21/2020 10:46:42 AM (UTC-05:00)
Subject: Interview with C&EN
EIDD-2801 science trans med.pdf

Dear Professor Menachery,

I hope this note finds you well in this challenging time.

I'm a reporter with Chemical & Engineering News, a weekly newsmagazine about chemistry. I am working on a story about the discovery of EIDD-2801, a compound currently in Phase I trials for COVID-19. I've attached a recent Science Translational Medicine paper about this compound. I am looking to speak with someone about the challenges of making antivirals in general and an oral antiviral specifically. Do you have a little time to chat with me this week? I don't think it would take more than 20 minutes. Just let me know when a good time to talk might be and what is the best number to reach you.

Thanks for your help,
Beth

Bethany Halford
Senior Correspondent
Chemical & Engineering News

Cite as:T. P. Sheahan *et al.*, *Sci. Transl. Med.* 10.1126/scitranslmed.abb5883 (2020).

CORONAVIRUS

An orally bioavailable broad-spectrum antiviral inhibits SARS-CoV-2 in human airway epithelial cell cultures and multiple coronaviruses in mice

Timothy P. Sheahan[1*†], Amy C. Sims[1$*], Shuntai Zhou[2], Rachel L. Graham[1], Andrea J. Pruijssers[3], Maria L. Agostini[3], Sarah R. Leist[1], Alexandra Schäfer[1], Kenneth H. Dinnon III[1,4], Laura J. Stevens[3], James D. Chappell[3], Xiaotao Lu[3], Tia M. Hughes[3], Amelia S. George[3], Collin S. Hill[2], Stephanie A. Montgomery[5], Ariane J. Brown[1], Gregory R. Bluemling[6,7], Michael G. Natchus[6], Manohar Saindane[6], Alexander A. Kolykhalov[6,7], George Painter[6,7,8], Jennifer Harcourt[9], Azaibi Tamin[9], Natalie J. Thornburg[9], Ronald Swanstrom[2,10], Mark R. Denison[3], Ralph S. Baric[1,4†]

[1]Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599, USA. [2]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599, USA. [3]Department of Pediatrics, Vanderbilt University Medical Center, Nashville, TN, TN, 37232,USA [4]Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, Chapel Hill, NC [5]Department of Pathology & Laboratory Medicine, University of North Carolina, Chapel Hill, NC, 27599, USA. [6]Emory Institute of Drug Development (EIDD), Emory University, Atlanta, GA, 30322, USA. [7]Drug Innovation Ventures at Emory (DRIVE), Atlanta, GA, 30322, USA. [8]Department of Pharmacology and Chemical Biology, Emory University, Atlanta, GA, 30322, USA. [9]Centers for Disease Control and Prevention, Division of Viral Diseases Atlanta GA [10]Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, Chapel Hill, NC

*Authors contributed equally.

$ Current address for A.C.S. is Chemical and Biological Signature Sciences, National Security Division, Pacific Northwest National Laboratory, Richland, WA 99352, USA.

†**Corresponding author. Email:** Timothy P. Sheahan sheahan@email.unc.edu and Ralph S. Baric rbaric@email.unc.edu

Coronaviruses (CoVs) traffic frequently between species resulting in novel disease outbreaks, most recently exemplified by the newly emerged SARS-CoV-2, the causative agent of COVID-19. Herein, we show that the ribonucleoside analog β-D-N^4-hydroxycytidine (NHC, EIDD-1931) has broad spectrum antiviral activity against SARS-CoV-2, MERS-CoV, SARS-CoV, and related zoonotic group 2b or 2c Bat-CoVs, as well as increased potency against a coronavirus bearing resistance mutations to the nucleoside analog inhibitor remdesivir. In mice infected with SARS-CoV or MERS-CoV, both prophylactic and therapeutic administration of EIDD-2801, an orally bioavailable NHC-prodrug (β-D-N^4-hydroxycytidine-5′-isopropyl ester), improved pulmonary function, and reduced virus titer and body weight loss. Decreased MERS-CoV yields in vitro and in vivo were associated with increased transition mutation frequency in viral but not host cell RNA, supporting a mechanism of lethal mutagenesis in CoV. The potency of NHC/EIDD-2801 against multiple coronaviruses and oral bioavailability highlight its potential utility as an effective antiviral against SARS-CoV-2 and other future zoonotic coronaviruses.

INTRODUCTION

The genetically diverse *Orthocoronavirinae* (coronavirus, CoV) family circulates in many avian and mammalian species. Phylogenetically, CoVs are divided into 4 genera: alpha (group 1), beta (group 2), gamma (group 3) and delta (group 4). Three new human CoV have emerged in the past 20 years with severe acute respiratory syndrome CoV (SARS-CoV) in 2002, Middle East respiratory syndrome CoV (MERS-CoV) in 2012, and now SARS-CoV-2 in 2019 (*1-3*). In fact, all human CoV are thought to have emerged originally as zoonoses (*4-6*). The ongoing SARS-CoV-2 pandemic (referred to as COVID-19, Coronavirus disease 2019) has caused over 500,000 infections and over 25,000 deaths in 199 countries. Like SARS- and MERS-CoV, the respiratory disease caused by SARS-CoV-2 can progress to acute lung injury (ALI), an end stage lung disease with limited treatment options and very poor prognoses(*3, 7, 8*). This emergence paradigm is not limited to humans. A novel group 1 CoV called swine acute diarrhea syndrome CoV (SADS-CoV) recently emerged from bats causing the loss of over 20,000 pigs in Guangdong Province, China (*9*). More alarmingly, many group 2 SARS-like and MERS-like coronaviruses are circulating in bat reservoir species that can use human receptors and replicate efficiently in primary human lung cells without adaptation(*9-12*). The presence of these "pre-epidemic" zoonotic strains foreshadow the emergence and epidemic potential of additional SARS-

like and MERS-like viruses in the future. Given the diversity of CoV strains in zoonotic reservoirs and a penchant for emergence, broadly active antivirals are clearly needed for rapid response to new CoV outbreaks in humans and domesticated animals.

Currently, there are no approved therapies specific for any human CoV. β-D-N4-hydroxycytidine (NHC, EIDD-1931) is orally bioavailable ribonucleoside analog with broad-spectrum antiviral activity against various unrelated RNA viruses including influenza, Ebola, CoV, and Venezuelan equine encephalitis virus (VEEV)(*13-16*). For VEEV, the mechanism of action (MOA) for NHC has been shown to be through lethal mutagenesis where deleterious transition mutations accumulate in viral RNA(*14, 17*). Thus, we sought to determine NHC's breadth of antiviral activity against multiple emerging CoV, its mechanism of action for CoV and its efficacy in mouse models of CoV pathogenesis.

RESULTS

NHC potently inhibits MERS-CoV and newly emerging SARS-CoV-2 replication

To determine whether NHC blocks the replication of highly pathogenic human CoV, we performed antiviral assays in cell lines with MERS-CoV and the newly emerging SARS-CoV-2. We first assessed the antiviral activity of NHC against MERS-CoV in the human lung epithelial cell line Calu-3 2B4 ("Calu3" cells). Using a recombinant MERS-CoV expressing nanoluciferase (MERS-nLUC)(*18*), we measured virus replication in cultures exposed to a dose range of drug for 48hr. NHC was potently antiviral with an average half-maximum effective concentration (IC_{50}) of 0.15 μM and no observed cytoxicity in similarly treated uninfected cultures across the dose range (50% cytotoxic concentration, CC_{50}, >10 μM) (Fig. 1A). The therapeutic index for NHC was >100. Using a clinical isolate of SARS-CoV2 (2019-nCoV/USA-WA1/2020), we performed antiviral assays in African green monkey kidney (Vero) cells and found NHC was potently antiviral with an IC_{50} of 0.3 μM and CC_{50} of >10 μM (Fig. 1B). We then determined the antiviral activity of NHC against SARS-CoV-2 in the Calu-3 cells through the measurement of infectious virus production and viral genomes. We observed a dose-dependent reduction in virus titers (Fig. 1C) with an IC_{50} of 0.08 μM. Viral genomic RNA was quantitated in clarified supernatants by qRT-PCR (Fig. 1D). Like the effect on infectious titers, we found a dose-dependent reduction in viral genomic RNA and a similar calculated IC_{50} of 0.09 μM. Collectively, these data demonstrate that NHC is potently antiviral against two genetically distinct emerging CoV.

NHC is highly active against SARS-CoV-2, MERS-CoV, and SARS-CoV in primary human airway epithelial cell cultures

To determine if NHC would be similarly antiviral in primary human cells, we performed a series of studies in primary airway epithelial (HAE) cell cultures. HAE model the architecture and cellular complexity of the conducting airway and are readily infected by multiple human and zoonotic CoV, including SARS- and MERS-CoV (*19*). We first assessed cytotoxicity of NHC in HAE treated with an extended dose range for 48hr using quantitative PCR of cell death-related gene transcripts as our metric. NHC treatment did not appreciably alter gene expression even at doses up to 100 μM (fig. S1). We then sought to determine if NHC would inhibit clinical isolate SARS-CoV-2 replication in HAE. We observed a dose dependent reduction in SARS-CoV-2 infectious virus production (Fig. 2A). In MERS-CoV infected HAE, NHC substantially reduced virus production with maximal titer reduction of > 5 logs at 10 μM (average IC_{50} = 0.024 μM), which correlated with reduced genomic (ORF1) and subgenomic (ORFN) RNA in paired samples (Fig. 2B). We observed similar trends in titer reduction (> 3 log at 10 μM, average IC_{50} = 0.14 μM) and in copies of genomic and subgenomic RNA in SARS-CoV- infected HAE (Fig. 2C). Thus, NHC was potently antiviral against SARS-CoV-2, MERS-CoV and SARS-CoV in primary human epithelial cell cultures without cytotoxicity.

NHC is effective against remdesivir (RDV)-resistant virus and multiple distinct zoonotic CoV

CoV are taxonomically divided into multiple genogroups (alpha, beta, gamma, delta) but human-infecting CoV are found in only the alpha and beta subgroups thus far (Fig. 3A). There is high sequence conservation in the RNA-dependent RNA polymerase (RdRp, nsp12) across CoV (Fig. 3A). For example, the RdRp of SARS-CoV-2 has 99.1% similarity and 96% amino acid identity to that of SARS-CoV (Fig. 3A). To gain insight into structural conservation of RdRp across the CoV family, we modeled the variation reflected in the RdRp dendrogram in Fig. 3A onto the structure of the SARS-CoV RdRp (*20*) (Fig. 3B). The core of the RdRp molecule and main structural motifs that all RdRp harbor (Fig. 3B and fig. S2) are highly conserved among CoV including SARS-CoV-2. We previously reported that CoV resistance to another broad spectrum nucleoside analog, RDV, was mediated by RdRp residues F480L and V557L in a model coronavirus mouse hepatitis virus (MHV) and in SARS-CoV, resulting in a 5-fold shift in IC_{50} (Fig. 3C)(*21*). Consequently, we tested whether RDV resistance mutations in MHV conferred cross-resistance to NHC. In fact, the two RDV resistance mutations, alone or together, conferred increased sensitivity to inhibition by NHC (Fig. 3D). As our previous studies have demonstrated a high genetic barrier to NHC for VEEV, influenza and CoV (*14-16*), the lack of cross-resistance further suggests that NHC and RDV may select for exclusive and mutually sensitizing resistance pathways.

To explore the breadth of antiviral efficacy against zoonotic CoV, we performed antiviral assays in HAE with three

zoonotic Bat-CoV: SHC014, HKU3, and HKU5. Closely related to the beta 2b SARS-CoV, Bat-CoV SHC014 is capable of replicating in human cells without adaptation(*11*), suggesting its potential for zoonotic emergence into humans. The more distantly related SARS-like beta 2b CoV, recombinant Bat-CoV HKU3, has a modified receptor binding domain to facilitate growth in cell culture (*22*). Lastly, Bat-CoV HKU5 is a MERS-like beta 2c CoV (*23*). NHC diminished infectious virus production and the levels of genomic/subgenomic viral RNA in HAE in a dose-dependent manner for all three Bat-CoVs (Fig. 4). Therefore, the antiviral activity of NHC was not limited by natural amino acid variation in the RdRp, which among the group 2b and group 2c CoV can vary by almost 20%. Moreover, these data suggest that if another SARS- or MERS-like virus were to spillover into humans in the future, they would likely be susceptible to the antiviral activity of NHC.

NHC antiviral activity is associated with increased viral mutation rates

It has recently been shown that NHC treatment increases the mutation rate in viral genomic RNA of RSV (*24*), VEEV (*14*), influenza (*24*), and our previous study used RNA seq to show that overall transition mutation frequency is increased during NHC treatment of MHV and MERS-CoV during infection in continuous cell lines(*16*). We sought to determine if NHC would increase the mutation frequency during MERS-CoV infection in human primary HAE. Using MERS-CoV-infected HAE treated with either vehicle or a dose range of NHC or RDV, we show that both drugs reduced virus titers in a dose-dependent manner (Fig. 5A). We then used a highly-sensitive high-fidelity deep sequencing approach (Primer ID NGS), which uses barcoded degenerate primers and Illumina indexed libraries to determine accurate mutation rates on viral RNA production (*25*). Using this approach, we analyzed a 538 bp region of viral genomic RNA in nonstructural protein 15 (nsp15). The error rates (#mutations/10,000 bases) in vehicle- (0.01) or RDV- (0.01) treated cultures were very low. RDV is reported to act via chain termination of nascent viral RNA, and thus the low error rates in RDV-treated cultures are in line with the proposed MOA (*26*). In contrast, the error rate was significantly increased in NHC-treated MERS-CoV RNA in a dose-dependent manner (Two-way ANOVA with Dunnett's multiple comparison test; 10-fold increase at 10 μM, $P < 0.0001$ at 24 and 48 hpi; 5-fold increase at 1μM, $P < 0.0001$ at 24 hpi and $P = 0.0015$ at 48 hpi) (Fig. 5C). The magnitude of the error rate in NHC-treated cultures correlated with virus titer reduction. At 48 hpi the respective error rate and virus titer was 0.015 and 3.96E+06 pfu/mL for vehicle treatment, 0.045 and 2.86E+04 pfu/mL with 1 μM NHC; and 0.090 and 1.5E+02 pfu/mL 10 μM NHC. Thus, with 1 μM NHC a 3-fold increase in error rate resulted in a 138-fold decrease in virus titer, while with 10 μM NHC a 6-fold increase in error rate resulted in a 26,000-fold decrease in virus titer.

We then examined the mutational spectra induced by NHC, which can be incorporated into viral RNA as a substitution for either cytosine (C) or uracil (U). RNA-mutagenic antivirals may incorporate in both nascent negative and positive sense RNA during genome replication (Fig. 5D). Adenine-to-guanine (A-to-G) and uracil-to-cytosine (U-to-C) transitions were enriched in MERS-CoV genomic RNA in an NHC dose-dependent manner (Fig. 5E). Collectively, these data used high-fidelity sequence analysis to demonstrate a specific enrichment for A:G and C:U transitions in MERS-CoV RNA after NHC treatment of primary HAE cell cultures.

Therapeutic EIDD-2801 reduces SARS-CoV replication and pathogenesis

Given the promising antiviral activity of NHC in vitro, we next evaluated its in vivo efficacy using EIDD-2801, an orally bioavailable prodrug of NHC (β-D-N^4-hydroxycytidine-5′-isopropyl ester), designed for improved in vivo pharmacokinetics and oral bioavailability in humans and non-human primates (*15*). Importantly, the plasma profiles of NHC and EIDD-2801 are similar in mice following oral delivery (*15*). We first performed a prophylactic dose escalation study in C57BL/6 mice where we orally administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or 50, 150, or 500 mg/kg EIDD-2801 2hr prior to intranasal infection with 5E+04 PFU of mouse-adapted SARS-CoV (SARS-MA15), and then vehicle or drug every 12 hours thereafter. Beginning on 3 days post-infection (dpi) and through the end of the study, body weight loss compared to vehicle treatment was significantly diminished (50 mg/kg) or prevented (150, 500 mg/kg) with EIDD-2801 prophylaxis (Two-way ANOVA with Dunnett's multiple comparison test, $P < 0.0001$) (fig. S3A). Lung hemorrhage was also significantly reduced 5 dpi with 500 mg/kg EIDD-2801 treatment (Kruskal-Wallis Test, $P = 0.010$, fig. S3B). Interestingly, there was a dose-dependent reduction in SARS-CoV lung titer (median titers: 50 mg/kg = 7E+03 pfu/mL, 150 mg/kg = 2.5E+03 pfu/mL, 500 mg/kg = 50 pfu/mL, vehicle = 6.5E+04 pfu/mL) with significant differences (Kruskal-Wallis with Dunn's multiple comparisons test) among the vehicle, 150 mg/kg ($P = 0.03$) and 500 mg/kg ($P = 0.006$) groups. Thus, prophylactic orally administered EIDD-2801 was robustly antiviral and able to prevent SARS-CoV replication and disease.

Since only the 500 mg/kg group significantly diminished weight loss, hemorrhage and reduced lung titer to near undetectable levels, we tested this dose under therapeutic treatment conditions to determine if EIDD-2801 could improve the outcomes of an ongoing CoV infection. As a control, we initiated oral vehicle or EIDD-2801 2 hours prior to infection with 1E+04 pfu SARS-MA15. For therapeutic conditions, we initiated EIDD-2801 treatment 12, 24, or 48 hours after infection. After initiating treatment, dosing for all groups was performed every 12 hours for the duration of the study. Both

prophylactic treatment initiated 2 hours prior to infection and therapeutic treatment initiated 12 hours after infection significantly (Two-way ANOVA with Tukey's multiple comparison test) prevented body weight loss following SARS-CoV infection on 2 dpi and thereafter (-2 hours: P = 0.0002 to <0.0001; +12 hours: P = 0.0289 to <0.0001) as compared to vehicle treated animals (Fig. 6A). Treatment initiated 24 hpi also significantly reduced body weight loss (3-5 dpi, P = 0.01 to <0.0001) although not to the same degree as the earlier treatment initiation groups. When initiated 48 hpi, body weight loss was only different from vehicle on 4 dpi (P = 0.037, Fig. 6A). Therapeutic EIDD-2801 significantly (Kruskal-Wallis with Dunnett's multiple comparison test) reduced lung hemorrhage when initiated up to 24 hours after infection (-2, +12, and +24 hours P < 0.0001) mirroring the body weight loss phenotypes (Fig. 6B). Interestingly, all EIDD-2801 treated mice had significantly (Kruskal-Wallis with Dunnett's multiple comparison test) reduced viral loads in the lungs even in the +48 hours group (All P < 0.0001, Fig. 6C), which experienced the least protection from body weight loss and lung hemorrhage. We also measured pulmonary function via whole body plethysmography (WBP). In Fig. 6D, we show the WBP enhanced pause (PenH) metric, which is a surrogate marker for bronchoconstriction or pulmonary obstruction (*27*), was significantly (Two-way ANOVA with Dunnett's multiple comparison test) improved throughout the course of the study if treatment was initiated up to 12 hours after infection (-2 hours: 2d pi to 5 dpi, P < 0.0001 to 0.019, +12 hours: 2 dpi to 5 dpi, P < 0.0001 to 0.0192) although the +24 hours group showed sporadic improvement as well (3 dpi P = 0.002) (Fig. 6D). Lastly, we blindly evaluated hematoxylin and eosin-stained lung tissue sections for histological features of ALI using two different and complementary scoring tools (*18*), which show that treatment initiated up to +12 hours significantly reduced ALI (Kruskal-Wallis with Dunn's multiple comparison test) (American Thoracic Society (ATS) Lung Injury Score: -2 hours P = 0.0004, +12 hours P = 0.0053, Diffuse alveolar damage (DAD) Score: -2 hours P = 0.0015, +12 hours P = 0.0004, Fig. 6E). Altogether, therapeutic EIDD-2801 was potently antiviral against SARS-CoV in vivo but the degree of clinical benefit was dependent on the time of initiation post-infection.

EIDD-2801 prophylactic and therapeutic efficacy correlates with increased MERS-CoV mutation rate

After obtaining promising in vivo efficacy data with SARS-CoV, we investigated whether EIDD-2801 would be effective against MERS-CoV. As the murine ortholog of the MERS-CoV receptor, dipeptidyl peptidase 4 (DPP4), does not support viral binding and entry, all in vivo studies were performed in genetically modified mice encoding a murine DPP4 receptor encoding two human residues at positions 288 and 330 (hDPP4 288/330 mice)(*18, 28*). Similar to our SARS-CoV data, all doses of prophylactic EIDD-2801 (50, 150 and 500 mg/kg) protected hDPP4 288/330 mice (fig. S4) from significant body weight loss (Two-way ANOVA with Dunnett's multiple comparison test, P = 0.03 to < 0.0001), lung hemorrhage (Kruskal-Wallis with Dunn's multiple comparison test, P = 0.01 to <0.0001), and virus replication which was undetectable (Kruskal-Wallis with Dunn's multiple comparison test, P < 0.0001) regardless of drug dose following intranasal infection with 5E+04 PFU mouse-adapted MERS-CoV (fig. S4).

We then evaluated the therapeutic efficacy EIDD-2801 following the promising results of our prophylactic studies. Similar to our SARS-CoV study, EIDD-2801 treatment administered before or 12 hours after intranasal mouse-adapted MERS-CoV infection (5E+04 PFU) prevented body weight loss from 2 through 6 dpi (Two-way ANOVA with Tukey's multiple comparison test, Fig. 7A, P = 0.02 to <0.0001) and lung hemorrhage on 6 dpi (Kruskal-Wallis with Dunn's multiple comparison test, P = 0.0004 to < 0.0001, Fig. 7B), but treatment initiated 24 or 48 hours did not offer similar protection. Unlike body weight loss and lung hemorrhage data which varied by treatment initiation time, virus lung titer on 6 dpi was significantly reduced to the limit of detection in all treatment groups (Kruskal-Wallis with Dunn's multiple comparison test, Fig. 7C, P < 0.0001). Interestingly, when viral genomic RNA was quantified in paired samples of lung tissue, EIDD-2801 significantly reduced quantities of viral RNA (One-way ANOVA with Dunnett's multiple comparison test, P <0.0001 to 0.017) in an initiation time-dependent manner for all groups except for +48 hours (Fig. 7D). The discrepancy among infectious titers and viral RNA suggests that accumulated mutations render the particles non-infectious and undetectable by plaque assay, consistent with the MOA. To gauge the effect of EIDD-2801 treatment on lung function, we assessed pulmonary function by WBP. Mirroring the body weight loss data, normal pulmonary function was only observed in groups where treatment was initiated prior to or 12 hours after infection (Two-way ANOVA with Tukey's multiple comparison test, -2hr: P < 0.0001 3 dpi, P = 0.0002 4 dpi, +12hr: P < 0.0001 3 dpi, P = 0.0008 4 dpi, Fig. 7E). Collectively, these data demonstrate that NHC prodrug, EIDD-2801, robustly reduces MERS-CoV infectious titers, viral RNA, and pathogenesis under both prophylactic and early therapeutic conditions.

To study the molecular mechanisms associated with drug performance in vivo, we investigated the correlation between infectious virus production and EIDD-2801-mediated mutagenesis of MERS-CoV RNA under therapeutic treatment conditions. Using Primer ID NGS, we measured the mutation rates of both viral genomic RNA (non-structural protein 10, nsp10) and host interferon stimulated gene 15 (*ISG15*) mRNA, a highly up-regulated innate immune-related gene after MERS-CoV infection (Fig. 7F). Primer ID NGS measures the

mutational frequency in single RNA molecules, each of which are represented by a single template consensus sequence (TCS) (*25*). Viral TCS were significantly reduced (Two-way ANOVA with Tukey's multiple comparison test, -2 hours P <0.0001, +12 hours P = 0.0001, +24 hours P = 0.02) in a treatment initiation time-dependent manner (Fig. 7G) similar to viral genomic RNA measured by qRT-PCR. In contrast, the numbers of ISG15 TCS were similar (P = 0.2 to 0.8) for all groups indicating that neither vehicle nor drug treatment significantly affected the levels of or mutated ISG15 mRNA transcripts (Fig. 7G). Similar to our TCS data in Fig. 6G, the total error rate in viral nsp10 was significantly increased (Two-way ANOVA with Tukey's multiple comparison test) in groups where treatment was initiated prior to (-2 hours, median error rate = 10.5 errors/10,000 bases, P < 0.0001) and up to 24 hours post infection (12 hours, median error rate = 8.2 errors/10,000 bases, P < 0.0001 ; +24 hours, median error rate = 5.4 errors/10,000 bases, P = 0.0003) but the error rates in ISG15 remained at baseline for all groups (Fig. 7H). In addition, nucleotide transitions observed in MERS-CoV genomes in vitro, were also observed in vivo in groups where treatment was initiated prior to and up to 12 hours post infection (Two-way ANOVA with Tukey's multiple comparison test, P = 0.0003 to < 0.0001) (Fig. 7I). Importantly, these transitions were not observed in host ISG15 mRNA (Fig. 7I). Lastly, the EIDD-2801 dose-dependent mutagenesis of viral RNA correlated with an increase in codon change frequency, including stop codons, in mice where treatment was initiated 12 hours or before (Two-way ANOVA with Tukey's multiple comparison test, vehicle median = 3.4; -2hr median = 22.8, P = 0.0035; +12 hours median = 20.0, P = 0.0004, Fig. 7J). Thus, approximately 20% of the mutations observed in the -2 hours and +12 hours groups resulted in a codon change and alteration of the nsp10 protein sequence. When extrapolating our results from nsp10 to the entirety of the 30kb MERS-CoV genome, EIDD-2801 likely causes between 15 (+24 hours treatment) and 30 (-2 hours treatment) mutations per genome, 10-20% of which result in amino acid coding changes. Altogether, our data demonstrates that EIDD-2801-driven mutagenesis correlates well with the reductions in viral load, strongly suggestive of an error catastrophe-driven mechanism of action under therapeutic conditions.

DISCUSSION

In the past 20 years, three novel human coronaviruses have emerged (*29, 30*). The group 2b SARS-like CoV represent an existential and future threat to global health as evidenced by the emergence of SARS-CoV and SARS-CoV-2. Zoonotic SARS-like bat CoV strains can use human angiotensin-converting enzyme 2 (ACE2) receptors, grow well in primary human airway cells, and vary by as much as 25% in key therapeutic and vaccine gene targets (*11, 31*). Thus, to address the current public health emergency of COVID-19 and to maximize pandemic preparedness in the future, broad-based vaccines and therapeutics, which are active against the higher risk RNA virus families prone to emergence, are desperately needed.

Small molecule antivirals can exert their antiviral effect through multiple mechanisms including blocking viral entry, inhibiting a virally encoded enzyme, blocking virus particle formation, or targeting a host factor required for replication (*32*). Multiple direct acting antivirals are currently under evaluation in randomized control trials to treat COVID-19 including hydroxychloroquine, remdesivir, lopinavir/ritonavir(*33-35*). Here, we report the broad-spectrum antiviral activity of NHC and its orally bioavailable prodrug EIDD-2801, against SARS-CoV, MERS-CoV, and the current pandemic strain SARS-CoV-2 in primary human airway epithelial cells. In addition to CoV, NHC is broadly active against multiple genetically distinct viruses including VEE, influenza A and B, Ebola, and Chikungunya viruses (*13-16, 19, 21, 24, 36-38*). Here, we show that prophylactic and therapeutic EIDD-2801 significantly reduced lung viral loads and improved pulmonary function in mouse models of both SARS- and MERS-CoV pathogenesis. Although the improvement in both SARS- and MERS-CoV outcomes diminished with the delay of treatment initiation time, it is important to note that the kinetics of disease in mice are compressed as compared to that in humans. Whereas SARS- and MERS-CoV lung titers peak on 1-2 dpi in mice concurrent with the onset of clinical signs and notable damage to the lung epithelium, in humans this occurs 7-10 days after the onset of symptoms (*19, 28, 39, 40*). Thus, in mice, the window within which to treat emerging CoV infection prior to peak replication is compressed (e.g., 24-48 hours). As with oseltamivir treatment for influenza which fails to provide a protective effect if administered >5 days after the onset of symptoms, the window in which to treat COVID-19 patients prior to peak virus replication is likely during the first week of symptoms when pharyngeal shedding is at its highest(*41, 42*). However, virus replication and shedding may continue for several weeks in the most severe COVID-19 patients(*34*). Thus, early intervention with an antiviral like EIDD-2801 is likely to provide the most clinical benefit although there may opportunities in severe patients where the duration of virus replication may be extended. Our current study is clearly limited by the lack of in vivo efficacy testing with SARS-CoV-2. Currently, robust mouse models that recapitulate the SARS-CoV-2 pathogenesis observed in humans do not yet exist due to a noted virus spike glycoprotein and mouse ACE2 receptor incompatibility complicating the evaluation of medical countermeasures(*43, 44*). In addition, SARS-CoV and MERS-CoV, SARS-CoV-2 disease severity increases with increasing age. Our studies are limited by the lack of drug efficacy testing in CoV aged mouse models that

recapitulate the age-related increase in pathogenesis observed in humans(*45*). The data provided in this manuscript suggest that EIDD-2801 should be quickly evaluated in primate models of human disease, using immediate models for MERS-CoV and SARS-CoV pathogenesis or newly described cynomolgus and rhesus macaque models for SARS-CoV-2 (*46-49*).

For VEE and influenza, NHC/EIDD-2801 exerts its antiviral activity on the RNA-dependent RNA polymerase leading to error catastrophe by inducing an error rate of replication that surpasses the error threshold allowed to sustain a virus population (*14, 15*). This process occurs when NHC is incorporated during RNA synthesis then subsequently misread thus increasing mutation rates. Therefore, for CoV, the NHC MOA would appear less likely to be affected by the RNA proofreading activity encoded by the nsp14 exonuclease function that otherwise limits misincorperation (*50*). Here, we present data using Primer ID NGS to quantitate the frequency and identity of the mutational spectra in the MERS-CoV genome in both drug-treated primary human airway cells and in mice at single genome resolution. As CoV are positive sense RNA viruses that replicate through a negative sense RNA intermediate, NHC incorporation as a C or a U can occur in both polarities of RNA. We found increased nucleotide transitions (A to G, G to A, C to U, U to C) consistent with those reported after influenza and VEE infections (*14, 15*). Under identical conditions, RDV did not alter the mutation rate in MERS-CoV genomic RNA, supporting its reported mechanism of action as a chain terminator of viral RNA synthesis (*26*). In primary human lung cell cultures and mice infected with MERS-CoV, the NHC mutation rates inversely correlated with a reduction in infectious virus. In addition, we found a positive correlation between increased mutation rates and the frequency of nonsynonymous mutations and the degree of therapeutic efficacy in mice. To explore the potential off-target effect in host mRNA which may contribute to drug toxicity, we also examined the impact of NHC treatment on *ISG15* transcripts, a gene highly induced following MERS-CoV infection. Although ISG15 transcripts are present in great abundance, an accumulation of mutations was not observed in *ISG15* in this model even at 500 mg/kg dosing. These data also support previous studies using RNAseq to demonstrate that the model coronavirus MHV displayed increased mutation frequencies following NHC treatment in vitro (*16*). With regard to nucleic acid specificity, ribonucleotides are efficiently removed from eukaryotic cell DNA; therefore, treating a viral infection with a mutagenic ribonucleoside analog should show a selectivity for incorporation into the viral genome and not be efficient at being incorporated into and inducing mutations into host cell DNA (*51*). All together, these data strongly support the notion that EIDD-2801 and its active nucleoside analog NHC exert their antiviral effect through the induction of error catastrophe in the targeted virus. While our data suggest that the MERS-CoV nsp14 proofreading activity appeared ineffective against NHC in vitro and EIDD-2801 in vivo, future studies should investigate the antiviral activity of NHC in the presence or absence of the nsp14 proofreading activity, as loss of this activity increased the sensitivity of MHV and SARS-CoV replication to RDV treatment (*50*).

Together, our data support the continued development of EIDD-2801 as a potent broad spectrum antiviral that could be useful in treating contemporary, newly emerged and emerging coronavirus infections of the future.

MATERIALS AND METHODS

Study Design

The primary goal of this study was to determine the antiviral activity of the nucleoside analog NHC (EIDD-1931) against multiple emerging CoV in vitro and antiviral efficacy of its prodrug, EIDD-2801, in mouse models of CoV pathogenesis. Coupling cell lines and primary HAE cell cultures, we evaluated the antiviral activity of NHC against the three most recently emerged human CoV: SARS-CoV, MERS-CoV, and SARS-CoV-2. For both SARS-CoV and MERS-CoV, the data presented for HAE studies are representative of those from 2-3 separate human donors. For SARS-CoV-2, the HAE were from a single human donor. We evaluated drug cytotoxicity in both Calu-3 2B4 and HAE cell cultures. Calu-3 and the SARS-CoV and MERS-CoV HAE studies were performed in biological triplicate. HAE studies with SARS-CoV-2 and the SARS- and MERS-like bat CoV were performed with two wells per condition. Drug effects were measured relative to vehicle controls in vitro and comparisons in vivo were performed to vehicle controls. We also aimed to determine the antiviral efficacy of EIDD-2801 in mouse models of CoV pathogenesis. These studies were intended to provide the preclinical data to justify nonhuman primate studies and human clinical trials. Mice were age- and sex-matched and randomly assigned into groups before infection and treatment. Pathology was scored blinded by a board-certified veterinary pathologist. Primary data for all studies are provided in data file S1.

Ethics regulation of laboratory animals

Efficacy studies were performed in animal biosafety level 3 facilities at UNC Chapel Hill. All work was conducted under protocols approved by the Institutional Animal Care and Use Committee at UNC Chapel Hill (IACUC protocol #16-284) according to guidelines set by the Association for the Assessment and Accreditation of Laboratory Animal Care and the U.S. Department of Agriculture.

Compounds

The parental compound β-D-N^4-hydroxycytidine (NHC, all in vitro studies) and its prodrug EIDD-2801 (all in vivo studies) was supplied by Emory University Institute for Drug

Discovery (EIDD). NHC was supplied as a 10 mM stock in DMSO and EIDD-2801 as a solid and solubilized in vehicle containing 10% PEG400, 2.5% Cremophor RH40 in water (10/2.5/87.5%, all v/v) prior to use. RDV was solubilized in 100% DMSO and provided by Gilead Sciences, Inc as previously described (*18, 19*).

Cell cultures

At UNC, the human lung epithelial cell line Calu-3 2B4 cells was maintained in Dulbecco's modified Eagle's medium (DMEM, Gibco), 20% fetal bovine serum (Hyclone) and 1x antibiotic/antimycotic (Gibco). At Vanderbilt University Medical Center (VUMC), Calu-3 2B4 were propagated in DMEM supplemented with 20% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). At VUMC, VeroE6 cells were cultured in DMEM supplemented with 10% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). At UNC, VeroE6 cells were cultured in DMEM supplemented with 10% Fetal Clone II (Hyclone) and 1x antibiotic/antimycotic (Gibco). Murine delayed brain tumor (DBT) cells were maintained in DMEM supplemented with 10% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). Primary human airway epithelial (HAE) cell cultures were obtained from the Tissue Procurement and Cell Culture Core Laboratory in the Marsico Lung Institute/Cystic Fibrosis Research Center at UNC and are described more thoroughly below (*52*).

Virus strains

Except for SARS-CoV-2, all viruses used for these studies were derived from infectious clones and isolated as previously described (*53*). SARS-CoV-2 clinical isolate was obtained at VUMC and UNC from the CDC (2019-nCoV/USA-WA1/2020 strain, GenBank accession no. MN985325.1) and passaged twice in Vero E6 cells at each respective institution to create a passage 5 working stock (*54*). Virus strains for in vitro experiments include SARS-CoV expressing the green fluorescent protein (GFP) in place of open reading frames 7a/b (ORF7a/b, SARS-GFP)(*53*), bat-spike receptor binding domain (Bat-SRBD)(*22*), a chimeric CoV strain derived from the HKU3 SARS-like bat coronavirus genomic sequence that has the wild type (Urbani SARS-CoV strain) RBD in the HKU3 spike gene to allow for virus replication in non-human primate cell lines and HAE cultures, SHC014 SARS-like bat coronavirus (*11*), MERS-CoV expressing nanoluciferase in the place of ORF3 (MERS-nLUC)(*19*), and MERS-CoV expressing the red fluorescent protein gene in the place of ORF 5 (RFP, MERS-RFP)(*55*). The virus stock utilized for MERS-CoV in vivo studies was derived from a plaque-purified isolate of the mouse-adapted MERS-CoV p35C4 strain (*56*). The virus stock utilized for SARS-CoV in vivo studies was derived from the infectious clone of the mouse-adapted SARS-CoV MA15 (MA15) strain (*57*). All work with MHV was performed using the recombinant WT strain MHV-A59 (GenBank accession no. AY910861)(*58*).

In vitro antiviral activity experiments

MERS-CoV nLUC in Calu-3: At 48 hours prior to infection, Calu-3 2B4 cells were plated in a 96-well black-walled clear bottom plate at $5x10^4$ cells/well. A 10 mM stock of NHC was serially diluted in 100% DMSO in 3-fold increments to obtain a ten-point dilution series. MERS-nLUC was diluted in DMEM supplemented with 10% FBS, and 1% Antibiotic-Antimycotic to achieve a multiplicity of infection (MOI) of 0.08. Cells were infected and concurrently treated with NHC in triplicate per drug dilution for 1hr, after which viral inoculum was aspirated, cultures were rinsed once and fresh medium containing drug or vehicle was added. At 48 hours post infection, nanoluciferase expression as a surrogate for virus replication was quantitated on a Spectramax plate reader (Molecular Devices) according to the manufacturer's instructions (Promega, NanoGlo). For the 100% inhibition control, diluted MERS-nLUC was exposed to short-wave UV light (UVP, LLC) for 6 min to inhibit the ability of the virus to replicate. For the 0% inhibition control, cells were infected in the presence of vehicle only. DMSO was kept constant in all conditions at 0.05%. Values from triplicate wells per condition were averaged and compared to controls to generate a percent inhibition value for each drug dilution. The IC_{50} value was defined as the concentration at which there was a 50% decrease in luciferase expression. Data were analyzed using GraphPad Prism 8.0. The IC_{50} values were calculated by nonlinear regression analysis using the dose-response (variable slope) equation (four parameter logistic equation): Y = Bottom + (Top-Bottom)/(1+10^((LogIC50-X)*HillSlope)). To measure cell viability to determine if there was any NHC-induced cytotoxicity, Calu-3 2B4 cells were plated and treated with NHC only as described above. Cells were exposed to the same ten-point dilution series created for the in vitro efficacy studies. As above, 0.05% DMSO-treated cells served as the 0% cytotoxicity control. Wells without cells served as the 100% cytotoxic positive control. After 48 hours, cell viability was measured on a Spectramax (Molecular Devices) via Cell-Titer Glo Assay (Promega) according to the manufacturer's protocol. Similar data were obtained in three independent experiments.

SARS-CoV-2 in Calu-3: Calu-3 2B4 cells were adsorbed with MOI 0.1 PFU/cell of SARS-CoV-2 (2019-nCoV/USA-WA1/2020 strain) at 37°C. Plates were manually rocked every 10 min to redistribute the inoculum. After 30 min, virus inoculum was removed, cells were washed with Phosphate buffered saline (PBS) once to remove unbound virus, medium containing NHC or vehicle control (DMSO) was added back onto the cells, and cells were incubated for 72 hours at 37°C.

SARS-CoV-2 in Vero E6: Vero E6 cells were plated at 20,000 cells/well in a 96-well plate. 24hr later, medium

containing a dose response of NHC was added concurrent with SARS-CoV-2 (2019-nCoV/USA-WA1/2020 strain) at an MOI of 0.05. 48 hours post infection, cell viability was measured by CellTiter Glo assay.

SARS-CoV, MERS-CoV, and SARS-CoV-2 in HAE: Human tracheobronchial epithelial cells provided by Dr. Scott Randell were obtained from airway specimens resected from patients undergoing surgery under University of North Carolina Institutional Review Board-approved protocols (#03-1396) by the Cystic Fibrosis Center Tissue Culture Core. Primary cells were expanded to generate passage 1 cells and passage 2 cells were plated at a density of 250,000 cells per well on Transwell-COL (12mm diameter) supports (Corning). Human airway epithelium cultures (HAE) were generated by provision of an air-liquid interface for 6 to 8 weeks to form well-differentiated, polarized cultures that resembled in vivo pseudostratified mucociliary epithelium (*59*).· At 48 hours prior to infection the apical surface of the culture was washed with 500 μL PBS for 1.5 hours at 37°C and the cultures moved into fresh air liquid interface (ALI) media. Immediately prior to infection, apical surfaces were washed twice to remove accumulated mucus with 500 μL of PBS with each wash lasting 30 min at 37°C and HAE cultures were moved into ALI media containing various concentrations of NHC ranging from 10 μM to 0.0016 μM as indicated for each experiment (final % DMSO < 0.05%). Upon removing the second PBS wash, 200 μL of viral inoculum (SARS-GFP, MERS-RFP or 2019-nCoV/USA-WA1/2020 strain) at an MOI of 0.5 was added to the apical surface and HAE cultures were incubated for 2 hours at 37°C. Viral inoculum was then removed, and the apical surface of the cultures were washed three times with 500μL PBS and then incubated at 37°C until 48 hours post infection (hpi). For all HAE cultures, infectious virus produced was collected by washing the apical surface of the culture with 100 μL PBS. Apical washes were stored at -80°C until analysis and titered by plaque assay as previously described (*19*).

qRT-PCR approach to assess cytotoxicity

Total RNA was isolated using the Zymo Direct-zol RNA MiniPrep Kit (Zymo Research Corp.) according to the manufacturer's directions. Cells were treated with 1μM staurosporine (Sigma-Aldrich) as a positive control. First-strand cDNA was generated using Superscript III reverse transcriptase (Life Technologies). For quantification of cellular markers of toxicity/apoptosis, real-time PCR was performed using commercially validated TaqMan-based primer-probe sets (**table S1**) and TaqMan Universal PCR Mix (Life Technologies). Results were then normalized as described above.

MERS-CoV genomic RNA qRT-PCR

Mouse lungs were stored in RNAlater (ThermoFisher) at -80°C until processed via homogenization in TRIzol (Invitrogen). Total RNA was isolated using Direct-zol RNA MiniPrep kit (Zymo Research). Previously published TaqMan primers were synthesized by Integrated DNA Technologies (IDT) to quantify MERS genomic RNA (targeting orf1a: Forward: 5′-GCACATCTGTGGTTCTCCTCTCT-3′, Probe (6-FAM/ZEN/IBFQ): 5′- TGCTCCAACAGTTACAC-3′, Reverse: 5′-AAGCCCAGGCCCTACTATTAGC)(*60*). qRT-PCR was performed using 100ng total RNA compared to an RNA standard curve using TaqMan Fast Virus 1-Step Master Mix (ThermoFisher) on a Quant Studio 3 (Applied Biosystems).

Quantification of SARS-CoV-2 viral RNA genome copy number by qRT-PCR

Cell supernatants were harvested in TRIzol LS reagent (Invitrogen), and RNA was purified following phase separation by chloroform as recommended by the manufacturer. The RNA in the aqueous phase was collected and further purified using PureLink RNA Mini Kits (Invitrogen) according to the manufacturer's protocol. Viral RNA was quantified using one-step quantitative reverse transcription PCR (qRT-PCR) on a StepOnePlus Real-Time PCR system (Applied Biosystems) by TaqMan Fast Virus 1-Step Master Mix chemistry (Applied Biosystems). SARS-CoV-2 N gene RNA was amplified using forward (5′-GACCCCAAAATCAGCGAAAT) and reverse (5′-TCTGGTTACTGCCAGTTGAATCTG) primers and probe (5′-FAM-ACCCCGCATTACGTTTGGTGGACC-BHQ1) designed by the United States Centers for Disease Control and Prevention (oligonucleotides produced by IDT, cat# 10006606). Copy numbers were interpolated from a standard curve produced with dilutions of N gene RNA. Briefly, SARS-CoV-2-N positive control plasmid DNA (IDT, cat# 10006625) was amplified using forward (5′-TAATACGACTCACTATAGGGATGTCTGATAATGGACCCCA) and reverse (5′- TTAGGCCTGAGTTGAGTCAG) primers, resulting in a 1280 nucleotide fragment containing a T7 promoter. The PCR product was purified by column (Promega) and in vitro transcribed using the mMESSAGE mMACHINE T7 Transcription Kit (Invitrogen) according to the manufacturer's protocol. Transcribed RNA was purified using RNeasy mini kit (Qiagen) according to the manufacturer's protocol, and serial 10-fold dilutions were quantified as described above.

Primer ID and deep sequencing

Primer ID NGS is designed to specifically identify and remove RT-PCR mutations, while facilitating highly accurate sequence determination of single RNA molecules, because each cDNA is created with a barcoded degenerate primer (N10, 4^{10} combinations) from which Illumina indexed libraries are made. We used a multiplexed Primer ID library prep approach and MiSeq sequencing to investigate the presence of mutations in the viral genomes and murine mRNA. We designed cDNA primers targeting multiple regions on the viral genome and murine mRNA, each with a block of random

nucleotides (11 bp long) as the Primer ID (*25, 61*) (**table S2**). Viral RNA was extracted using QIAamp viral RNA kit. A pre-amplification titration of templates was performed to estimate the amount of template to use. We used SuperScript III to make cDNA with multiplexed cDNA primers based on the regions to be sequenced. We used 41R_PID11 for the pilot sequencing and titration determination. For the MERS-CoV sequencing, we multiplexed nsp10_PID11, nsp12_PID11 and nsp14_PID11 for the cDNA reaction; for the murine mRNA sequencing, we used mixed primers of nsp10_PID11, ifit3_PID11, isg15_PID11. After bead purification, we amplified the cDNA with a mixture of forward primers (based on the described schemes) and a universal reverse primer, followed by another round of PCR to incorporate Illumina sequencing adaptors and barcodes in the amplicons. After gel-purification and quantification, we pooled 24 libraries for MiSeq 300 base paired-end sequencing. The TCS pipeline version 1.38 (https://github.com/SwanstromLab/PID) was used to process the Primer ID sequencing data and construct template consensus sequences (TCSs) to represent each individual input templates, and the sequences of each region in the pool was de-multiplexed. The RUBY package viral_seq version 1.0.6 (https://rubygems.org/gems/viral_seq) was used to calculate the mutation rate at each position. NCBI SRA Accession numbers for sequence data are as follows: PRJNA613261 (Fig. 5) and PRJNA613454 (Fig. 7).

In vivo experiments

We performed 4 mouse studies to evaluate the in vivo efficacy of the NHC prodrug (EIDD-2801). First, we performed prophylactic dose escalation studies for both SARS- and MERS-CoV to determine the most efficacious dose of EIDD-2801 per virus. For SARS-CoV, in cohorts of equivalent numbers of male and female 20-29 week old SPF C57BL/6J (Stock 000664 Jackson Labs) mice (n = 10/dose group), we administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or 50, 150 or 500 mg/kg EIDD-2801 by oral gavage 2 hours prior to intranasal infection with 1E+04 PFU mouse-adapted SARS-CoV strain MA15 in 50μl. Mice were anaesthetized with a mixture of ketamine/xylazine prior to intranasal infection. Vehicle or drug was administered every 12hr for the remainder of the study. Body weight and pulmonary function by whole body plethysmography were measured daily. On 5 dpi, animals were sacrificed by isoflurane overdose, lungs were scored for lung hemorrhage, and the inferior right lobe was frozen at −80°C for viral titration via plaque assay. Briefly, 500,000 Vero E6 cells/well were seeded in 6-well plates. The following day, medium was removed and serial dilutions of clarified lung homogenate were added per plate (10^{-1} to 10^{-6} dilutions) and incubated at 37°C for 1hr after which wells were overlaid with 1X DMEM, 5% Fetal Clone 2 serum, 1X antibiotic/antimycotic, 0.8% agarose. Two days after, plaques were enumerated to generate a plaque/ml value. Lung hemorrhage is a gross pathological phenotype readily observed by the naked eye driven by the degree of virus replication where the coloration of the lung changes from pink to dark red (*62, 63*). The large left lobe was placed in 10% buffered formalin and stored at 4°C for 1-3 weeks until histological sectioning and analysis. For MERS-CoV, the prophylactic dose escalation studies we performed similarly as done for SARS-CoV with our recently developed a mouse model for MERS-CoV, which has a humanized DPP4 receptor (hDPP4) (*28*). We performed all in vivo studies with EIDD-2801 in equivalent numbers of 10-14 week old female and male C57BL/6J hDPP4 mice. Second, we intranasally infected mice with 5E+04 PFU mouse-adapted MERS-CoV strain M35C4 in 50μl. Third, to titer lungs by plaque assay, Vero CCL81 cells were used and plaques were enumerated 3 dpi.

To determine the time at which therapeutic administration of EIDD-2801 would fail to improve outcomes with SARS-CoV or MERS-CoV infection, we performed therapeutic efficacy studies in mice where we initiated treatment 2 hours prior to infection or 12, 24 or 48 hours after infection. As 500 mg/kg provided the most complete protection from disease in prophylactic SARS-CoV studies, this dose was used for both therapeutic efficacy studies. Vehicle or EIDD-2801 was given via oral gavage twice daily following initiation of treatment. For both SARS-CoV and MERS-CoV, the infectious dose for the therapeutic studies and the mouse strains were the same as that used in the prophylactic studies. The numbers of mice per group for the SARS-CoV studies were as follows: Vehicle (n = 10), -2 hours (n = 10), +12 hours (n = 10), +24 hours (n = 10), +48 hours (n = 10). The numbers of mice per group for the MERS-CoV therapeutic studies were as follows: Vehicle (n = 9), -2 hours (n = 9), +12 hours (n = 9), +24 hours (n = 7), +48 hours (n = 10). As described above, each day mouse body weight and pulmonary function were quantitated. On 5 dpi for SARS-CoV and 6 dpi for MERS-CoV, animals were humanely sacrificed and tissues were harvested and analyzed as described above. In addition, for the MERS-CoV study, lung tissue was harvested and stored in RNAlater (Thermo Fisher) at -80°C and then thawed, homogenized in Trizol reagent (Invitrogen) and total RNA was isolated using a Direct-zol RNA MiniPrep kit (Zymo Research). This total RNA was then used for Primer ID and qRT-PCR.

Whole body plethysmography

Pulmonary function was monitored once daily via whole-body plethysmography (Buxco Respiratory Solutions, DSI Inc.). Mice intended for this analysis were randomly chosen prior to the initiation of the study. Briefly, after a 30-min acclimation time in the plethysmograph, data for 11 parameters was recorded every 2 s for 5 min.

Acute lung injury histological assessment tools

Two different and complementary quantitative histologic tools were used to determine if antiviral treatments

diminished the histopathologic features associated with lung injury. Both analyses and scoring were performed by a Board Certified Veterinary Pathologist who was blinded to the treatment groups.

American Thoracic Society lung injury scoring tool. In order to help quantitate histological features of ALI observed in mouse models and increase their translation to the human condition, we used the ATS scoring tool (*63*). In a blinded manner, we chose three random diseased fields of lung tissue at high power (60 ×), which were scored for the following: (A) neutrophils in the alveolar space (none = 0, 1–5 cells = 1, > 5 cells = 2), (B) neutrophils in the interstitial space/ septae (none = 0, 1–5 cells = 1, > 5 cells = 2), (C) hyaline membranes (none = 0, one membrane = 1, > 1 membrane = 2), (D) Proteinaceous debris in air spaces (none = 0, one instance = 1, > 1 instance = 2), (E) alveolar septal thickening (< 2× mock thickness = 0, 2–4× mock thickness = 1, > 4× mock thickness = 2). To obtain a lung injury score per field, the scores for A–E were then put into the following formula, which contains multipliers that assign varying levels of importance for each phenotype of the disease state.: score = [(20x A) + (14 x B) + (7 x C) + (7 x D) + (2 x E)]/100. The scores for the three fields per mouse were averaged to obtain a final score ranging from 0 to and including 1.

Diffuse Alveolar Damage (DAD) tool. The second histological tool to quantitate lung injury was reported by Schmidt *et al.*(*64*). DAD is the pathological hallmark of ALI (*63, 64*). Three random diseased fields of lung tissue were scored at high power (60 ×) for the following in a blinded manner: 1 = absence of cellular sloughing and necrosis, 2 = Uncommon solitary cell sloughing and necrosis (1–2 foci/field), 3 = multifocal (3 + foci) cellular sloughing and necrosis with uncommon septal wall hyalinization, or 4 = multifocal (>75% of field) cellular sloughing and necrosis with common and/or prominent hyaline membranes. The scores for the three fields per mouse were averaged to get a final DAD score per mouse.

nsp12 phylogenetic analysis and conservation modeling

Coronavirus RdRp (nsp12) protein sequence alignments and phylogenetic trees were generated using Geneious Tree Builder in Geneious Prime (version 2020.0.5) and visualized using Evolview (https://www.evolgenius.info/evolview/). Protein similarity scores were calculated using Blosom62 matrix. The accession numbers used were: PDCoV (KR265858), AIBV (NC_001451), HCoV-229E (JX503060), PEDV (NC_003436), MHV (AY700211), HCoV-HKU1 (DQ415904), HCoV-NL63 (JX504050), HCOV-OC43 (AY903460), HKU5-1 (NC_009020), MERS-CoV (JX869059), HKU9-4 (EF065516), 2019-nCoV (MN996528), HKU3-1 (DQ022305), SHC014 (KC881005), WIV1 (KF367457), SARS-CoV (AY278741). Amino acid conservation scores of coronavirus RdRp were generated using ConSurf Server (https://consurf.tau.ac.il/) using the protein alignment described above and visualized on the SARS-CoV RdRp structure (PDB: 6NUR) in PyMol (version 1.8.6.0)(*20, 65*).

Statistical analysis

All statistical data analyses were performed in Graphpad Prism 8. Statistical significance for each endpoint was determined with specific statistical tests. In general, for metrics with multiple treatment groups with longitudinal data (e.g., mouse weight loss or pulmonary function over time), two-way ANOVA was performed with the suggested multiple comparison test as advised by Prism. For comparative data with for a single timepoint (e.g., lung titer) Kruskal-Wallis or one-way ANOVA was performed with the suggested multiple comparison test. For each test, a p-value <0.05 was considered significant. Specific tests are noted in each figure legend.

SUPPLEMENTARY MATERIALS

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Supplementary Figure 1. Assessment of cytotoxicity of NHC in primary human epithelial cell cultures by qRT-PCR.

Supplementary Figure 2. High conservation of RdRp functional domains for SARS-CoV-2.

Supplementary Figure 3. Prophylactic EIDD-2801 reduces SARS-CoV replication and pathogenesis.

Supplementary Figure 4. Prophylactic EIDD-2801 reduces MERS-CoV replication and pathogenesis.

Supplementary Table 1. Real-time PCR primer/probe sets for indicators of cellular apoptosis/toxicity.

Supplementary Table 2. Primers used for MiSeq library prep and sequencing.

Data file S1. Primary data.

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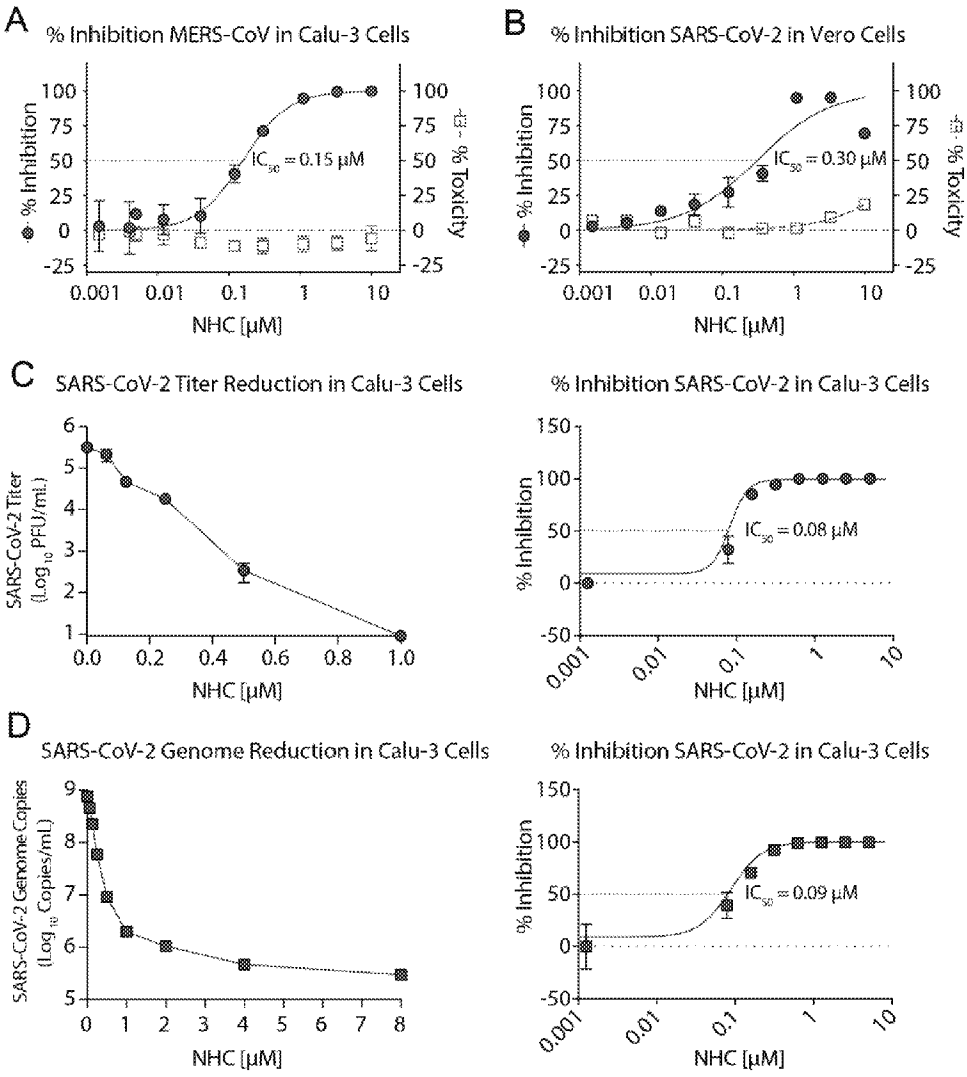

Fig. 1. NHC potently inhibits MERS-CoV and newly emerging SARS-CoV-2 replication. (A) Percent inhibition of MERS-CoV replication and NHC cytotoxicity in Calu-3 cells. Calu-3 cells were infected in triplicate with MERS-CoV nanoluciferase (nLUC) at a multiplicity of infection (MOI) of 0.08 in the presence of a range of drug for 48 hours, after which replication was measured through quantitation of MERS-CoV–expressed nLUC. Cytotoxicity was measured in similarly treated but uninfected cultures via Cell-Titer-Glo assay. Data are combined from 3 independent experiments. **(B)** NHC antiviral activity and cytotoxicity in Vero E6 cells infected with SARS-CoV-2. Vero E6 cells were infected in duplicate with SARS-CoV-2 clinical isolate 2019-nCoV/USA-WA1/2020 virus at an MOI of 0.05 in the presence of a range of drug for 48 hours, after which replication was measured through quantitation of cell viability by Cell-Titer-Glo assay. Cytotoxicity was measured as in **A**. Data are combined from 2 independent experiments. **(C)** SARS-CoV-2 titer reduction (left) and percent inhibition (right) in Calu-3 cells. Cells were infected with at an MOI of 0.1 for 30 min, washed and exposed to a dose response of NHC in triplicate per condition. 72 hours post infection, virus production was measured by plaque assay. **(D)** SARS-CoV-2 genomic RNA reduction (left) and percent inhibition (right) in Calu-3 cells. Viral RNA was isolated from clarified supernatants from the study in panel **C**. Genome copy numbers were quantitated by qRT-PCR with primer/probes targeting the N gene. For **A-D**, the symbol is at the mean and the error bars represent the standard deviation.

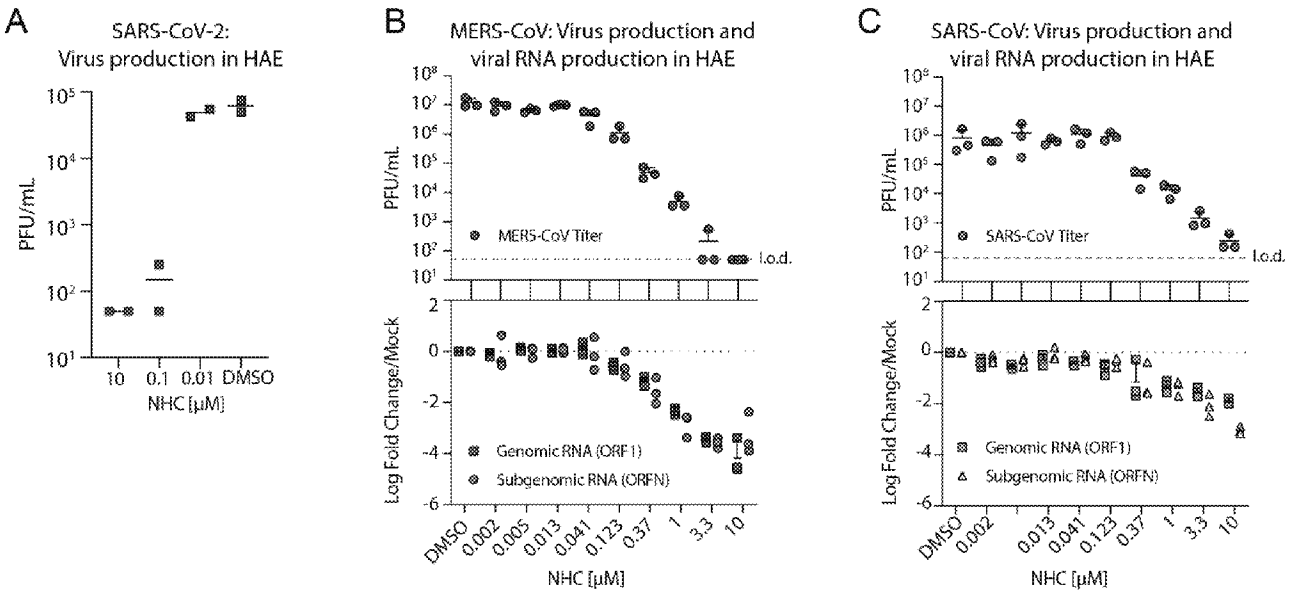

Fig. 2. NHC is highly active against SARS-CoV-2, MERS-CoV, and SARS-CoV in primary human airway epithelial cell cultures. (A) HAE were infected at an MOI of 0.5 with clinical isolate SARS-CoV-2 for 2 hours in the presence of NHC in duplicate after which virus was removed and cultures were washed in incubated in NHC for 48 hours when apical washes were collected for virus titration by plaque assay. The line is at the mean. Each symbol represents the titer from a single well. **(B)** HAE cells were infected with MERS-CoV red fluorescent protein (RFP) at an MOI of 0.5 in triplicate and treated similarly to **A**. qRT-PCR for MERS-CoV ORF1 and ORFN mRNA. Total RNA was isolated from cultures in **C** for qRT-PCR analysis. Representative data from three separate experiments with three different cell donors are displayed. PFU, plaque-forming units. **(C)** Studies performed as in **A** but with SARS-CoV green fluorescent protein (GFP). Representative data from two separate experiments with two different cell donors are displayed. Each symbol represents the data from one HAE culture, the line is at the mean and the error bars represent the standard deviation.

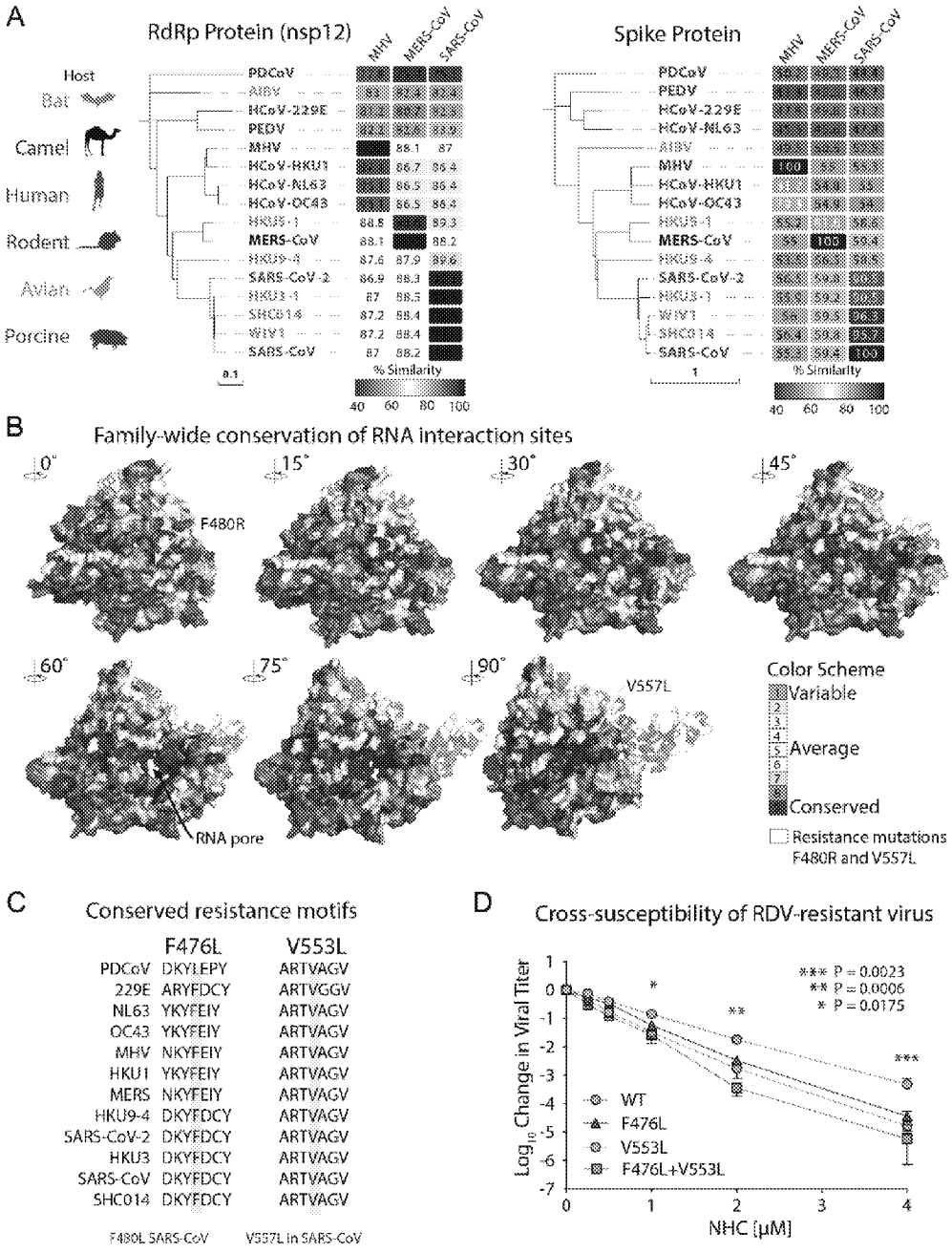

Fig. 3. Remdesivir (RDV) resistance mutations in the highly conserved RNA-dependent RNA polymerase increase susceptibility to NHC. (A) Neighbor-joining trees created with representatives from all four CoV genogroups showing the genetic similarity of CoV nsp12 (RdRp) and CoV spike glycoprotein, which mediates host tropism and entry into cells. Text color of the virus strain label corresponds to virus host species on the left. The heatmap adjacent to each neighbor-joining tree depicts percent amino acid identity (% A.A. similarity) against mouse hepatitis virus (MHV), SARS-CoV, or MERS-CoV. **(B)** The variation encompassed in panel **A** was modeled onto the RdRp structure of the SARS-CoV RdRp. **(C)** Amino acid sequence of CoV in panel **A** at known resistance alleles to antiviral drug RDV. **(D)** Virus titer reduction assay in DBT cells across a range of NHC with recombinant MHV bearing resistance mutations to RDV. Data shown are combined from three independent experiments performed with biological duplicates or triplicates per condition. Asterisks indicate statistically significant differences by Mann-Whitney test as indicated on the graph.

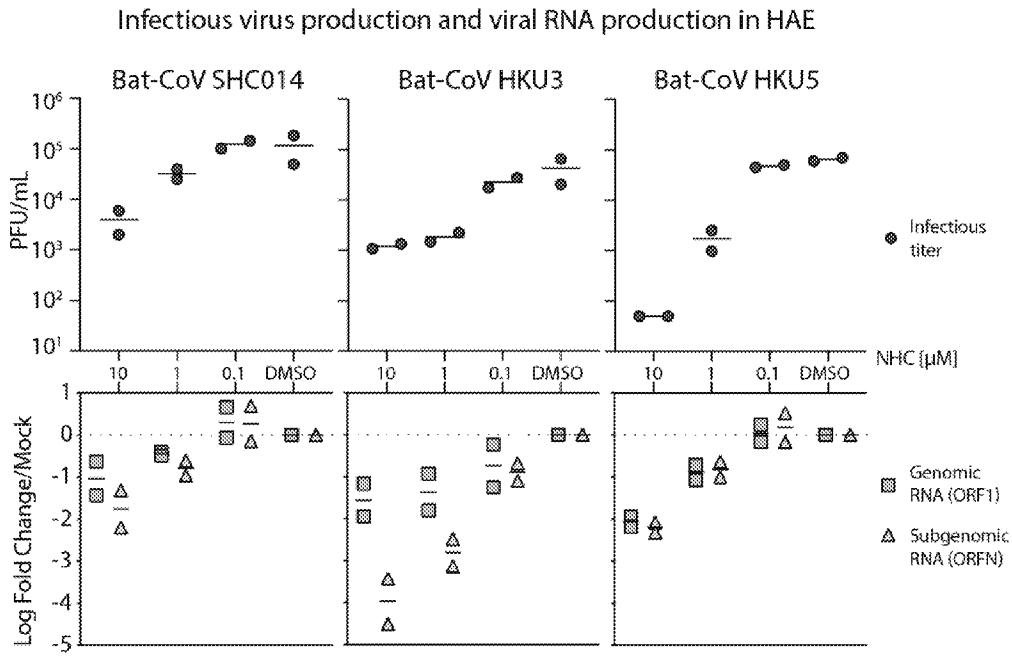

Fig. 4. NHC is effective against multiple genetically distinct Bat-CoV. Top: Antiviral efficacy of NHC in HAE cells against SARS-like (HKU3, SHC014, group 2b) and MERS-like (HKU5, group 2c) bat-CoV. HAE cells were infected at an MOI of 0.5 in the presence of NHC in duplicate. After 48 hours, virus produced was titrated via plaque assay. Each data point represents the titer per culture. Bottom: qRT-PCR for CoV ORF1 and ORFN mRNA in total RNA from cultures in the top panel. Mock, mock-treated. Representative data from two separate experiments with two different cell donors are displayed.

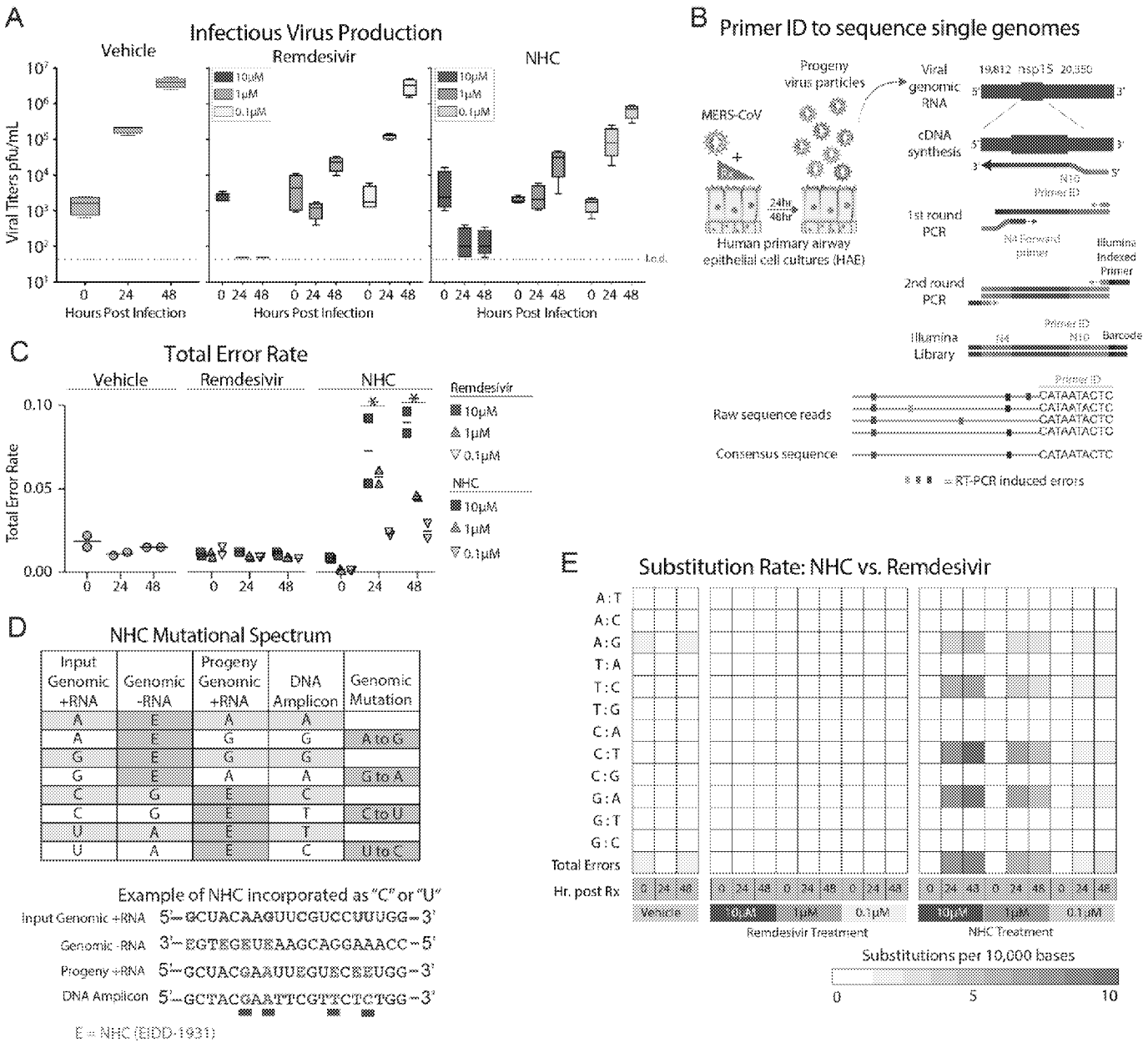

Fig. 5. NHC antiviral activity is associated with increased viral mutation rates. (**A**) HAE cultures were infected with MERS-CoV red fluorescent protein (RFP) at an MOI of 0.5 in duplicate in the presence of vehicle, RDV, or NHC for 48 hours, after which apical washes were collected for virus titration. Data are combined from two independent studies. The boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range. **(B)** Schematic of Primer ID deep sequencing for single RNA genomes of MERS-CoV. **(C)** The total error rate for MERS-CoV RNA isolated from cultures in panel **A** as determined by Primer ID. Error rate values are # mutations per 10,000 bases. Asterisks indicate significant differences as compared to untreated group by two-way ANOVA with a Dunnett's multiple comparison test. **(D)** Description of potential NHC mutational spectra on both positive and negative sense viral RNA. **(E)** Nucleotide transitions in cDNA derived from MERS-CoV genomic RNA.

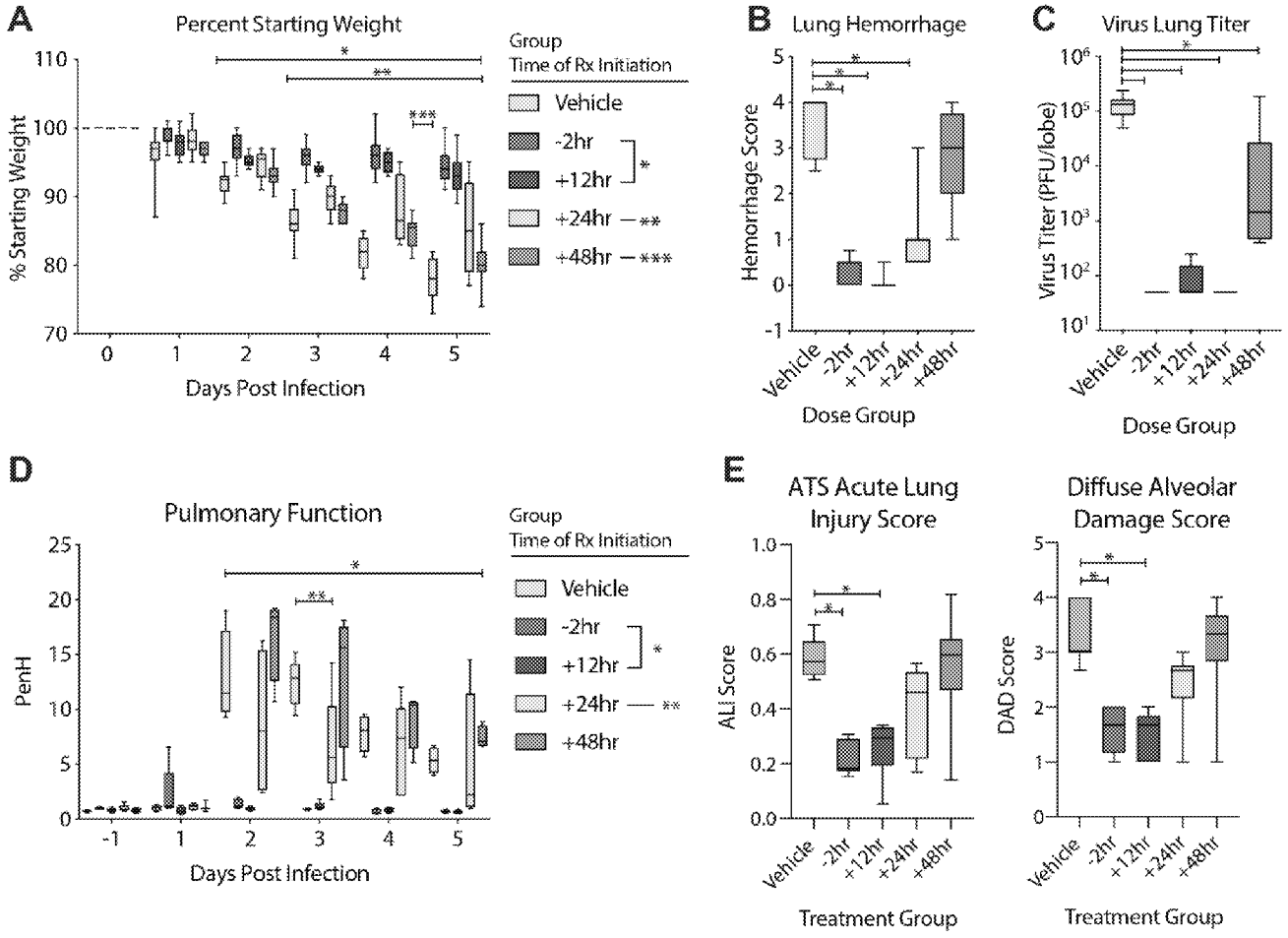

Fig. 6. Prophylactic and therapeutic EIDD-2801 reduces SARS-CoV replication and pathogenesis. Equivalent numbers of 25-29 week old male and female C57BL/6 mice were administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or NHC prodrug EIDD-2801 beginning at -2 hours, +12, +24 or +48 hours post infection and every 12 hours thereafter by oral gavage (n = 10/group). Mice were intranasally infected with 1E+04 PFU mouse-adapted SARS-CoV MA15 strain. **(A)** Percent starting weight. Asterisks indicate differences from vehicle treated by two-way ANOVA with Tukey's multiple comparison test. **(B)** Lung hemorrhage in mice from panel **A** scored on a scale of 0-4 where 0 is a normal pink healthy lung and 4 is a diffusely discolored dark red lung. **(C)** Virus lung titer in mice from panel **A** as determined by plaque assay. Asterisks in both panel **B** and **C** indicate differences from vehicle by one-way ANOVA with a Dunnett's multiple comparison test. **(D)** Pulmonary function by whole body plethysmography was performed daily on five animals per group. Asterisks indicate differences from vehicle by two-way ANOVA with a Dunnett's multiple comparison test. **(E)** The histological features of acute lung injury (ALI) were blindly scored using the American Thoracic Society Lung Injury Scoring system and a Diffuse Alveolar Damage Scoring System. Three randomly chosen high power (60X) fields of diseased lung were assessed per mouse. The numbers of mice scored per group: Vehicle N = 7, -2 hours N = 9, +12 hours N = 9, +24 hours N = 10, +48 hours N = 9. Asterisks indicate statistical significance compared to vehicle by Kruskal-Wallis with a Dunn's multiple comparison test. For all panels, the boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range. *, -2 hours and +12 hours compared to vehicle; **, +24 hours compared to vehicle; ***, +48 hours compared to vehicle.

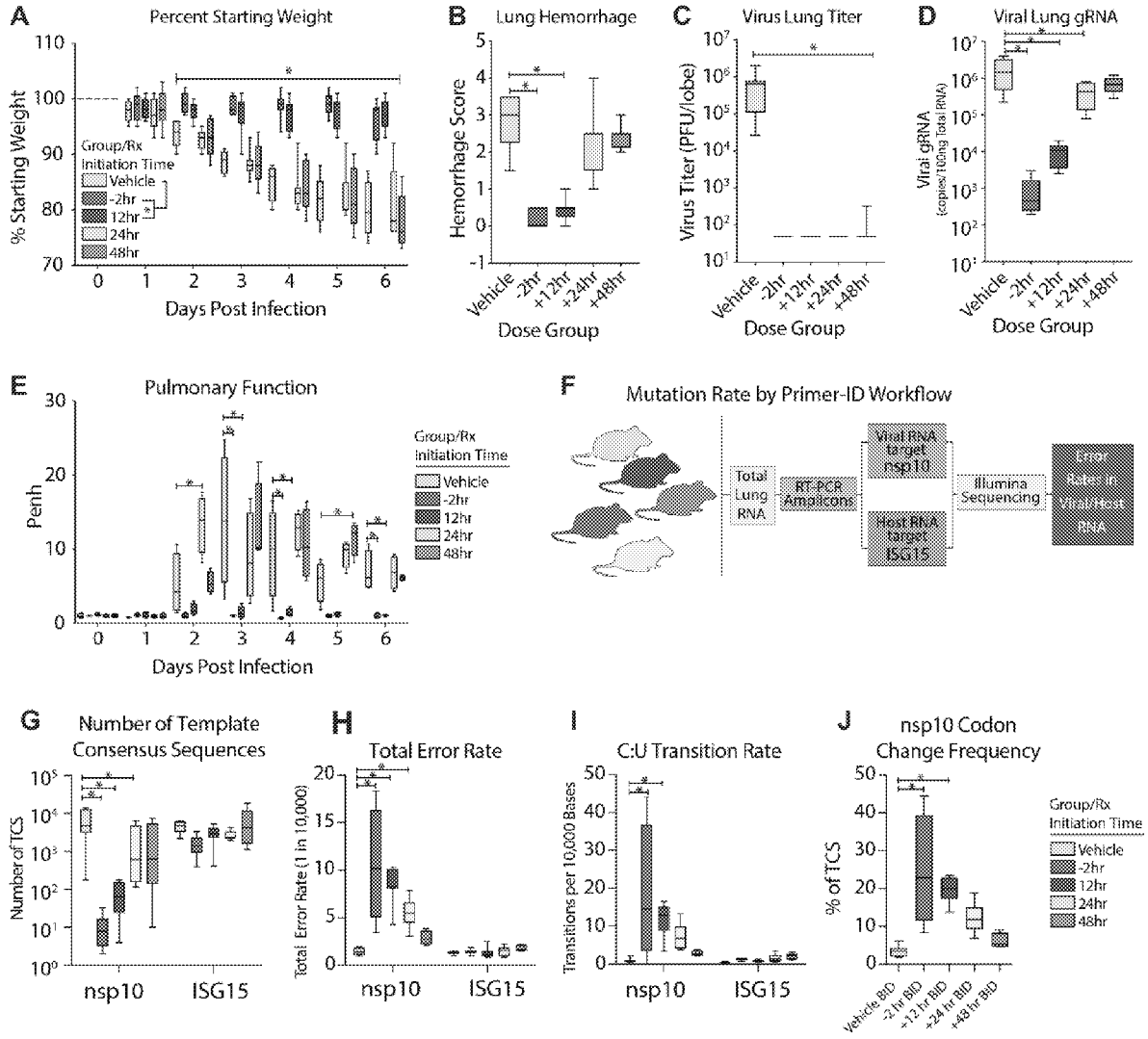

Fig. 7. Prophylactic and therapeutic EIDD-2801 reduces MERS-CoV replication and pathogenesis coincident with increased viral mutation rates. Equivalent numbers of 10-14 week old male and female C57BL/6 hDPP4 mice were administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or NHC prodrug EIDD-2801 beginning at -2 hours, +12, +24 or +48 hours post infection and every 12 hours thereafter by oral gavage (n = 10/group). Mice were intranasally infected with 5E+04 PFU mouse-adapted MERS-CoV M35C4 strain. (**A**) Percent starting weight. Asterisks indicate differences between -2 hours and +12 hours group from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**B**) Lung hemorrhage in mice from panel **A** scored on a scale of 0-4 where 0 is a normal pink healthy lung and 4 is a diffusely discolored dark red lung. (**C**) Virus lung titer in mice from panel **A** as determined by plaque assay. Asterisks in both panel **B** and **C** indicate differences from vehicle by Kruskal-Wallis with Dunn's multiple comparison test. (**D**) MERS-CoV genomic RNA in lung tissue by qRT-PCR. Asterisks indicate differences by one-way ANOVA with a Dunnett's multiple comparison test. (**E**) Pulmonary function by whole body plethysmography was performed daily on four animals per group. Asterisks indicate differences from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**F**) Workflow to measure mutation rate in MERS-CoV RNA and host transcript ISG15 by Primer ID in mouse lung tissue. (**G**) Number of template consensus sequences (TCS) for MERS-CoV nsp10 and ISG15. (**H**) Total error rate in MERS-CoV nsp10 and ISG15. (**I**) The cytosine to uridine transition rate in MERS-CoV nsp10 and ISG15. In panels **G-I,** asterisks indicate differences from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**J**) Codon change frequency in MERS-CoV nsp10. Asterisks indicate differences from vehicle by Kruskal-Wallis with Dunn's multiple comparison test. For all panels, the boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range.

From: Bård Erik Hansen [barderik1970@hotmail.no]
Sent: 3/10/2020 4:29:23 AM
To: wiv@wh.iov.cn; Menachery, Vineet [vimenach@UTMB.EDU]
Subject: Covid-19 and your research published in Nature 2015.

Did you do this?

https://www.nature.com/articles/nm.3985?fbclid=IwAR0_e9zAK67BfLNKPfrAPSDcbfp-E_RROtjFpSr2Yx7TbOGixx2k0RZ1WWc

This is an article with collaboration bethin Wuhan University and University of North Carolina at Chapel Hill,

Read the article. Did your virus get out of the lab?

From: Banu Guven [banuguv@gmail.com]
Sent: 3/22/2020 6:46:16 AM
To: Menachery, Vineet [vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com
Subject: Reg. your article from 2015 on "A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence"

Dear Dr. Menachery,

My name is Banu Güven and I am a journalist from Turkey, residing in Germany, working mainly for WDR Cosmo and DW Turkish and other online news media.

In Turkey, a doctor (oncologist) is using your article "A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence" from 2015 to suggest that COVID19 was man-made. His videos go viral, shared in WhatsApp groups etc. Please check 04'46"

https://www.instagram.com/tv/B-B_FwojLcz/?igshid=t1xm9m9rgd1w

Here he is showing the article and suggesting that the virus is man-made in cooperation with a biotech laboratory in Wuhan and academics in the USA and was leaked outside, accidentally or on purpose.

I am a journalist, and I understand what I read, but what I don't understand is, how he came to this conclusion.

In order to give an answer to people who are texting me, I would like to have your comment. I also think it is important for you to know, that your article is being shown as "evidence" to the thesis that the virus was man-made.

Although some of them may sound crazy, I have to ask you these questions:

Is the virus you have created with other co-scientists SARS Cov 2?

Your opinion on conspiracy theories on viruses and particularly SARS Cov 2?

What is your article from 2015 saying?

Have you foreseen this pandemic coming in 2015?

What could have been done since then to prevent it or cure the symptoms?

Your opinion on WHO's and govts' responses to combat SARS cov2?

Thank you and best regards,

Banu Güven
Journalist
+491722510888
Twitter: @banuguven

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][jjohnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]
From: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Sent: Tue 4/7/2020 8:06:51 AM (UTC-05:00)
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Erik

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CORONAVIRUS

An orally bioavailable broad-spectrum antiviral inhibits SARS-CoV-2 in human airway epithelial cell cultures and multiple coronaviruses in mice

Timothy P. Sheahan[1*†], Amy C. Sims[1$*], Shuntai Zhou[2], Rachel L. Graham[1], Andrea J. Pruijssers[3], Maria L. Agostini[3], Sarah R. Leist[1], Alexandra Schäfer[1], Kenneth H. Dinnon III[1,4], Laura J. Stevens[3], James D. Chappell[3], Xiaotao Lu[3], Tia M. Hughes[3], Amelia S. George[3], Collin S. Hill[2], Stephanie A. Montgomery[5], Ariane J. Brown[1], Gregory R. Bluemling[6,7], Michael G. Natchus[6], Manohar Saindane[6], Alexander A. Kolykhalov[6,7], George Painter[6,7,8], Jennifer Harcourt[9], Azaibi Tamin[9], Natalie J. Thornburg[9], Ronald Swanstrom[2,10], Mark R. Denison[3], Ralph S. Baric[1,4†]

[1]Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599, USA. [2]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599, USA. [3]Department of Pediatrics, Vanderbilt University Medical Center, Nashville, TN, TN, 37232,USA [4]Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, Chapel Hill, NC [5]Department of Pathology & Laboratory Medicine, University of North Carolina, Chapel Hill, NC, 27599, USA. [6]Emory Institute of Drug Development (EIDD), Emory University, Atlanta, GA, 30322, USA. [7]Drug Innovation Ventures at Emory (DRIVE), Atlanta, GA, 30322, USA. [8]Department of Pharmacology and Chemical Biology, Emory University, Atlanta, GA, 30322, USA. [9]Centers for Disease Control and Prevention, Division of Viral Diseases Atlanta GA [10]Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, Chapel Hill, NC

*Authors contributed equally.

$ Current address for A.C.S. is Chemical and Biological Signature Sciences, National Security Division, Pacific Northwest National Laboratory, Richland, WA 99352, USA.

†**Corresponding author. Email:** Timothy P. Sheahan sheahan@email.unc.edu and Ralph S. Baric rbaric@email.unc.edu

Coronaviruses (CoVs) traffic frequently between species resulting in novel disease outbreaks, most recently exemplified by the newly emerged SARS-CoV-2, the causative agent of COVID-19. Herein, we show that the ribonucleoside analog β-D-N^4-hydroxycytidine (NHC, EIDD-1931) has broad spectrum antiviral activity against SARS-CoV-2, MERS-CoV, SARS-CoV, and related zoonotic group 2b or 2c Bat-CoVs, as well as increased potency against a coronavirus bearing resistance mutations to the nucleoside analog inhibitor remdesivir. In mice infected with SARS-CoV or MERS-CoV, both prophylactic and therapeutic administration of EIDD-2801, an orally bioavailable NHC-prodrug (β-D-N^4-hydroxycytidine-5′-isopropyl ester), improved pulmonary function, and reduced virus titer and body weight loss. Decreased MERS-CoV yields in vitro and in vivo were associated with increased transition mutation frequency in viral but not host cell RNA, supporting a mechanism of lethal mutagenesis in CoV. The potency of NHC/EIDD-2801 against multiple coronaviruses and oral bioavailability highlight its potential utility as an effective antiviral against SARS-CoV-2 and other future zoonotic coronaviruses.

INTRODUCTION

The genetically diverse *Orthocoronavirinae* (coronavirus, CoV) family circulates in many avian and mammalian species. Phylogenetically, CoVs are divided into 4 genera: alpha (group 1), beta (group 2), gamma (group 3) and delta (group 4). Three new human CoV have emerged in the past 20 years with severe acute respiratory syndrome CoV (SARS-CoV) in 2002, Middle East respiratory syndrome CoV (MERS-CoV) in 2012, and now SARS-CoV-2 in 2019 (*1-3*). In fact, all human CoV are thought to have emerged originally as zoonoses (*4-6*). The ongoing SARS-CoV-2 pandemic (referred to as COVID-19, Coronavirus disease 2019) has caused over 500,000 infections and over 25,000 deaths in 199 countries. Like SARS- and MERS-CoV, the respiratory disease caused by SARS-CoV-2 can progress to acute lung injury (ALI), an end stage lung disease with limited treatment options and very poor prognoses(*3, 7, 8*). This emergence paradigm is not limited to humans. A novel group 1 CoV called swine acute diarrhea syndrome CoV (SADS-CoV) recently emerged from bats causing the loss of over 20,000 pigs in Guangdong Province, China (*9*). More alarmingly, many group 2 SARS-like and MERS-like coronaviruses are circulating in bat reservoir species that can use human receptors and replicate efficiently in primary human lung cells without adaptation(*9-12*). The presence of these "pre-epidemic" zoonotic strains foreshadow the emergence and epidemic potential of additional SARS-

like and MERS-like viruses in the future. Given the diversity of CoV strains in zoonotic reservoirs and a penchant for emergence, broadly active antivirals are clearly needed for rapid response to new CoV outbreaks in humans and domesticated animals.

Currently, there are no approved therapies specific for any human CoV. β-D-N4-hydroxycytidine (NHC, EIDD-1931) is orally bioavailable ribonucleoside analog with broad-spectrum antiviral activity against various unrelated RNA viruses including influenza, Ebola, CoV, and Venezuelan equine encephalitis virus (VEEV)(*13-16*). For VEEV, the mechanism of action (MOA) for NHC has been shown to be through lethal mutagenesis where deleterious transition mutations accumulate in viral RNA(*14, 17*). Thus, we sought to determine NHC's breadth of antiviral activity against multiple emerging CoV, its mechanism of action for CoV and its efficacy in mouse models of CoV pathogenesis.

RESULTS

NHC potently inhibits MERS-CoV and newly emerging SARS-CoV-2 replication

To determine whether NHC blocks the replication of highly pathogenic human CoV, we performed antiviral assays in cell lines with MERS-CoV and the newly emerging SARS-CoV-2. We first assessed the antiviral activity of NHC against MERS-CoV in the human lung epithelial cell line Calu-3 2B4 ("Calu3" cells). Using a recombinant MERS-CoV expressing nanoluciferase (MERS-nLUC)(*18*), we measured virus replication in cultures exposed to a dose range of drug for 48hr. NHC was potently antiviral with an average half-maximum effective concentration (IC_{50}) of 0.15 μM and no observed cytoxicity in similarly treated uninfected cultures across the dose range (50% cytotoxic concentration, CC_{50}, >10 μM) (Fig. 1A). The therapeutic index for NHC was >100. Using a clinical isolate of SARS-CoV2 (2019-nCoV/USA-WA1/2020), we performed antiviral assays in African green monkey kidney (Vero) cells and found NHC was potently antiviral with an IC_{50} of 0.3 μM and CC_{50} of >10 μM (Fig. 1B). We then determined the antiviral activity of NHC against SARS-CoV-2 in the Calu-3 cells through the measurement of infectious virus production and viral genomes. We observed a dose-dependent reduction in virus titers (Fig. 1C) with an IC_{50} of 0.08 μM. Viral genomic RNA was quantitated in clarified supernatants by qRT-PCR (Fig. 1D). Like the effect on infectious titers, we found a dose-dependent reduction in viral genomic RNA and a similar calculated IC_{50} of 0.09 μM. Collectively, these data demonstrate that NHC is potently antiviral against two genetically distinct emerging CoV.

NHC is highly active against SARS-CoV-2, MERS-CoV, and SARS-CoV in primary human airway epithelial cell cultures

To determine if NHC would be similarly antiviral in primary human cells, we performed a series of studies in primary airway epithelial (HAE) cell cultures. HAE model the architecture and cellular complexity of the conducting airway and are readily infected by multiple human and zoonotic CoV, including SARS- and MERS-CoV (*19*). We first assessed cytotoxicity of NHC in HAE treated with an extended dose range for 48hr using quantitative PCR of cell death-related gene transcripts as our metric. NHC treatment did not appreciably alter gene expression even at doses up to 100 μM (fig. S1). We then sought to determine if NHC would inhibit clinical isolate SARS-CoV-2 replication in HAE. We observed a dose dependent reduction in SARS-CoV-2 infectious virus production (Fig. 2A). In MERS-CoV infected HAE, NHC substantially reduced virus production with maximal titer reduction of > 5 logs at 10 μM (average IC_{50} = 0.024 μM), which correlated with reduced genomic (ORF1) and subgenomic (ORFN) RNA in paired samples (Fig. 2B). We observed similar trends in titer reduction (> 3 log at 10 μM, average IC_{50} = 0.14 μM) and in copies of genomic and subgenomic RNA in SARS-CoV- infected HAE (Fig. 2C). Thus, NHC was potently antiviral against SARS-CoV-2, MERS-CoV and SARS-CoV in primary human epithelial cell cultures without cytotoxicity.

NHC is effective against remdesivir (RDV)-resistant virus and multiple distinct zoonotic CoV

CoV are taxonomically divided into multiple genogroups (alpha, beta, gamma, delta) but human-infecting CoV are found in only the alpha and beta subgroups thus far (Fig. 3A). There is high sequence conservation in the RNA-dependent RNA polymerase (RdRp, nsp12) across CoV (Fig. 3A). For example, the RdRp of SARS-CoV-2 has 99.1% similarity and 96% amino acid identity to that of SARS-CoV (Fig. 3A). To gain insight into structural conservation of RdRp across the CoV family, we modeled the variation reflected in the RdRp dendrogram in Fig. 3A onto the structure of the SARS-CoV RdRp (*20*) (Fig. 3B). The core of the RdRp molecule and main structural motifs that all RdRp harbor (Fig. 3B and fig. S2) are highly conserved among CoV including SARS-CoV-2. We previously reported that CoV resistance to another broad spectrum nucleoside analog, RDV, was mediated by RdRp residues F480L and V557L in a model coronavirus mouse hepatitis virus (MHV) and in SARS-CoV, resulting in a 5-fold shift in IC_{50} (Fig. 3C)(*21*). Consequently, we tested whether RDV resistance mutations in MHV conferred cross-resistance to NHC. In fact, the two RDV resistance mutations, alone or together, conferred increased sensitivity to inhibition by NHC (Fig. 3D). As our previous studies have demonstrated a high genetic barrier to NHC for VEEV, influenza and CoV (*14-16*), the lack of cross-resistance further suggests that NHC and RDV may select for exclusive and mutually sensitizing resistance pathways.

To explore the breadth of antiviral efficacy against zoonotic CoV, we performed antiviral assays in HAE with three

zoonotic Bat-CoV: SHC014, HKU3, and HKU5. Closely related to the beta 2b SARS-CoV, Bat-CoV SHC014 is capable of replicating in human cells without adaptation(*11*), suggesting its potential for zoonotic emergence into humans. The more distantly related SARS-like beta 2b CoV, recombinant Bat-CoV HKU3, has a modified receptor binding domain to facilitate growth in cell culture (*22*). Lastly, Bat-CoV HKU5 is a MERS-like beta 2c CoV (*23*). NHC diminished infectious virus production and the levels of genomic/subgenomic viral RNA in HAE in a dose-dependent manner for all three Bat-CoVs (Fig. 4). Therefore, the antiviral activity of NHC was not limited by natural amino acid variation in the RdRp, which among the group 2b and group 2c CoV can vary by almost 20%. Moreover, these data suggest that if another SARS- or MERS-like virus were to spillover into humans in the future, they would likely be susceptible to the antiviral activity of NHC.

NHC antiviral activity is associated with increased viral mutation rates

It has recently been shown that NHC treatment increases the mutation rate in viral genomic RNA of RSV (*24*), VEEV (*14*), influenza (*24*), and our previous study used RNA seq to show that overall transition mutation frequency is increased during NHC treatment of MHV and MERS-CoV during infection in continuous cell lines(*16*). We sought to determine if NHC would increase the mutation frequency during MERS-CoV infection in human primary HAE. Using MERS-CoV-infected HAE treated with either vehicle or a dose range of NHC or RDV, we show that both drugs reduced virus titers in a dose-dependent manner (Fig. 5A). We then used a highly-sensitive high-fidelity deep sequencing approach (Primer ID NGS), which uses barcoded degenerate primers and Illumina indexed libraries to determine accurate mutation rates on viral RNA production (*25*). Using this approach, we analyzed a 538 bp region of viral genomic RNA in nonstructural protein 15 (nsp15). The error rates (#mutations/10,000 bases) in vehicle- (0.01) or RDV- (0.01) treated cultures were very low. RDV is reported to act via chain termination of nascent viral RNA, and thus the low error rates in RDV-treated cultures are in line with the proposed MOA (*26*). In contrast, the error rate was significantly increased in NHC-treated MERS-CoV RNA in a dose-dependent manner (Two-way ANOVA with Dunnett's multiple comparison test; 10-fold increase at 10 μM, $P < 0.0001$ at 24 and 48 hpi; 5-fold increase at 1μM, $P < 0.0001$ at 24 hpi and $P = 0.0015$ at 48 hpi) (Fig. 5C). The magnitude of the error rate in NHC-treated cultures correlated with virus titer reduction. At 48 hpi the respective error rate and virus titer was 0.015 and 3.96E+06 pfu/mL for vehicle treatment, 0.045 and 2.86E+04 pfu/mL with 1 μM NHC; and 0.090 and 1.5E+02 pfu/mL 10 μM NHC. Thus, with 1 μM NHC a 3-fold increase in error rate resulted in a 138-fold decrease in virus titer, while with 10 μM NHC a 6-fold increase in error rate resulted in a 26,000-fold decrease in virus titer.

We then examined the mutational spectra induced by NHC, which can be incorporated into viral RNA as a substitution for either cytosine (C) or uracil (U). RNA-mutagenic antivirals may incorporate in both nascent negative and positive sense RNA during genome replication (Fig. 5D). Adenine-to-guanine (A-to-G) and uracil-to-cytosine (U-to-C) transitions were enriched in MERS-CoV genomic RNA in an NHC dose-dependent manner (Fig. 5E). Collectively, these data used high-fidelity sequence analysis to demonstrate a specific enrichment for A:G and C:U transitions in MERS-CoV RNA after NHC treatment of primary HAE cell cultures.

Therapeutic EIDD-2801 reduces SARS-CoV replication and pathogenesis

Given the promising antiviral activity of NHC in vitro, we next evaluated its in vivo efficacy using EIDD-2801, an orally bioavailable prodrug of NHC (β-D-N^4-hydroxycytidine-5′-isopropyl ester), designed for improved in vivo pharmacokinetics and oral bioavailability in humans and non-human primates (*15*). Importantly, the plasma profiles of NHC and EIDD-2801 are similar in mice following oral delivery (*15*). We first performed a prophylactic dose escalation study in C57BL/6 mice where we orally administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or 50, 150, or 500 mg/kg EIDD-2801 2hr prior to intranasal infection with 5E+04 PFU of mouse-adapted SARS-CoV (SARS-MA15), and then vehicle or drug every 12 hours thereafter. Beginning on 3 days post-infection (dpi) and through the end of the study, body weight loss compared to vehicle treatment was significantly diminished (50 mg/kg) or prevented (150, 500 mg/kg) with EIDD-2801 prophylaxis (Two-way ANOVA with Dunnett's multiple comparison test, $P < 0.0001$) (fig. S3A). Lung hemorrhage was also significantly reduced 5 dpi with 500 mg/kg EIDD-2801 treatment (Kruskal-Wallis Test, $P = 0.010$, fig. S3B). Interestingly, there was a dose-dependent reduction in SARS-CoV lung titer (median titers: 50 mg/kg = 7E+03 pfu/mL, 150 mg/kg = 2.5E+03 pfu/mL, 500 mg/kg = 50 pfu/mL, vehicle = 6.5E+04 pfu/mL) with significant differences (Kruskal-Wallis with Dunn's multiple comparisons test) among the vehicle, 150 mg/kg ($P = 0.03$) and 500 mg/kg ($P = 0.006$) groups. Thus, prophylactic orally administered EIDD-2801 was robustly antiviral and able to prevent SARS-CoV replication and disease.

Since only the 500 mg/kg group significantly diminished weight loss, hemorrhage and reduced lung titer to near undetectable levels, we tested this dose under therapeutic treatment conditions to determine if EIDD-2801 could improve the outcomes of an ongoing CoV infection. As a control, we initiated oral vehicle or EIDD-2801 2 hours prior to infection with 1E+04 pfu SARS-MA15. For therapeutic conditions, we initiated EIDD-2801 treatment 12, 24, or 48 hours after infection. After initiating treatment, dosing for all groups was performed every 12 hours for the duration of the study. Both

prophylactic treatment initiated 2 hours prior to infection and therapeutic treatment initiated 12 hours after infection significantly (Two-way ANOVA with Tukey's multiple comparison test) prevented body weight loss following SARS-CoV infection on 2 dpi and thereafter (-2 hours: P = 0.0002 to <0.0001; +12 hours: P = 0.0289 to <0.0001) as compared to vehicle treated animals (Fig. 6A). Treatment initiated 24 hpi also significantly reduced body weight loss (3-5 dpi, P = 0.01 to <0.0001) although not to the same degree as the earlier treatment initiation groups. When initiated 48 hpi, body weight loss was only different from vehicle on 4 dpi (P = 0.037, Fig. 6A). Therapeutic EIDD-2801 significantly (Kruskal-Wallis with Dunnett's multiple comparison test) reduced lung hemorrhage when initiated up to 24 hours after infection (-2, +12, and +24 hours P < 0.0001) mirroring the body weight loss phenotypes (Fig. 6B). Interestingly, all EIDD-2801 treated mice had significantly (Kruskal-Wallis with Dunnett's multiple comparison test) reduced viral loads in the lungs even in the +48 hours group (All P < 0.0001, Fig. 6C), which experienced the least protection from body weight loss and lung hemorrhage. We also measured pulmonary function via whole body plethysmography (WBP). In Fig. 6D, we show the WBP enhanced pause (PenH) metric, which is a surrogate marker for bronchoconstriction or pulmonary obstruction (*27*), was significantly (Two-way ANOVA with Dunnett's multiple comparison test) improved throughout the course of the study if treatment was initiated up to 12 hours after infection (-2 hours: 2d pi to 5 dpi, P < 0.0001 to 0.019, +12 hours: 2 dpi to 5 dpi, P < 0.0001 to 0.0192) although the +24 hours group showed sporadic improvement as well (3 dpi P = 0.002) (Fig. 6D). Lastly, we blindly evaluated hematoxylin and eosin-stained lung tissue sections for histological features of ALI using two different and complementary scoring tools (*18*), which show that treatment initiated up to +12 hours significantly reduced ALI (Kruskal-Wallis with Dunn's multiple comparison test) (American Thoracic Society (ATS) Lung Injury Score: -2 hours P = 0.0004, +12 hours P = 0.0053, Diffuse alveolar damage (DAD) Score: -2 hours P = 0.0015, +12 hours P = 0.0004, Fig. 6E). Altogether, therapeutic EIDD-2801 was potently antiviral against SARS-CoV in vivo but the degree of clinical benefit was dependent on the time of initiation post-infection.

EIDD-2801 prophylactic and therapeutic efficacy correlates with increased MERS-CoV mutation rate

After obtaining promising in vivo efficacy data with SARS-CoV, we investigated whether EIDD-2801 would be effective against MERS-CoV. As the murine ortholog of the MERS-CoV receptor, dipeptidyl peptidase 4 (DPP4), does not support viral binding and entry, all in vivo studies were performed in genetically modified mice encoding a murine DPP4 receptor encoding two human residues at positions 288 and 330 (hDPP4 288/330 mice)(*18, 28*). Similar to our SARS-CoV data, all doses of prophylactic EIDD-2801 (50, 150 and 500 mg/kg) protected hDPP4 288/330 mice (fig. S4) from significant body weight loss (Two-way ANOVA with Dunnett's multiple comparison test, P = 0.03 to < 0.0001), lung hemorrhage (Kruskal-Wallis with Dunn's multiple comparison test, P = 0.01 to <0.0001), and virus replication which was undetectable (Kruskal-Wallis with Dunn's multiple comparison test, P < 0.0001) regardless of drug dose following intranasal infection with 5E+04 PFU mouse-adapted MERS-CoV (fig. S4).

We then evaluated the therapeutic efficacy EIDD-2801 following the promising results of our prophylactic studies. Similar to our SARS-CoV study, EIDD-2801 treatment administered before or 12 hours after intranasal mouse-adapted MERS-CoV infection (5E+04 PFU) prevented body weight loss from 2 through 6 dpi (Two-way ANOVA with Tukey's multiple comparison test, Fig. 7A, P = 0.02 to <0.0001) and lung hemorrhage on 6 dpi (Kruskal-Wallis with Dunn's multiple comparison test, P = 0.0004 to < 0.0001, Fig. 7B), but treatment initiated 24 or 48 hours did not offer similar protection. Unlike body weight loss and lung hemorrhage data which varied by treatment initiation time, virus lung titer on 6 dpi was significantly reduced to the limit of detection in all treatment groups (Kruskal-Wallis with Dunn's multiple comparison test, Fig. 7C, P < 0.0001). Interestingly, when viral genomic RNA was quantified in paired samples of lung tissue, EIDD-2801 significantly reduced quantities of viral RNA (One-way ANOVA with Dunnett's multiple comparison test, P <0.0001 to 0.017) in an initiation time-dependent manner for all groups except for +48 hours (Fig. 7D). The discrepancy among infectious titers and viral RNA suggests that accumulated mutations render the particles non-infectious and undetectable by plaque assay, consistent with the MOA. To gauge the effect of EIDD-2801 treatment on lung function, we assessed pulmonary function by WBP. Mirroring the body weight loss data, normal pulmonary function was only observed in groups where treatment was initiated prior to or 12 hours after infection (Two-way ANOVA with Tukey's multiple comparison test, -2hr: P < 0.0001 3 dpi, P = 0.0002 4 dpi, +12hr: P < 0.0001 3 dpi, P = 0.0008 4 dpi, Fig. 7E). Collectively, these data demonstrate that NHC prodrug, EIDD-2801, robustly reduces MERS-CoV infectious titers, viral RNA, and pathogenesis under both prophylactic and early therapeutic conditions.

To study the molecular mechanisms associated with drug performance in vivo, we investigated the correlation between infectious virus production and EIDD-2801-mediated mutagenesis of MERS-CoV RNA under therapeutic treatment conditions. Using Primer ID NGS, we measured the mutation rates of both viral genomic RNA (non-structural protein 10, nsp10) and host interferon stimulated gene 15 (*ISG15*) mRNA, a highly up-regulated innate immune-related gene after MERS-CoV infection (Fig. 7F). Primer ID NGS measures the

mutational frequency in single RNA molecules, each of which are represented by a single template consensus sequence (TCS) (*25*). Viral TCS were significantly reduced (Two-way ANOVA with Tukey's multiple comparison test, -2 hours P <0.0001, +12 hours P = 0.0001, +24 hours P = 0.02) in a treatment initiation time-dependent manner (Fig. 7G) similar to viral genomic RNA measured by qRT-PCR. In contrast, the numbers of ISG15 TCS were similar (P = 0.2 to 0.8) for all groups indicating that neither vehicle nor drug treatment significantly affected the levels of or mutated ISG15 mRNA transcripts (Fig. 7G). Similar to our TCS data in Fig. 6G, the total error rate in viral nsp10 was significantly increased (Two-way ANOVA with Tukey's multiple comparison test) in groups where treatment was initiated prior to (-2 hours, median error rate = 10.5 errors/10,000 bases, P < 0.0001) and up to 24 hours post infection (12 hours, median error rate = 8.2 errors/10,000 bases, P < 0.0001 ; +24 hours, median error rate = 5.4 errors/10,000 bases, P = 0.0003) but the error rates in ISG15 remained at baseline for all groups (Fig. 7H). In addition, nucleotide transitions observed in MERS-CoV genomes in vitro, were also observed in vivo in groups where treatment was initiated prior to and up to 12 hours post infection (Two-way ANOVA with Tukey's multiple comparison test, P = 0.0003 to < 0.0001) (Fig. 7I). Importantly, these transitions were not observed in host ISG15 mRNA (Fig. 7I). Lastly, the EIDD-2801 dose-dependent mutagenesis of viral RNA correlated with an increase in codon change frequency, including stop codons, in mice where treatment was initiated 12 hours or before (Two-way ANOVA with Tukey's multiple comparison test, vehicle median = 3.4; -2hr median = 22.8, P = 0.0035; +12 hours median = 20.0, P = 0.0004, Fig. 7J). Thus, approximately 20% of the mutations observed in the -2 hours and +12 hours groups resulted in a codon change and alteration of the nsp10 protein sequence. When extrapolating our results from nsp10 to the entirety of the 30kb MERS-CoV genome, EIDD-2801 likely causes between 15 (+24 hours treatment) and 30 (-2 hours treatment) mutations per genome, 10-20% of which result in amino acid coding changes. Altogether, our data demonstrates that EIDD-2801-driven mutagenesis correlates well with the reductions in viral load, strongly suggestive of an error catastrophe-driven mechanism of action under therapeutic conditions.

DISCUSSION

In the past 20 years, three novel human coronaviruses have emerged (*29, 30*). The group 2b SARS-like CoV represent an existential and future threat to global health as evidenced by the emergence of SARS-CoV and SARS-CoV-2. Zoonotic SARS-like bat CoV strains can use human angiotensin-converting enzyme 2 (ACE2) receptors, grow well in primary human airway cells, and vary by as much as 25% in key therapeutic and vaccine gene targets (*11, 31*). Thus, to address the current public health emergency of COVID-19 and to maximize pandemic preparedness in the future, broad-based vaccines and therapeutics, which are active against the higher risk RNA virus families prone to emergence, are desperately needed.

Small molecule antivirals can exert their antiviral effect through multiple mechanisms including blocking viral entry, inhibiting a virally encoded enzyme, blocking virus particle formation, or targeting a host factor required for replication (*32*). Multiple direct acting antivirals are currently under evaluation in randomized control trials to treat COVID-19 including hydroxychloroquine, remdesivir, lopinavir/ritonavir(*33-35*). Here, we report the broad-spectrum antiviral activity of NHC and its orally bioavailable prodrug EIDD-2801, against SARS-CoV, MERS-CoV, and the current pandemic strain SARS-CoV-2 in primary human airway epithelial cells. In addition to CoV, NHC is broadly active against multiple genetically distinct viruses including VEE, influenza A and B, Ebola, and Chikungunya viruses (*13-16, 19, 21, 24, 36-38*). Here, we show that prophylactic and therapeutic EIDD-2801 significantly reduced lung viral loads and improved pulmonary function in mouse models of both SARS- and MERS-CoV pathogenesis. Although the improvement in both SARS- and MERS-CoV outcomes diminished with the delay of treatment initiation time, it is important to note that the kinetics of disease in mice are compressed as compared to that in humans. Whereas SARS- and MERS-CoV lung titers peak on 1-2 dpi in mice concurrent with the onset of clinical signs and notable damage to the lung epithelium, in humans this occurs 7-10 days after the onset of symptoms (*19, 28, 39, 40*). Thus, in mice, the window within which to treat emerging CoV infection prior to peak replication is compressed (e.g., 24-48 hours). As with oseltamivir treatment for influenza which fails to provide a protective effect if administered >5 days after the onset of symptoms, the window in which to treat COVID-19 patients prior to peak virus replication is likely during the first week of symptoms when pharyngeal shedding is at its highest(*41, 42*). However, virus replication and shedding may continue for several weeks in the most severe COVID-19 patients(*34*). Thus, early intervention with an antiviral like EIDD-2801 is likely to provide the most clinical benefit although there may opportunities in severe patients where the duration of virus replication may be extended. Our current study is clearly limited by the lack of in vivo efficacy testing with SARS-CoV-2. Currently, robust mouse models that recapitulate the SARS-CoV-2 pathogenesis observed in humans do not yet exist due to a noted virus spike glycoprotein and mouse ACE2 receptor incompatibility complicating the evaluation of medical countermeasures(*43, 44*). In addition, SARS-CoV and MERS-CoV, SARS-CoV-2 disease severity increases with increasing age. Our studies are limited by the lack of drug efficacy testing in CoV aged mouse models that

recapitulate the age-related increase in pathogenesis observed in humans(*45*). The data provided in this manuscript suggest that EIDD-2801 should be quickly evaluated in primate models of human disease, using immediate models for MERS-CoV and SARS-CoV pathogenesis or newly described cynomolgus and rhesus macaque models for SARS-CoV-2 (*46-49*).

For VEE and influenza, NHC/EIDD-2801 exerts its antiviral activity on the RNA-dependent RNA polymerase leading to error catastrophe by inducing an error rate of replication that surpasses the error threshold allowed to sustain a virus population (*14, 15*). This process occurs when NHC is incorporated during RNA synthesis then subsequently misread thus increasing mutation rates. Therefore, for CoV, the NHC MOA would appear less likely to be affected by the RNA proofreading activity encoded by the nsp14 exonuclease function that otherwise limits misincorperation (*50*). Here, we present data using Primer ID NGS to quantitate the frequency and identity of the mutational spectra in the MERS-CoV genome in both drug-treated primary human airway cells and in mice at single genome resolution. As CoV are positive sense RNA viruses that replicate through a negative sense RNA intermediate, NHC incorporation as a C or a U can occur in both polarities of RNA. We found increased nucleotide transitions (A to G, G to A, C to U, U to C) consistent with those reported after influenza and VEE infections (*14, 15*). Under identical conditions, RDV did not alter the mutation rate in MERS-CoV genomic RNA, supporting its reported mechanism of action as a chain terminator of viral RNA synthesis (*26*). In primary human lung cell cultures and mice infected with MERS-CoV, the NHC mutation rates inversely correlated with a reduction in infectious virus. In addition, we found a positive correlation between increased mutation rates and the frequency of nonsynonymous mutations and the degree of therapeutic efficacy in mice. To explore the potential off-target effect in host mRNA which may contribute to drug toxicity, we also examined the impact of NHC treatment on *ISG15* transcripts, a gene highly induced following MERS-CoV infection. Although ISG15 transcripts are present in great abundance, an accumulation of mutations was not observed in *ISG15* in this model even at 500 mg/kg dosing. These data also support previous studies using RNAseq to demonstrate that the model coronavirus MHV displayed increased mutation frequencies following NHC treatment in vitro (*16*). With regard to nucleic acid specificity, ribonucleotides are efficiently removed from eukaryotic cell DNA; therefore, treating a viral infection with a mutagenic ribonucleoside analog should show a selectivity for incorporation into the viral genome and not be efficient at being incorporated into and inducing mutations into host cell DNA (*51*). All together, these data strongly support the notion that EIDD-2801 and its active nucleoside analog NHC exert their antiviral effect through the induction of error catastrophe in the targeted virus. While our data suggest that the MERS-CoV nsp14 proofreading activity appeared ineffective against NHC in vitro and EIDD-2801 in vivo, future studies should investigate the antiviral activity of NHC in the presence or absence of the nsp14 proofreading activity, as loss of this activity increased the sensitivity of MHV and SARS-CoV replication to RDV treatment (*50*).

Together, our data support the continued development of EIDD-2801 as a potent broad spectrum antiviral that could be useful in treating contemporary, newly emerged and emerging coronavirus infections of the future.

MATERIALS AND METHODS

Study Design

The primary goal of this study was to determine the antiviral activity of the nucleoside analog NHC (EIDD-1931) against multiple emerging CoV in vitro and antiviral efficacy of its prodrug, EIDD-2801, in mouse models of CoV pathogenesis. Coupling cell lines and primary HAE cell cultures, we evaluated the antiviral activity of NHC against the three most recently emerged human CoV: SARS-CoV, MERS-CoV, and SARS-CoV-2. For both SARS-CoV and MERS-CoV, the data presented for HAE studies are representative of those from 2-3 separate human donors. For SARS-CoV-2, the HAE were from a single human donor. We evaluated drug cytotoxicity in both Calu-3 2B4 and HAE cell cultures. Calu-3 and the SARS-CoV and MERS-CoV HAE studies were performed in biological triplicate. HAE studies with SARS-CoV-2 and the SARS- and MERS-like bat CoV were performed with two wells per condition. Drug effects were measured relative to vehicle controls in vitro and comparisons in vivo were performed to vehicle controls. We also aimed to determine the antiviral efficacy of EIDD-2801 in mouse models of CoV pathogenesis. These studies were intended to provide the preclinical data to justify nonhuman primate studies and human clinical trials. Mice were age- and sex-matched and randomly assigned into groups before infection and treatment. Pathology was scored blinded by a board-certified veterinary pathologist. Primary data for all studies are provided in data file S1.

Ethics regulation of laboratory animals

Efficacy studies were performed in animal biosafety level 3 facilities at UNC Chapel Hill. All work was conducted under protocols approved by the Institutional Animal Care and Use Committee at UNC Chapel Hill (IACUC protocol #16-284) according to guidelines set by the Association for the Assessment and Accreditation of Laboratory Animal Care and the U.S. Department of Agriculture.

Compounds

The parental compound β-D-N^4-hydroxycytidine (NHC, all in vitro studies) and its prodrug EIDD-2801 (all in vivo studies) was supplied by Emory University Institute for Drug

Discovery (EIDD). NHC was supplied as a 10 mM stock in DMSO and EIDD-2801 as a solid and solubilized in vehicle containing 10% PEG400, 2.5% Cremophor RH40 in water (10/2.5/87.5%, all v/v) prior to use. RDV was solubilized in 100% DMSO and provided by Gilead Sciences, Inc as previously described (*18, 19*).

Cell cultures

At UNC, the human lung epithelial cell line Calu-3 2B4 cells was maintained in Dulbecco's modified Eagle's medium (DMEM, Gibco), 20% fetal bovine serum (Hyclone) and 1x antibiotic/antimycotic (Gibco). At Vanderbilt University Medical Center (VUMC), Calu-3 2B4 were propagated in DMEM supplemented with 20% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). At VUMC, VeroE6 cells were cultured in DMEM supplemented with 10% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). At UNC, VeroE6 cells were cultured in DMEM supplemented with 10% Fetal Clone II (Hyclone) and 1x antibiotic/antimycotic (Gibco). Murine delayed brain tumor (DBT) cells were maintained in DMEM supplemented with 10% FBS (Gibco), 100 U/ml penicillin and streptomycin (Gibco), and 0.25 μM amphotericin B (Corning). Primary human airway epithelial (HAE) cell cultures were obtained from the Tissue Procurement and Cell Culture Core Laboratory in the Marsico Lung Institute/Cystic Fibrosis Research Center at UNC and are described more thoroughly below (*52*).

Virus strains

Except for SARS-CoV-2, all viruses used for these studies were derived from infectious clones and isolated as previously described (*53*). SARS-CoV-2 clinical isolate was obtained at VUMC and UNC from the CDC (2019-nCoV/USA-WA1/2020 strain, GenBank accession no. MN985325.1) and passaged twice in Vero E6 cells at each respective institution to create a passage 5 working stock (*54*). Virus strains for in vitro experiments include SARS-CoV expressing the green fluorescent protein (GFP) in place of open reading frames 7a/b (ORF7a/b, SARS-GFP)(*53*), bat-spike receptor binding domain (Bat-SRBD)(*22*), a chimeric CoV strain derived from the HKU3 SARS-like bat coronavirus genomic sequence that has the wild type (Urbani SARS-CoV strain) RBD in the HKU3 spike gene to allow for virus replication in non-human primate cell lines and HAE cultures, SHC014 SARS-like bat coronavirus (*11*), MERS-CoV expressing nanoluciferase in the place of ORF3 (MERS-nLUC)(*19*), and MERS-CoV expressing the red fluorescent protein gene in the place of ORF 5 (RFP, MERS-RFP)(*55*). The virus stock utilized for MERS-CoV in vivo studies was derived from a plaque-purified isolate of the mouse-adapted MERS-CoV p35C4 strain (*56*). The virus stock utilized for SARS-CoV in vivo studies was derived from the infectious clone of the mouse-adapted SARS-CoV MA15 (MA15) strain (*57*). All work with MHV was performed using the recombinant WT strain MHV-A59 (GenBank accession no. AY910861)(*58*).

In vitro antiviral activity experiments

MERS-CoV nLUC in Calu-3: At 48 hours prior to infection, Calu-3 2B4 cells were plated in a 96-well black-walled clear bottom plate at $5x10^4$ cells/well. A 10 mM stock of NHC was serially diluted in 100% DMSO in 3-fold increments to obtain a ten-point dilution series. MERS-nLUC was diluted in DMEM supplemented with 10% FBS, and 1% Antibiotic-Antimycotic to achieve a multiplicity of infection (MOI) of 0.08. Cells were infected and concurrently treated with NHC in triplicate per drug dilution for 1hr, after which viral inoculum was aspirated, cultures were rinsed once and fresh medium containing drug or vehicle was added. At 48 hours post infection, nanoluciferase expression as a surrogate for virus replication was quantitated on a Spectramax plate reader (Molecular Devices) according to the manufacturer's instructions (Promega, NanoGlo). For the 100% inhibition control, diluted MERS-nLUC was exposed to short-wave UV light (UVP, LLC) for 6 min to inhibit the ability of the virus to replicate. For the 0% inhibition control, cells were infected in the presence of vehicle only. DMSO was kept constant in all conditions at 0.05%. Values from triplicate wells per condition were averaged and compared to controls to generate a percent inhibition value for each drug dilution. The IC_{50} value was defined as the concentration at which there was a 50% decrease in luciferase expression. Data were analyzed using GraphPad Prism 8.0. The IC_{50} values were calculated by nonlinear regression analysis using the dose-response (variable slope) equation (four parameter logistic equation): Y = Bottom + (Top-Bottom)/(1+10^((LogIC50-X)*HillSlope)). To measure cell viability to determine if there was any NHC-induced cytotoxicity, Calu-3 2B4 cells were plated and treated with NHC only as described above. Cells were exposed to the same ten-point dilution series created for the in vitro efficacy studies. As above, 0.05% DMSO-treated cells served as the 0% cytotoxicity control. Wells without cells served as the 100% cytotoxic positive control. After 48 hours, cell viability was measured on a Spectramax (Molecular Devices) via Cell-Titer Glo Assay (Promega) according to the manufacturer's protocol. Similar data were obtained in three independent experiments.

SARS-CoV-2 in Calu-3: Calu-3 2B4 cells were adsorbed with MOI 0.1 PFU/cell of SARS-CoV-2 (2019-nCoV/USA-WA1/2020 strain) at 37°C. Plates were manually rocked every 10 min to redistribute the inoculum. After 30 min, virus inoculum was removed, cells were washed with Phosphate buffered saline (PBS) once to remove unbound virus, medium containing NHC or vehicle control (DMSO) was added back onto the cells, and cells were incubated for 72 hours at 37°C.

SARS-CoV-2 in Vero E6: Vero E6 cells were plated at 20,000 cells/well in a 96-well plate. 24hr later, medium

containing a dose response of NHC was added concurrent with SARS-CoV-2 (2019-nCoV/USA-WA1/2020 strain) at an MOI of 0.05. 48 hours post infection, cell viability was measured by CellTiter Glo assay.

SARS-CoV, MERS-CoV, and SARS-CoV-2 in HAE: Human tracheobronchial epithelial cells provided by Dr. Scott Randell were obtained from airway specimens resected from patients undergoing surgery under University of North Carolina Institutional Review Board-approved protocols (#03-1396) by the Cystic Fibrosis Center Tissue Culture Core. Primary cells were expanded to generate passage 1 cells and passage 2 cells were plated at a density of 250,000 cells per well on Transwell-COL (12mm diameter) supports (Corning). Human airway epithelium cultures (HAE) were generated by provision of an air-liquid interface for 6 to 8 weeks to form well-differentiated, polarized cultures that resembled in vivo pseudostratified mucociliary epithelium (*59*).· At 48 hours prior to infection the apical surface of the culture was washed with 500 μL PBS for 1.5 hours at 37°C and the cultures moved into fresh air liquid interface (ALI) media. Immediately prior to infection, apical surfaces were washed twice to remove accumulated mucus with 500 μL of PBS with each wash lasting 30 min at 37°C and HAE cultures were moved into ALI media containing various concentrations of NHC ranging from 10 μM to 0.0016 μM as indicated for each experiment (final % DMSO < 0.05%). Upon removing the second PBS wash, 200 μL of viral inoculum (SARS-GFP, MERS-RFP or 2019-nCoV/USA-WA1/2020 strain) at an MOI of 0.5 was added to the apical surface and HAE cultures were incubated for 2 hours at 37°C. Viral inoculum was then removed, and the apical surface of the cultures were washed three times with 500μL PBS and then incubated at 37°C until 48 hours post infection (hpi). For all HAE cultures, infectious virus produced was collected by washing the apical surface of the culture with 100 μL PBS. Apical washes were stored at -80°C until analysis and titered by plaque assay as previously described (*19*).

qRT-PCR approach to assess cytotoxicity

Total RNA was isolated using the Zymo Direct-zol RNA MiniPrep Kit (Zymo Research Corp.) according to the manufacturer's directions. Cells were treated with 1μM staurosporine (Sigma-Aldrich) as a positive control. First-strand cDNA was generated using Superscript III reverse transcriptase (Life Technologies). For quantification of cellular markers of toxicity/apoptosis, real-time PCR was performed using commercially validated TaqMan-based primer-probe sets (**table S1**) and TaqMan Universal PCR Mix (Life Technologies). Results were then normalized as described above.

MERS-CoV genomic RNA qRT-PCR

Mouse lungs were stored in RNAlater (ThermoFisher) at -80°C until processed via homogenization in TRIzol (Invitrogen). Total RNA was isolated using Direct-zol RNA MiniPrep kit (Zymo Research). Previously published TaqMan primers were synthesized by Integrated DNA Technologies (IDT) to quantify MERS genomic RNA (targeting orf1a: Forward: 5′-GCACATCTGTGGTTCTCCTCTCT-3′, Probe (6-FAM/ZEN/IBFQ): 5′- TGCTCCAACAGTTACAC-3′, Reverse: 5′-AAGCCCAGGCCCTACTATTAGC)(*60*). qRT-PCR was performed using 100ng total RNA compared to an RNA standard curve using TaqMan Fast Virus 1-Step Master Mix (ThermoFisher) on a Quant Studio 3 (Applied Biosystems).

Quantification of SARS-CoV-2 viral RNA genome copy number by qRT-PCR

Cell supernatants were harvested in TRIzol LS reagent (Invitrogen), and RNA was purified following phase separation by chloroform as recommended by the manufacturer. The RNA in the aqueous phase was collected and further purified using PureLink RNA Mini Kits (Invitrogen) according to the manufacturer's protocol. Viral RNA was quantified using one-step quantitative reverse transcription PCR (qRT-PCR) on a StepOnePlus Real-Time PCR system (Applied Biosystems) by TaqMan Fast Virus 1-Step Master Mix chemistry (Applied Biosystems). SARS-CoV-2 N gene RNA was amplified using forward (5′-GACCCCAAAATCAGCGAAAT) and reverse (5′-TCTGGTTACTGCCAGTTGAATCTG) primers and probe (5′-FAM-ACCCCGCATTACGTTTGGTGGACC-BHQ1) designed by the United States Centers for Disease Control and Prevention (oligonucleotides produced by IDT, cat# 10006606). Copy numbers were interpolated from a standard curve produced with dilutions of N gene RNA. Briefly, SARS-CoV-2-N positive control plasmid DNA (IDT, cat# 10006625) was amplified using forward (5′-TAATACGACTCACTATAGGGATGTCTGATAATGGACCCCA) and reverse (5′- TTAGGCCTGAGTTGAGTCAG) primers, resulting in a 1280 nucleotide fragment containing a T7 promoter. The PCR product was purified by column (Promega) and in vitro transcribed using the mMESSAGE mMACHINE T7 Transcription Kit (Invitrogen) according to the manufacturer's protocol. Transcribed RNA was purified using RNeasy mini kit (Qiagen) according to the manufacturer's protocol, and serial 10-fold dilutions were quantified as described above.

Primer ID and deep sequencing

Primer ID NGS is designed to specifically identify and remove RT-PCR mutations, while facilitating highly accurate sequence determination of single RNA molecules, because each cDNA is created with a barcoded degenerate primer (N10, 4^{10} combinations) from which Illumina indexed libraries are made. We used a multiplexed Primer ID library prep approach and MiSeq sequencing to investigate the presence of mutations in the viral genomes and murine mRNA. We designed cDNA primers targeting multiple regions on the viral genome and murine mRNA, each with a block of random

nucleotides (11 bp long) as the Primer ID (*25, 61*) (**table S2**). Viral RNA was extracted using QIAamp viral RNA kit. A pre-amplification titration of templates was performed to estimate the amount of template to use. We used SuperScript III to make cDNA with multiplexed cDNA primers based on the regions to be sequenced. We used 41R_PID11 for the pilot sequencing and titration determination. For the MERS-CoV sequencing, we multiplexed nsp10_PID11, nsp12_PID11 and nsp14_PID11 for the cDNA reaction; for the murine mRNA sequencing, we used mixed primers of nsp10_PID11, ifit3_PID11, isg15_PID11. After bead purification, we amplified the cDNA with a mixture of forward primers (based on the described schemes) and a universal reverse primer, followed by another round of PCR to incorporate Illumina sequencing adaptors and barcodes in the amplicons. After gel-purification and quantification, we pooled 24 libraries for MiSeq 300 base paired-end sequencing. The TCS pipeline version 1.38 (https://github.com/SwanstromLab/PID) was used to process the Primer ID sequencing data and construct template consensus sequences (TCSs) to represent each individual input templates, and the sequences of each region in the pool was de-multiplexed. The RUBY package viral_seq version 1.0.6 (https://rubygems.org/gems/viral_seq) was used to calculate the mutation rate at each position. NCBI SRA Accession numbers for sequence data are as follows: PRJNA613261 (Fig. 5) and PRJNA613454 (Fig. 7).

In vivo experiments

We performed 4 mouse studies to evaluate the in vivo efficacy of the NHC prodrug (EIDD-2801). First, we performed prophylactic dose escalation studies for both SARS- and MERS-CoV to determine the most efficacious dose of EIDD-2801 per virus. For SARS-CoV, in cohorts of equivalent numbers of male and female 20-29 week old SPF C57BL/6J (Stock 000664 Jackson Labs) mice (n = 10/dose group), we administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or 50, 150 or 500 mg/kg EIDD-2801 by oral gavage 2 hours prior to intranasal infection with 1E+04 PFU mouse-adapted SARS-CoV strain MA15 in 50μl. Mice were anaesthetized with a mixture of ketamine/xylazine prior to intranasal infection. Vehicle or drug was administered every 12hr for the remainder of the study. Body weight and pulmonary function by whole body plethysmography were measured daily. On 5 dpi, animals were sacrificed by isoflurane overdose, lungs were scored for lung hemorrhage, and the inferior right lobe was frozen at −80°C for viral titration via plaque assay. Briefly, 500,000 Vero E6 cells/well were seeded in 6-well plates. The following day, medium was removed and serial dilutions of clarified lung homogenate were added per plate (10^{-1} to 10^{-6} dilutions) and incubated at 37°C for 1hr after which wells were overlaid with 1X DMEM, 5% Fetal Clone 2 serum, 1X antibiotic/antimycotic, 0.8% agarose. Two days after, plaques were enumerated to generate a plaque/ml value. Lung hemorrhage is a gross pathological phenotype readily observed by the naked eye driven by the degree of virus replication where the coloration of the lung changes from pink to dark red (*62, 63*). The large left lobe was placed in 10% buffered formalin and stored at 4°C for 1-3 weeks until histological sectioning and analysis. For MERS-CoV, the prophylactic dose escalation studies we performed similarly as done for SARS-CoV with our recently developed a mouse model for MERS-CoV, which has a humanized DPP4 receptor (hDPP4) (*28*). We performed all in vivo studies with EIDD-2801 in equivalent numbers of 10-14 week old female and male C57BL/6J hDPP4 mice. Second, we intranasally infected mice with 5E+04 PFU mouse-adapted MERS-CoV strain M35C4 in 50μl. Third, to titer lungs by plaque assay, Vero CCL81 cells were used and plaques were enumerated 3 dpi.

To determine the time at which therapeutic administration of EIDD-2801 would fail to improve outcomes with SARS-CoV or MERS-CoV infection, we performed therapeutic efficacy studies in mice where we initiated treatment 2 hours prior to infection or 12, 24 or 48 hours after infection. As 500 mg/kg provided the most complete protection from disease in prophylactic SARS-CoV studies, this dose was used for both therapeutic efficacy studies. Vehicle or EIDD-2801 was given via oral gavage twice daily following initiation of treatment. For both SARS-CoV and MERS-CoV, the infectious dose for the therapeutic studies and the mouse strains were the same as that used in the prophylactic studies. The numbers of mice per group for the SARS-CoV studies were as follows: Vehicle (n = 10), -2 hours (n = 10), +12 hours (n = 10), +24 hours (n = 10), +48 hours (n = 10). The numbers of mice per group for the MERS-CoV therapeutic studies were as follows: Vehicle (n = 9), -2 hours (n = 9), +12 hours (n = 9), +24 hours (n = 7), +48 hours (n = 10). As described above, each day mouse body weight and pulmonary function were quantitated. On 5 dpi for SARS-CoV and 6 dpi for MERS-CoV, animals were humanely sacrificed and tissues were harvested and analyzed as described above. In addition, for the MERS-CoV study, lung tissue was harvested and stored in RNAlater (Thermo Fisher) at -80°C and then thawed, homogenized in Trizol reagent (Invitrogen) and total RNA was isolated using a Direct-zol RNA MiniPrep kit (Zymo Research). This total RNA was then used for Primer ID and qRT-PCR.

Whole body plethysmography

Pulmonary function was monitored once daily via whole-body plethysmography (Buxco Respiratory Solutions, DSI Inc.). Mice intended for this analysis were randomly chosen prior to the initiation of the study. Briefly, after a 30-min acclimation time in the plethysmograph, data for 11 parameters was recorded every 2 s for 5 min.

Acute lung injury histological assessment tools

Two different and complementary quantitative histologic tools were used to determine if antiviral treatments

diminished the histopathologic features associated with lung injury. Both analyses and scoring were performed by a Board Certified Veterinary Pathologist who was blinded to the treatment groups.

American Thoracic Society lung injury scoring tool. In order to help quantitate histological features of ALI observed in mouse models and increase their translation to the human condition, we used the ATS scoring tool (*63*). In a blinded manner, we chose three random diseased fields of lung tissue at high power (60 ×), which were scored for the following: (A) neutrophils in the alveolar space (none = 0, 1–5 cells = 1, > 5 cells = 2), (B) neutrophils in the interstitial space/ septae (none = 0, 1–5 cells = 1, > 5 cells = 2), (C) hyaline membranes (none = 0, one membrane = 1, > 1 membrane = 2), (D) Proteinaceous debris in air spaces (none = 0, one instance = 1, > 1 instance = 2), (E) alveolar septal thickening (< 2× mock thickness = 0, 2–4× mock thickness = 1, > 4× mock thickness = 2). To obtain a lung injury score per field, the scores for A–E were then put into the following formula, which contains multipliers that assign varying levels of importance for each phenotype of the disease state.: score = [(20x A) + (14 x B) + (7 x C) + (7 x D) + (2 x E)]/100. The scores for the three fields per mouse were averaged to obtain a final score ranging from 0 to and including 1.

Diffuse Alveolar Damage (DAD) tool. The second histological tool to quantitate lung injury was reported by Schmidt *et al.*(*64*). DAD is the pathological hallmark of ALI (*63, 64*). Three random diseased fields of lung tissue were scored at high power (60 ×) for the following in a blinded manner: 1 = absence of cellular sloughing and necrosis, 2 = Uncommon solitary cell sloughing and necrosis (1–2 foci/field), 3 = multifocal (3 + foci) cellular sloughing and necrosis with uncommon septal wall hyalinization, or 4 = multifocal (>75% of field) cellular sloughing and necrosis with common and/or prominent hyaline membranes. The scores for the three fields per mouse were averaged to get a final DAD score per mouse.

nsp12 phylogenetic analysis and conservation modeling

Coronavirus RdRp (nsp12) protein sequence alignments and phylogenetic trees were generated using Geneious Tree Builder in Geneious Prime (version 2020.0.5) and visualized using Evolview (https://www.evolgenius.info/evolview/). Protein similarity scores were calculated using Blosom62 matrix. The accession numbers used were: PDCoV (KR265858), AIBV (NC_001451), HCoV-229E (JX503060), PEDV (NC_003436), MHV (AY700211), HCoV-HKU1 (DQ415904), HCoV-NL63 (JX504050), HCOV-OC43 (AY903460), HKU5-1 (NC_009020), MERS-CoV (JX869059), HKU9-4 (EF065516), 2019-nCoV (MN996528), HKU3-1 (DQ022305), SHC014 (KC881005), WIV1 (KF367457), SARS-CoV (AY278741). Amino acid conservation scores of coronavirus RdRp were generated using ConSurf Server (https://consurf.tau.ac.il/) using the protein alignment described above and visualized on the SARS-CoV RdRp structure (PDB: 6NUR) in PyMol (version 1.8.6.0)(*20, 65*).

Statistical analysis

All statistical data analyses were performed in Graphpad Prism 8. Statistical significance for each endpoint was determined with specific statistical tests. In general, for metrics with multiple treatment groups with longitudinal data (e.g., mouse weight loss or pulmonary function over time), two-way ANOVA was performed with the suggested multiple comparison test as advised by Prism. For comparative data with for a single timepoint (e.g., lung titer) Kruskal-Wallis or one-way ANOVA was performed with the suggested multiple comparison test. For each test, a p-value <0.05 was considered significant. Specific tests are noted in each figure legend.

SUPPLEMENTARY MATERIALS

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Supplementary Figure 1. Assessment of cytotoxicity of NHC in primary human epithelial cell cultures by qRT-PCR.

Supplementary Figure 2. High conservation of RdRp functional domains for SARS-CoV-2.

Supplementary Figure 3. Prophylactic EIDD-2801 reduces SARS-CoV replication and pathogenesis.

Supplementary Figure 4. Prophylactic EIDD-2801 reduces MERS-CoV replication and pathogenesis.

Supplementary Table 1. Real-time PCR primer/probe sets for indicators of cellular apoptosis/toxicity.

Supplementary Table 2. Primers used for MiSeq library prep and sequencing.

Data file S1. Primary data.

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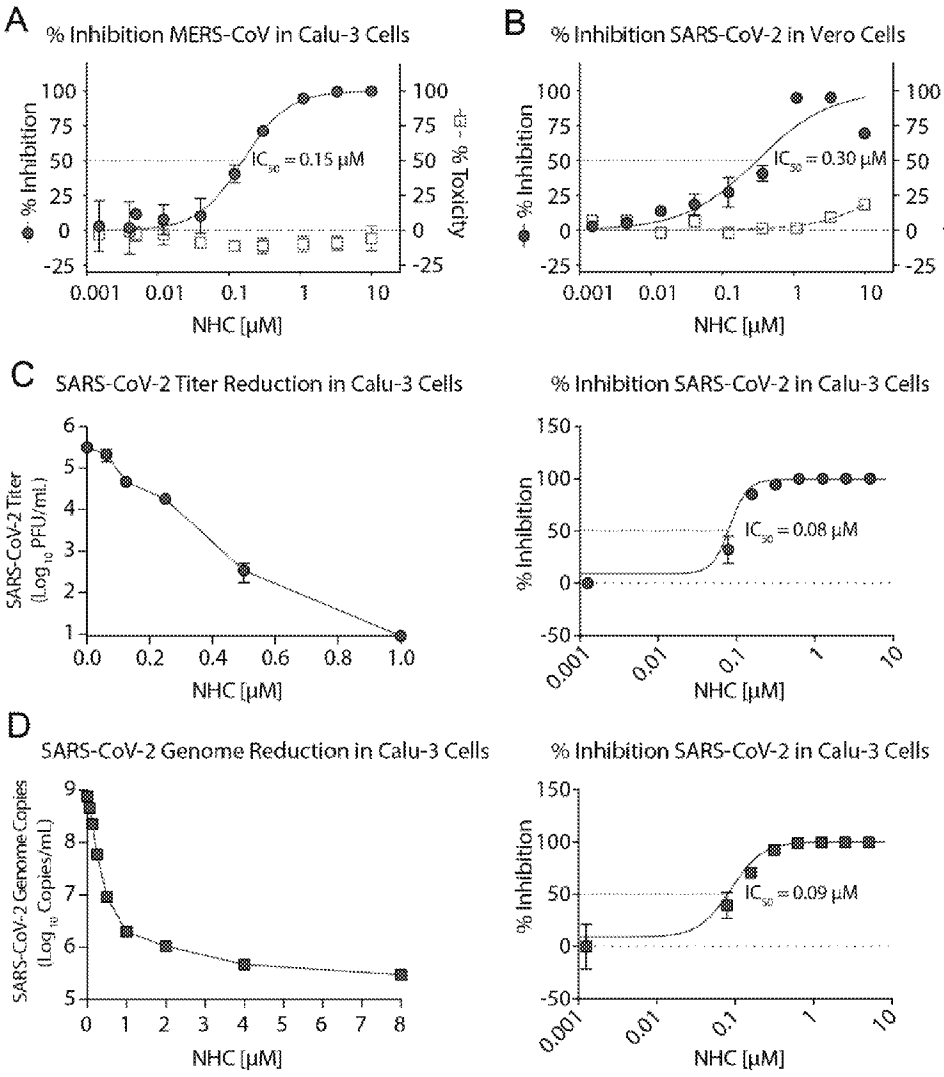

Fig. 1. NHC potently inhibits MERS-CoV and newly emerging SARS-CoV-2 replication. (A) Percent inhibition of MERS-CoV replication and NHC cytotoxicity in Calu-3 cells. Calu-3 cells were infected in triplicate with MERS-CoV nanoluciferase (nLUC) at a multiplicity of infection (MOI) of 0.08 in the presence of a range of drug for 48 hours, after which replication was measured through quantitation of MERS-CoV–expressed nLUC. Cytotoxicity was measured in similarly treated but uninfected cultures via Cell-Titer-Glo assay. Data are combined from 3 independent experiments. **(B)** NHC antiviral activity and cytotoxicity in Vero E6 cells infected with SARS-CoV-2. Vero E6 cells were infected in duplicate with SARS-CoV-2 clinical isolate 2019-nCoV/USA-WA1/2020 virus at an MOI of 0.05 in the presence of a range of drug for 48 hours, after which replication was measured through quantitation of cell viability by Cell-Titer-Glo assay. Cytotoxicity was measured as in **A**. Data are combined from 2 independent experiments. **(C)** SARS-CoV-2 titer reduction (left) and percent inhibition (right) in Calu-3 cells. Cells were infected with at an MOI of 0.1 for 30 min, washed and exposed to a dose response of NHC in triplicate per condition. 72 hours post infection, virus production was measured by plaque assay. **(D)** SARS-CoV-2 genomic RNA reduction (left) and percent inhibition (right) in Calu-3 cells. Viral RNA was isolated from clarified supernatants from the study in panel **C**. Genome copy numbers were quantitated by qRT-PCR with primer/probes targeting the N gene. For **A-D**, the symbol is at the mean and the error bars represent the standard deviation.

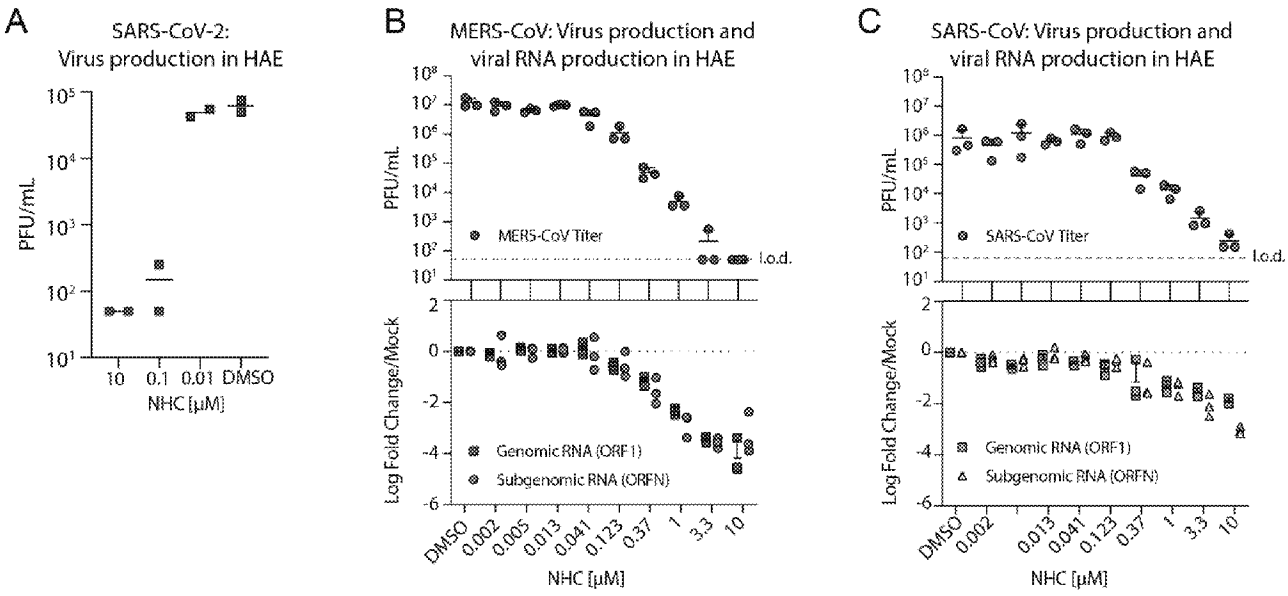

Fig. 2. NHC is highly active against SARS-CoV-2, MERS-CoV, and SARS-CoV in primary human airway epithelial cell cultures. (A) HAE were infected at an MOI of 0.5 with clinical isolate SARS-CoV-2 for 2 hours in the presence of NHC in duplicate after which virus was removed and cultures were washed in incubated in NHC for 48 hours when apical washes were collected for virus titration by plaque assay. The line is at the mean. Each symbol represents the titer from a single well. **(B)** HAE cells were infected with MERS-CoV red fluorescent protein (RFP) at an MOI of 0.5 in triplicate and treated similarly to **A**. qRT-PCR for MERS-CoV ORF1 and ORFN mRNA. Total RNA was isolated from cultures in **C** for qRT-PCR analysis. Representative data from three separate experiments with three different cell donors are displayed. PFU, plaque-forming units. **(C)** Studies performed as in **A** but with SARS-CoV green fluorescent protein (GFP). Representative data from two separate experiments with two different cell donors are displayed. Each symbol represents the data from one HAE culture, the line is at the mean and the error bars represent the standard deviation.

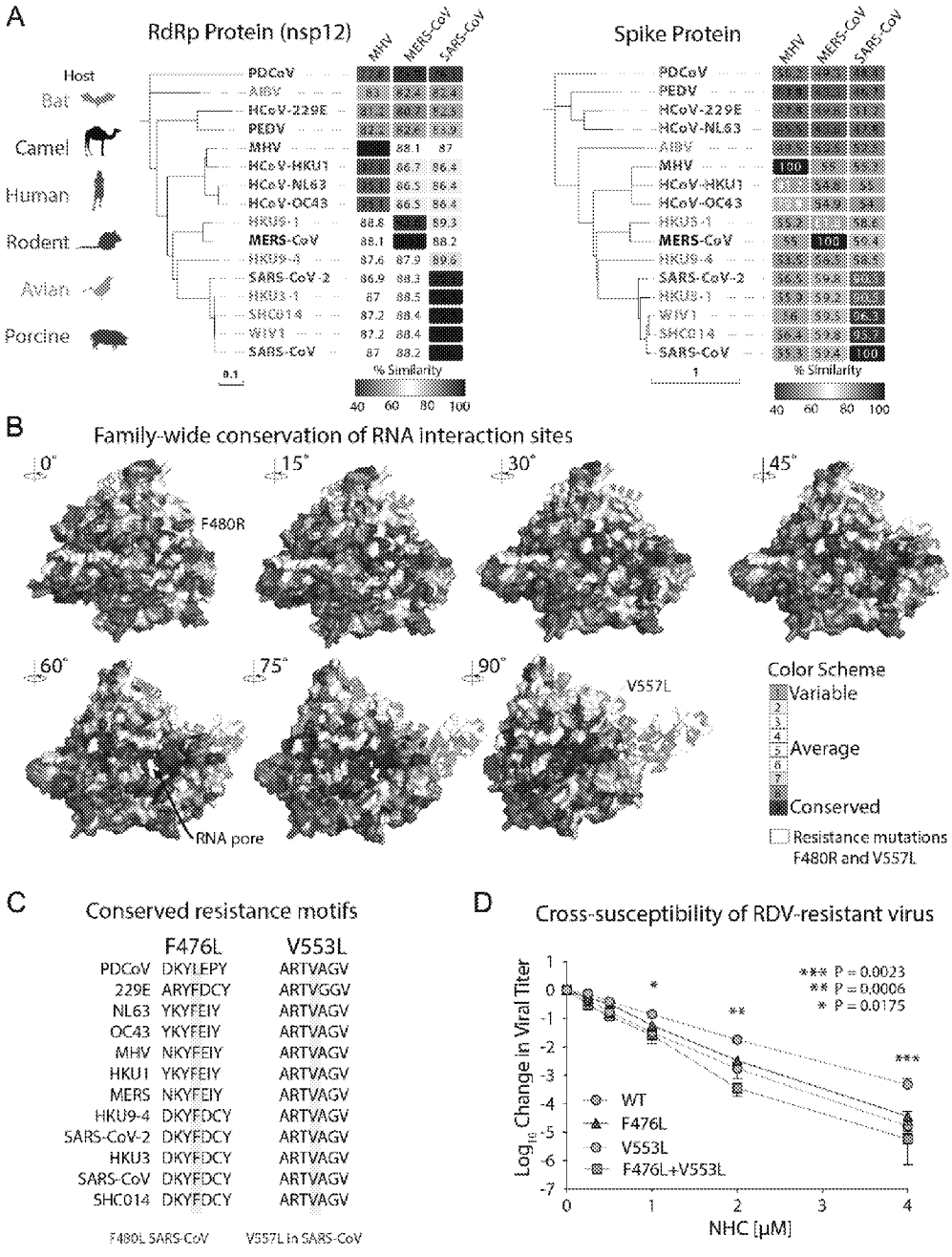

Fig. 3. Remdesivir (RDV) resistance mutations in the highly conserved RNA-dependent RNA polymerase increase susceptibility to NHC. (A) Neighbor-joining trees created with representatives from all four CoV genogroups showing the genetic similarity of CoV nsp12 (RdRp) and CoV spike glycoprotein, which mediates host tropism and entry into cells. Text color of the virus strain label corresponds to virus host species on the left. The heatmap adjacent to each neighbor-joining tree depicts percent amino acid identity (% A.A. similarity) against mouse hepatitis virus (MHV), SARS-CoV, or MERS-CoV. **(B)** The variation encompassed in panel **A** was modeled onto the RdRp structure of the SARS-CoV RdRp. **(C)** Amino acid sequence of CoV in panel **A** at known resistance alleles to antiviral drug RDV. **(D)** Virus titer reduction assay in DBT cells across a range of NHC with recombinant MHV bearing resistance mutations to RDV. Data shown are combined from three independent experiments performed with biological duplicates or triplicates per condition. Asterisks indicate statistically significant differences by Mann-Whitney test as indicated on the graph.

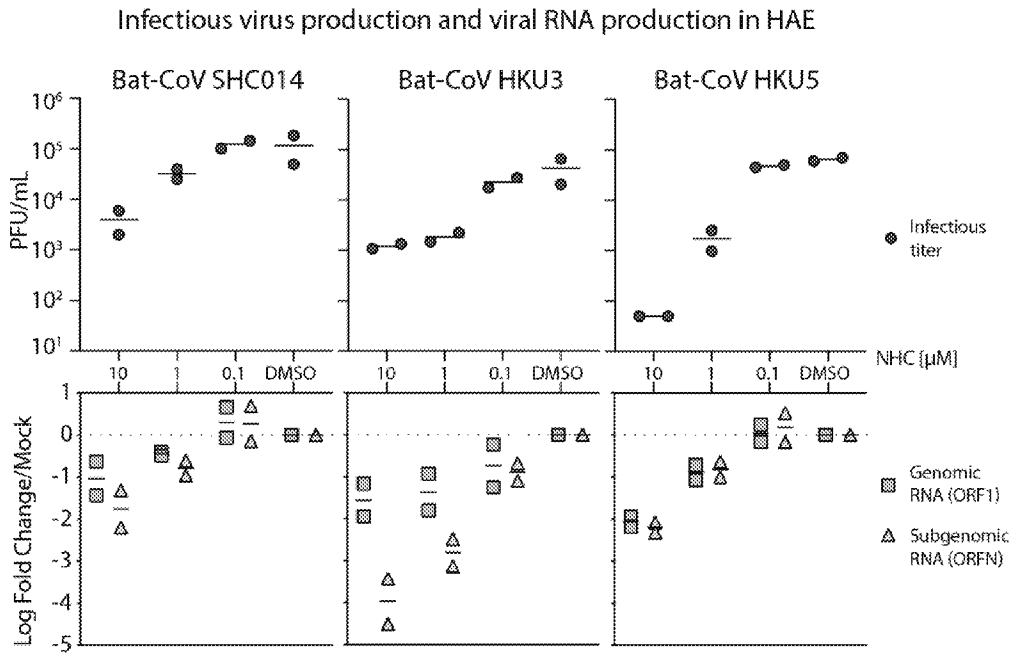

Fig. 4. NHC is effective against multiple genetically distinct Bat-CoV. Top: Antiviral efficacy of NHC in HAE cells against SARS-like (HKU3, SHC014, group 2b) and MERS-like (HKU5, group 2c) bat-CoV. HAE cells were infected at an MOI of 0.5 in the presence of NHC in duplicate. After 48 hours, virus produced was titrated via plaque assay. Each data point represents the titer per culture. Bottom: qRT-PCR for CoV ORF1 and ORFN mRNA in total RNA from cultures in the top panel. Mock, mock-treated. Representative data from two separate experiments with two different cell donors are displayed.

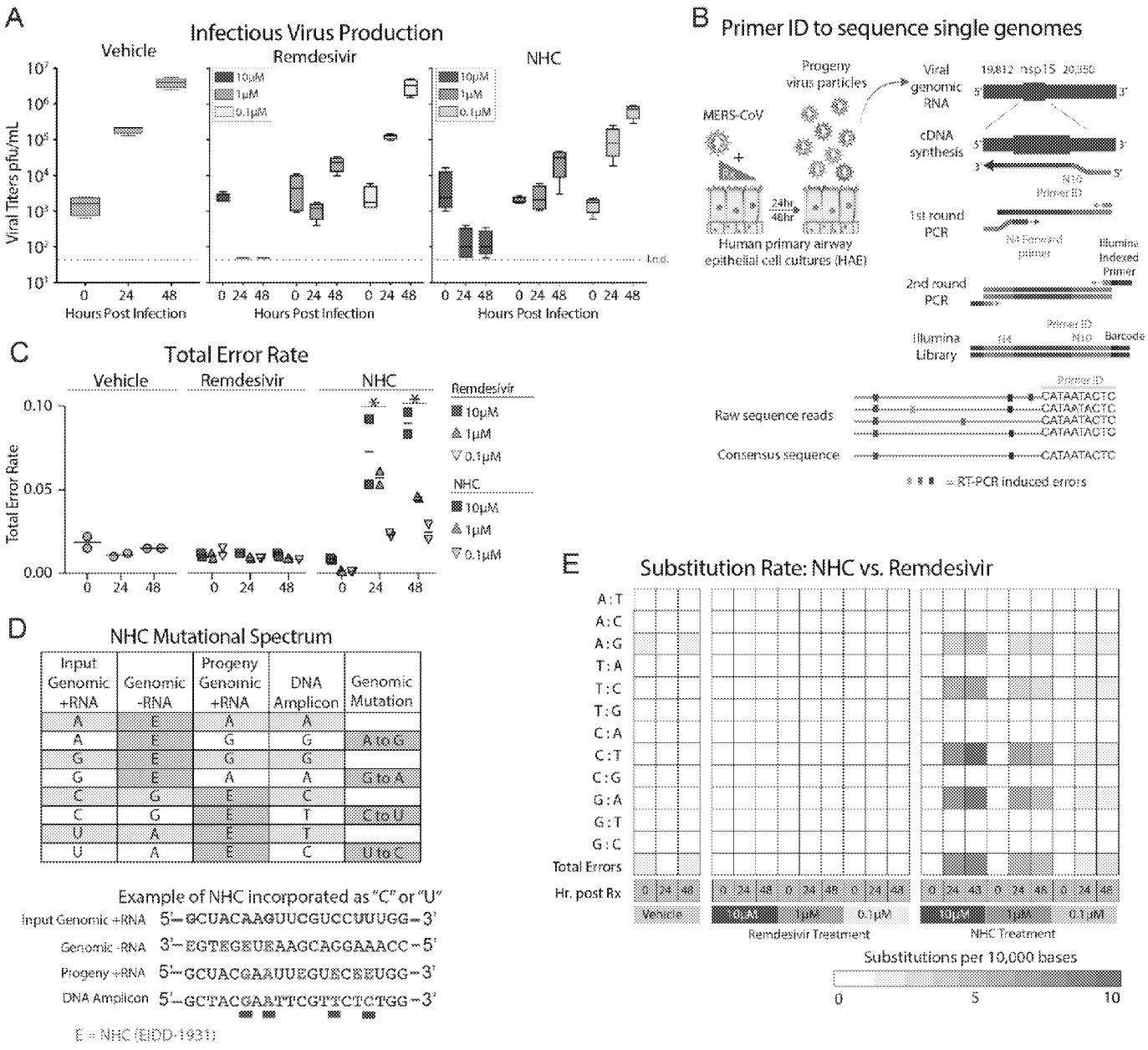

Fig. 5. NHC antiviral activity is associated with increased viral mutation rates. (**A**) HAE cultures were infected with MERS-CoV red fluorescent protein (RFP) at an MOI of 0.5 in duplicate in the presence of vehicle, RDV, or NHC for 48 hours, after which apical washes were collected for virus titration. Data are combined from two independent studies. The boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range. **(B)** Schematic of Primer ID deep sequencing for single RNA genomes of MERS-CoV. **(C)** The total error rate for MERS-CoV RNA isolated from cultures in panel **A** as determined by Primer ID. Error rate values are # mutations per 10,000 bases. Asterisks indicate significant differences as compared to untreated group by two-way ANOVA with a Dunnett's multiple comparison test. **(D)** Description of potential NHC mutational spectra on both positive and negative sense viral RNA. **(E)** Nucleotide transitions in cDNA derived from MERS-CoV genomic RNA.

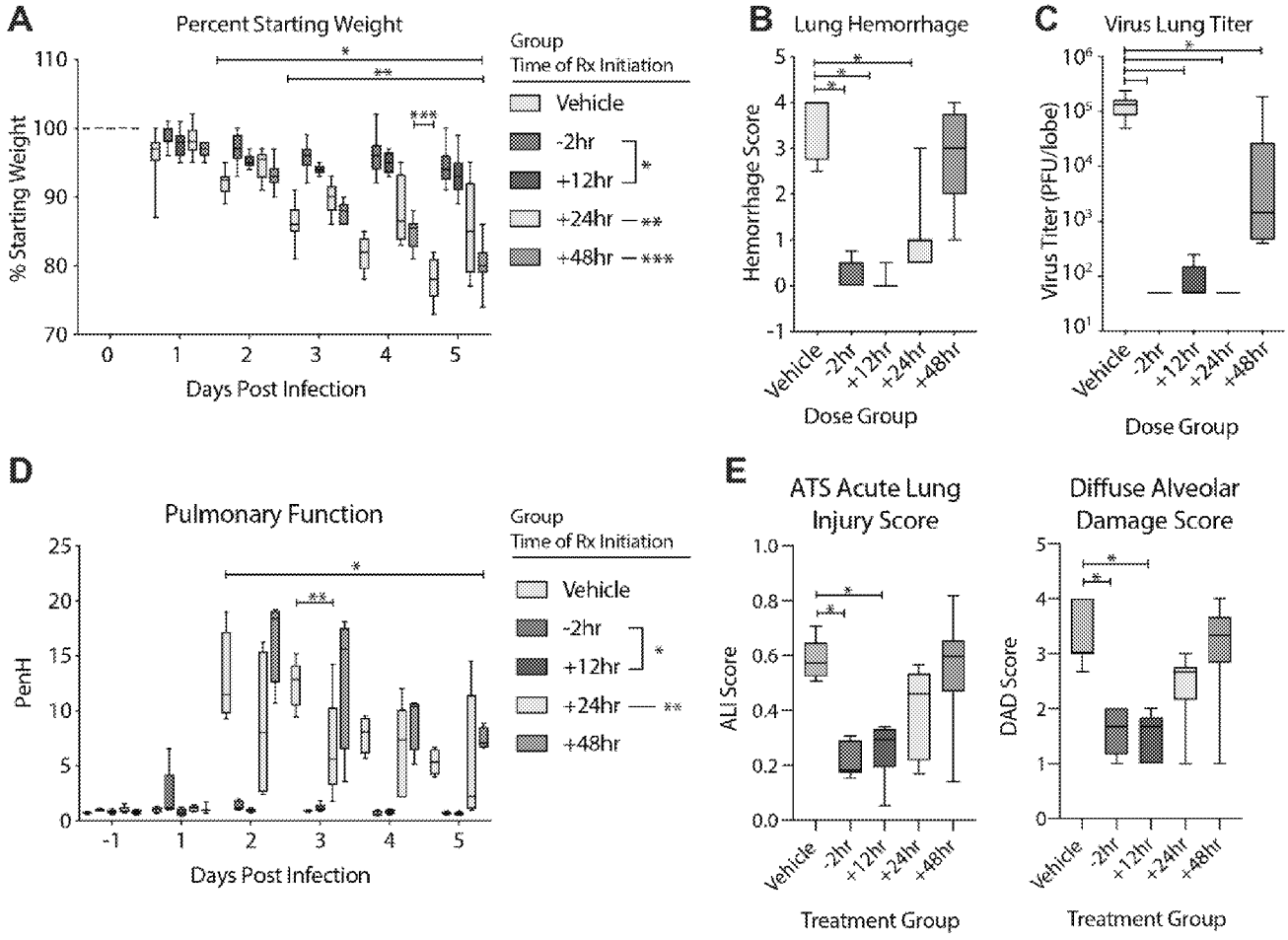

Fig. 6. Prophylactic and therapeutic EIDD-2801 reduces SARS-CoV replication and pathogenesis. Equivalent numbers of 25-29 week old male and female C57BL/6 mice were administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or NHC prodrug EIDD-2801 beginning at -2 hours, +12, +24 or +48 hours post infection and every 12 hours thereafter by oral gavage (n = 10/group). Mice were intranasally infected with 1E+04 PFU mouse-adapted SARS-CoV MA15 strain. **(A)** Percent starting weight. Asterisks indicate differences from vehicle treated by two-way ANOVA with Tukey's multiple comparison test. **(B)** Lung hemorrhage in mice from panel **A** scored on a scale of 0-4 where 0 is a normal pink healthy lung and 4 is a diffusely discolored dark red lung. **(C)** Virus lung titer in mice from panel **A** as determined by plaque assay. Asterisks in both panel **B** and **C** indicate differences from vehicle by one-way ANOVA with a Dunnett's multiple comparison test. **(D)** Pulmonary function by whole body plethysmography was performed daily on five animals per group. Asterisks indicate differences from vehicle by two-way ANOVA with a Dunnett's multiple comparison test. **(E)** The histological features of acute lung injury (ALI) were blindly scored using the American Thoracic Society Lung Injury Scoring system and a Diffuse Alveolar Damage Scoring System. Three randomly chosen high power (60X) fields of diseased lung were assessed per mouse. The numbers of mice scored per group: Vehicle N = 7, -2 hours N = 9, +12 hours N = 9, +24 hours N = 10, +48 hours N = 9. Asterisks indicate statistical significance compared to vehicle by Kruskal-Wallis with a Dunn's multiple comparison test. For all panels, the boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range. *, -2 hours and +12 hours compared to vehicle; **, +24 hours compared to vehicle; ***, +48 hours compared to vehicle.

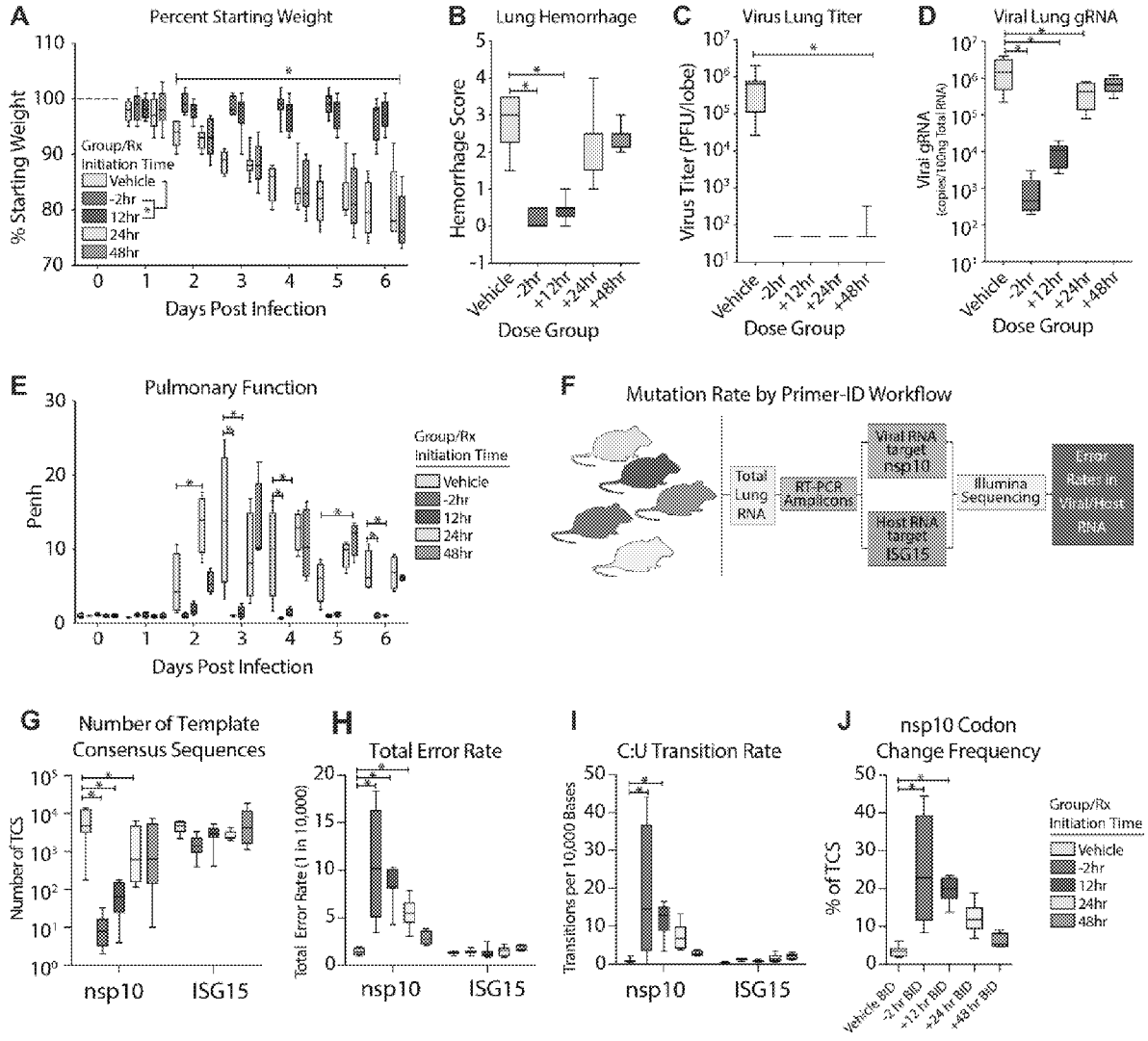

Fig. 7. Prophylactic and therapeutic EIDD-2801 reduces MERS-CoV replication and pathogenesis coincident with increased viral mutation rates. Equivalent numbers of 10-14 week old male and female C57BL/6 hDPP4 mice were administered vehicle (10% PEG, 2.5% Cremophor RH40 in water) or NHC prodrug EIDD-2801 beginning at -2 hours, +12, +24 or +48 hours post infection and every 12 hours thereafter by oral gavage (n = 10/group). Mice were intranasally infected with 5E+04 PFU mouse-adapted MERS-CoV M35C4 strain. (**A**) Percent starting weight. Asterisks indicate differences between -2 hours and +12 hours group from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**B**) Lung hemorrhage in mice from panel **A** scored on a scale of 0-4 where 0 is a normal pink healthy lung and 4 is a diffusely discolored dark red lung. (**C**) Virus lung titer in mice from panel **A** as determined by plaque assay. Asterisks in both panel **B** and **C** indicate differences from vehicle by Kruskal-Wallis with Dunn's multiple comparison test. (**D**) MERS-CoV genomic RNA in lung tissue by qRT-PCR. Asterisks indicate differences by one-way ANOVA with a Dunnett's multiple comparison test. (**E**) Pulmonary function by whole body plethysmography was performed daily on four animals per group. Asterisks indicate differences from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**F**) Workflow to measure mutation rate in MERS-CoV RNA and host transcript ISG15 by Primer ID in mouse lung tissue. (**G**) Number of template consensus sequences (TCS) for MERS-CoV nsp10 and ISG15. (**H**) Total error rate in MERS-CoV nsp10 and ISG15. (**I**) The cytosine to uridine transition rate in MERS-CoV nsp10 and ISG15. In panels **G-I,** asterisks indicate differences from vehicle by two-way ANOVA with Tukey's multiple comparison test. (**J**) Codon change frequency in MERS-CoV nsp10. Asterisks indicate differences from vehicle by Kruskal-Wallis with Dunn's multiple comparison test. For all panels, the boxes encompass the 25th to 75th percentile, the line is at the median, while the whiskers represent the range.

Science Translational Medicine

An orally bioavailable broad-spectrum antiviral inhibits SARS-CoV-2 in human airway epithelial cell cultures and multiple coronaviruses in mice

Timothy P. Sheahan, Amy C. Sims, Shuntai Zhou, Rachel L. Graham, Andrea J. Pruijssers, Maria L. Agostini, Sarah R. Leist, Alexandra Schäfer, Kenneth H. Dinnon III, Laura J. Stevens, James D. Chappell, Xiaotao Lu, Tia M. Hughes, Amelia S. George, Collin S. Hill, Stephanie A. Montgomery, Ariane J. Brown, Gregory R. Bluemling, Michael G. Natchus, Manohar Saindane, Alexander A. Kolykhalov, George Painter, Jennifer Harcourt, Azaibi Tamin, Natalie J. Thornburg, Ronald Swanstrom, Mark R. Denison and Ralph S. Baric

Sci Transl Med published online 6 April 2020

To: LeDuc, James W.[jwleduc@UTMB.EDU]
Cc: Reyes, Raul[rareyes@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]
From: Menachery, Vineet[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=e8de7da558c24fa08b25d7643703d2db-Menachery,]
Sent: Thur 4/16/2020 10:28:31 AM (UTC-05:00)
Subject: Re: WIV questions

A few of the questions are about the WIV facility. Since I have never been there, I didn't want to comment. I know you interacted with them in the planning stages.

I'll forward those requests to Raul and Connie.

Thanks

VDM

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Thursday, April 16, 2020 10:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Reyes, Raul <rareyes@UTMB.EDU>; Holubar, Connie J. <cjholuba@UTMB.EDU>
Subject: RE: WIV questions

Me too…Probably best to refer to Raul and Connie who are managing responses unless there are specific questions that you feel we should/can address.

Thanks, Jim

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, April 16, 2020 10:22 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: WIV questions

Hey Jim,

I have been getting more questions about the Wuhan Institute of Virology and my interactions with them. I am not particularly interested in talking about them and have only had limited interactions. I have been sending a few to you. I just wanted to make sure you are ok with me deflecting those questions to you.

Thanks

VDM

To: Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Tesh Robert[rbtesh22@gmail.com]; Holubar, Connie J.[cjholuba@UTMB.EDU]; Erdman Dean[derdman05@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 1/23/2020 9:09:07 AM (UTC-06:00)
Subject: Re: Snakes could be the source of the Wuhan coronavirus outbreak

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From: Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Sent: Thursday, January 23, 2020 8:23 AM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Tesh Robert <rbtesh22@gmail.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Erdman Dean <derdman05@gmail.com>
Subject: RE: Snakes could be the source of the Wuhan coronavirus outbreak

Interesting. But snakes are very commonly found in wet-markets throughout China and Southeast Asia though.

-----Original Message-----
From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Wednesday, January 22, 2020 11:20 PM
To: LeDuc, James W. <jwleduc@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Tesh Robert <rbtesh22@gmail.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Erdman Dean <derdman05@gmail.com>
Subject: Snakes could be the source of the Wuhan coronavirus outbreak

????????
Snakes could be the source of the Wuhan coronavirus outbreak https://www.cnn.com/2020/01/22/health/snakes-wuhan-coronavirus-outbreak-conversation-partner/index.html

Tom Ksiazek

Sent from a portable device

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: 1/9/2020 8:02:57 AM
To: Menachery, Vineet [vimenach@UTMB.EDU]
Subject: RE: New CoV

HI Vineet, thanks for the Info regarding Anne. Looks like it is a 2B CoV. Good to know whether UTMB wants to be aggressive. Hope you had a nice holiday as well. Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, January 8, 2020 10:13 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: New CoV

Hey,

I chatted with Anne over email. I told her I'd send her my comments and suggestions and she can work on the paper further. She said it might take awhile since she has to work on it in the evenings.

Do you have info on the new virus in Wuhan? I heard that it's a CoV and maybe even a 2B virus. Nothing concrete or that I trust. I assume we'll read about it in a George Gao paper shortly.

I am going to gauge the UTMB funding structure to see if there is money to rapidly respond. Generally, they've been able to shake free money for NHP and other animal models for emerging virus outbreaks. I imagine Kent would be lead on that, but I am sure I'd be included.

We got your Christmas card. Congrats on the new grand child. Everyone looks great.

VDM

From: Linyou Cao [lcao2@ncsu.edu]
Sent: 2/3/2020 11:23:22 PM
To: rbaric@email.unc.edu; Menachery, Vineet [vimenach@UTMB.EDU]
Subject: Inquiry of your Nature Medicine paper on CoronaVirus
Attachments: nm.3985.pdf

Dear Prof. Baric and Prof. Menachery,

I am writing to kindly seek some clarification about the paper you published at Nature Medicine as attached. In particular, I was hoping to know if the CoronaVirus now widely spreading in China and worldwide is the same or any format of mutation of the virus studied in the paper. This information would be extremely important for the development of efficient strategy to control or eventual stop the spreading and also for the development of medical treatment . I would truly appreciate your response for the well being of billions of people in China whose are suffering tremendous mental and physical pain even loss of life.

Many thanks,

Linyou

--

Linyou Cao, PhD
Associate Professor
Department of Materials Science and Engineering
Department of Electrical and Computer Engineering(Affiliated)
Department of Physics (Affiliated)
North Carolina State University
911 Partners Way
Rm. 3070A, EB1
Tel. 919-515-5407
lcao2@ncsu.edu
https://www.mse.ncsu.edu/cao/

nature medicine

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Vineet D Menachery[1], Boyd L Yount Jr[1], Kari Debbink[1,2], Sudhakar Agnihothram[3], Lisa E Gralinski[1], Jessica A Plante[1], Rachel L Graham[1], Trevor Scobey[1], Xing-Yi Ge[4], Eric F Donaldson[1], Scott H Randell[5,6], Antonio Lanzavecchia[7], Wayne A Marasco[8,9], Zhengli-Li Shi[4] & Ralph S Baric[1,2]

The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations[1]. Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve *in vitro* titers equivalent to epidemic strains of SARS-CoV. Additionally, *in vivo* experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis. Evaluation of available SARS-based immune-therapeutic and prophylactic modalities revealed poor efficacy; both monoclonal antibody and vaccine approaches failed to neutralize and protect from infection with CoVs using the novel spike protein. On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both *in vitro* and *in vivo*. Our work suggests a potential risk of SARS-CoV re-emergence from viruses currently circulating in bat populations.

The emergence of SARS-CoV heralded a new era in the cross-species transmission of severe respiratory illness with globalization leading to rapid spread around the world and massive economic impact[3,4]. Since then, several strains—including influenza A strains H5N1, H1N1 and H7N9 and MERS-CoV—have emerged from animal populations, causing considerable disease, mortality and economic hardship for the afflicted regions[5]. Although public health measures were able to stop the SARS-CoV outbreak[4], recent metagenomics studies have identified sequences of closely related SARS-like viruses circulating in Chinese bat populations that may pose a future threat[1,6]. However, sequence data alone provides minimal insights to identify and prepare for future prepandemic viruses. Therefore, to examine the emergence potential (that is, the potential to infect humans) of circulating bat CoVs, we built a chimeric virus encoding a novel, zoonotic CoV spike protein—from the RsSHC014-CoV sequence that was isolated from Chinese horseshoe bats[1]—in the context of the SARS-CoV mouse-adapted backbone. The hybrid virus allowed us to evaluate the ability of the novel spike protein to cause disease independently of other necessary adaptive mutations in its natural backbone. Using this approach, we characterized CoV infection mediated by the SHC014 spike protein in primary human airway cells and *in vivo*, and tested the efficacy of available immune therapeutics against SHC014-CoV. Together, the strategy translates metagenomics data to help predict and prepare for future emergent viruses.

The sequences of SHC014 and the related RsWIV1-CoV show that these CoVs are the closest relatives to the epidemic SARS-CoV strains (**Fig. 1a,b**); however, there are important differences in the 14 residues that bind human ACE2, the receptor for SARS-CoV, including the five that are critical for host range: Y442, L472, N479, T487 and Y491 (ref. 7). In WIV1, three of these residues vary from the epidemic SARS-CoV Urbani strain, but they were not expected to alter binding to ACE2 (**Supplementary Fig. 1a,b** and **Supplementary Table 1**). This fact is confirmed by both pseudotyping experiments that measured the ability of lentiviruses encoding WIV1 spike proteins to enter cells expressing human ACE2 (**Supplementary Fig. 1**) and by *in vitro* replication assays of WIV1-CoV (ref. 1). In contrast, 7 of 14 ACE2-interaction residues in SHC014 are different from those in SARS-CoV, including all five residues critical for host range (**Supplementary Fig. 1c** and **Supplementary Table 1**). These changes, coupled with

[1]Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [2]Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [3]National Center for Toxicological Research, Food and Drug Administration, Jefferson, Arkansas, USA. [4]Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China. [5]Department of Cell Biology and Physiology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [6]Cystic Fibrosis Center, Marsico Lung Institute, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [7]Institute for Research in Biomedicine, Bellinzona Institute of Microbiology, Zurich, Switzerland. [8]Department of Cancer Immunology and AIDS, Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts, USA. [9]Department of Medicine, Harvard Medical School, Boston, Massachusetts, USA. Correspondence should be addressed to R.S.B. (rbaric@email.unc.edu) or V.D.M. (vineet@email.unc.edu).

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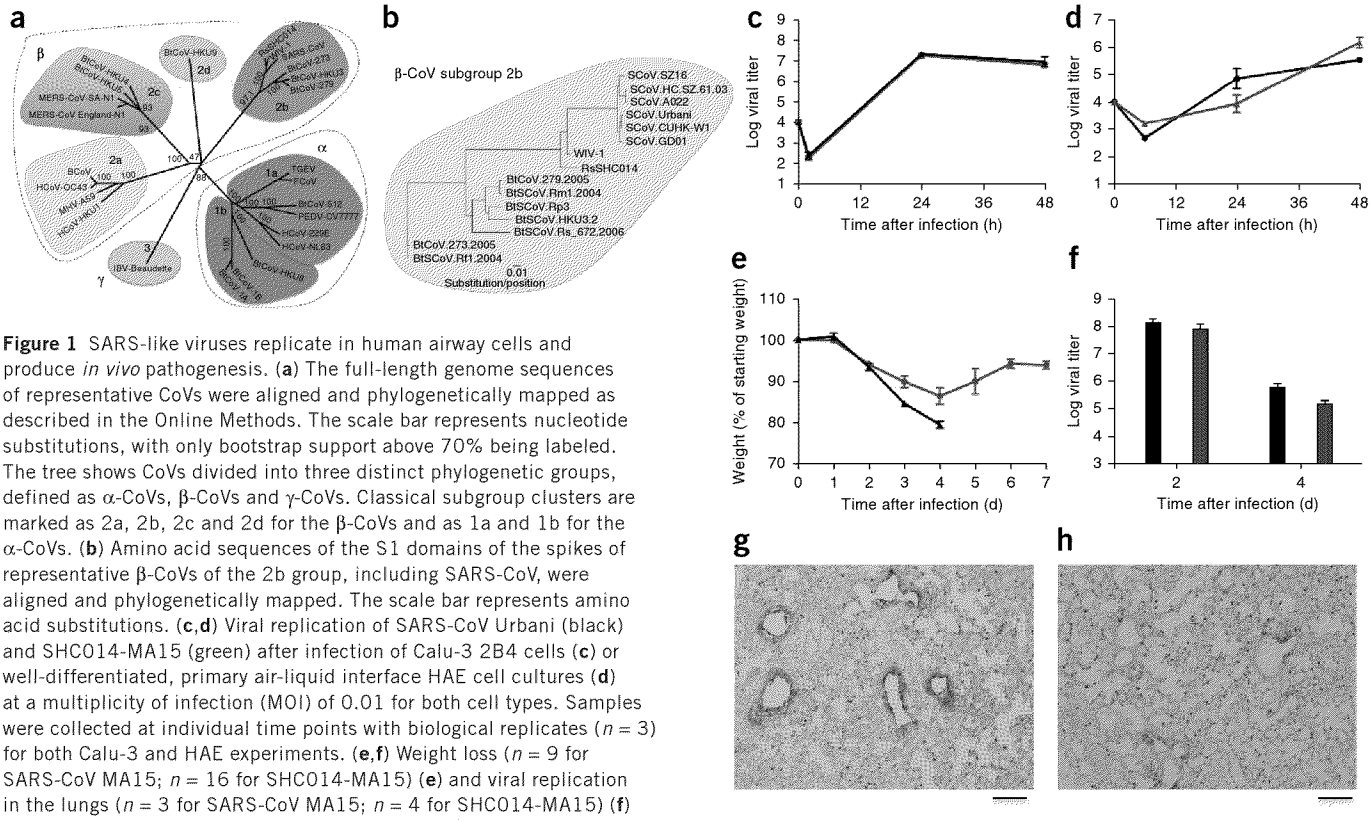

Figure 1 SARS-like viruses replicate in human airway cells and produce *in vivo* pathogenesis. (**a**) The full-length genome sequences of representative CoVs were aligned and phylogenetically mapped as described in the Online Methods. The scale bar represents nucleotide substitutions, with only bootstrap support above 70% being labeled. The tree shows CoVs divided into three distinct phylogenetic groups, defined as α-CoVs, β-CoVs and γ-CoVs. Classical subgroup clusters are marked as 2a, 2b, 2c and 2d for the β-CoVs and as 1a and 1b for the α-CoVs. (**b**) Amino acid sequences of the S1 domains of the spikes of representative β-CoVs of the 2b group, including SARS-CoV, were aligned and phylogenetically mapped. The scale bar represents amino acid substitutions. (**c**,**d**) Viral replication of SARS-CoV Urbani (black) and SHC014-MA15 (green) after infection of Calu-3 2B4 cells (**c**) or well-differentiated, primary air-liquid interface HAE cell cultures (**d**) at a multiplicity of infection (MOI) of 0.01 for both cell types. Samples were collected at individual time points with biological replicates ($n = 3$) for both Calu-3 and HAE experiments. (**e**,**f**) Weight loss ($n = 9$ for SARS-CoV MA15; $n = 16$ for SHC014-MA15) (**e**) and viral replication in the lungs ($n = 3$ for SARS-CoV MA15; $n = 4$ for SHC014-MA15) (**f**) of 10-week-old BALB/c mice infected with 1×10^4 p.f.u. of mouse-adapted SARS-CoV MA15 (black) or SHC014-MA15 (green) via the intranasal (i.n.) route. (**g**,**h**) Representative images of lung sections stained for SARS-CoV N antigen from mice infected with SARS-CoV MA15 ($n = 3$ mice) (**g**) or SHC014-MA15 ($n = 4$ mice) (**h**) are shown. For each graph, the center value represents the group mean, and the error bars define the s.e.m. Scale bars, 1 mm.

the failure of pseudotyped lentiviruses expressing the SHC014 spike to enter cells (**Supplementary Fig. 1d**), suggested that the SHC014 spike is unable to bind human ACE2. However, similar changes in related SARS-CoV strains had been reported to allow ACE2 binding[7,8], suggesting that additional functional testing was required for verification. Therefore, we synthesized the SHC014 spike in the context of the replication-competent, mouse-adapted SARS-CoV backbone (we hereafter refer to the chimeric CoV as SHC014-MA15) to maximize the opportunity for pathogenesis and vaccine studies in mice (**Supplementary Fig. 2a**). Despite predictions from both structure-based modeling and pseudotyping experiments, SHC014-MA15 was viable and replicated to high titers in Vero cells (**Supplementary Fig. 2b**). Similarly to SARS, SHC014-MA15 also required a functional ACE2 molecule for entry and could use human, civet and bat ACE2 orthologs (**Supplementary Fig. 2c,d**). To test the ability of the SHC014 spike to mediate infection of the human airway, we examined the sensitivity of the human epithelial airway cell line Calu-3 2B4 (ref. 9) to infection and found robust SHC014-MA15 replication, comparable to that of SARS-CoV Urbani (**Fig. 1c**). To extend these findings, primary human airway epithelial (HAE) cultures were infected and showed robust replication of both viruses (**Fig. 1d**). Together, the data confirm the ability of viruses with the SHC014 spike to infect human airway cells and underscore the potential threat of cross-species transmission of SHC014-CoV.

To evaluate the role of the SHC014 spike in mediating infection *in vivo*, we infected 10-week-old BALB/c mice with 10^4 plaque-forming units (p.f.u.) of either SARS-MA15 or SHC014-MA15 (**Fig. 1e–h**). Animals infected with SARS-MA15 experienced rapid weight loss and lethality by 4 d post infection (d.p.i.); in contrast, SHC014-MA15 infection produced substantial weight loss (10%) but no lethality in mice (**Fig. 1e**). Examination of viral replication revealed nearly equivalent viral titers from the lungs of mice infected with SARS-MA15 or SHC014-MA15 (**Fig. 1f**). Whereas lungs from the SARS-MA15–infected mice showed robust staining in both the terminal bronchioles and the lung parenchyma 2 d.p.i. (**Fig. 1g**), those of SHC014-MA15–infected mice showed reduced airway antigen staining (**Fig. 1h**); in contrast, no deficit in antigen staining was observed in the parenchyma or in the overall histology scoring, suggesting differential infection of lung tissue for SHC014-MA15 (**Supplementary Table 2**). We next analyzed infection in more susceptible, aged (12-month-old) animals. SARS-MA15–infected animals rapidly lost weight and succumbed to infection (**Supplementary Fig. 3a,b**). SHC014-MA15 infection induced robust and sustained weight loss, but had minimal lethality. Trends in the histology and antigen staining patterns that we observed in young mice were conserved in the older animals (**Supplementary Table 3**). We excluded the possibility that SHC014-MA15 was mediating infection through an alternative receptor on the basis of experiments using *Ace2*$^{-/-}$ mice, which did not show weight loss or antigen staining after SHC014-MA15 infection (**Supplementary Fig. 4a,b** and **Supplementary Table 2**). Together, the data indicate that viruses with the SHC014 spike are capable of inducing weight loss in mice in the context of a virulent CoV backbone.

Given the preclinical efficacy of Ebola monoclonal antibody therapies, such as ZMApp[10], we next sought to determine the efficacy of SARS-CoV monoclonal antibodies against infection with

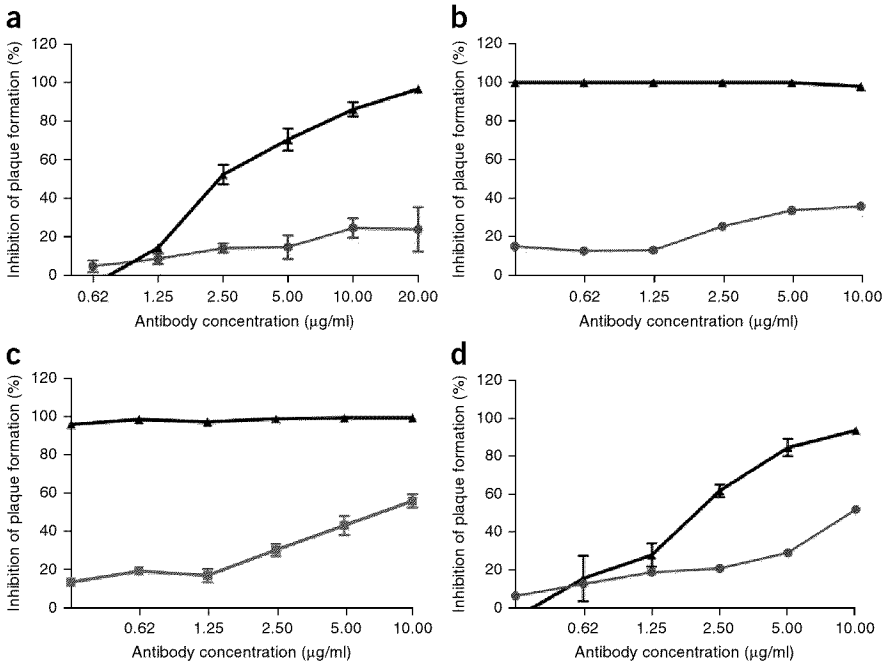

Figure 2 SARS-CoV monoclonal antibodies have marginal efficacy against SARS-like CoVs. (**a**–**d**) Neutralization assays evaluating efficacy (measured as reduction in the number of plaques) of a panel of monoclonal antibodies, which were all originally generated against epidemic SARS-CoV, against infection of Vero cells with SARS-CoV Urbani (black) or SHC014-MA15 (green). The antibodies tested were fm6 ($n = 3$ for Urbani; $n = 5$ for SHC014-MA15)[11,12] (**a**), 230.15 ($n = 3$ for Urbani; $n = 2$ for SHC014-MA15) (**b**), 227.15 ($n = 3$ for Urbani; $n = 5$ for SHC014-MA15) (**c**) and 109.8 ($n = 3$ for Urbani; $n = 2$ for SHC014-MA15)[13] (**d**). Each data point represents the group mean and error bars define the s.e.m. Note that the error bars in SARS-CoV Urbani–infected Vero cells in **b**,**c** are overlapped by the symbols and are not visible.

SHC014-MA15. Four broadly neutralizing human monoclonal antibodies targeting SARS-CoV spike protein had been previously reported and are probable reagents for immunotherapy[11–13]. We examined the effect of these antibodies on viral replication (expressed as percentage inhibition of viral replication) and found that whereas wild-type SARS-CoV Urbani was strongly neutralized by all four antibodies at relatively low antibody concentrations (**Fig. 2a–d**), neutralization varied for SHC014-MA15. Fm6, an antibody generated by phage display and escape mutants[11,12], achieved only background levels of inhibition of SHC014-MA15 replication (**Fig. 2a**). Similarly, antibodies 230.15 and 227.14, which were derived from memory B cells of SARS-CoV–infected patients[13], also failed to block SHC014-MA15 replication (**Fig. 2b,c**). For all three antibodies, differences between the SARS and SHC014 spike amino acid sequences corresponded to direct or adjacent residue changes found in SARS-CoV escape mutants (fm6 N479R; 230.15 L443V; 227.14 K390Q/E), which probably explains the absence of the antibodies' neutralizing activity against SHC014. Finally, monoclonal antibody 109.8 was able to achieve 50% neutralization of SHC014-MA15, but only at high concentrations (10 μg/ml) (**Fig. 2d**). Together, the results demonstrate that broadly neutralizing antibodies against SARS-CoV may only have marginal efficacy against emergent SARS-like CoV strains such as SHC014.

To evaluate the efficacy of existing vaccines against infection with SHC014-MA15, we vaccinated aged mice with double-inactivated whole SARS-CoV (DIV). Previous work showed that DIV could neutralize and protect young mice from challenge with a homologous virus[14]; however, the vaccine failed to protect aged animals in which augmented immune pathology was also observed, indicating the possibility of the animals being harmed because of the vaccination[15]. Here we found that DIV did not provide protection from challenge with SHC014-MA15 with regards to weight loss or viral titer (**Supplementary Fig. 5a,b**). Consistent with a previous report with other heterologous group 2b CoVs[15], serum from DIV-vaccinated, aged mice also failed to neutralize SHC014-MA15 (**Supplementary Fig. 5c**). Notably, DIV vaccination resulted in robust immune pathology (**Supplementary Table 4**) and eosinophilia (**Supplementary Fig. 5d–f**). Together, these results confirm that the DIV vaccine would not be protective against infection with SHC014 and could possibly augment disease in the aged vaccinated group.

In contrast to vaccination of mice with DIV, the use of SHC014-MA15 as a live, attenuated vaccine showed potential cross-protection against challenge with SARS-CoV, but the results have important caveats. We infected young mice with 10^4 p.f.u. of SHC014-MA15 and observed them for 28 d. We then challenged the mice with SARS-MA15 at day 29 (**Supplementary Fig. 6a**). The prior infection of the mice with the high dose of SHC014-MA15 conferred protection against challenge with a lethal dose of SARS-MA15, although there was only a minimal SARS-CoV neutralization response from the antisera elicited 28 d after SHC014-MA15 infection (**Supplementary Fig. 6b**, 1:200). In the absence of a secondary antigen boost, 28 d.p.i. represents the expected peak of antibody titers and implies that there will be diminished protection against SARS-CoV over time[16,17]. Similar results showing protection against challenge with a lethal dose of SARS-CoV were observed in aged BALB/c mice with respect to weight loss and viral replication (**Supplementary Fig. 6c,d**). However, the SHC014-MA15 infection dose of 10^4 p.f.u. induced >10% weight loss and lethality in some aged animals (**Fig. 1** and **Supplementary Fig. 3**). We found that vaccination with a lower dose of SHC014-MA15 (100 p.f.u.), did not induce weight loss, but it also failed to protect aged animals from a SARS-MA15 lethal dose challenge (**Supplementary Fig. 6e,f**). Together, the data suggest that SHC014-MA15 challenge may confer cross-protection against SARS-CoV through conserved epitopes, but the required dose induces pathogenesis and precludes use as an attenuated vaccine.

Having established that the SHC014 spike has the ability to mediate infection of human cells and cause disease in mice, we next synthesized a full-length SHC014-CoV infectious clone based on the approach used for SARS-CoV (**Fig. 3a**)[2]. Replication in Vero cells revealed no deficit for SHC014-CoV relative to that for SARS-CoV (**Fig. 3b**); however, SHC014-CoV was significantly ($P < 0.01$) attenuated in primary HAE cultures at both 24 and 48 h after infection (**Fig. 3c**). *In vivo* infection of mice demonstrated no significant weight loss but showed reduced viral replication in lungs of full-length SHC014-CoV infection, as compared to SARS-CoV Urbani (**Fig. 3d,e**). Together, the results establish the viability of full-length

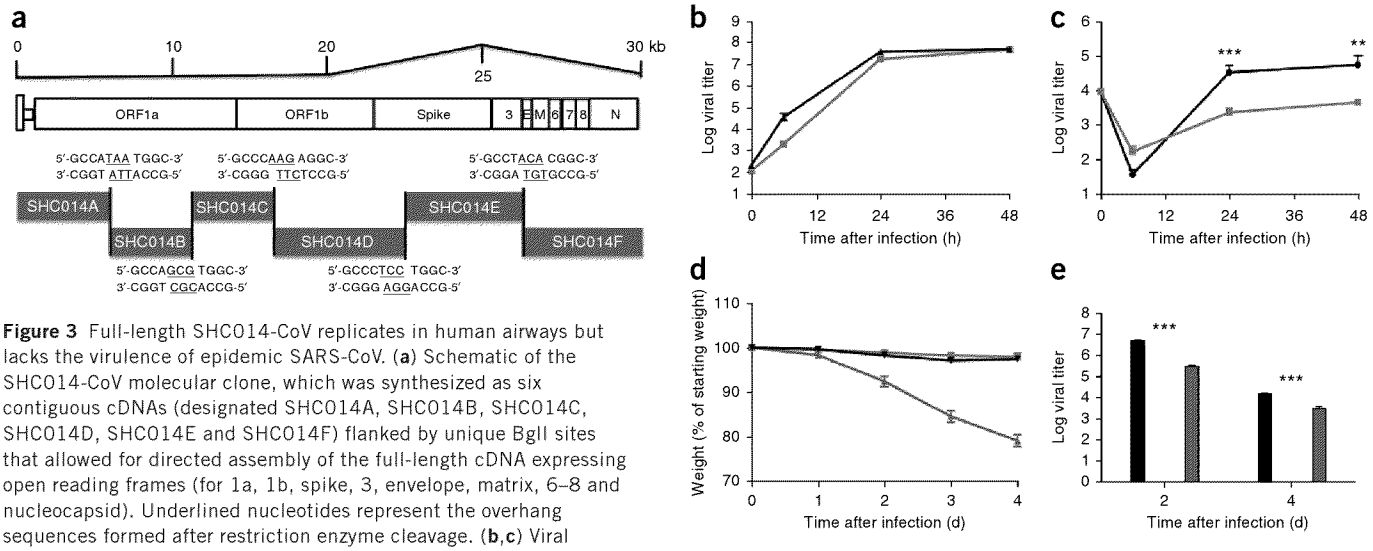

Figure 3 Full-length SHC014-CoV replicates in human airways but lacks the virulence of epidemic SARS-CoV. (**a**) Schematic of the SHC014-CoV molecular clone, which was synthesized as six contiguous cDNAs (designated SHC014A, SHC014B, SHC014C, SHC014D, SHC014E and SHC014F) flanked by unique BglI sites that allowed for directed assembly of the full-length cDNA expressing open reading frames (for 1a, 1b, spike, 3, envelope, matrix, 6–8 and nucleocapsid). Underlined nucleotides represent the overhang sequences formed after restriction enzyme cleavage. (**b**,**c**) Viral replication of SARS-CoV Urbani (black) or SHC014-CoV (green) after infection of Vero cells (**b**) or well-differentiated, primary air-liquid interface HAE cell cultures (**c**) at an MOI of 0.01. Samples were collected at individual time points with biological replicates ($n = 3$) for each group. Data represent one experiment for both Vero and HAE cells. (**d**,**e**) Weight loss ($n = 3$ for SARS-CoV MA15, $n = 7$ for SHC014-CoV; $n = 6$ for SARS-Urbani) (**d**) and viral replication in the lungs ($n = 3$ for SARS-Urbani and SHC014-CoV) (**e**) of 10-week-old BALB/c mice infected with 1×10^5 p.f.u. of SARS-CoV MA15 (gray), SHC014-CoV (green) or SARS-CoV Urbani (black) via the i.n. route. Each data point represents the group mean, and error bars define the s.e.m. $^{**}P < 0.01$ and $^{***}P < 0.001$ using two-tailed Student's *t*-test of individual time points.

SHC014-CoV, but suggest that further adaptation is required for its replication to be equivalent to that of epidemic SARS-CoV in human respiratory cells and in mice.

During the SARS-CoV epidemic, links were quickly established between palm civets and the CoV strains that were detected in humans[4]. Building on this finding, the common emergence paradigm argues that epidemic SARS-CoV originated as a bat virus, jumped to civets and incorporated changes within the receptor-binding domain (RBD) to improve binding to civet Ace2 (ref. 18). Subsequent exposure to people in live-animal markets permitted human infection with the civet strain, which, in turn, adapted to become the epidemic strain (**Fig. 4a**). However, phylogenetic analysis suggests that early human SARS strains appear more closely related to bat strains than to civet strains[18]. Therefore, a second paradigm argues that direct bat-human transmission initiated SARS-CoV emergence and that palm civets served as a secondary host and reservoir for continued infection (**Fig. 4b**)[19]. For both paradigms, spike adaptation in a secondary host is seen as a necessity, with most mutations expected to occur within the RBD, thereby facilitating improved infection. Both theories imply that pools of bat CoVs are limited and that host-range mutations are

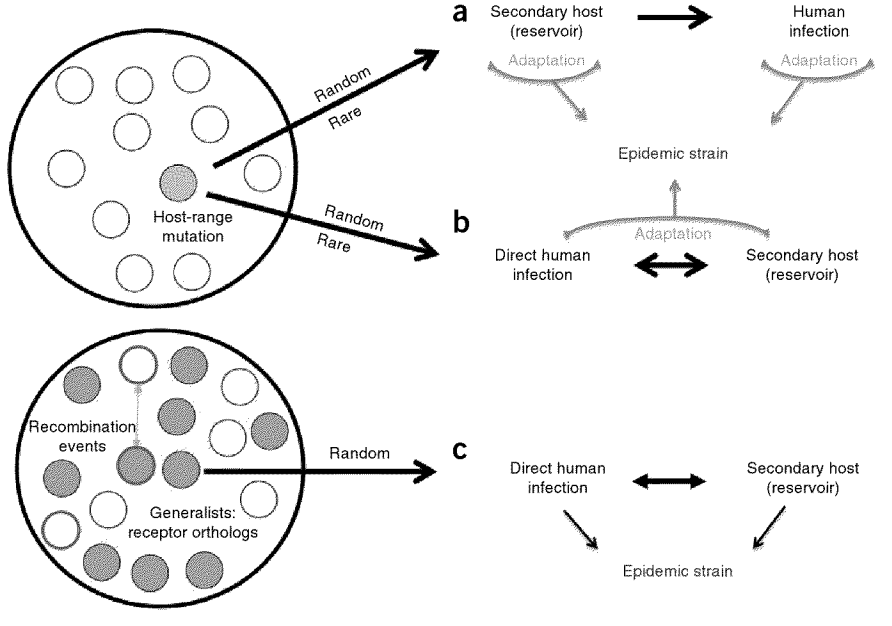

Figure 4 Emergence paradigms for coronaviruses. Coronavirus strains are maintained in quasi-species pools circulating in bat populations. (**a**,**b**) Traditional SARS-CoV emergence theories posit that host-range mutants (red circle) represent random and rare occurrences that permit infection of alternative hosts. The secondary-host paradigm (**a**) argues that a nonhuman host is infected by a bat progenitor virus and, through adaptation, facilitates transmission to humans; subsequent replication in humans leads to the epidemic viral strain. The direct paradigm (**b**) suggests that transmission occurs between bats and humans without the requirement of an intermediate host; selection then occurs in the human population with closely related viruses replicating in a secondary host, permitting continued viral persistence and adaptation in both. (**c**) The data from chimeric SARS-like viruses argue that the quasi-species pools maintain multiple viruses capable of infecting human cells without the need for mutations (red circles). Although adaptations in secondary or human hosts may be required for epidemic emergence, if SHC014 spike–containing viruses recombined with virulent CoV backbones (circles with green outlines), then epidemic disease may be the result in humans. Existing data support elements of all three paradigms.

both random and rare, reducing the likelihood of future emergence events in humans.

Although our study does not invalidate the other emergence routes, it does argue for a third paradigm in which circulating bat CoV pools maintain 'poised' spike proteins that are capable of infecting humans without mutation or adaptation (**Fig. 4c**). This hypothesis is illustrated by the ability of a chimeric virus containing the SHC014 spike in a SARS-CoV backbone to cause robust infection in both human airway cultures and in mice without RBD adaptation. Coupled with the observation of previously identified pathogenic CoV backbones[3,20], our results suggest that the starting materials required for SARS-like emergent strains are currently circulating in animal reservoirs. Notably, although full-length SHC014-CoV probably requires additional backbone adaption to mediate human disease, the documented high-frequency recombination events in CoV families underscores the possibility of future emergence and the need for further preparation.

To date, genomics screens of animal populations have primarily been used to identify novel viruses in outbreak settings[21]. The approach here extends these data sets to examine questions of viral emergence and therapeutic efficacy. We consider viruses with the SHC014 spike a potential threat owing to their ability to replicate in primary human airway cultures, the best available model for human disease. In addition, the observed pathogenesis in mice indicates a capacity for SHC014-containing viruses to cause disease in mammalian models, without RBD adaptation. Notably, differential tropism in the lung as compared to that with SARS-MA15 and attenuation of full-length SHC014-CoV in HAE cultures relative to SARS-CoV Urbani suggest that factors beyond ACE2 binding—including spike processivity, receptor bio-availability or antagonism of the host immune responses—may contribute to emergence. However, further testing in nonhuman primates is required to translate these finding into pathogenic potential in humans. Importantly, the failure of available therapeutics defines a critical need for further study and for the development of treatments. With this knowledge, surveillance programs, diagnostic reagents and effective treatments can be produced that are protective against the emergence of group 2b–specific CoVs, such as SHC014, and these can be applied to other CoV branches that maintain similarly heterogeneous pools.

In addition to offering preparation against future emerging viruses, this approach must be considered in the context of the US government–mandated pause on gain-of-function (GOF) studies[22]. On the basis of previous models of emergence (**Fig. 4a,b**), the creation of chimeric viruses such as SHC014-MA15 was not expected to increase pathogenicity. Although SHC014-MA15 is attenuated relative to its parental mouse-adapted SARS-CoV, similar studies examining the pathogenicity of CoVs with the wild-type Urbani spike within the MA15 backbone showed no weight loss in mice and reduced viral replication[23]. Thus, relative to the Urbani spike–MA15 CoV, SHC014-MA15 shows a gain in pathogenesis (**Fig. 1**). On the basis of these findings, scientific review panels may deem similar studies building chimeric viruses based on circulating strains too risky to pursue, as increased pathogenicity in mammalian models cannot be excluded. Coupled with restrictions on mouse-adapted strains and the development of monoclonal antibodies using escape mutants, research into CoV emergence and therapeutic efficacy may be severely limited moving forward. Together, these data and restrictions represent a crossroads of GOF research concerns; the potential to prepare for and mitigate future outbreaks must be weighed against the risk of creating more dangerous pathogens. In developing policies moving forward, it is important to consider the value of the data generated by these studies and whether these types of chimeric virus studies warrant further investigation versus the inherent risks involved.

Overall, our approach has used metagenomics data to identify a potential threat posed by the circulating bat SARS-like CoV SHC014. Because of the ability of chimeric SHC014 viruses to replicate in human airway cultures, cause pathogenesis *in vivo* and escape current therapeutics, there is a need for both surveillance and improved therapeutics against circulating SARS-like viruses. Our approach also unlocks the use of metagenomics data to predict viral emergence and to apply this knowledge in preparing to treat future emerging virus infections.

METHODS

Methods and any associated references are available in the online version of the paper.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper.

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AUTHOR CONTRIBUTIONS

V.D.M. designed, coordinated and performed experiments, completed analysis and wrote the manuscript. B.L.Y. designed the infectious clone and recovered chimeric viruses; S.A. completed neutralization assays; L.E.G. helped perform mouse experiments; T.S. and J.A.P. completed mouse experiments and plaque assays; X.-Y.G. performed pseudotyping experiments; K.D. generated structural figures and predictions; E.F.D. generated phylogenetic analysis; R.L.G. completed RNA analysis; S.H.R. provided primary HAE cultures; A.L. and W.A.M. provided critical monoclonal antibody reagents; and Z.-L.S. provided SHC014 spike sequences and plasmids. R.S.B. designed experiments and wrote manuscript.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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ONLINE METHODS

Viruses, cells, *in vitro* infection and plaque assays. Wild-type SARS-CoV (Urbani), mouse-adapted SARS-CoV (MA15) and chimeric SARS-like CoVs were cultured on Vero E6 cells (obtained from United States Army Medical Research Institute of Infectious Diseases), grown in Dulbecco's modified Eagle's medium (DMEM) (Gibco, CA) and 5% fetal clone serum (FCS) (Hyclone, South Logan, UT) along with antibiotic/antimycotic (Gibco, Carlsbad, CA). DBT cells (Baric laboratory, source unknown) expressing *ACE2* orthologs have been previously described for both human and civet; bat *Ace2* sequence was based on that from *Rhinolophus leschenaulti*, and DBT cells expressing bat *Ace2* were established as described previously[8]. Pseudotyping experiments were similar to those using an HIV-based pseudovirus, prepared as previously described[10], and examined on HeLa cells (Wuhan Institute of Virology) that expressed *ACE2* orthologs. HeLa cells were grown in minimal essential medium (MEM) (Gibco, CA) supplemented with 10% FCS (Gibco, CA) as previously described[24]. Growth curves in Vero E6, DBT, Calu-3 2B4 and primary human airway epithelial cells were performed as previously described[8,25]. None of the working cell line stocks were authenticated or tested for mycoplasma recently, although the original seed stocks used to create the working stocks are free from contamination. Human lungs for HAE cultures were procured under University of North Carolina at Chapel Hill Institutional Review Board–approved protocols. HAE cultures represent highly differentiated human airway epithelium containing ciliated and non-ciliated epithelial cells as well as goblet cells. The cultures are also grown on an air-liquid interface for several weeks before use, as previously described[26]. Briefly, cells were washed with PBS and inoculated with virus or mock-diluted in PBS for 40 min at 37 °C. After inoculation, cells were washed three times and fresh medium was added to signify time '0'. Three or more biological replicates were harvested at each described time point. No blinding was used in any sample collections nor were samples randomized. All virus cultivation was performed in a biosafety level (BSL) 3 laboratory with redundant fans in the biosafety cabinets, as described previously by our group[2]. All personnel wore powered air purifying respirators (Breathe Easy, 3M) with Tyvek suits, aprons and booties and were double-gloved.

Sequence clustering and structural modeling. The full-length genomic sequences and the amino acid sequences of the S1 domains of the spike of representative CoVs were downloaded from Genbank or Pathosystems Resource Integration Center (PATRIC), aligned with ClustalX and phylogenetically compared by using maximum likelihood estimation using 100 bootstraps or by using the PhyML (https://code.google.com/p/phyml/) package, respectively. The tree was generated using maximum likelihood with the PhyML package. The scale bar represents nucleotide substitutions. Only nodes with bootstrap support above 70% are labeled. The tree shows that CoVs are divided into three distinct phylogenetic groups defined as α-CoVs, β-CoVs and γ-CoVs. Classical subgroup clusters are marked as 2a, 2b, 2c and 2d for β-CoVs, and 1a and 1b for the α-CoVs. Structural models were generated using Modeller (Max Planck Institute Bioinformatics Toolkit) to generate homology models for SHC014 and Rs3367 of the SARS RBD in complex with ACE2 based on crystal structure 2AJF (Protein Data Bank). Homology models were visualized and manipulated in MacPyMol (version 1.3).

Construction of SARS-like chimeric viruses. Both wild-type and chimeric viruses were derived from either SARS-CoV Urbani or the corresponding mouse-adapted (SARS-CoV MA15) infectious clone (ic) as previously described[27]. Plasmids containing spike sequences for SHC014 were extracted by restriction digest and ligated into the E and F plasmid of the MA15 infectious clone. The clone was designed and purchased from Bio Basic as six contiguous cDNAs using published sequences flanked by unique class II restriction endonuclease sites (BglI). Thereafter, plasmids containing wild-type, chimeric SARS-CoV and SHC014-CoV genome fragments were amplified, excised, ligated and purified. *In vitro* transcription reactions were then preformed to synthesize full-length genomic RNA, which was transfected into Vero E6 cells as previously described[2]. The medium from transfected cells was harvested and served as seed stocks for subsequent experiments. Chimeric and full-length viruses were confirmed by sequence analysis before use in these studies. Synthetic construction of chimeric mutant and full-length SHC014-CoV was approved by the University of North Carolina Institutional Biosafety Committee and the Dual Use Research of Concern committee.

Ethics statement. This study was carried out in accordance with the recommendations for the care and use of animals by the Office of Laboratory Animal Welfare (OLAW), NIH. The Institutional Animal Care and Use Committee (IACUC) of The University of North Carolina at Chapel Hill (UNC, Permit Number A-3410-01) approved the animal study protocol (IACUC #13-033) used in these studies.

Mice and *in vivo* infection. Female, 10-week-old and 12-month-old BALB/cAnNHsD mice were ordered from Harlan Laboratories. Mouse infections were done as previously described[20]. Briefly, animals were brought into a BSL3 laboratory and allowed to acclimate for 1 week before infection. For infection and live-attenuated virus vaccination, mice were anesthetized with a mixture of ketamine and xylazine and infected intranasally, when challenged, with 50 μl of phosphate-buffered saline (PBS) or diluted virus with three or four mice per time point, per infection group per dose as described in the figure legends. For individual mice, notations for infection including failure to inhale the entire dose, bubbling of inoculum from the nose, or infection through the mouth may have led to exclusion of mouse data at the discretion of the researcher; post-infection, no other pre-established exclusion or inclusion criteria are defined. No blinding was used in any animal experiments, and animals were not randomized. For vaccination, young and aged mice were vaccinated by footpad injection with a 20-μl volume of either 0.2 μg of double-inactivated SARS-CoV vaccine with alum or mock PBS; mice were then boosted with the same regimen 22 d later and challenged 21 d thereafter. For all groups, as per protocol, animals were monitored daily for clinical signs of disease (hunching, ruffled fur and reduced activity) for the duration of the experiment. Weight loss was monitored daily for the first 7 d, after which weight monitoring continued until the animals recovered to their initial starting weight or displayed weight gain continuously for 3 d. All mice that lost greater than 20% of their starting body weight were ground-fed and further monitored multiple times per day as long as they were under the 20% cutoff. Mice that lost greater than 30% of their starting body weight were immediately sacrificed as per protocol. Any mouse deemed to be moribund or unlikely to recover was also humanely sacrificed at the discretion of the researcher. Euthanasia was performed using an isoflurane overdose and death was confirmed by cervical dislocation. All mouse studies were performed at the University of North Carolina (Animal Welfare Assurance #A3410-01) using protocols approved by the UNC Institutional Animal Care and Use Committee (IACUC).

Histological analysis. The left lung was removed and submerged in 10% buffered formalin (Fisher) without inflation for 1 week. Tissues were embedded in paraffin and 5-μm sections were prepared by the UNC Lineberger Comprehensive Cancer Center histopathology core facility. To determine the extent of antigen staining, sections were stained for viral antigen using a commercially available polyclonal SARS-CoV anti-nucleocapsid antibody (Imgenex) and scored in a blinded manner by for staining of the airway and parenchyma as previously described[20]. Images were captured using an Olympus BX41 microscope with an Olympus DP71 camera.

Virus neutralization assays. Plaque reduction neutralization titer assays were performed with previously characterized antibodies against SARS-CoV, as previously described[11–13]. Briefly, neutralizing antibodies or serum was serially diluted twofold and incubated with 100 p.f.u. of the different infectious clone SARS-CoV strains for 1 h at 37 °C. The virus and antibodies were then added to a 6-well plate with 5×10^5 Vero E6 cells/well with multiple replicates ($n \geq 2$). After a 1-h incubation at 37 °C, cells were overlaid with 3 ml of 0.8% agarose in medium. Plates were incubated for 2 d at 37 °C, stained with neutral red for 3 h and plaques were counted. The percentage of plaque reduction was calculated as (1 − (no. of plaques with antibody/no. of plaques without antibody)) × 100.

doi:10.1038/nm.3985

Corrigendum: Multiphoton imaging reveals a new leukocyte recruitment paradigm in the glomerulus

Sapna Devi, Anqi Li, Clare L V Westhorpe, Camden Y Lo, Latasha D Abeynaike, Sarah L Snelgrove, Pam Hall, Joshua D Ooi, Christopher G Sobey, A Richard Kitching & Michael J Hickey
Nat. Med. **19**, 107–112 (2013); published online 16 December 2012; corrected after print 12 August 2015

In the published article, in the Online Methods section, it is stated that the dose of DHE used is 20 mg/kg, when in fact DHE was administered at 2 mg/kg. The error has been corrected in the HTML and PDF versions of the article.

Corrigendum: PAR1 signaling regulates the retention and recruitment of EPCR-expressing bone marrow hematopoietic stem cells

Shiri Gur-Cohen, Tomer Itkin, Sagarika Chakrabarty, Claudine Graf, Orit Kollet, Aya Ludin, Karin Golan, Alexander Kalinkovich, Guy Ledergor, Eitan Wong, Elisabeth Niemeyer, Ziv Porat, Ayelet Erez, Irit Sagi, Charles T Esmon, Wolfram Ruf & Tsvee Lapidot
Nat. Med. **21**, 1307–1317 (2015); published online 12 October 2015; corrected after print 18 November 2015

In the version of this article initially published, the first author's name was incorrect. The error has been corrected in the HTML and PDF versions of the article.

Corrigendum: Myeloid-derived growth factor (C19orf10) mediates cardiac repair following myocardial infarction

Mortimer Korf-Klingebiel, Marc R Reboll, Stefanie Klede, Torben Brod, Andreas Pich, Felix Polten, L Christian Napp, Johann Bauersachs, Arnold Ganser, Eva Brinkmann, Ines Reimann, Tibor Kempf, Hans W Niessen, Jacques Mizrahi, Hans-Joachim Schönfeld, Antonio Iglesias, Maria Bobadilla, Yong Wang & Kai C Wollert
Nat. Med. **21**, 140–149 (2015); published online 12 January 2015; corrected after print 19 November 2015

In the version of this article initially published, the article number in reference 13 is incorrectly stated as '100ra190' and should be '100ra90'. The error has been corrected in the HTML and PDF versions of the article.

Corrigendum: A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Vineet D Menachery, Boyd L Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E Gralinski, Jessica A Plante, Rachel L Graham, Trevor Scobey, Xing-Yi Ge, Eric F Donaldson, Scott H Randell, Antonio Lanzavecchia, Wayne A Marasco, Zhengli-Li Shi & Ralph S Baric
Nat. Med.; doi:10.1038/nm.3985; corrected 20 November 2015

In the version of this article initially published online, the authors omitted to acknowledge a funding source, USAID-EPT-PREDICT funding from EcoHealth Alliance, to Z.-L.S. The error has been corrected for the print, PDF and HTML versions of this article.

Corrigendum: Long-term glycemic control using polymer-encapsulated human stem cell–derived beta cells in immune-competent mice

Arturo J Vegas, Omid Veiseh, Mads Gürtler, Jeffrey R Millman, Felicia W Pagliuca, Andrew R Bader, Joshua C Doloff, Jie Li, Michael Chen, Karsten Olejnik, Hok Hei Tam, Siddharth Jhunjhunwala, Erin Langan, Stephanie Aresta-Dasilva, Srujan Gandham, James J McGarrigle, Matthew A Bochenek, Jennifer Hollister-Lock, Jose Oberholzer, Dale L Greiner, Gordon C Weir, Douglas A Melton, Robert Langer & Daniel G Anderson
Nat. Med.; doi:10.1038/nm.4030; corrected online 18 February 2016

In the version of this article initially published online, the authors omitted acknowledgment recognizing the histology core of the Harvard Stem Cell Institute and several individuals for their assistance. The error has been corrected for the print, PDF and HTML versions of this article.

From: Menachery, Vineet [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: 1/27/2020 2:35:28 PM
To: Baric, Ralph S [rbaric@email.unc.edu]
Subject: Re: New CoV

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, January 27, 2020 2:33 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: New CoV

552.117

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Monday, January 27, 2020 2:33 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: New CoV

Number?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, January 27, 2020 3:32 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: New CoV

I can talk now.

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Monday, January 27, 2020 1:52 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: New CoV

You have time for a quick call at 4PM EST?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, January 8, 2020 10:13 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: New CoV

Hey,

I chatted with Anne over email. I told her I'd send her my comments and suggestions and she can work on the paper further. She said it might take awhile since she has to work on it in the evenings.

Do you have info on the new virus in Wuhan? I heard that it's a CoV and maybe even a 2B virus. Nothing concrete or that I trust. I assume we'll read about it in a George Gao paper shortly.

I am going to gauge the UTMB funding structure to see if there is money to rapidly respond. Generally, they've been able to shake free money for NHP and other animal models for emerging virus outbreaks. I imagine Kent would be lead on that, but I am sure I'd be included.

We got your Christmas card. Congrats on the new grand child. Everyone looks great.

VDM

From: Liu, Shan-Lu <liu.6244@osu.edu>
Sent: Thursday, November 28, 2019 9:58 AM
To: zhengzhiming4
@gmail.com;haitguo@iupui.edu;tzhou@mail.nih.gov;GCheng@mednet.ucla.edu;liangy
@umn.edu;rli@vcu.edu;wjma@ksu.edu;xjmeng@vt.edu;Zhijian.Chen@UTSouthwester
n.edu;mluo@gsu.edu;zhangyj@umd.edu;xzhu1
@umd.edu;jqiu@kumc.edu;lijun@uic.edu;fengwei.bai@usm.edu;andyu@iupui.edu;rea
chxw@vt.edu;gluo@uab.edu;ldu@nybc.org;hxu@tulane.edu;liu_fy@berkeley.edu;shita
o.li@okstate.edu;Shan.lu@umassmed.edu;Hu, Haitao;wenzheho@temple.edu;Qfeng4
@central.uh.edu;tang@bio.fsu.edu;feng.li@sdstate.edu;ruilu@lsu.edu;sxiang2
@unl.edu;qiyi.tang@howard.edu;dingsw@ucr.edu;guohua@missouri.edu;bling@tulan
e.edu;junwang@pharmacy.arizona.edu;lifang@umn.edu;wang518@umd.edu;gaos8
@upmc.edu;pewang@uchc.edu;xiangy@uthscsa.edu;fzhu@bio.fsu.edu;chen.liang@mc
gill.ca;lyuan@vt.edu;fgao@duke.edu;wangjw28@163.com;xfyu1
@zju.edu.cn;bzhao@partners.org;jianw@musc.edu;zyang@ksu.edu;yu.cong@nih.gov;
weiming.yuan@usc.edu;Zongdi.feng@nationwidechildrens.org;juh13
@psu.edu;hengx@missouri.edu;lsu@med.unc.edu;ywu8
@gmu.edu;jwu@whu.edu.cn;tshuo@uic.edu;Shibojiang@fudan.edu.cn;sjiang@nybc.or
g;pinwang@usc.edu;rzhao@som.umaryland.edu;shuylong@mail.sysu.edu.cn;xuefeng.li
u@georgetown.edu;yuxingli@som.umaryland.edu;shixia.wang@umassmed.edu;yhe@i
pbcams.ac.cn;Pinghui.feng@usc.edu;ju-
tao.guo@bblumberg.org;lin.liu@okstate.edu;hua.zhu@rutgers.edu;Jinhong.chang@bb
lumberg.org;jianzhu1012@gmail.com;ronghai@ucr.edu;jun.zhu@nih.gov;jliu4
@uams.edu;xiangpeng.kong@med.nyu.edu;haoquanwu@outlook.com;Wenjun.liu@de
fence.gov.au;Liang.shan@wustl.edu;hliao@duke.edu;yuan2
@upenn.edu;zxing@umn.edu;hongmin.li@health.ny.gov;pzheng@ihv.umaryland.edu;y
aliu@ihv.umaryland.edu;jxw103@case.edu;xiangguo.qiu@canada.ca;Feng
Shao;zlshi@wh.iov.cn;klan@whu.edu.cn;zengmsh@mail.sysu.edu.cn;Nan Yan;Zhang,
Rong;liliwang@upenn.edu;Linheng Li;kli1
@uthsc.edu;tsx@case.edu;ssun@mdanderson.org;ysang@tnstate.edu;Liu, Shan-
Lu;wu@crystal.harvard.edu;Sun.Jie@mayo.edu;peijun@strubi.ox.ac.uk;jiayu@coh.org;b
chen@crystal.harvard.edu;Wen, Haitao;Qu, Feng;Hezhao.Ji@umanitoba.ca;Li,
Zihai;zhengyo@msu.edu;zhanglinqi@tsinghua.edu.cn;wxiao@temple.edu;Whu@templ
e.edu;RSun@mednet.ucla.edu;Guangping.Gao@umassmed.edu;PZheng@ihv.umarylan
d.edu;GMSWANG@nus.edu.sg;Shi, Pei yong;yaliu@ihv.umaryland.edu;ziying-
yan@uiowa.edu;lqiao@luc.edu;yong.xiong@yale.edu;Wang,
Qiuhong;shuping_tong_md@brown.edu;pinghuif@usc.edu;gaof@im.ac.cn
Subject: Happy Thanksgiving and meeting next year, June 12-13, 2020
Attachments: Meeting report_ACVA_SCBA-virology_Kunming.pdf; Junming_1.JPG; Kunming_2.JPG;
Kunming_3.JPG; Kunming_4.JPG

Dear friends and colleagues,

I wish you all a great Thanksgiving holiday!

A few updates:

1. We will have our first scientific meeting on June 12-13, 2020, right before the ASV annual meeting (June 13-17) in Fort Collins, Colorado State University. Organizing and scientific committees will be formed soon.
2. I am excited to share that Dr. Xiang-Jin (XJ) Meng of Virginia Tech, a distinguished virology and a member of the US National Academy of Science, will be the keynote speaker of this meeting. Details will follow.
3. In addition to scientific programs, we will also hold an election; a new leadership team will be elected to serve our community for the next two years.
4. Attached please find a brief report of our Kunming meeting, along with a few photos.

Please let me know if you have comments and suggestions.

All best wishes, and happy holidays!

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

SCBA-Virology Division Workshop Held in Kunming

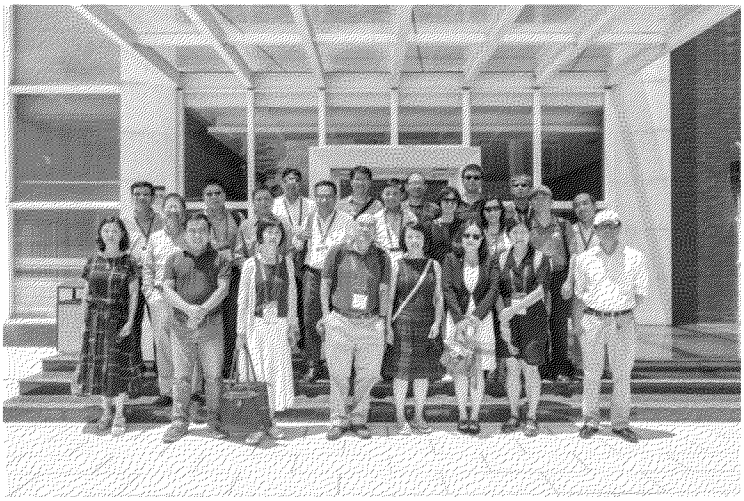
The SCBA-Virology Division held a scientific workshop on July 28, 2019 after the 17th SCBA International Symposium in Kunming, China. The workshop was co-organized by Drs. Genhong Cheng, Haitao Guo, Shan-Lu Liu and Tongqing Zhou of the SCBA-virology Division and by Dr. Qihan Li at the Institute of Medical Biology (IMB), Chinese Academy of Medical Sciences (CAMS).

The meeting was opened by an introductory speech by Prof. Qihan Li, Director of IMB, followed by scientific presentations. The workshop had three sessions, which covered the topics of "Immunity to Viral Infection", "Viral Pathogenesis", and "Vaccine and Primate Models". More than 50 people attended the workshop, many from IMB. Speakers, session chairs, and panelists include: Tian Wang, Shan-Lu Liu, Haitao Hu, Jie Sun, Wenzhe Ho, Lishan Su, Wei Jiang, Xuefeng Liu, Hongyu Deng, Yuntao Wu, Jianming Hu, Genhong Cheng, Lanying Du, Yuan Yan, Kui Li, Shou-Wei Ding, Qi Huang, etc.

Before the scientific sessions, meeting attendees were given a guided tour of the National Medical Primate Research Center located in IMB, CAMS, which hosts the largest P4 primate research facility in China and plays a leading role in breeding, reproduction, disease control, genetic studies of primates in the world. In addition to IMB of CAMS, the workshop was also supported by Drs. Yuelong Shu and Musheng Zeng at Sun Yat-sen University (SYSU), China, Dr. Yuntao Wu at Virongy, LLC and George Mason University, as well as Immune Technology Corp.

This is the first scientific event after the official establishment of the SCBA-Virology Division in 2018. During the 2019 SCBA international symposium and the SCBA-Virology satellite workshop, we also organized opportunities for social networking.


The 17th SCBA
International Symposium
Bioscience for All, All for Bioscience
全球華人生物學家大會
暨第十七屆美洲华人生物科学学会学术研讨会
— 病毒学分会卫星会 —
17th SCBA
病毒学分会卫星会




The 17th SCBA
2019年7月28日
July 28th, 2019
中国 昆明
Kunming, China
International Symposium
Bioscience for All,
All for Bioscience
全球華人生物學家大會
暨第十七届美洲华人生物科学学会学术研讨会
— 病毒学分会卫星会 —
中国医学科学院医学生物学研究所
云南省重大传染病疫苗工程技术中心
云南省重大传染病疫苗研发重点实验室
云南省传染病疫苗研发及产业化国际科技合作基地
病毒学分会卫星会


宴安會堂


IMBCAMS
IMBCAMS

Suryanarayanan2_TPIA_0000000347

From: Liu, Shan-Lu <liu.6244@osu.edu>
Sent: Sunday, December 29, 2019 8:56 AM
To: zhengzhiming4
@gmail.com;haitguo@iupui.edu;tzhou@mail.nih.gov;GCheng@mednet.ucla.edu;liangy
@umn.edu;rli@vcu.edu;wjma@ksu.edu;xjmeng@vt.edu;Zhijian.Chen@UTSouthwester
n.edu;mluo@gsu.edu;zhangyj@umd.edu;xzhu1
@umd.edu;jqiu@kumc.edu;lijun@uic.edu;fengwei.bai@usm.edu;andyu@iupui.edu;rea
chxw@vt.edu;gluo@uab.edu;ldu@nybc.org;hxu@tulane.edu;liu_fy@berkeley.edu;shita
o.li@okstate.edu;Shan.lu@umassmed.edu;Hu, Haitao;wenzheho@temple.edu;Qfeng4
@central.uh.edu;tang@bio.fsu.edu;feng.li@sdstate.edu;ruilu@lsu.edu;sxiang2
@unl.edu;qiyi.tang@howard.edu;dingsw@ucr.edu;guohua@missouri.edu;bling@tulan
e.edu;junwang@pharmacy.arizona.edu;lifang@umn.edu;wang518@umd.edu;gaos8
@upmc.edu;pewang@uchc.edu;xiangy@uthscsa.edu;fzhu@bio.fsu.edu;chen.liang@mc
gill.ca;lyuan@vt.edu;fgao@duke.edu;wangjw28@163.com;xfyu1
@zju.edu.cn;bzhao@partners.org;jianw@musc.edu;zyang@ksu.edu;yu.cong@nih.gov;
weiming.yuan@usc.edu;Zongdi.feng@nationwidechildrens.org;juh13
@psu.edu;hengx@missouri.edu;lsu@med.unc.edu;ywu8
@gmu.edu;jwu@whu.edu.cn;tshuo@uic.edu;Shibojiang@fudan.edu.cn;sjiang@nybc.or
g;pinwang@usc.edu;rzhao@som.umaryland.edu;shuylong@mail.sysu.edu.cn;xuefeng.li
u@georgetown.edu;yuxingli@som.umaryland.edu;shixia.wang@umassmed.edu;yhe@i
pbcams.ac.cn;Pinghui.feng@usc.edu;ju-
tao.guo@bblumberg.org;lin.liu@okstate.edu;hua.zhu@rutgers.edu;Jinhong.chang@bb
lumberg.org;jianzhu1012@gmail.com;ronghai@ucr.edu;jun.zhu@nih.gov;jliu4
@uams.edu;xiangpeng.kong@med.nyu.edu;haoquanwu@outlook.com;Wenjun.liu@de
fence.gov.au;Liang.shan@wustl.edu;hliao@duke.edu;yuan2
@upenn.edu;zxing@umn.edu;hongmin.li@health.ny.gov;pzheng@ihv.umaryland.edu;y
aliu@ihv.umaryland.edu;jxw103@case.edu;xiangguo.qiu@canada.ca;Feng
Shao;zlshi@wh.iov.cn;klan@whu.edu.cn;zengmsh@mail.sysu.edu.cn;Nan Yan;Zhang,
Rong;liliwang@upenn.edu;Linheng Li;kli1
@uthsc.edu;tsx@case.edu;ssun@mdanderson.org;ysang@tnstate.edu;Liu, Shan-
Lu;wu@crystal.harvard.edu;Sun.Jie@mayo.edu;peijun@strubi.ox.ac.uk;jiayu@coh.org;b
chen@crystal.harvard.edu;Wen, Haitao;Qu, Feng;Hezhao.Ji@umanitoba.ca;Li,
Zihai;zhengyo@msu.edu;zhanglinqi@tsinghua.edu.cn;wxiao@temple.edu;Whu@templ
e.edu;RSun@mednet.ucla.edu;Guangping.Gao@umassmed.edu;PZheng@ihv.umarylan
d.edu;GMSWANG@nus.edu.sg;Shi, Pei yong;yaliu@ihv.umaryland.edu;ziying-
yan@uiowa.edu;lqiao@luc.edu;yong.xiong@yale.edu;Wang,
Qiuhong;shuping_tong_md@brown.edu;pinghuif@usc.edu;gaof@im.ac.cn;zihai@musc
.edu;zqin@uams.edu;guodeyin@www.sysu.edu.cn
Subject: ACVA/SCBA-Virology Division: 2019 Year in Review
Attachments: ACVASCBA-Virology 2019 year in review.pdf

Dear Colleagues and Friends:

Happy new year! I wish you all a healthy and productive 2020!

I would like to share the below summary on our major activities in 2019.

ACVA/SCBA-Virology Division: 2019 Year in Review (chronologically)

1. Continuous and focused discussion on the Science letter "Racial Profiling Harms Science" (original title "Racial Profiling Harms American Science and Innovation").

2. Seven Chinese or Chinese American scientists, including 5 members of ACVA/SCBA-Virology Division, elected to the American Academy of Microbiology (AAM) - Genhong Cheng（程根宏）, Pinghui Feng （冯平辉）, Guangping Gao (高光坪）, Jake T Liang （連展阳）, Zhengli Shi （石正丽）, Yumei Wen (闻玉梅), Richard Zhao （赵玉琪）.

3. Themed discussion on the universal influenza vaccine, vectored ImmunoProphylaxis, and attenuated influenza vaccine.

4. Themed discussion of Open Access journal publishing.

5. Debate and discussion on the definition of "racial profiling": Chinese translations, differences between "racial profiling" and "racial discrimination", and differences in Chinese translations: " 种族标签，种族偏见，种族歧视".

6. Themed discussion on virus-host evolutionary arms races: HIV and others.

7. Ultimate publication of the Science letter on March 21, 2019 (online) – sagas and stories behind the scenes.

8. Responses to the Science letter and media reports – "The Scientist", "知识分子", and others.

9. Discussion and responses to US institution's statements, Emory/MD Anderson faculty firing, and NIH's foreign influences and FBI investigations.

10. Establishment of the ACVA/SCBA-Virology Division website (https://sites.google.com/view/scba-virology/home), as well as collection and distribution of membership list (https://sites.google.com/view/scba-virology/members).

11. Dr. George F. Gao elected to the US National Academy of Sciences as International Member (formerly called Foreign Associate).

12. Dr. Zongdi Feng (冯枞棣) won the 2019 ASV's Ann Palmenberg Junior Investigator's award.

13. ACVA/SCBA-Virology participation in the 17th SCBA International Symposium, Kunming, July 24-28, 2019, and scientific workshop and social gathering at the 2nd ACVA/SCBA-virology meeting in Kunming, July 28, 2019.

14. Response and discussion on the role of $\alpha 4\beta 7$ antibody in the control of HIV/SIV infection: 3 Science papers with all negative results - what has gone wrong and what is next?

15. Dr. Feng Shao won the 2019 Future Scientific Prize in Biological Sciences: congratulations and discussions on the scientific evaluation systems in China – ideas and solutions.

16. Three members among the 2019 Journal of Virology top 25 reviewers: Drs. Dongdi Feng (冯枞棣), Bin He (何斌), and Dong-Yan Jin (金冬雁); note that Dr. Bin He is PhD advisor of Dr. Feng, and both have been on the list multiple times, including 2018 (Drs. Ju-tao Guo and Jianming Hu were among the 2018's JVI top 25 reviewers)

17. Response and discussion about the 2019 Lasker award for the discovery of T and B development.

18. Overwhelming responses to Dr. Xuetao Cao's publication issues raised by Pubpeer.com, and heated discussion on scientific misconduct in general.

19. Heated discussion on publishing in CNS (Cell, Nature and Science), selection of conference speakers, and scientific community networking.

20. Themed discussion on self-plagiarism and direct feedback from Editor in Chiefs of Journal of Virology (Roz Sandri-Goldin), Journal of Immunology (Gene Oltz), Viruses (Eric Freed), Emerging Microbes and Infections (Shan Lu), etc.

21. Themed discussion on publications of structural biology studies in CNS - a scientific favor or true advance in biology?

22. Themed discussion on US patents and institution royalties - why are they different?

23. Themed discussion on viral entry: definition of viral receptors – requirements and pitfalls.

Shan-Lu Liu, MD, PhD
President of ACVA/SCBA-Virology
The Ohio State University

Dear Colleagues and Friends:

Happy new year! I wish you all a healthy and productive 2020!

I would like to share the below summary on our major activities in 2019.

ACVA/SCBA-Virology Division: 2019 Year in Review (chronologically)

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23. Themed discussion on viral entry: definition of viral receptors – requirements and pitfalls.

From: Sun, Jie, Ph.D. <Sun.Jie@mayo.edu>
Sent: Thursday, November 28, 2019 11:37 AM
To: Liu, Shan-Lu;zhengzhiming4@gmail.com;haitguo@iupui.edu;tzhou@mail.nih.gov;GCheng@mednet.ucla.edu;liangy@umn.edu;rli@vcu.edu;wjma@ksu.edu;xjmeng@vt.edu;Zhijian.Chen@UTSouthwestern.edu;mluo@gsu.edu;zhangyj@umd.edu;xzhu1@umd.edu;jqiu@kumc.edu;lijun@uic.edu;fengwei.bai@usm.edu;andyu@iupui.edu;reachxw@vt.edu;gluo@uab.edu;ldu@nybc.org;hxu@tulane.edu;liu_fy@berkeley.edu;shitao.li@okstate.edu;Shan.lu@umassmed.edu;Hu, Haitao;wenzheho@temple.edu;Qfeng4@central.uh.edu;tang@bio.fsu.edu;feng.li@sdstate.edu;ruilu@lsu.edu;sxiang2@unl.edu;qiyi.tang@howard.edu;dingsw@ucr.edu;guohua@missouri.edu;bling@tulane.edu;junwang@pharmacy.arizona.edu;lifang@umn.edu;wang518@umd.edu;gaos8@upmc.edu;pewang@uchc.edu;xiangy@uthscsa.edu;fzhu@bio.fsu.edu;chen.liang@mcgill.ca;lyuan@vt.edu;fgao@duke.edu;wangjw28@163.com;xfyu1@zju.edu.cn;bzhao@partners.org;jianw@musc.edu;zyang@ksu.edu;yu.cong@nih.gov;weiming.yuan@usc.edu;Zongdi.feng@nationwidechildrens.org;juh13@psu.edu;hengx@missouri.edu;lsu@med.unc.edu;ywu8@gmu.edu;jwu@whu.edu.cn;tshuo@uic.edu;Shibojiang@fudan.edu.cn;sjiang@nybc.org;pinwang@usc.edu;rzhao@som.umaryland.edu;shuylong@mail.sysu.edu.cn;xuefeng.liu@georgetown.edu;yuxingli@som.umaryland.edu;shixia.wang@umassmed.edu;yhe@ipbcams.ac.cn;Pinghui.feng@usc.edu;ju-tao.guo@bblumberg.org;lin.liu@okstate.edu;hua.zhu@rutgers.edu;Jinhong.chang@bblumberg.org;jianzhu1012@gmail.com;ronghai@ucr.edu;jun.zhu@nih.gov;jliu4@uams.edu;xiangpeng.kong@med.nyu.edu;haoquanwu@outlook.com;Wenjun.liu@defence.gov.au;Liang.shan@wustl.edu;hliao@duke.edu;yuan2@upenn.edu;zxing@umn.edu;hongmin.li@health.ny.gov;pzheng@ihv.umaryland.edu;yaliu@ihv.umaryland.edu;jxw103@case.edu;xiangguo.qiu@canada.ca;Feng Shao;zlshi@wh.iov.cn;klan@whu.edu.cn;zengmsh@mail.sysu.edu.cn;Nan Yan;Zhang, Rong;liliwang@upenn.edu;Linheng Li;kli1@uthsc.edu;tsx@case.edu;ssun@mdanderson.org;ysang@tnstate.edu;wu@crystal.harvard.edu;peijun@strubi.ox.ac.uk;jiayu@coh.org;bchen@crystal.harvard.edu;Wen, Haitao;Qu, Feng;Hezhao.Ji@umanitoba.ca;Li, Zihai;zhengyo@msu.edu;zhanglinqi@tsinghua.edu.cn;wxiao@temple.edu;Whu@temple.edu;RSun@mednet.ucla.edu;Guangping.Gao@umassmed.edu;PZheng@ihv.umaryland.edu;GMSWANG@nus.edu.sg;Shi, Pei yong;yaliu@ihv.umaryland.edu;ziying-yan@uiowa.edu;lqiao@luc.edu;yong.xiong@yale.edu;Wang, Qiuhong;shuping_tong_md@brown.edu;pinghuif@usc.edu;gaof@im.ac.cn
Subject: Re: [EXTERNAL] Happy Thanksgiving and meeting next year, June 12-13, 2020

Thanks for sharing. Happy Thanksgiving to everyone!

Best wishes,

Jie

Jie Sun, Ph.D.
Associate Professor
Department of Medicine
Department of Immunology
Mayo Clinic
Stabile 8-26
200 1st St SW
Rochester, MN 55905
Tel: 507-284-9503
Email: Sun.Jie@mayo.edu
http://www.mayo.edu/research/faculty/sun-jie-ph-d/bio-20348662

From: "Liu, Shan-Lu" <liu.6244@osu.edu>
Date: Thursday, November 28, 2019 at 10:54 AM
To: "zhengzhiming4@gmail.com" <zhengzhiming4@gmail.com>, "haitguo@iupui.edu" <haitguo@iupui.edu>, "tzhou@mail.nih.gov" <tzhou@mail.nih.gov>, "GCheng@mednet.ucla.edu" <GCheng@mednet.ucla.edu>, "liangy@umn.edu" <liangy@umn.edu>, "rli@vcu.edu" <rli@vcu.edu>, "wjma@ksu.edu" <wjma@ksu.edu>, "xjmeng@vt.edu" <xjmeng@vt.edu>, "Zhijian.Chen@UTSouthwestern.edu" <Zhijian.Chen@UTSouthwestern.edu>, "mluo@gsu.edu" <mluo@gsu.edu>, "zhangyj@umd.edu" <zhangyj@umd.edu>, "xzhu1@umd.edu" <xzhu1@umd.edu>, "jqiu@kumc.edu" <jqiu@kumc.edu>, "lijun@uic.edu" <lijun@uic.edu>, "fengwei.bai@usm.edu" <fengwei.bai@usm.edu>, "andyu@iupui.edu" <andyu@iupui.edu>, "reachxw@vt.edu" <reachxw@vt.edu>, "gluo@uab.edu" <gluo@uab.edu>, "ldu@nybc.org" <ldu@nybc.org>, "hxu@tulane.edu" <hxu@tulane.edu>, "liu_fy@berkeley.edu" <liu_fy@berkeley.edu>, "shitao.li@okstate.edu" <shitao.li@okstate.edu>, "Shan.lu@umassmed.edu" <Shan.lu@umassmed.edu>, "haihu@UTMB.edu" <haihu@UTMB.edu>, "wenzheho@temple.edu" <wenzheho@temple.edu>, "Qfeng4@central.uh.edu" <Qfeng4@central.uh.edu>, "tang@bio.fsu.edu" <tang@bio.fsu.edu>, "feng.li@sdstate.edu" <feng.li@sdstate.edu>, "ruilu@lsu.edu" <ruilu@lsu.edu>, "sxiang2@unl.edu" <sxiang2@unl.edu>, "qiyi.tang@howard.edu" <qiyi.tang@howard.edu>, "dingsw@ucr.edu" <dingsw@ucr.edu>, "guohua@missouri.edu" <guohua@missouri.edu>, "bling@tulane.edu" <bling@tulane.edu>, "junwang@pharmacy.arizona.edu" <junwang@pharmacy.arizona.edu>, "lifang@umn.edu" <lifang@umn.edu>, "wang518@umd.edu" <wang518@umd.edu>, "gaos8@upmc.edu" <gaos8@upmc.edu>, "pewang@uchc.edu" <pewang@uchc.edu>, "xiangy@uthscsa.edu" <xiangy@uthscsa.edu>, "fzhu@bio.fsu.edu" <fzhu@bio.fsu.edu>, "chen.liang@mcgill.ca" <chen.liang@mcgill.ca>, "lyuan@vt.edu" <lyuan@vt.edu>, "fgao@duke.edu" <fgao@duke.edu>, "wangjw28@163.com" <wangjw28@163.com>, "xfyu1@zju.edu.cn" <xfyu1@zju.edu.cn>, "bzhao@partners.org" <bzhao@partners.org>, "jianw@musc.edu" <jianw@musc.edu>, "zyang@ksu.edu" <zyang@ksu.edu>, "yu.cong@nih.gov" <yu.cong@nih.gov>, "weiming.yuan@usc.edu" <weiming.yuan@usc.edu>, "Zongdi.feng@nationwidechildrens.org" <Zongdi.feng@nationwidechildrens.org>, "juh13@psu.edu" <juh13@psu.edu>, "hengx@missouri.edu" <hengx@missouri.edu>, "lsu@med.unc.edu" <lsu@med.unc.edu>, "ywu8@gmu.edu" <ywu8@gmu.edu>, "jwu@whu.edu.cn" <jwu@whu.edu.cn>, "tshuo@uic.edu" <tshuo@uic.edu>, "Shibojiang@fudan.edu.cn" <Shibojiang@fudan.edu.cn>, "sjiang@nybc.org" <sjiang@nybc.org>, "pinwang@usc.edu" <pinwang@usc.edu>, "rzhao@som.umaryland.edu" <rzhao@som.umaryland.edu>, "shuylong@mail.sysu.edu.cn" <shuylong@mail.sysu.edu.cn>, "xuefeng.liu@georgetown.edu" <xuefeng.liu@georgetown.edu>, "yuxingli@som.umaryland.edu" <yuxingli@som.umaryland.edu>, "shixia.wang@umassmed.edu" <shixia.wang@umassmed.edu>, "yhe@ipbcams.ac.cn" <yhe@ipbcams.ac.cn>, "Pinghui.feng@usc.edu" <Pinghui.feng@usc.edu>, "ju-tao.guo@bblumberg.org" <ju-tao.guo@bblumberg.org>, "lin.liu@okstate.edu"

<lin.liu@okstate.edu>, "hua.zhu@rutgers.edu" <hua.zhu@rutgers.edu>, "Jinhong.chang@bblumberg.org" <Jinhong.chang@bblumberg.org>, "jianzhu1012@gmail.com" <jianzhu1012@gmail.com>, "ronghai@ucr.edu" <ronghai@ucr.edu>, "jun.zhu@nih.gov" <jun.zhu@nih.gov>, "jliu4@uams.edu" <jliu4@uams.edu>, "xiangpeng.kong@med.nyu.edu" <xiangpeng.kong@med.nyu.edu>, "haoquanwu@outlook.com" <haoquanwu@outlook.com>, "Wenjun.liu@defence.gov.au" <Wenjun.liu@defence.gov.au>, "Liang.shan@wustl.edu" <Liang.shan@wustl.edu>, "hliao@duke.edu" <hliao@duke.edu>, "yuan2@upenn.edu" <yuan2@upenn.edu>, "zxing@umn.edu" <zxing@umn.edu>, "hongmin.li@health.ny.gov" <hongmin.li@health.ny.gov>, "pzheng@ihv.umaryland.edu" <pzheng@ihv.umaryland.edu>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "jxw103@case.edu" <jxw103@case.edu>, "xiangguo.qiu@canada.ca" <xiangguo.qiu@canada.ca>, Feng Shao <shaofeng@nibs.ac.cn>, "zlshi@wh.iov.cn" <zlshi@wh.iov.cn>, "klan@whu.edu.cn" <klan@whu.edu.cn>, "zengmsh@mail.sysu.edu.cn" <zengmsh@mail.sysu.edu.cn>, Nan Yan <Nan.Yan@UTSouthwestern.edu>, "Zhang, Rong" <rongzhang@wustl.edu>, "liliwang@upenn.edu" <liliwang@upenn.edu>, Linheng Li <LIL@stowers.org>, "kli1@uthsc.edu" <kli1@uthsc.edu>, "tsx@case.edu" <tsx@case.edu>, "ssun@mdanderson.org" <ssun@mdanderson.org>, "ysang@tnstate.edu" <ysang@tnstate.edu>, "Liu, Shan-Lu" <liu.6244@osu.edu>, "wu@crystal.harvard.edu" <wu@crystal.harvard.edu>, "Sun, Jie, Ph.D." <Sun.Jie@mayo.edu>, "peijun@strubi.ox.ac.uk" <peijun@strubi.ox.ac.uk>, "jiayu@coh.org" <jiayu@coh.org>, "bchen@crystal.harvard.edu" <bchen@crystal.harvard.edu>, "Wen, Haitao" <Haitao.Wen@osumc.edu>, "Qu, Feng" <qu.28@osu.edu>, "Hezhao.Ji@umanitoba.ca" <Hezhao.Ji@umanitoba.ca>, "Li, Zihai" <zihai@musc.edu>, "zhengyo@msu.edu" <zhengyo@msu.edu>, "zhanglinqi@tsinghua.edu.cn" <zhanglinqi@tsinghua.edu.cn>, "wxiao@temple.edu" <wxiao@temple.edu>, "Whu@temple.edu" <Whu@temple.edu>, "RSun@mednet.ucla.edu" <RSun@mednet.ucla.edu>, "Guangping.Gao@umassmed.edu" <Guangping.Gao@umassmed.edu>, "PZheng@ihv.umaryland.edu" <PZheng@ihv.umaryland.edu>, "GMSWANG@nus.edu.sg" <GMSWANG@nus.edu.sg>, "peshi@UTMB.EDU" <peshi@UTMB.EDU>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "ziying-yan@uiowa.edu" <ziying-yan@uiowa.edu>, "lqiao@luc.edu" <lqiao@luc.edu>, "yong.xiong@yale.edu" <yong.xiong@yale.edu>, "Wang, Qiuhong" <wang.655@osu.edu>, "shuping_tong_md@brown.edu" <shuping_tong_md@brown.edu>, "pinghuif@usc.edu" <pinghuif@usc.edu>, "gaof@im.ac.cn" <gaof@im.ac.cn>
Subject: [EXTERNAL] Happy Thanksgiving and meeting next year, June 12-13, 2020

Dear friends and colleagues,

I wish you all a great Thanksgiving holiday!

A few updates:

1. We will have our first scientific meeting on June 12-13, 2020, right before the ASV annual meeting (June 13-17) in Fort Collins, Colorado State University. Organizing and scientific committees will be formed soon.
2. I am excited to share that Dr. Xiang-Jin (XJ) Meng of Virginia Tech, a distinguished virology and a member of the US National Academy of Science, will be the keynote speaker of this meeting. Details will follow.
3. In addition to scientific programs, we will also hold an election; a new leadership team will be elected to serve our community for the next two years.
4. Attached please find a brief report of our Kunming meeting, along with a few photos.

Please let me know if you have comments and suggestions.

All best wishes, and happy holidays!

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

From: Jiang, Wei <jianw@musc.edu>
Sent: Thursday, November 28, 2019 11:14 AM
To: Liu, Shan-Lu;zhengzhiming4@gmail.com;haitguo@iupui.edu;tzhou@mail.nih.gov;GCheng@mednet.ucla.edu;liangy@umn.edu;rli@vcu.edu;wjma@ksu.edu;xjmeng@vt.edu;Zhijian.Chen@UTSouthwestern.edu;mluo@gsu.edu;zhangyj@umd.edu;xzhu1@umd.edu;jqiu@kumc.edu;lijun@uic.edu;fengwei.bai@usm.edu;andyu@iupui.edu;reachxw@vt.edu;gluo@uab.edu;ldu@nybc.org;hxu@tulane.edu;liu_fy@berkeley.edu;shitao.li@okstate.edu;Shan.lu@umassmed.edu;Hu, Haitao;wenzheho@temple.edu;Qfeng4@central.uh.edu;tang@bio.fsu.edu;feng.li@sdstate.edu;ruilu@lsu.edu;sxiang2@unl.edu;qiyi.tang@howard.edu;dingsw@ucr.edu;guohua@missouri.edu;bling@tulane.edu;junwang@pharmacy.arizona.edu;lifang@umn.edu;wang518@umd.edu;gaos8@upmc.edu;pewang@uchc.edu;xiangy@uthscsa.edu;fzhu@bio.fsu.edu;chen.liang@mcgill.ca;lyuan@vt.edu;fgao@duke.edu;wangjw28@163.com;xfyu1@zju.edu.cn;bzhao@partners.org;zyang@ksu.edu;yu.cong@nih.gov;weiming.yuan@usc.edu;Zongdi.feng@nationwidechildrens.org;juh13@psu.edu;hengx@missouri.edu;lsu@med.unc.edu;ywu8@gmu.edu;jwu@whu.edu.cn;tshuo@uic.edu;Shibojiang@fudan.edu.cn;sjiang@nybc.org;pinwang@usc.edu;rzhao@som.umaryland.edu;shuylong@mail.sysu.edu.cn;xuefeng.liu@georgetown.edu;yuxingli@som.umaryland.edu;shixia.wang@umassmed.edu;yhe@ipbcams.ac.cn;Pinghui.feng@usc.edu;ju-tao.guo@bblumberg.org;lin.liu@okstate.edu;hua.zhu@rutgers.edu;Jinhong.chang@bblumberg.org;jianzhu1012@gmail.com;ronghai@ucr.edu;jun.zhu@nih.gov;jliu4@uams.edu;xiangpeng.kong@med.nyu.edu;haoquanwu@outlook.com;Wenjun.liu@defence.gov.au;Liang.shan@wustl.edu;hliao@duke.edu;yuan2@upenn.edu;zxing@umn.edu;hongmin.li@health.ny.gov;pzheng@ihv.umaryland.edu;yaliu@ihv.umaryland.edu;jxw103@case.edu;xiangguo.qiu@canada.ca;Feng Shao;zlshi@wh.iov.cn;klan@whu.edu.cn;zengmsh@mail.sysu.edu.cn;Nan Yan;Zhang, Rong;liliwang@upenn.edu;Linheng Li;kli1@uthsc.edu;tsx@case.edu;ssun@mdanderson.org;ysang@tnstate.edu;wu@crystal.harvard.edu;Sun.Jie@mayo.edu;peijun@strubi.ox.ac.uk;jiayu@coh.org;bchen@crystal.harvard.edu;Wen, Haitao;Qu, Feng;Hezhao.Ji@umanitoba.ca;Li, Zihai;zhengyo@msu.edu;zhanglinqi@tsinghua.edu.cn;wxiao@temple.edu;Whu@temple.edu;RSun@mednet.ucla.edu;Guangping.Gao@umassmed.edu;pzheng@ihv.umaryland.edu;GMSWANG@nus.edu.sg;Shi, Pei yong;yaliu@ihv.umaryland.edu;ziying-yan@uiowa.edu;lqiao@luc.edu;yong.xiong@yale.edu;Wang, Qiuhong;shuping_tong_md@brown.edu;pinghuif@usc.edu;gaof@im.ac.cn
Subject: Re: Happy Thanksgiving and meeting next year, June 12-13, 2020

Thank you for sharing the information, this was a fantastic meeting, I did enjoy it at Kunming!

Wei Jiang, M.D. & M.S
Associate Professor

Department of Microbiology and Immunology
Division of Infectious Diseases, Department of Medicine
Medical University of South Carolina
173 Ashley Ave. BSB208D
Charleston, SC 29425
Lab phone 843-876-2457
jianw@musc.edu

From: Liu, Shan-Lu <liu.6244@osu.edu>
Sent: Thursday, November 28, 2019 10:57 AM
To: zhengzhiming4@gmail.com <zhengzhiming4@gmail.com>; haitguo@iupui.edu <haitguo@iupui.edu>; tzhou@mail.nih.gov <tzhou@mail.nih.gov>; GCheng@mednet.ucla.edu <GCheng@mednet.ucla.edu>; liangy@umn.edu <liangy@umn.edu>; rli@vcu.edu <rli@vcu.edu>; wjma@ksu.edu <wjma@ksu.edu>; xjmeng@vt.edu <xjmeng@vt.edu>; Zhijian.Chen@UTSouthwestern.edu <Zhijian.Chen@UTSouthwestern.edu>; mluo@gsu.edu <mluo@gsu.edu>; zhangyj@umd.edu <zhangyj@umd.edu>; xzhu1@umd.edu <xzhu1@umd.edu>; jqiu@kumc.edu <jqiu@kumc.edu>; lijun@uic.edu <lijun@uic.edu>; fengwei.bai@usm.edu <fengwei.bai@usm.edu>; andyu@iupui.edu <andyu@iupui.edu>; reachxw@vt.edu <reachxw@vt.edu>; gluo@uab.edu <gluo@uab.edu>; ldu@nybc.org <ldu@nybc.org>; hxu@tulane.edu <hxu@tulane.edu>; liu_fy@berkeley.edu <liu_fy@berkeley.edu>; shitao.li@okstate.edu <shitao.li@okstate.edu>; Shan.lu@umassmed.edu <Shan.lu@umassmed.edu>; haihu@UTMB.edu <haihu@UTMB.edu>; wenzheho@temple.edu <wenzheho@temple.edu>; Qfeng4@central.uh.edu <Qfeng4@central.uh.edu>; tang@bio.fsu.edu <tang@bio.fsu.edu>; feng.li@sdstate.edu <feng.li@sdstate.edu>; ruilu@lsu.edu <ruilu@lsu.edu>; sxiang2@unl.edu <sxiang2@unl.edu>; qiyi.tang@howard.edu <qiyi.tang@howard.edu>; dingsw@ucr.edu <dingsw@ucr.edu>; guohua@missouri.edu <guohua@missouri.edu>; bling@tulane.edu <bling@tulane.edu>; junwang@pharmacy.arizona.edu <junwang@pharmacy.arizona.edu>; lifang@umn.edu <lifang@umn.edu>; wang518@umd.edu <wang518@umd.edu>; gaos8@upmc.edu <gaos8@upmc.edu>; pewang@uchc.edu <pewang@uchc.edu>; xiangy@uthscsa.edu <xiangy@uthscsa.edu>; fzhu@bio.fsu.edu <fzhu@bio.fsu.edu>; chen.liang@mcgill.ca <chen.liang@mcgill.ca>; lyuan@vt.edu <lyuan@vt.edu>; fgao@duke.edu <fgao@duke.edu>; wangjw28@163.com <wangjw28@163.com>; xfyu1@zju.edu.cn <xfyu1@zju.edu.cn>; bzhao@partners.org <bzhao@partners.org>; Jiang, Wei <jianw@musc.edu>; zyang@ksu.edu <zyang@ksu.edu>; yu.cong@nih.gov <yu.cong@nih.gov>; weiming.yuan@usc.edu <weiming.yuan@usc.edu>; Zongdi.feng@nationwidechildrens.org <Zongdi.feng@nationwidechildrens.org>; juh13@psu.edu <juh13@psu.edu>; hengx@missouri.edu <hengx@missouri.edu>; lsu@med.unc.edu <lsu@med.unc.edu>; ywu8@gmu.edu <ywu8@gmu.edu>; jwu@whu.edu.cn <jwu@whu.edu.cn>; tshuo@uic.edu <tshuo@uic.edu>; Shibojiang@fudan.edu.cn <Shibojiang@fudan.edu.cn>; sjiang@nybc.org <sjiang@nybc.org>; pinwang@usc.edu <pinwang@usc.edu>; rzhao@som.umaryland.edu <rzhao@som.umaryland.edu>; shuylong@mail.sysu.edu.cn <shuylong@mail.sysu.edu.cn>; xuefeng.liu@georgetown.edu <xuefeng.liu@georgetown.edu>; yuxingli@som.umaryland.edu <yuxingli@som.umaryland.edu>; shixia.wang@umassmed.edu <shixia.wang@umassmed.edu>; yhe@ipbcams.ac.cn <yhe@ipbcams.ac.cn>; Pinghui.feng@usc.edu <Pinghui.feng@usc.edu>; ju-tao.guo@bblumberg.org <ju-tao.guo@bblumberg.org>; lin.liu@okstate.edu <lin.liu@okstate.edu>; hua.zhu@rutgers.edu <hua.zhu@rutgers.edu>; Jinhong.chang@bblumberg.org <Jinhong.chang@bblumberg.org>; jianzhu1012@gmail.com <jianzhu1012@gmail.com>; ronghai@ucr.edu <ronghai@ucr.edu>; jun.zhu@nih.gov <jun.zhu@nih.gov>; jliu4@uams.edu <jliu4@uams.edu>; xiangpeng.kong@med.nyu.edu <xiangpeng.kong@med.nyu.edu>; haoquanwu@outlook.com <haoquanwu@outlook.com>; Wenjun.liu@defence.gov.au <Wenjun.liu@defence.gov.au>; Liang.shan@wustl.edu <Liang.shan@wustl.edu>; hliao@duke.edu <hliao@duke.edu>; yuan2@upenn.edu <yuan2@upenn.edu>; zxing@umn.edu <zxing@umn.edu>; hongmin.li@health.ny.gov <hongmin.li@health.ny.gov>; pzheng@ihv.umaryland.edu <pzheng@ihv.umaryland.edu>; yaliu@ihv.umaryland.edu <yaliu@ihv.umaryland.edu>; jxw103@case.edu <jxw103@case.edu>; xiangguo.qiu@canada.ca <xiangguo.qiu@canada.ca>; Feng Shao <shaofeng@nibs.ac.cn>; zlshi@wh.iov.cn <zlshi@wh.iov.cn>; klan@whu.edu.cn <klan@whu.edu.cn>; zengmsh@mail.sysu.edu.cn <zengmsh@mail.sysu.edu.cn>; Nan Yan <Nan.Yan@UTSouthwestern.edu>; Zhang, Rong <rongzhang@wustl.edu>; liliwang@upenn.edu <liliwang@upenn.edu>; Linheng Li <LIL@stowers.org>; kli1@uthsc.edu <kli1@uthsc.edu>; tsx@case.edu <tsx@case.edu>; ssun@mdanderson.org <ssun@mdanderson.org>; ysang@tnstate.edu <ysang@tnstate.edu>; Liu, Shan-Lu <liu.6244@osu.edu>; wu@crystal.harvard.edu <wu@crystal.harvard.edu>; Sun.Jie@mayo.edu <Sun.Jie@mayo.edu>; peijun@strubi.ox.ac.uk <peijun@strubi.ox.ac.uk>;

jiayu@coh.org <jiayu@coh.org>; bchen@crystal.harvard.edu <bchen@crystal.harvard.edu>; Wen, Haitao <Haitao.Wen@osumc.edu>; Qu, Feng <qu.28@osu.edu>; Hezhao.Ji@umanitoba.ca <Hezhao.Ji@umanitoba.ca>; Li, Zihai <zihai@musc.edu>; zhengyo@msu.edu <zhengyo@msu.edu>; zhanglinqi@tsinghua.edu.cn <zhanglinqi@tsinghua.edu.cn>; wxiao@temple.edu <wxiao@temple.edu>; Whu@temple.edu <Whu@temple.edu>; RSun@mednet.ucla.edu <RSun@mednet.ucla.edu>; Guangping.Gao@umassmed.edu <Guangping.Gao@umassmed.edu>; PZheng@ihv.umaryland.edu <PZheng@ihv.umaryland.edu>; GMSWANG@nus.edu.sg <GMSWANG@nus.edu.sg>; peshi@UTMB.EDU <peshi@UTMB.EDU>; yaliu@ihv.umaryland.edu <yaliu@ihv.umaryland.edu>; ziying-yan@uiowa.edu <ziying-yan@uiowa.edu>; lqiao@luc.edu <lqiao@luc.edu>; yong.xiong@yale.edu <yong.xiong@yale.edu>; Wang, Qiuhong <wang.655@osu.edu>; shuping_tong_md@brown.edu <shuping_tong_md@brown.edu>; pinghuif@usc.edu <pinghuif@usc.edu>; gaof@im.ac.cn <gaof@im.ac.cn>
Subject: Happy Thanksgiving and meeting next year, June 12-13, 2020

Dear friends and colleagues,

I wish you all a great Thanksgiving holiday!

A few updates:

1. We will have our first scientific meeting on June 12-13, 2020, right before the ASV annual meeting (June 13-17) in Fort Collins, Colorado State University. Organizing and scientific committees will be formed soon.
2. I am excited to share that Dr. Xiang-Jin (XJ) Meng of Virginia Tech, a distinguished virology and a member of the US National Academy of Science, will be the keynote speaker of this meeting. Details will follow.
3. In addition to scientific programs, we will also hold an election; a new leadership team will be elected to serve our community for the next two years.
4. Attached please find a brief report of our Kunming meeting, along with a few photos.

Please let me know if you have comments and suggestions.

All best wishes, and happy holidays!

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

From: LeDuc, James W.
Sent: Friday, April 3, 2020 12:48 PM
To: Shi, Pei yong;Yuan Zhiming;zlshi
Subject: How did covid-19 begin? Its initial origin story is shaky. from The Washington Post

https://www.washingtonpost.com/opinions/global-opinions/how-did-covid-19-begin-its-initial-origin-story-is-shaky/2020/04/02/1475d488-7521-11ea-87da-77a8136c1a6d_story.html

Please see link to article that appeared today in the Washington Post. I've has inquiries already. Any information you might have to address the work done in the Wuhan CDC would be helpful. BSL2 work there on coronaviruses? True?

Thanks, and I hope you are all well. Things are heating up here but so far everyone is well.

Best wishes, Jim

To: Wang Linfa[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Lim Sandie[sandie.lim@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Mon 1/6/2020 1:45:20 AM (UTC-06:00)
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Prof Wang,
Noted with thanks.

Dear Pei Yong,
Many thanks for accepting our invitation. We will send you a letter of invite for your visit from 16 March to 21 March and follow up with you with more information.

Thank you and we look forward to seeing you in March.

Regards,
Yih-Shin

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Monday, 6 January 2020 10:14 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Pei-Yong,

That is wonderful!

Dear Yih Sin,
Can you follow up with flight/hotel booking, seminar, etc with Pei-Yong?

Many thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Sunday, 5 January, 2020 9:00 PM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Linfa,

Happy 2020!

Many thanks for the kind invitation. I am excited about the visit and the retreat. I could arrive on Monday and give a seminar on Tuesday and leave on Saturday.

I'm glad you are helping with the "Wuhan pneumonia" investigation. Please let me know if there is anything I could help.

All the best from Galveston!

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, January 4, 2020 6:45 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Forgot to mention: you will be invited under the "distinguished professor" title and you are also required to give a seminar to the whole school either on Tue or Wed before the retreat, so you need to plan a 4-5 day visit.

Thanks

LF

PS: as you may be aware, the "Wuhan pneumonia" investigation is ongoing and highly "explosive". I will be in Wuhan on 15-18 Jan.

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Wang Linfa
Sent: Sunday, 5 January 2020 8:43 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Invitation as a guest speaker for the EID retreat 2020

Dear Pei Yong,

Happy 2020!

We are planning a BIG retreat for EID on 19-20 March 2020, first time to have a 2-day retreat.

We are going to invite all past PIs (Duane, Veronika, etc) and will officially farewell Mariano.

We thought it will be a good idea to give Mariano a surprise by inviting you as a guest speaker.

Duke-NUS will of course cover the return business class airfare and all associated costs.

Do let me know if you are available and able to do that.

Thanks in advance.

Cheers,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Sun 1/5/2020 8:13:43 PM (UTC-06:00)
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Pei-Yong,

That is wonderful!

Dear Yih Sin,
Can you follow up with flight/hotel booking, seminar, etc with Pei-Yong?

Many thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Sunday, 5 January, 2020 9:00 PM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Linfa,

Happy 2020!

Many thanks for the kind invitation. I am excited about the visit and the retreat. I could arrive on Monday and give a seminar on Tuesday and leave on Saturday.

I'm glad you are helping with the "Wuhan pneumonia" investigation. Please let me know if there is anything I could help.

All the best from Galveston!

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, January 4, 2020 6:45 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Forgot to mention: you will be invited under the "distinguished professor" title and you are also required to give a seminar to the whole school either on Tue or Wed before the retreat, so you need to plan a 4-5 day visit.

Thanks

LF

PS: as you may be aware, the "Wuhan pneumonia" investigation is ongoing and highly "explosive". I will be in Wuhan on 15-18 Jan.

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Wang Linfa
Sent: Sunday, 5 January 2020 8:43 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Invitation as a guest speaker for the EID retreat 2020

Dear Pei Yong,

Happy 2020!

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We thought it will be a good idea to give Mariano a surprise by inviting you as a guest speaker.

Duke-NUS will of course cover the return business class airfare and all associated costs.

Do let me know if you are available and able to do that.

Thanks in advance.

Cheers,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Wednesday, May 20, 2020 10:44 PM
To: 'relman@stanford.edu';'rbaric@email.unc.edu';'saif.2@osu.edu';'stanley-perlman@uiowa.edu';'daszak@ecohealthalliance.org';'harvey.fineberg@moore.org';'dgriffi6@jhmi.edu';'peggy@hbfam.net';LeDuc, James W.;Shi, Pei yong;Dzau, Victor J.
Cc: 'fsharples_3@hotmail.com';Lowenthal, Micah;'antoinette_baric@med.unc.edu';'andre@ecohealthalliance.org';'jennifer.ryan@moore.org';Bowman, Katherine;Kanarek, Morgan;'Raymond JEANLOZ';Hare, Hope;'davidrfranz@gmail.com'
Subject: 3rd Virtual U.S. China dialogue meeting on COVID-19
Attachments: Immunity topics for 3rd China U.S. Dialogue.docx

Greetings,

As we discussed during our meeting on Monday we hope to hold a third virtual dialogue meeting with CAS and CCDC experts to discuss what is known about COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

We have proposed to CAS that this meeting take place on **Tuesday evening, May 26 from 9:00 -11:00 PM ET for the Americans** (and the morning of Wednesday, May 27 for the Chinese). I have attached the list of questions on these topics we sent to CAS for your information. **Please let me know if you are interested and available to participate in the 3rd virtual dialogue meeting.**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 18, 2020 10:18 AM
To: Hare, Hope <HHare@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>

Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
3) Ideas for topics (and additional American experts) for future virtual dialogue sessions
4) Discussion of George Gao's joint statement idea
5) CAS idea to post a blurb about the meetings on the CAS website
6) Other issues, concerns

I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: [redacted] **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 4:26 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Cc: Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
Here is the Zoom link for this meeting: [redacted] **552.136**
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

The National Academies of
SCIENCES · ENGINEERING · MEDICINE

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

Questions:

Immune Response and Immunotherapy

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection
  - How is immune response being measured?
  - Was there standardization of testing tools?
- What can be said about the characterization of the
  - Innate immune responses?
  - humoral immune response?
  - cellular immune response?
- What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection?
  - Is the use of immune plasma effective?
  - Have there been any complications?
- What has been China's experience with human monoclonal antibodies for treatment and prevention?
  - Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?
- What immunopathologies are evident in the patients with COVID-19?
  - Are there any biomarkers in patients who develop systemic inflammation?
  - What is the most effective treatment for patients who develop a cytokine storm?

Immunity

- After recovery, what types of antiviral immune responses are present?
- Do these immune responses protect from re-infection?
- What is known about the durability of neutralizing antibody and longevity of protective immunity?
  Did recovery from SARS provide any protection from infection with SARS-CoV-2?

Reactivation or Reinfection of Recovered Patients

- Has reactivation of latent virus or re-infection been seen among survivors?
- Is reactivation/reinfection a concern with respect to a fall resurgence?
- What steps should be taken in anticipation of a fall resurgence in transmission?

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Fri 1/17/2020 9:10:07 AM (UTC-06:00)
Subject: Re: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

In the airport flying back to SG now.
Let's chat when I am back in office

Sent from my iPhone

On 17 Jan 2020, at 10:31 PM, Shi, Pei yong <peshi@utmb.edu> wrote:

Hi Linfa,
Hope your trip to Wuhan is exciting.
Let's talk when you get a chance.
Best,

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Thursday, January 16, 2020 10:03 PM
To: Shi, Pei yong <peshi@UTMB.EDU>; Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

Great, many thanks!

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, 15 January 2020 10:47 AM
To: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

Dear Linfa,

Please see the attached support letter and feel free to give any suggestions.
Best, Pei-Yong

From: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Sent: Monday, January 13, 2020 9:21 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

~ Sent on behalf of Professor Linfa Wang, Programme Director, Programme in EID, Duke-NUS Medical School ~

Dear Prof Shi,

The National Medical Excellence Awards (NMEA), organised by Singapore's National Medical Research Council (NMRC), is a series of awards that aims to recognise and celebrate healthcare professionals who have made significant contributions to medical excellence in Singapore, be it in the fields of research, knowledge translation, clinical practice or healthcare delivery.

The Core Leaders of Singhealth Duke-NUS Academic Medical Center has proposed for Professor Eng Eong Ooi to be nominated for the NMEA Outstanding Clinician Scientist Award for his contributions in translation research. Prof Ooi is a three-time recipient of the NMRC Clinician-Scientist Senior Investigator Award and led several investigator-initiated clinical trials.

We will be grateful if you could provide a reference letter for Prof Ooi's nomination for this prestigious national award. It would be helpful if you would comment on the following:

1. Prof Ooi's contributions towards healthcare research resulting or will result in healthcare benefits for the Singapore community;
2. His involvement in the translational and/or clinical research and how his basic research impacts the clinical and commercialisation outcomes;
3. The impact of his contributions and recognition on the international level;
4. Any additional ins insights that may be helpful in strengthening this nomination

Attached is a copy of his CV for your reference. We would appreciate a reply by 7 Feb 2020, if at all possible. Please send your letter to me (linfa.wang@duke-nus.edu.sg) and our programme manager (yihshin.lai@duke-nus.edu.sg). Thank you in advance for taking time to do this. Your response will be maintained in confidence.

Yours sincerely,

<image001.jpg>

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: zlshi <zlshi@wh.iov.cn>
Sent: Sunday, June 9, 2019 8:59 PM
To: dyjin;tlying;Shi, Pei yong
Cc: Rong Lijun
Subject: Fw: SCBA session speakers

Dear all,

Would you please see the following email and register in the meeting.

Thanks and see you soon.

Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China
Tel & Fax: (0086) 27 87197240
Email: zlshi@wh.iov.cn

From: Li, Linheng
Date: 2019-06-06 22:39
To: btsang@ohri.ca; bgao@mail.nih.gov; byang@sri.utoronto.ca; Yu, Ron; chgzou@ynu.edu.cn; clyang@genetics.ac.cn; cpeng@yorku.ca; Changqing.Ju@uth.tmc.edu; dann@coh.org; ld2567@cumc.columbia.edu; dewang@mcw.edu; dyu@mdanderson.org; dongwang@ucsd.edu; fxia@uams.edu; liuf@ioz.ac.cn; liuf@hotmail.com; gcheng@mednet.ucla.edu; gonghong.wei@oulu.fi; HLiang1@mdanderson.org; Hansen.He@uhnresearch.ca; hss.sun@utoronto.ca; yanghuanming@genomics.cn; huiz@bcm.edu; hulin@wakehealth.edu; Huiping.Zhou@vcuhealth.org; minglam@uw.edu; juh13@psu.edu; jxu@bcm.edu; jianping_jin@zju.edu.cn; jie.qiao@263.net; Jindan-yu@northwestern.edu; jchen@emory.edu; jsli@sibcb.ac.cn; jliu@mdanderson.org; jzhang@luc.edu; jchiang@neomed.edu; jhuang@zju.edu.cn; Ji@medicine.tamhsc.edu; klan@whu.edu.cn; XuK3@uthscsa.edu; llan1@mgh.harvard.edu; lijun@uic.edu; Lcheng2@jhmi.edu; Lcheng2@jhmi.edu; lsu@med.unc.edu; weilixin_smmu@163.com; qinlx@fudan.edu.cn; wmeng@bcm.edu; myou@neomed.edu; luominmin@nibs.ac.cn; homi@mail.nih.gov; psun@wakehealth.edu; perchen@163.com; pzhang@neomed.edu; qi.cao@northwestern.edu; rjzhou@whu.edu.cn; ren@brandeis.edu; rzhang27@Central.UH.EDU; sz2296@cumc.columbia.edu; ssun@mdanderson.org; shaomeng@umich.edu; gaoshaorong@tongji.edu.cn; Sheng.Zhang@uth.tmc.edu; chengs@mail.nih.gov; shc2034@med.cornell.edu; lantian012345@163.com; thchuang@nhri.org.tw; weizhang@uoguelph.ca; zongwx@pharmacy.rutgers.edu; weiwei.dang@bcm.edu; wxding@kumc.edu; wswei@pku.edu.cn; wh221@cinj.rutgers.edu; wwei2@bidmc.harvard.edu; xwwu@mdanderson.org; XJ.Wang@ucdenver.edu; Xiaobo.zhou@channing.harvard.edu; xyu@coh.org; xiaodong.cheng@uth.tmc.edu; xiaohwu@scripps.edu; xw3u@nih.gov; bianxiuwu@263.net; sean.li@childrens.harvard.edu; jzhang@cm.utexas.edu; Yang.Xia@uth.tmc.edu; liyi@bcm.edu; yisheng@yorku.ca; sunyi@umich.edu; yisun@zju.edu.cn; zhangyin@mail.nih.gov; yinghao@sibs.ac.cn; liy2@ccf.org; yongx@bcm.edu; liy2@mskcc.org; yfshi@suda.edu.cn; yuncai@lji.org; chris.lau@ucsf.edu; fengzh@cinj.rutgers.edu; zlshi@wh.iov.cn; lou.zhenkun@mayo.edu; shenzh@cinj.rutgers.edu; zp.feng@utoronto.ca; zdu@genetics.ac.cn
CC: 莫明和; Xu, Jianming; Li, Linheng
Subject: SCBA session speakers

Dear Cochairs,

The meeting local organizers received many e-mails asking about the traveling and lodging things. I was asked to
Send this note again to you as co-chairs and please do forward it to your session speakers to let them know how to handle
Registration, traveling and lodging things.

1. Please register (http://scba.medmeeting.org/8579?lang=en) and select speaker category, your registration fee is waived, However,
2. If you are a domestic speaker please pay your registration fee (http://scba.medmeeting.org) but the meeting will give you lecture fee.
3. You will be responsible for your own traveling including the airport-hotel transportation and reserving hotel room.

Thanks
We are looking forward to seeing you in Kunming.

Linheng

To: Duane J Gubler[duane.gubler@duke-nus.edu.sg]; Soman Abraham, Ph.D.[soman.abraham@duke.edu]; Greg Gray, M.D.[gregory.gray@duke.edu]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; Messling von, Veronika /6[Veronika.vonMessling@bmbf.bund.de]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Wang Linfa[linfa.wang@duke-nus.edu.sg]; Howe Shiqin[shiqin.howe@duke-nus.edu.sg]; Lim Sandie[sandie.lim@duke-nus.edu.sg]; Loh Jian Yun[jianyun.loh@duke-nus.edu.sg]; Stephanie Shirley William[shirleywilliam@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Fri 2/14/2020 12:09:50 AM (UTC-06:00)
Subject: [Postponed] EID Scientific Retreat 2020

Dear all,

We would like to thank you for agreeing to attend the EID retreat 2020 on 19 and 20 March. We were looking forward to seeing all of you at the retreat, however in view of the current COVID-19 situation, we had decided to postpone the retreat till further notice. NUS has also informed us that all events involving more than 50 participants should be cancelled.

We will update all of you once we have a confirmed date when the situation improves and hope you will be able to make it.

Thank you for your understanding.

Regards,
Yih-Shin

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Thur 2/13/2020 6:12:21 PM (UTC-06:00)
Subject: Re: Singapore visit in March

Ok thanks

Sent from my iPhone

On 14 Feb 2020, at 8:09 AM, Shi, Pei yong <peshi@utmb.edu> wrote:

Dear Linfa,

Thanks. I will be available to talk at your convenience over the weekend.

I have attached my WeChat QR code for connection.

Best,

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Thursday, February 13, 2020 5:57 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: Singapore visit in March

Dear Pei-Yong,

You beat me by 3 hours! We have made the decision to postpone the retreat, but I will first announce it at our PI meeting in one hr's time. I was going to then send the postpone notice to all guests!

Extremely busy, but a lot to chat about. So I will try to give you a call on the weekend. Let me know what is a good time and your number.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857

Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Friday, 14 February 2020 3:22 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: Singapore visit in March

Hi Linfa,

Congratulations for the very nice commentary at Lancet!

I'm writing to see if we should postpone the trip to Singapore. If so, Yih Shin needs to help me cancel the flight and hotel reservations.

Hope all well in Singapore. We could catch up over phone when you get a chance.

Best wishes from Galveston!

Pei-Yong

<Pei Yong WeChat QR code.png>

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Sun 5/3/2020 12:54:06 AM (UTC-05:00)
Subject: RE: Support letter for World Reference Center for Emerging Viruses and Arboviruses
200503-Support Letter for WRCEVA-Scott W.pdf

Here it is.

I am sure that you are watching closely the WIV saga being played out in the highest US political level and it is now in Australia as well!

Very sad indeed! I am worried that this will be another WMD scandal: found "evidence" at any cost, even if fabrication is required!

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, 28 April 2020 10:19 PM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Support letter for World Reference Center for Emerging Viruses and Arboviruses

Thanks, Linfa
I'm helping Scott Weaver for this grant.
Best, Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Tuesday, April 28, 2020 8:44 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Support letter for World Reference Center for Emerging Viruses and Arboviruses

OK will do

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>

Sent: Tuesday, 28 April 2020 7:29 PM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: FW: Support letter for World Reference Center for Emerging Viruses and Arboviruses

- External Email -

Dear Linfa,

I'm writing for a support letter for an NIH grant I'm participating. The grant is to support the World Reference Center for Emerging Viruses and Arboviruses (WRCEVA) at UTMB. The WRCEVA collects more than 7,000 viruses and distribute to global research on emerging viruses, particularly arboviruses. We are asking a few prominent scientists who have been collaborators of WRCEVA faculty or major customers of our repositories to write letters of support to include in the application. It is critical for us to demonstrate the impact of the WRCEVA to the virology community, so these letters will be important components of the application,

If you are willing to write a letter, feel free to use the attached template or guide you, or of course you may choose to write something more personal.

If possible, please send your letter electronically on letterhead by May 5th.

Many thanks for your support.

Best regards,
Pei-Yong

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

DukeNUS
Medical School

03 May 2020

Dr. Scott C. Weaver, Director
World Reference Center for Emerging Viruses and Arboviruses
Institute for Human Infections and Immunity
University of Texas Medical Branch
Galveston, Texas 77555-0610
USA

RE: Support Letter for the World Reference Center for Emerging Viruses and Arboviruses (WRCEVA)

Dear Scott,

I am writing to express my enthusiastic support for your NIH R24 renewal application in support of the World Reference Center for Emerging Viruses and Arboviruses (WRCEVA). As you know, the Duke-NUS Medical School has been a major beneficiary of the WRCEVA for many years as the recipient of critical virus strains, antibodies, and other reagents for our research programs. Your unique collection of viruses and associated reagents has been essential to many aspects of our work, including our rapid response to the Zika virus outbreak in Singapore. We have benefitted from several highly productive scientific collaborations leading to our world class findings about the virus structure and rapid development of Zika vaccine candidates. I also want to confirm that my institution will continue to rely on the WRCEVA for assistance with the identification and characterization of new viruses and strains as needed, and we will contribute samples to your collection in order to help maintain its unique value to the scientific community.

Yours sincerely,

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director, Programme in Emerging Infectious Diseases

8 College Road, Singapore 169857
T 6516 7666 F 6221 7396
www.duke-nus.edu.sg
A school of the National University of Singapore (RCB No: 200604346E)

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Wang Linfa[linfa.wang@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Tue 1/14/2020 9:20:43 PM (UTC-06:00)
Subject: RE: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

Dear Pei Yong,

Received with thanks!

Regards,
Yih-Shin

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, 15 January 2020 10:47 AM
To: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

Dear Linfa,
Please see the attached support letter and feel free to give any suggestions.
Best, Pei-Yong

From: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Sent: Monday, January 13, 2020 9:21 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)

~ Sent on behalf of Professor Linfa Wang, Programme Director, Programme in EID, Duke-NUS Medical School ~

Dear Prof Shi,

The National Medical Excellence Awards (NMEA), organised by Singapore's National Medical Research Council (NMRC), is a series of awards that aims to recognise and celebrate healthcare professionals who have made significant contributions to medical excellence in Singapore, be it in the fields of research, knowledge translation, clinical practice or healthcare delivery.

The Core Leaders of Singhealth Duke-NUS Academic Medical Center has proposed for Professor Eng Eong Ooi to be nominated for the NMEA Outstanding Clinician Scientist Award for his contributions in translation research. Prof Ooi is a three-time recipient of the NMRC Clinician-Scientist Senior Investigator Award and led several investigator-initiated clinical trials.

We will be grateful if you could provide a reference letter for Prof Ooi's nomination for this prestigious national award. It would be helpful if you would comment on the following:

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3. The impact of his contributions and recognition on the international level;

4. Any additional ins insights that may be helpful in strengthening this nomination

Attached is a copy of his CV for your reference. We would appreciate a reply by 7 Feb 2020, if at all possible. Please send your letter to me (linfa.wang@duke-nus.edu.sg) and our programme manager (yihshin.lai@duke-nus.edu.sg). Thank you in advance for taking time to do this. Your response will be maintained in confidence.

Yours sincerely,

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School

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To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Wang Linfa[linfa.wang@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Mon 1/13/2020 9:21:26 PM (UTC-06:00)
Subject: Requesting for reference letter - Eng Eong Ooi (Nomination for National Medical Excellence Awards)
CV NMEA (Eng Eong OOI).doc

~ Sent on behalf of Professor Linfa Wang, Programme Director, Programme in EID, Duke-NUS Medical School ~

Dear Prof Shi,

The National Medical Excellence Awards (NMEA), organised by Singapore's National Medical Research Council (NMRC), is a series of awards that aims to recognise and celebrate healthcare professionals who have made significant contributions to medical excellence in Singapore, be it in the fields of research, knowledge translation, clinical practice or healthcare delivery.

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2. His involvement in the translational and/or clinical research and how his basic research impacts the clinical and commercialisation outcomes;
3. The impact of his contributions and recognition on the international level;
4. Any additional ins insights that may be helpful in strengthening this nomination

Attached is a copy of his CV for your reference. We would appreciate a reply by 7 Feb 2020, if at all possible. Please send your letter to me (linfa.wang@duke-nus.edu.sg) and our programme manager (yihshin.lai@duke-nus.edu.sg). Thank you in advance for taking time to do this. Your response will be maintained in confidence.

Yours sincerely,

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School

Curriculum vitae

Name: Ooi Eng Eong
Title: Professor
Email: [HYPERLINK "mailto:engeong.ooi@duke-nus.edu.sg"] **Contact No**: 6516 8594
Office Mailing Address: Duke-NUS Medical School, 8 College Road, Singapore 169857
Current Position: Professor & Deputy Director, Programme in Emerging Infectious Diseases, Duke-NUS Medical School

Joint Positions:
Professor, SingHealth Duke-NUS Global Health Institute
Professor, Saw Swee Hock School of Public Health, National University of Singapore
Professor, Department of Microbiology & Immunology, National University of Singapore
Co-Director, Viral Research and Experimental Medicine Centre, SingHealth Duke-NUS Academic Medical Centre
Co-Founder, Tychan Pte Ltd

Academic qualifications (Indicate the degree's title, year of award and name of the institution that conferred the degree)

B.M., B.S.	University of Nottingham (1993)
Ph.D.	National University of Singapore (1998)
FRCPath.	Royal College of Pathologists, UK. (2013)

Research interests
The global emergence of epidemic dengue is fuelled partly by an incomplete understanding of the determinants of both dengue immunity and pathogenesis. My background in clinical medicine and molecular biology enables me to position my research at the interface between clinical epidemiology and trials with basic virology and immunology. Specifically, my research interests are to define how antibodies either protect against or enhance dengue virus infection and the molecular determinants of clinical and epidemiological fitness of dengue viruses. By understanding these mechanisms, I hope to contribute to the development of effective vaccines and therapeutics against dengue and other flaviviruses.

I am also interested in translational research. I co-founded Tychan Private Limited, a Singapore-based Temasek owned clinical-stage biotechnology company that develops therapeutic antibodies for emerging viruses. I have also co-founded the Viral Research and Experimental Medicine Centre at SingHealth Duke-NUS Academic Medical Centre (ViREMiCS), which aims to develop molecular endpoints to accelerate therapeutic and vaccine trials for both academia and industry.

Selected Professional Memberships and Contributions

1994-	Singapore Medical Council – full registration
2003-	Fellow of the Royal Society of Tropical Medicine and Hygiene
2006-	Member, American Society of Tropical Medicine and Hygiene
2006	WHO Temporary Adviser, UNICEF/UNDP/World Bank/WHO Special Programme for Research and Training in Tropical Diseases Scientific Working Group on Dengue
2009-2020	Member, Local Review Panel, National Medical Research Council, Singapore
2013-	Fellow of the Royal College of Pathologists, UK
2014-2016	Member of the Dengue Vaccine Scientific Advisory Board for Sanofi Pasteur
2015	Co-founder of Tychan Pte Ltd (a clinical stage biotechnology company in Singapore)
2017-2022	Editor, Journal of General Virology
2019	Director, Global Dengue and Aedes-transmitted Diseases Consortium
2019	Member, Dengue Vaccine Immunology Advisory Board, Takeda Vaccines Inc.
2019	Chair, Dengue Vaccine Efficacy Advisory Board, Takeda Vaccines Inc.
2019-2020	Co-Chair, Lancet Commission on *Aedes*-Transmitted Diseases

Honours

2010 NMRC Clinician-Scientist Award (Senior Investigator)
2013 Fellow of the Royal College of Pathologists, UK (by published works)
2014 NMRC Clinician-Scientist Award (Senior Investigator)
2016 1st Prize in SingHealth- Duke-NUS Research Team Award
2017 Fellow of the Academy of Medicine, Singapore
2019 NMRC Clinician-Scientist Award (Senior Investigator)
2019 1st Prize in SingHealth- Duke-NUS Research Team Award
2019 National Healthcare Group Research Impact Award

Selected Publications (full list can be found at: https://orcid.org/0000-0002-0520-1544)

1. Low JG*, Sung C*, Wijaya L*, Wei Y, Rathore AP, Watanabe S, Tan BH, Toh L, Chua LT, Hou Y, Chow A, Howe S, Chan WK, Tan KH, Chung JS, Cherng BP, Lye DC, Tambyah PA, Ng LC, Connolly J, Hibberd M, Leo YS, Cheung YB, Ooi EE*, Vasudevan SG (2014). Efficacy and safety of celgosivir, an alpha-glucosidase inhibitor, in dengue fever patients evaluated in a randomized, double-blind, placebo controlled proof-of-concept clinical trial. **Lancet Infect Dis** 14:706-15. *Equal contribution.
2. Robinson LN, Tharakaraman K, Rowley KJ, Costa VV, Chan KR, Wong YH, Ong LC, Tan HC, Koch T, Cain D, Kirloskar R, Viswanathan K, Liew CW, Tissire H, Ramakrishnan R, Myette JR, Babcock GJ, Sasisekharan V, Alonso S, Chen J, Lescar J, Shriver Z, Ooi EE, Sasisekharan R (2015). Structure-guided design of an antibody against dengue virus directed to a non-immunodominant epitope. **Cell**, 162:493-504.
3. Manokaran G, Finol E, Wang C, Gunaratne J, Bahl J, Ong EZ, Tan HC, Sessions OM, Ward AM, Gubler DJ, Harris E, Garcia-Blanco M, Ooi EE (2015). Dengue subgenomic RNA binds TRIM25 to inhibit interferon expression for epidemiological fitness. **Science**, 350:217-21.
4. Chan KR, Wang X, Saron WA, Gan ES, Tan HC, Mok DL, Zhang SL, Lee YH, Liang C, Wijaya L, Ghosh S, Cheung YB, Tannenbaum SR, Abraham SN, St John AL, Low JG, Ooi EE (2016). Cross-reactive antibodies enhance live attenuated virus infection for increased immunogenicity. **Nat Microbiol**, 1:16164.
5. Gan ES, Cheong WF, Chan KR, Ong EZ, Chai X, Tan HC, Ghosh S, Wenk MR, Ooi EE (2017). Hypoxia enhances antibody-dependent dengue virus infection. **EMBO J**, 36:1348-63.
6. Kwek SS, Watanabe S, Chan KR, Ong EZ, Tan HC, Ng WC, Nguyen MTX, Gan ES, Zhang SL, Chan KWK, Tan JH, Sessions OM, Manuel M, Pompon J, Chua C, Hazirah S, Tryggvason K, Vasudevan SG, Ooi EE (2018). A systematic approach to the development of a safe live attenuated zika vaccine. **Nat Commun**, 9:1031.
7. Tharakaraman K, Watanabe S, Chan KR, Huan J, Subramaniam V, Chionh YH, Raguram A, Quinlan D, McBee M, Ong EZ, Gan ES, Tan HC, Tyagi A, Bhushan S, Lescar J, Vasudevan SG, Ooi EE*, Sasisekharan R* (2018). Rational design and characterization of a Zika virus neutralizing antibody that targets a quaternary epitope. **Cell Host Microbe**, 23:618-27. *Co-corresponding authors.
8. Wilder-Smith A, Ooi EE, Horstick O, Wills B (2019). Dengue. **Lancet**, 393:350-363.
9. Chan KR, Gan ES, Chan CYY, Liang C, Low JZH, Zhang SL, Ong EZ, Bhatta A, Wijaya L, Lee YH, Low JG, Ooi EE (2019). Metabolic perturbations and cellular stress underpin susceptibility to symptomatic live attenuated yellow fever infection. **Nat Med**, 25;1218-1224.
10. Ng KH, Zhang SL, Tan HC, Kwek SS, Sessions OM, Chan CY, Liu ID, Lee CK, Tambyah PA, Ooi EE*, Yap HK* (2019). Persistent dengue virus infection in an immunosuppressed host reveals the roles of humoral and cellular immune responses. **Cell Host Microbe**, 26:601-605. *Equal contribution.

Patents held (related or unrelated to the study)

1) US Patent Application No 10/564,617, 2004. Diagnostics for SARS virus. Inventors: Kwang J, Ling A, Ooi EE, Chng H.

2) US Patent Application No PCT/SG2007/000310. Hemagglutinin antibody and uses thereof. Inventors: Hanson BJ, Lim AP, Ooi EE, Boon AC, Webby RJ. Filing date: 03 Jan 2010.
3) International Patent Application No PCT/SG2013/000455. Assay for the parallel detection of biological material based on PCR. Inventors: Wang L, Ooi EE, Sessions OM, Anderson DE. Filing date: 22 Oct 2013.
4) International Patent Publication No. WO2014/143907 A1. Novel dosing regimens of celgosivir for the treatment of dengue. Dow GS, Morrish G, Reid M, Vasudevan SG, Sung C, Rathore A, Watanabe S, Low J, Ooi EE. Publication date: 18 Sep 2014.
5) Singapore Patent Application 10201602980W. Rapid method of generating live attenuated vaccines. Ooi EE, Goh KC, Kwek SS, Tang CK. Filing date: 04 May 2016.
6) US Patent Serial No. 62/408020. Antibodies that bind zika virus envelope protein and uses thereof. Sasisekharan R, Tharakaraman K, Chan KR, Watanabe S, Vasudevan SG, Ooi EE. Filing date: 13 October 2016.

Summary of research outcomes from NMRC grants

Various grants from NMRC have enabled my laboratory to investigate the mechanistic basis of antibody-dependent dengue virus infection, including demonstration of this hypothesis in an experimental medicine trial. My laboratory has also led the way in showing how a small number of genetic differences can have profound effects on the epidemiological fitness of dengue virus. The latter understanding has now enabled us to develop a rapid approach to deriving attenuated flaviviruses for further exploration as vaccine candidates. These studies that mostly interface clinical and laboratory approaches have been published in well-respected journals. Several patents based on these findings have also either been granted or are at the national phase.

The translational focus of my research has also enabled me to play leading roles in several investigator-initiated clinical trials. One was a phase 2 trial that tested the efficacy of cholorquine as a prophylactic drug for influenza (published in *Lancet Infectious Diseases* in 2011). This trial was motivated by my laboratory's bench-based research findings. The second was to test the efficacy of celgosivir as an anti-dengue drug (published in *Lancet Infectious Diseases* in 2014) and the third was a phase I trial on a virus-like particle-based influenza vaccine (published in *Vaccine* in 2015). The final one was to test the effect of cross-reactive antibodies on the immunogenicity of live attenuated yellow fever vaccination. Primary and exploratory findings from this trial, which for the first time tested a long-standing hypothesis on antibody-dependent enhancement of virus infection through a proof-of-concept clinical trial, were published in *Nature Microbiology*, *JCI Insight* and *Nature Medicine*. Notably, of these 4 clinical trials, 3 were directly as a consequence of the basic virologic and immunologic investigations in my laboratory. My laboratory has also supported industry-sponsored therapeutic and vaccine development, including a pan-dengue therapeutic antibody against dengue (Visterra Inc, now licensed to Serum Institute of India), Zika and yellow fever (developed by Tychan Pte Ltd). We are currently in discussions with Takeda Vaccines and Janssen Pharmaceutica on collaborative clinical trials to evaluate their dengue vaccine and antiviral drug candidates using the laboratory tools that we have developed.

To: Shi, Pei yong[peshi@UTMB.EDU]; Wang Linfa[linfa.wang@duke-nus.edu.sg]
Cc: Lim Sandie[sandie.lim@duke-nus.edu.sg]; Stephanie Shirley William[shirleywilliam@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Wed 1/8/2020 7:12:49 PM (UTC-06:00)
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Pei Yong,

Received with thanks. We will start sourcing for tickets and will get back to you soon.

Regards,
Yih-Shin

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, 8 January 2020 7:51 AM
To: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>; Wang Linfa <linfa.wang@duke-nus.edu.sg>
Cc: Lim Sandie <sandie.lim@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Yih-Shin,

Thanks for help with the logistics. I could depart Houston on March 14 or 15 and leave Singapore on 21 afternoon/evening. I have attached my passport for flight/hotel booking.

Regards,
Pei-Yong

Pei-Yong Shi, Ph.D.
I.H. Kempner Professor of Human Genetics
Vice Chair for Innovation and Commercialization
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555
Phone: 409-772-6370

From: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Sent: Monday, January 6, 2020 1:45 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lim Sandie <sandie.lim@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Prof Wang,
Noted with thanks.

Dear Pei Yong,
Many thanks for accepting our invitation. We will send you a letter of invite for your visit from 16 March to 21 March and follow up with you with more information.

Thank you and we look forward to seeing you in March.

Regards,
Yih-Shin

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Monday, 6 January 2020 10:14 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Pei-Yong,

That is wonderful!

Dear Yih Sin,
Can you follow up with flight/hotel booking, seminar, etc with Pei-Yong?

Many thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Sunday, 5 January, 2020 9:00 PM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Dear Linfa,

Happy 2020!

Many thanks for the kind invitation. I am excited about the visit and the retreat. I could arrive on Monday and give a seminar on Tuesday and leave on Saturday.

I'm glad you are helping with the "Wuhan pneumonia" investigation. Please let me know if there is anything I could help.

All the best from Galveston!

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, January 4, 2020 6:45 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Invitation as a guest speaker for the EID retreat 2020

Forgot to mention: you will be invited under the "distinguished professor" title and you are also required to give a seminar to the whole school either on Tue or Wed before the retreat, so you need to plan a 4-5 day visit.

Thanks

LF

PS: as you may be aware, the "Wuhan pneumonia" investigation is ongoing and highly "explosive". I will be in Wuhan on 15-18 Jan.

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Wang Linfa
Sent: Sunday, 5 January 2020 8:43 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Invitation as a guest speaker for the EID retreat 2020

Dear Pei Yong,

Happy 2020!

We are planning a BIG retreat for EID on 19-20 March 2020, first time to have a 2-day retreat.

We are going to invite all past PIs (Duane, Veronika, etc) and will officially farewell Mariano.

We thought it will be a good idea to give Mariano a surprise by inviting you as a guest speaker.

Duke-NUS will of course cover the return business class airfare and all associated costs.

Do let me know if you are available and able to do that.

Thanks in advance.

Cheers,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Shi, Pei yong[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=8906C46397AE48488FCC55537DC5D6D3-SHI, PEI YO]

Location: WeChat

Importance: Normal

Subject: Collaboration discussion

Start Time: Sat 3/28/2020 8:00:00 AM (UTC-05:00)

End Time: Sat 3/28/2020 9:00:00 AM (UTC-05:00)

Required Attendees: Shi, Pei yong; Wang Linfa

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 3/11/2020 2:22:52 PM (UTC-05:00)
Subject: Pilot Projects
Defilippis_Pilot.pdf
DEFILIPPIS_RR_Budget.pdf
Jonsson_UTHSC_Proposal_submitted.pdf
Lesage_Sylvie_Pilot Budget.pdf
Lesage_Sylvie_Pilot.pdf
Parrish_Pilot.pdf
ParrishRR_Budget 030320.pdf
Smith Pilot Application.pdf
Smith RR_Budget10_1_4_A30-V1.4.pdf
Streblow Moorman_Pilot Project.pdf
Wang_Pilot.pdf
Wang_Pilot_budget_v5.pdf
Review Template.docx

Good afternoon all,
As promised this morning, I am sending you the 2020 Pilot projects. Please return your reviews by April 1 at the latest. I have also attached the review template.
Thank you,

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

LEAVE BLANK—FOR PHS USE ONLY.		
Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
The Collaborative Cross Mouse Model as a Tool for Dissecting Innate Immune Correlates of Vaccine Efficacy

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☒ YES
(If "Yes," state number and title)
Number: Title: Pilot Project: CSBIO

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Victor R. DeFilippis	PhD	defilipp

3c. POSITION TITLE
Associate Professor

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Vaccine and Gene Therapy Institute

3f. MAJOR SUBDIVISION

3d. MAILING ADDRESS *(Street, city, state, zip code)*
505 NW 185th Ave. Mail Code: VGTI
Beaverton, Oregon 97006-3448

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: 503-481-2575 FAX: 503-481-2719

E-MAIL ADDRESS:
defilipp@ohsu.edu

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☐ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☐ No ☐ Yes	☐ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No. A3304-01

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
9/1/2020	8/31/2021	74,675	115,000	74,675	115,000

9. APPLICANT ORGANIZATION
Name: Oregon Health & Science University
Address: 3181 SW Sam Jackson Park Road
Portland, Oregon 97239-3098

10. TYPE OF ORGANIZATION
Public: → ☐ Federal ☒ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
1931176109A1
DUNS NO. 09-699-7515 Cong. District OR-001

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name: Elizabeth Salvatierra
Title: Grants & Contracts Administrator
Address: 3181 SW Sam Jackson Park Road L106OPAM
Portland, Oregon 97239-3098
Tel: 503-494-0627 FAX: 503-494-
E-Mail: salvatie@ohsu.edu

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name: Kellie Guentert
Title: Director
Address: 3181 SW Sam Jackson Park Road L106OPAM
Portland, Oregon 97239-3098
Tel: 503-494-7784 FAX: 503-494-7787
E-Mail: orserv@ohsu.edu

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.

SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)* DATE

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: DeFilippis, Victor R., Ph.D.

eRA COMMONS USER NAME (credential, e.g., agency login): defilipp

POSITION TITLE: Associate Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Montana, Missoula, MT	B.A.	05/93	Zoology
Wayne State University, Detroit, MI	M.S.	08/95	Biology
University of California, Irvine, CA	Ph.D.	03/01	Biology
Oregon Health & Science Univ., Portland, OR	Postdoctoral	06/05	Virology/Immunology

A. Personal Statement

My research career has involved investigating numerous and diverse phenomena related to innate immunity, molecular biology, and viral disease. This includes exploring the biology of pattern recognition receptor signaling, the type I interferon response, and the mechanistic roles of innately activated transcription factors. Early in my career I focused on these topics largely in the context of virus-mediated activation, direct antiviral responses, and viral immune evasion. Recently my efforts have shifted to investigating the function and roles of innate immune processes for establishment of adaptive immunity. This includes examination of the specific signaling pathways and factors that potentiate antigen presentation and T cell activity but also the harnessing of these responses for beneficial clinical outcomes. In light of this my work now commonly employs techniques of drug discovery and development to identify and characterize novel compounds that elicit precisely targeted innate immune reactions useful in the contexts of vaccine enhancement, anti-tumor immunity, and broad-spectrum antiviral activity. This has led to the identification and characterization of novel IRF-activating molecules and a multi-investigator effort to understand how these can be employed in the context of immunotherapeutics. Experimentally I have employed and adapted a broad range of model types including *in vitro* and *ex vivo* culture of mammalian cells, mice, and nonhuman primates. I have also utilized and mastered a range of investigative and high content exploratory platforms including transcriptomics (RNAseq and hybridization array), proteomics, and high throughput chemical screening. I also routinely employ and customize numerous cutting-edge molecular methodologies such as viral expression vectors, transposon-mediated transgenics, cell reporters, CRISPR/Cas9-driven genome editing, protein techniques, and viral mutagenesis. My work has integrated these approaches with *in vivo* examination of adaptive immune responses including antibody and T lymphocyte activities. This scientific background has allowed me to accumulate a valuable infrastructure of reagents, equipment, and intellectual resources. As such, I am well positioned to lead the studies outlined in this proposal.

B. Positions and Honors

Positions and Employment

1993-1995	Research Asst., Dept. of Biological Sciences, Wayne State University, Detroit, MI
1995-1996	Teaching Asst., Dept. of Ecology & Evolutionary Biology, University of California, Irvine
1997-2001	Research Asst., Dept. of Ecology & Evolutionary Biology, University of California, Irvine
2001-2005	Postdoctoral Fellow, OHSU Vaccine and Gene Therapy Institute, Beaverton, OR
2005-2011	Research Assistant Professor, OHSU Vaccine and Gene Therapy Institute, Beaverton, OR
2011-2016	Assistant Scientist, OHSU Vaccine and Gene Therapy Institute, Beaverton, OR
2013-Present	Adjunct Faculty, OHSU Dept. of Molecular Microbiology and Immunology, Portland, OR

2016-2019 Assistant Professor, OHSU Vaccine and Gene Therapy Institute, Beaverton, OR
2019-Present Assistant Professor, Division of Pathobiology and Immunology, Oregon National Primate Research Center, Beaverton, OR
2019-Present Associate Professor, OHSU Vaccine and Gene Therapy Institute, Beaverton, OR

Professional Activities

2010-2011 Faculty of 1000 Associate Member
2012 NIAID Scientific Review Program for RFA-AI-12-020 "Partnerships for Interventions to Treat Chronic, Persistent and Latent Infections"
2014 Reviewer, California National Primate Research Center Pilot Research Program
2016 NIAID Scientific Review Program for PAR-16-106 "Rapid Assessment of Zika Virus (ZIKV) Complications"
2016 NIAID Scientific Review Program for RFP-NIAID-DMID-NIHAI2016059 "Pre-clinical Models of Infectious Diseases"
2018 Reviewer, Wellcome Trust DBT Fellowship
2018 Reviewer, Israeli Science Foundation
2020 NIAID Scientific Review Program for PHS-2020-1 "Adjuvant Development for Vaccines against Infectious or Immune-mediated Diseases"
2011-2013 Board of Directors, Buck Buck Foundation for Cytomegalovirus Awareness
2014-2019 Scientific Consultant, Tomegavax, Inc.
2015-2019 Scientific Advisor, NeuraLexo, Inc.
2013-Present Editorial Board Member, Journal of Virology
2017-Present Associate Editor, Frontiers in Cellular and Infection Microbiology
2019-Present Editorial Board Member, Cytokines

C. Contributions to Science (***Corresponding Author***)

1. Discovery and Characterization of Novel Innate Immune Stimulating Compounds.
Targeted activation of innate immune responses by small molecules has proven to be a powerful strategy for achieving beneficial clinical outcomes related to anti-cancer therapeutics, vaccine adjuvanticity, and broad-spectrum antiviral activity. My work has focused on leveraging these responses for immunotherapeutic purposes while identifying new molecular entities that may function as potential drug leads or research tools to facilitate dissection of associated innate immune processes. For this my group has employed high throughput screening that utilizes custom reporter cell lines constructed in our laboratory using sophisticated transgenic tools. Novel compounds discovered in this way are then characterized with respect to the transcriptional profiles they generate, phenotypes they elicit, and host targets required for their effects. To achieve these ends my group has pioneered the use of CRISPR/Cas9-mediated genome editing to construct a library of cells lacking targeted innate immune signaling and effector proteins that is used to identify essential cellular factors via loss of function assays. This technology also allows us to quickly dissect the molecular mechanistic bases of innate immune phenotypes. Additionally, we use medicinal and computational chemistry approaches to construct compound analogs and understand structure-activity relationships. This work has led to the identification and molecular characterization of the first novel small molecule agonists of the STING pathway as well as a novel TRIF-activating molecule. I served as the senior investigator for these relevant studies:

1. Gall B, Pryke K, Abraham J, Mizuno N, Botto S, Sali TM, Broeckel R, Haese N, Nilsen A, Placzek A, Morrison T, Heise M, Streblow D, ***DeFilippis VR**. 2018. Emerging Alphaviruses Are Sensitive to Cellular States Induced by a Novel Small-Molecule Agonist of the STING Pathway. Journal of Virology 92:8.2. PMCID: PMC5827377

2. Gall BJ, ***DeFilippis VR**. 2017. High-Throughput Screening for Identification of Novel Innate Immune Activators. Methods Mol Biol 1656:183–193. PMID: 28808971

3. Pryke KM, Abraham J, Sali TM, Gall BJ, Archer I, Liu A, Bambina S, Baird J, Gough M, Chakhtoura M, Haddad EK, Kirby IT, Nilsen A, Streblow DN, Hirsch AJ, Smith JL, ***DeFilippis VR**. 2017. A Novel Agonist of the TRIF Pathway Induces a Cellular State Refractory to Replication of Zika, Chikungunya, and Dengue Viruses. mBio 83 e00452-17. PMCID: PMC5414005

4. Sali, T, K Pryke, R Broeckel, J Staverosky, J Abraham, A Liu, J Smith, A Al-Shammari, L Amsler, K Sheridan, A Nilsen, DN Streblow, *DeFilippis VR. 2015. Characterization of a Novel Human-Specific STING Agonist that Elicits Antiviral Activity Against Emerging Alphaviruses. PLoS Pathogens. 11(12):e1005324. PMCID: PMC4672893

2. Innate Detection of Cytoplasmic DNA in the Context of Viral Infection.
Human cytomegalovirus is a ubiquitous beta-herpesvirus that infects hosts for life. While generally asymptomatic in immunologically healthy people, it can be a dangerous opportunistic infection during immunocompromise and represents a leading infectious cause of birth defects. The innate immune response to cytomegalovirus is a poorly understood phenomenon but involves induction of the type I interferon and inflammasome systems and, prominently, is fundamentally triggered by the sensing of cytoplasmic DNA. My work has led to characterization of processes and host factors involved in this response including the first demonstration that STING is required for cytomegalovirus innate immune recognition. This has involved the use of reverse genetics and functional genomics to allow an understanding of the importance of innate signaling pathways during infection. I served as a primary investigator for these relevant studies:

1. Botto S, Abraham J, Mizuno N, Pryke K, Gall B, Landais I, Streblow DN, Früh KJ, *DeFilippis VR. 2019. Human Cytomegalovirus Immediate Early 86-kDa Protein Blocks Transcription and Induces Degradation of the Immature Interleukin-1β Protein during Virion-Mediated Activation of the AIM2 Inflammasome. mBio **10**:257. PMCID: PMC6372796

2. *DeFilippis VR, Sali T, Alvarado D, White L, Bresnahan W, Früh KJ. 2010. Activation of the interferon response by human cytomegalovirus occurs via cytoplasmic double-stranded DNA but not glycoprotein B. Journal of Virology 84:8913–8925. PMCID: PMC2919031.

3. *DeFilippis VR, Alvarado D, Sali T, Rothenburg S, Früh K. 2010. Human cytomegalovirus induces the interferon response via the DNA sensor ZBP1. Journal of Virology 84:585–598. PMCID: PMC2798427

4. DeFilippis VR, Robinson B, Keck TM, Hansen SG, Nelson JA, Früh KJ. 2006. Interferon regulatory factor 3 is necessary for induction of antiviral genes during human cytomegalovirus infection. Journal of Virology 80:1032–1037. PMCID: PMC1346858.

3. Biology and Evolution of DNA Tumor Viruses.
DNA viruses such as Kaposi Sarcoma virus and papillomaviruses represent significant etiological sources of human cancers. Understanding the fundamental biology and evolution of these pathogens is not only crucial to our efforts to treat and eradicate them but also brings to light important phenomena regarding tumor biology and their co-evolution with human hosts. I have made contributions to studies that examine both virus-host biology of these agents but also their epidemiological and evolutionary histories, which has required the use of sophisticated techniques of computational molecular data analysis. I served as a primary or co-investigator for these relevant studies:

1. Xi LF, Schiffman M, Koutsky LA, Hulbert A, Lee S-K, DeFilippis VR, Shen Z, Kiviat NB. 2012. Association of human papillomavirus type 31 variants with risk of cervical intraepithelial neoplasia grades 2-3. Int J Cancer 131:2300–2307. PMID: 22396129

2. Rose PP, Carroll JM, Carroll PA, DeFilippis VR, Lagunoff M, Moses AV, Roberts CT, Fruh K. 2007. The insulin receptor is essential for virus-induced tumorigenesis of Kaposi's sarcoma. Oncogene 26:1995–2005. PMID: 17001305

3. McAllister SC, Hansen SG, Ruhl RA, Raggo CM, DeFilippis VR, Greenspan D, Früh K, Moses AV. 2004. Kaposi sarcoma-associated herpesvirus (KSHV) induces heme oxygenase-1 expression and activity in KSHV-infected endothelial cells. Blood 103:3465–3473. PMID: 14726403

4. *DeFilippis VR, Ayala FJ, Villarreal LP. 2002. Evidence of diversifying selection in human papillomavirus type 16 E6 but not E7 oncogenes. J Mol Evol 55:491–499. PMID: 12355268

4. Development and Utilization of Nonhuman Primate Models of Viral Disease and Immunity.
Nonhuman primates (NHP) represent a unique and powerful model for understanding the impacts of and responses to viral infection. I have been pivotally involved in multiple studies that have led to establishment of new research models that employ NHP, revealed novel phenomena regarding emerging Zika ang Chikungunya virus biology, and led to unexpected discoveries in cytomegalovirus replication. Ultimately, this work has served to mold my skills and direct my ability to leverage NHP models for acquiring impactful research outcomes. I served as a co-investigator for these relevant studies:

1. Hirsch AJ, Roberts VHJ, Grigsby PL, Haese N, Schabel MC, Wang X, Lo JO, Liu Z, Kroenke CD, Smith JL, Kelleher M, Broeckel R, Kreklywich CN, Parkins CJ, Denton M, Smith P, **DeFilippis VR**, Messer W, Nelson JA, Hennebold JD, Grafe M, Colgin L, Lewis A, Ducore R, Swanson T, Legasse AW, Axthelm MK, MacAllister R, Moses AV, Morgan TK, Frias AE, Streblow DN. 2018. Zika virus infection in pregnant rhesus macaques causes placental dysfunction and immunopathology. Nature Communications 1–15. PMCID: PMC5772047

2. Hirsch AJ, Smith JL, Haese NN, Broeckel RM, Parkins CJ, Kreklywich C, **DeFilippis VR**, Denton M, Smith PP, Messer WB, Colgin LMA, Ducore RM, Grigsby PL, Hennebold JD, Swanson T, Legasse AW, Axthelm MK, MacAllister R, Wiley CA, Nelson JA, Streblow DN. 2017. Zika Virus infection of rhesus macaques leads to viral persistence in multiple tissues. PLoS Pathog 13:e1006219. PMCID: PMC5344528

3. Malouli D, Hansen SG, Nakayasu ES, Marshall EE, Hughes CM, Ventura AB, Gilbride RM, Lewis MS, Xu G, Kreklywich C, Whizin N, Fischer M, Legasse AW, Viswanathan K, Siess D, Camp DG, Axthelm MK, Kahl C, **DeFilippis VR**, Smith RD, Streblow DN, Picker LJ, Früh K. 2014. Cytomegalovirus pp65 limits dissemination but is dispensable for persistence. J Clin Invest 124:1928–1944. PMCID: PMC4002596

4. Messaoudi I, Vomaske J, Totonchy T, Kreklywich, CN, Haberthur K, Springgay L, Brien JD, Diamond, MS, **DeFilippis, VR**, Streblow DN. 2013. Chikungunya virus infection results in higher and persistent viral replication in aged rhesus macaques due to defects in anti-viral immunity. PLoS Negl Trop Dis 7:e2343. PMCID: PMC3723534

5. Infection by and Immunity to Emerging Alpha- and Flaviviruses.
Mosquito-transmitted viruses that are currently undergoing widespread and explosive outbreaks throughout equatorial regions of the world include members of the flavivirus (e.g. Dengue, West Nile, and Zika) and alphavirus (e.g. Chikungunya) clades. Unfortunately, a deficiency of knowledge exists regarding the immunobiology, pathogenesis, and antiviral strategies to which these viruses are susceptible. This includes an understanding of how the viruses activate and evade innate immunity and what factors control tissue dissemination and control. My work has made multiple contributions to these fields including description of an unusual nearly global host transcription and translational shutoff mechanism exhibited by the Chikungunya virus in human cells. In addition, I was involved in characterization of a novel RIG-I agonist that confers broad-spectrum antiviral efficacy. Ultimately this work will facilitate identification of immune-based strategies that can be used to combat viral disease and spread. I served as a primary or co-investigator for these relevant studies:

1. White LK, Sali T, Alvarado D, Gatti E, Pierre P, Streblow D, *__DeFilippis VR__. 2011. Chikungunya virus induces IPS-1-dependent innate immune activation and protein kinase R-independent translational shutoff. Journal of Virology 85:606–620. PMCID: PMC3014158.

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D. Additional Information: Research Support and/or Scholastic Performance

Complete Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/victor.defilippis.1/bibliography/public/

D. Research Support

Ongoing Research Support

R01 AI143660 (DeFilippis, PI) 01/23/2019 – 12/31/2023
NIH/NIAID
Mechanistic Exploration of cGAS-STING-Mediated Vaccine Enhancement
cGAS and STING comprise a cellular signaling pathway crucial to generating innate and adaptive immune responses against microbe-infected cells that can elicit beneficial vaccine outcomes when stimulated by adjuvants. The goals of this work include detailed characterization of the molecular and immunological effects of STING activation using a combination of biochemical, murine, and nonhuman primate experimental models. Results we generate will have a transformative impact on our understanding of the biological role of STING and its immunotherapeutic potential as a pharmacologic target.
Role: Principal Investigator

HHSN272201400055C (Nelson, PI) 10/01/2019 – 09/30/2024
NIH/NIAID
Adjuvant Discovery Program
The goal of this work is to identify novel small molecules capable of stimulating activation of STING that can be used to enhance immunogenicity of flavivirus and alphavirus vaccines. This is undertaken in a partnership with Inimmune, Inc. and focuses on high throughput screening of chemical libraries to reveal and ultimately develop new innate activating compounds to enhance vaccine immunogenicity. There is no overlap with the current proposal.
Role: Co-Investigator

HHSN272201400055C (Nelson, PI) 09/30/2014 – 09/29/2020
NIH/NIAID
Adjuvant Discovery Program
The goal of this work is to identify novel small molecules capable of stimulating activation of IRF1, IRF3, or IRF5 that can be used to enhance immunogenicity of flavivirus vaccines. This is undertaken in a partnership with Inimmune, Inc. and focuses on high throughput screening of chemical libraries to reveal and ultimately develop new innate activating compounds to enhance vaccine immunogenicity. There is no overlap with the current proposal.
Role: Co-Investigator

U19 AI109680 (Whitley, PI) 03/01/2019 – 02/28/2024
NIH/NIAID
Antiviral Drug Discovery and Development Center: Project 2: Novel Therapeutic Strategies Targeting Re-emerging Alphaviruses
The main goal of this project is to develop novel nucleoside and nucleotide inhibitors directed against alphaviruses including Chikungunya virus and Venezuelan Equine Encephalitis virus. This work involves identifying antiviral molecules in a high throughput in vitro virus replication screen, validating their efficacy and nontoxicity in vitro, and optimizing their utility to clear virus replication in mouse models of infection. There is no overlap with the current proposal.
Role: Co-Investigator

Scope of Work

The goal of the work outlined in this pilot proposal is development of a powerful *in vivo* tool to mechanistically explore innate immune correlates of and genotype-associated variation in vaccine-mediated immune responses. Vaccination represents the most efficient tactic for combating infectious disease. Unfortunately, the immune activity elicited by vaccines can vary greatly between individuals and surprising gaps exist in our knowledge regarding how they work to enhance immunogenicity. The Collaborative Cross (CC) mouse model was devised to enable systems genetics and predictive biology approaches in an *in vivo* platform that recapitulates the phenotypic diversity of human populations. Preliminary work from our group utilized a panel of CC-derived lines to demonstrate striking variation in response to an adjuvanted protein vaccine against Zika virus. Based on this we predict that the CC model will be highly valuable as a tool for characterizing molecular and immunological correlates of vaccine efficacy. This pilot proposal aims to acquire experimental observations that serve as an important proof of principle supporting this idea. We therefore plan to undertake an investigation of the CC lines used in our previous study to characterize innate immune processes associated with diversity of vaccine-induced reactivity. Innate immune function is closely linked with the establishment of protective adaptive immune responses, especially those elicited by vaccination. Moreover, genotypic and phenotypic variation in innate immune genes and processes is evident in human populations. We aim to characterize vaccine-induced secretion of cyto/chemokines as well as innate cell trafficking to understand how they correlate with particular immune outcomes. These data can then be used to devise mechanistic models and allow novel hypotheses to be formed about their functional importance in vaccine efficacy. This will also facilitate further development of the CC model for dissecting genotype-associated vaccine responses.

Specific Aims

The goal of the work outlined in this pilot proposal is development of a powerful *in vivo* tool to mechanistically explore innate immune correlates of and genotype-associated variation in vaccine-mediated immune responses. Ultimately this will allow hypothesis-driven and clinically impactful investigation of causal links between vaccination outcomes and organism-specific attributes such as gene loci and immunological processes. Vaccination represents the most efficient and adaptable tactic for combating infectious disease. Vaccine platforms comprised of non-replicating immunogenic microbial antigens are extremely safe but elicit weaker immunity, a condition mitigated through co-administration of immune-enhancing molecules termed adjuvants. *Importantly, the immune activity elicited by vaccines can vary greatly between individuals with non-responsiveness to or reactogenicity associated with vaccination being demonstrable in patient populations*. While this diversity is influenced by numerous parameters (e.g. age, race, and socioeconomic conditions), genetic makeup contributes substantially to vaccine efficacy. However, basic and surprising gaps exist in our knowledge regarding how adjuvanted vaccines work to enhance immunogenicity. Obtaining a functional understanding of the relationship between the response to vaccination and underlying variables associated with genetic variability will require a model that is experimentally tractable, recapitulates key aspects of human outcomes, and can be used to probe cellular and molecular correlates. Examination of immune-related phenomena using human tissues and populations can be informative but these are not ideal for mechanistic characterization of vaccine success or operation. Contrastingly, laboratory mice are desirable to investigate immune function since they are easy to handle, can be maintained in a controlled setting, and allow for large sample sizes. Moreover, mice and humans share >90% of the same genes and thus successful genetic discovery efforts in humans often originate in murine studies. However, efforts that employ individual inbred mouse strains (e.g. C57BL/6) fail to recapitulate the phenotypic diversity exhibited by human populations, greatly reducing translatability of acquired results. In response to this insufficiency, the Collaborative Cross (CC) mouse model was devised to enable systems genetics and predictive biology approaches in an *in vivo* platform. CC mice comprise a panel of recombinant inbred (RI) lines derived from sequential breeding of eight founder strains chosen to maximize genetic and thus phenotypic variability, resulting in representation of millions of uniformly distributed polymorphisms. This gives rise to a reproducible set of genetic clones that can be exploited as both a powerful forward genetics tool as well as a generator of phenotypic diversity mimicking that displayed by outbred populations such as humans. Preliminary work from our group has utilized a set of eleven CC-derived RI lines to demonstrate striking variation in response to an adjuvanted protein-based vaccine against Zika virus. *Based on this we predict that the CC model will be highly valuable as a tool for characterizing molecular and immunological correlates of vaccine efficacy.* This pilot proposal aims to acquire experimental observations that serve as an important proof of principle supporting this idea. Our ultimate hope is that a straightforward and cost-effective model of vaccine response diversity in CC mice can be developed that will allow: 1) detailed characterization of the associated innate and adaptive mechanisms; and 2) identification of genes pivotal for establishment of protective immunity. We plan to accomplish this in the following specific aim:

***Specific Aim*: Characterize innate processes associated with vaccine response diversity**

Our preliminary data indicate that CC-RI lines exist that exhibit a phenotypic range with respect to vaccine-mediated antibody titers. As such, these represent a distinct and potentially highly informative set of models that are likely to yield valuable information about the physiological mechanisms responsible for this disparity. We therefore plan to undertake a comparative characterization of molecular and immunological processes associated with substantial differences in vaccine-induced reactivity. We aim to identify secreted cyto/chemokines and or innate immune processes that correlate with particular outcomes that can then be used to devise models and allow novel hypotheses to be formed about their functional importance in vaccine efficacy.

Background and Significance

Vaccines are essential for diminishing pathogen-mediated illness. Yet the potency of protective responses they elicit varies greatly between individuals. While these responses are influenced by many parameters, genetic makeup contributes substantially[1-7]. Genome-wide association studies have identified many polymorphisms in protein coding regions that link innate and adaptive immune functions crucial to vaccine efficacy[4,7,13,14]. This includes receptors, cytokines, and antimicrobial effectors as well as proteins involved in antigen presentation. Vaccines comprised of inert antigen are the safest immunization platform since no microbial growth occurs. However, since their administration and exposure are localized and transient, these do not activate as many facets of the immune response and can lead to weaker, shorter-lived immunity. This is mitigated through the co-administration of molecules termed adjuvants that augment immunogenicity by stimulating innate immune processes, often mimicking those triggered by infection. As such, innate immunity is essential to adjuvant-dependent elicitation of protective immunity[8]. In addition, innate immune genes exhibit high diversity as a result of host-pathogen co-evolution[9]. Moreover, reactogenic and adverse effects of vaccination often involve dysfunctional innate responses to vaccine components, for which evidence of a genetic link also exists[10]. *Unfortunately, a large knowledge deficit exists regarding the mechanistic link between polymorphism in immune-related genes, their molecular phenotypes, and vaccine responsiveness*[11]. Furthermore, models are lacking that both recapitulate the diversity of vaccine effects in humans and are tractable for hypothesis-based study. Mice reproduce key aspects of the human immune system (including innate reactivity[12]) and allow great flexibility of experimental parameters. However, inbred strains do not display the diversity of phenotypes present in human populations. The CC model is a set of recombinant inbred (RI) mouse lines developed to enable systems genetics and predictive biology *in vivo*[13,14]. These were derived through breeding of eight diverse founder strains, and, as such, up to eight variant alleles may be present at any locus. Individual CC-RI lines, like other inbred strains, comprise a population of genetic clones, allowing for repeat measures and comparative studies across the model. In addition to facilitating discovery of genetic factors associated with phenotypes, the CC model can also be harnessed to explore the mechanistic bases of vaccine response variation. *We hypothesize that this will be applicable as an impactful model to study variability in immune responses to vaccination, especially with respect to: 1) innate immune activation by characterized adjuvants; and 2) potentially adverse reactions to vaccines.* This will enable development of an innovative rational approach to vaccinology and ultimately facilitate strategies that are safer, more effective, and personalized to patient biology.

Preliminary Data

We utilized a replication-defective virus-like particle (VLP) antigen from Zika virus (ZIKVLP) to explore vaccine responses in CC-RI mice[15,16]. This was chosen based on its clinical importance and well-described patterns of replication and immunity in mice[17,18]. We screened the genotype-associated range of antibody (Ab) responses using eleven genetically diverse CC-RI lines in the absence or presence of immunologically dissimilar adjuvants. Mice were vaccinated with ZIKVLP alone, ZIKVLP + cyclic di-AMP (CDA; agonist of the STING pathway[19]), or ZIKVLP + Pam3CSK4 (TLR2 agonist[20]) using intramuscular (IM) prime/boost. Zika-specific total IgG was examined by ELISA using sera (currently banked) collected from mice at 3w post boost (6w post prime). *In all CC-RI lines, ZIKVLP alone led to significantly lower Ab responses than when administered with an adjuvant* (**Figure 1**). Intriguingly, while CDA improved Ab titers to a statistically significant degree in all CC-RI lines, Pam3CSK4 only did so in five of eleven lines. Moreover, mean IgG titers per vaccine type also varied *between CC-RI lines by nearly three logs*, with lines CC040 and CC031 displaying the extremes. Finally, the degree to which adjuvants enhanced IgG titers also varied greatly between lines. *Given the crucial role of innate responses in the establishment of adaptive immunity, we hypothesize that the CC model as utilized here represents a powerful tool for understanding adjuvant-associated processes that correlate with elicitation of protective immunity and perhaps reactogenicity.*

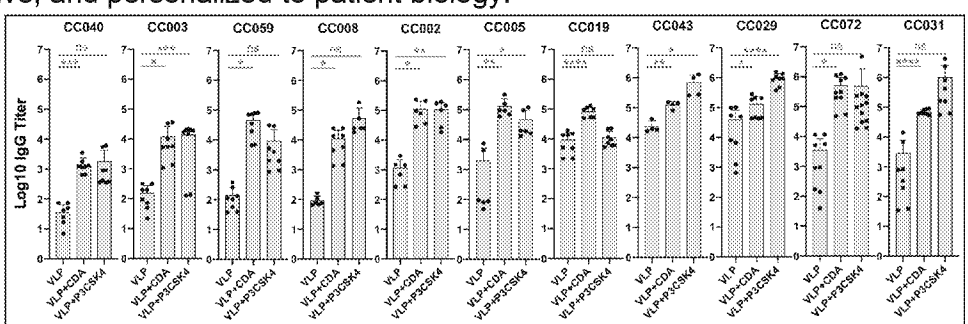

Figure 1. Zika-specific total IgG elicited by ZIKVLP in the absence or presence of CDA or Pam3CSK4 across CC-RI lines. CC-RI lines (as indicated) were vaccinated by a prime-boost strategy as described in the text and harvested at 6w post prime. Sandwich ELISA was then used to quantify antibodies reactive to Zika virus particles in duplicate. Data presented are average geometric mean titers ±SD for each vaccine cohort (n = 4 in most cases). Students T-test was then used to compare results from animals vaccinated with and without adjuvant (*p<0.05; **p<0.01; ***p<0.001; ****p<0.0001).

Specific Aim: Characterize innate processes associated with vaccine response diversity

Hypothesis: We hypothesize that innate immunological processes induced by adjuvanted vaccines are identifiable as dissimilar between CC-RI lines that display differences in induced Ab levels (**Fig. 1**). This is likely to include disparities in cytokine secretion profiles and localized immune cell recruitment and migration.

Rationale: Ab responses to adjuvanted vaccination in CC-RI lines are diverse and adjuvant-specific (**Fig. 1**). As such, these constitute a unique model from which exceptionally informative data regarding the underlying

physiological mechanisms can be retrieved. Adjuvant function correlates with transcriptomic patterns specific to tissue type as well as cytokine secretion and immune cell infiltration[21-23]. We plan to undertake an unbiased characterization of innate immunological processes associated with the differences seen in vaccine-induced reactivity. Findings can then be used in future work to test novel hypotheses about their functional importance.

Approach: We will utilize CC-RI lines described above (**Fig. 1**). First, secretion of local and systemic cytokines will be measured following vaccination with ZIKVLP with or without CDA or Pam3CSK4. Second, we will compare migration of immune cells to the vaccine site of injection (SOI). Our goal is to characterize the immediate innate immune changes that occur as a reaction to vaccine administration between CC-RI lines to identify distinguishing phenotypes that can investigated for their mechanistic roles in follow on studies.

1) Vaccine-induced cytokine profiling. Vaccines adjuvanted with innate inducers elicit secretion of immunomodulatory cytokines systemically as well as at the SOI[17-22]. Evidence indicates this facilitates transient inflammatory processes that attract antigen presenting cells (APC), enable antigen loading and delivery, and polarize adaptive immune responses. We hypothesize that the vaccine response variation observed between CC-RI lines will be reflected in levels of CDA- and Pam3CSK4-induced cytokines in injected muscle between the CC-RI lines. For this, we will vaccinate mice from each of the eleven CC-RI lines (n = 4/treatment; 2 of each sex) with PBS vehicle, ZIKVLP, ZIKVLP + Alum, or ZIKVLP + Pam3CSK4 and euthanize at 6h post vaccination (timepoint shown to represent peak induction over a time course[17,22]). Sera will be harvested and injected and contralateral (control) quadriceps will be homogenized and treated with protease inhibitor[24]. An aliquot of homogenate will also be saved for RNA isolation to allow mRNA quantitation. Next, we will use a Luminex multiplex assay to measure levels of Eotaxin, VEGF, TNF-α, RANTES, MIP-2, MIP-1β, MIP-1α, MIG, M-CSF, MCP-1, LIX, LIF, KC-like, IP-10, IL-17, IL-15, IL-13, IL-12 (p70), IL-12 (p40), IL-10, IL-9, IL-7, IL-6, IL-5, IL-4, IL-3, IL-2, IL-1β, IL-1α, IFN-γ, GM-CSF, and G-CSF in these tissues. Induction of each will be compared between vaccines and CC-RI lines using standard statistical methods. We aim to identify individual or classes of cytokines that are differentially secreted in response to specific vaccinations within and between CC-RI lines.

2) Injection site immune cell migration. Innate reactions to adjuvanted IM vaccines drive localized recruitment of immune cells to the SOI[25-28]. The magnitude and quality of recruited cells dictates antigen loading, trafficking, and presentation in draining lymph node (dLN) and correlates with establishment of adaptive immunity. To assess vaccine- and CC-RI-associated differences in this innate process, we will use flow cytometry to quantify accumulation of macrophages ($F4/80^{high}CD11b^{+}SSC^{high}$), monocytes ($CD11b^{+}Ly6C^{high}Ly6G\text{-}F4/80^{int}$), myeloid DCs ($MHCII^{high}CD11c^{+}F4/80^{low}$), plasmacytoid DCs ($120G8^{+}CD11b^{dim}CD11c^{int}$), granulocytes ($CD11b^{+}GR1^{+}$), neutrophils ($CD11b^{+}Ly6C^{+}Ly6G^{high}F4/80^{-}$), and eosinophils ($CD11b^{+}Ly6C^{int}Ly6G^{int}F4/80^{int}$) in injected muscles at 72h post-vaccination[24,25,27,28]. For this we will select a subset of CC-RI lines to examine that represent phenotypic extremes in terms of Ab response and cytokine secretion (maximum of eight lines). For instance, we will include two lines that exhibit the largest (i.e. CC059, CC008) and smallest (i.e. CC019, CC029) disparity in IgG titers between adjuvanted and nonadjuvanted VLP. We will also select four lines that display the most disparate collective patterns of cytokine secretion as determined above. Mice will be treated as described for cytokine experiments. Injected and contralateral muscle tissue will be excised and digested in IMDM containing collagenase, DNAseI, and BSA and filtered through 70 μm nylon mesh. Cells will be stained with monoclonal Ab listed above and sorted on a BD LSR-II. Data analysis and visualization will be performed using FlowJo. Contralateral muscles and those injected with PBS or VLP alone will serve as controls that will allow determination of adjuvant- and VLP-associated changes. We will then statistically compare absolute numbers of each cell type between CC-RI lines to establish whether significant differences are detectable.

Analysis of Results and Future Work: Our goal is to demonstrate that genotype-associated differences in adjuvanted vaccine immunogenicity (**Fig. 1**) correlate with innate phenotypes. This will establish CC mice as a unique platform for both: 1) discovery of immunological and genetic traits associated with vaccine efficacy; and 2) directly testing hypotheses regarding mechanistic relationships. As a proof of principle, we propose to examine cytokine induction and immune cell trafficking, two innate processes that are simple to evaluate yet fundamental to vaccine function. Given the diversity in IgG titers between CC-RI lines and vaccine types we anticipate detecting associated differences in innate immune processes. In addition to the rapid and direct induction of cytokine synthesis by STING and TLR2 activity, signaling proteins in both pathways are known to exhibit polymorphisms that affect function. We thus predict that differences will be evident in the cytokine profiles between vaccine types and CC-RI lines. Profiles will likely differ in overall magnitude of detection or predicted immune impact (e.g. Th polarization, chemotactic properties, etc.). These will also constitute important targets for follow up study. Moreover, the concurrent collection of tissue RNA will allow follow up transcriptomic work on target genes of interest. By focusing on CC-RI lines that exhibit the most dissimilar responses for immune cell assessment, we maximize the probability that differences in the underlying variables are detectable. We also expect that these results will reveal differences in cells that link innate and adaptive immune processes and thus reveal potential functional targets for follow up studies. Our long-term goal is the maturation of the CC model as a unique system for investigating processes, factors, and genes associated with vaccine reactivity. Work completed here will be both an important proof of concept and a source of targets for future hypothesis testing.

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BUDGET JUSTIFICATION

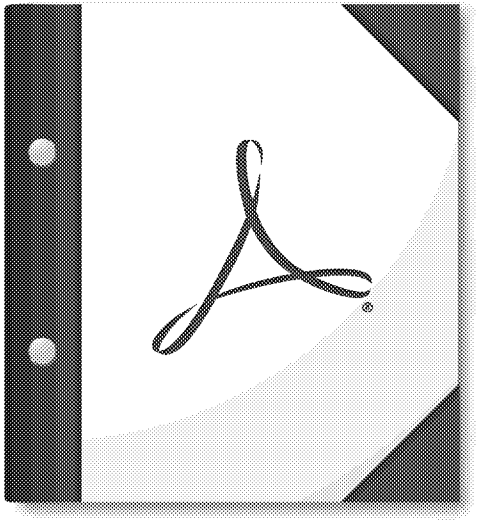
KEY PERSONNEL:

Victor DeFilippis, Ph.D., Principal Investigator, 1% effort (0.12 calendar months). Dr. DeFilippis will provide the oversight to ensure proper coordination and efficient execution of research activities. Dr. DeFilippis will hold the primary role in promoting scientific direction, ensuring research progress, and facilitating communication. Dr. DeFilippis will be responsible for maintaining compliance with all institutional, federal, and NIH regulations as well as the safety and security of data, and managing materials, facilities and resources of the program.

NON-KEY PERSONNEL:

Dylan Boehm, Ph.D., Postdoctoral Researcher, 15% effort (1.8 calendar months). Dr. Boehm is a postdoctoral scientist in the DeFilippis laboratory. He is an accomplished mouse immunologist with skills and experience related to all in vivo portions of the proposal. He will be working in consultation with Dr. DeFilippis regarding the design, execution, and analysis of all mouse experiments. This includes mouse handling and vaccination, tissue processing and storage, analysis of cytokine induction, and cell infiltration assays.

Supplies and Reagents
We are requesting funds for 228 CC-RI mice ($215 each = $49,020) as well as necessary per diems. Additional procurement of Luminex multiplex cytokine kits, antibodies for flow staining, and plasticware will also be required.



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Department of Health and Human Services
Public Health Services

Grant Application

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Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
Exploration of the Collaborative Cross for Study of Hantavirus Pathogenesis

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☒ YES
(If "Yes," state number and title)
Number: Title: http://www.systemsimmunogenetics.org/announcement.html

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Jonsson, Colleen B	PhD	Jonsson

3c. POSITION TITLE
Professor

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Microbiology, Immunology, Biochemistry

3f. MAJOR SUBDIVISION

3d. MAILING ADDRESS *(Street, city, state, zip code)*
Molecular Sciences Building
858 Madison
Memphis, TN 38163

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: 8654569866 FAX:

E-MAIL ADDRESS:
cjonsson@uthsc.edu

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☒ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
FWA00002301	☒ No ☐ Yes	☒ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No. A3325-01

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
9/1/2020	8/31/2021	115,000	115,000		115,000

9. APPLICANT ORGANIZATION
Name University of Tennessee Health Science Center
Address

10. TYPE OF ORGANIZATION
Public: → ☐ Federal ☒ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
1-626001636
DUNS NO. 941884009 Cong. District

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name
Title
Address
Tel: FAX:
E-Mail:

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name
Title
Address
Tel: FAX:
E-Mail:

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.	SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)*	DATE 2/24/20

BIOGRAPHICAL SKETCH

NAME: Briana M. Spruill-Harrell

eRA COMMONS USER NAME (credential, e.g., agency login): SPRUILL-HARRELL

POSITION TITLE: Graduate Student, University of Tennessee Health Science Center

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
Norfolk State University-Norfolk, VA	BA	05/2017	Biology

A. Personal Statement

I am a graduate student at the University of Tennessee Health Science Center. I began graduate school in the Fall of 2017 where I joined Dr. Colleen Jonsson's lab that next year. Over the past few years, my studies have been focused on the study of hantaviruses (now genus *Orthohantavirus*, family *Hantaviridae*). Our lab conducts *in vitro* and field-based studies on the biology, ecology and evolution of hantavirus and I was fascinated by how these rodent-borne viruses cause disease in human however establish persistence in their reservoir hosts without causing disease. In reviewing the literature, I realized that there were fundamental gaps in our understanding of the pathogenesis of these viruses in rodent and human host. First, studies on human pathogenesis were limited to *in vitro* and clinical findings as there are no animal models that fully recapitulate human disease outcomes. Secondly, there is limited research on rodent-reservoir hosts because of the lack of genetic and immunological tools for these wild rodent species, the lack of rodent colonies and the requirements to have an ABSL-4 facility for New World Rodents. Therefore, my thesis research is focused on developing mouse models to study hantavirus pathogenesis and persistence. The dichotomous infection outcomes observed in rodents and humans provides a unique opportunity to examine the mechanisms mediating disease or persistence. Moreover, these models will be useful for preclinical testing of antivirals or vaccines.

I have the motivation and resources necessary to successfully carry out the proposed research project. My previous undergraduate research experience has enabled me to develop analytical, technical, and communication skills which has benefited my progression throughout the graduate program. Additionally, Dr. Colleen Jonsson's expertise, leadership, and guidance will greatly aid in these efforts.

B. Positions and Honors

2014	Summer Research Intern with Dr. Regina Oyesanya, Norfolk State University, Department of Biology.
2015-17	Undergraduate Researcher with Dr. Regina Oyesanya, Norfolk State University, Department of Biology.
2016	Defense Intelligence Agency Student Intern; Office of Advance Technologies Intelligence Biological Sciences Branch with Major Tracy Clinton, Charlottesville, VA
2017-present	Member, Graduate Program in Immunology, Biochemistry and Molecular Biology, UTHSC
2019-present	Member, American Society for Virology

Honors and Awards

2013-17	Dozoretz National Institute for Mathematics and Applied Science (DNIMAS) Scholar
2013-17	Dean's List, Norfolk State University
2014	Annual Biomedical Research Conference for Minority Students Travel Award
2014	Norfolk State University Special Recognition Award for Poster Presentation
2015	Intelligence Community Centers of Academic Excellence (IC-CAE) National Security Certificate Award

C. Contributions to Science

Topic 1. **Ecology and Evolution of Hantaviruses.** As a Ph.D. student in Dr. Colleen Jonsson's lab, I learned and optimized an indirect immunofluorescence assay for screening hantaviral IgG antibodies. My experience with this technique allowed me to screen blood samples collected from wild rodents captured in the Interior Atlantic Forest of Paraguay. Previously, an experimental field study was conducted by our group to test whether food resources and/or landscape composition promote the emergence of hantaviruses harbored by rodent reservoirs within their native ecosystem. For our pending manuscript, I provided data showing rodent population dynamics, rodent demographics and viral prevalence. I also assisted with statistical analysis. We found that the addition of food resources increased rodent species diversity but did not affect hantaviral prevalence. For *Akodon montensis* species, the rodent reservoirs of *Jabora Orthohantavirus*, we detected a strong statistical association between antibody-positive animals and habitat degradation. From these studies, we found that the relationship between rodent biodiversity and hantaviral prevalence depends upon the specific host-pathogen ecology. I presented this work at the 2019 American Society for Virology conference and am listed as second author. The skills obtained from this project will be useful for the development of my research project, as outlined in the Research Strategy.

1. Camp, J.V., Spruill-Harrell, B., Owen, R.D., Solà-Rierae, C., Williams, E.P., Eastwood, G., Sawyer, A.M., Jonsson, C.B. (2020). Mixed Effects of Habitat Degradation and Resources on Species Diversity and Epidemiology of Orthohantavirus in Sympatric Wild Rodent Reservoirs within a Neotropical Forest. PLOS Neglected Tropical Diseases. Manuscript submitted for publication.

BIOGRAPHICAL SKETCH

NAME: Colleen B. Jonsson

eRA COMMONS USER NAME (credential, e.g., agency login): JONSSON

POSITION TITLE: Professor, Van Vleet Chair of Excellence in Virology; Director, UTHSC Regional Biocontainment Laboratory

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
University of Missouri—St. Louis, St. Louis, MO	BA	05/1983	Biology
University of Missouri—St. Louis, St. Louis, MO	BA	05/1983	Chemistry
Purdue University, W. Lafayette, IN	PhD	08/1990	Biochemistry
University of Medicine and Dentistry of New Jersey, Piscataway, NJ	Postdoc	08/1993	Virology/Biochemistry
United States Army Medical Institute of Infectious Disease (ORISE Sabbatical Fellow)	Sabbatical	08/2000	Virology

A. Personal Statement

I am a Professor in the Department of Microbiology, Immunology and Biochemistry, Director of the Institute for Study of Host-Pathogen Interactions, Director of the Regional Biocontainment Laboratory at the University of Tennessee Health Science Center. During the early years of my academic career, I focused on studies to elucidate that structure-function activities of retroviral and hantaviral proteins using a combination of biochemical, virology, cell biology approaches and techniques. Over the years, these efforts have segued into a much broader, multidisciplinary research program that include laboratory and field-based efforts in the biology, ecology and evolution of hantaviruses, and drug discovery research into several emerging RNA viruses. Additionally, I have worked on the development of various small animal models for the testing of therapeutics. Lastly, I have engaged in scientific capacity building in the area of infectious disease diagnostics in several developing countries; Paraguay, Honduras, Brazil and most recently, Ukraine.

My research in the study of hantaviruses (now genus *Orthohantavirus*, family *Hantaviridae*) began in 1995 as a new Assistant Professor at New Mexico State University. I started this position during the 1993 outbreak of hantavirus pulmonary syndrome in the Four Corners region of the USA. I found the sudden appearance of this new, rodent-borne virus fascinating. In review of the literature, I quickly realized fundamental gaps in our understanding of these viruses. First, there were (and still are) no therapeutics for treatment of hantaviruses and their diseases in humans; second, there was little known regarding the structure-function of virion proteins; and third, we knew little of the dynamics of virus populations in the reservoir rodent species or during the course of infection in humans. I describe briefly our accomplishments and then summarize the current focus of my lab in international research.

Our structure-function studies of the hantaviral N protein showed the protein recognized the viral genomic RNA with fairly high affinity and we mapped the RNA binding domain to a central conserved region. Subsequent research focused on cellular trafficking on N and we were the first to show the virus trafficked to the ERGIC and required microtubules, specifically dynein. We also discovered that hantaviruses differ in their cellular components required for cellular entry/trafficking. Finally, we have worked with Rossman's group at Purdue to define the structure of the Hantaan virion by cryoelectron microscopy and we have continued these efforts with Jason Lanman at Purdue for several of the New World hantaviruses (publications in progress).

The intensive efforts of my lab in structure-function studies enabled my transition into field work. I was able to establish both ELISA and strip-based tests for hantaviruses that were used in surveys of human and animal populations. While much of the published research has been focused in Paraguay and Brazil, I led several workshops in Paraguay, Honduras, El Salvador to enable participants to conduct sero-surveillance of hantaviruses. This type of work has recently expanded to Ukraine.

Our research into therapeutics has primarily focused on defining the mechanism of action of ribavirin for HTNV. The motivation to address this question was that ribavirin is the only antiviral for treatment of hantaviral infection (open label); and we hypothesized that if we understood why it was so effective (an potent) that understanding its mechanism would open the door to better antivirals for treatment. Our studies revealed that ribavirin increased the mutation frequency (Mf) of HTNV. We learned that HTNV has a lethal threshold of Mf, past which it no longer can survive *in vitro*. We tested this in vivo in a lethal mouse model and observed that ribavirin increased Mf, but this correlates with persistence in the host, and an increase in positively-selected amino acids. In contrast, the untreated, HTNV-infected mice, showed a decrease in Mf (as compared to preexisting standing genetic variation suggesting negative selection of the virus. These findings motivated the question, how do hantaviruses spill over and adapt to new hosts? This is one of the main questions being addressed now in the lab and field studies and will be discussed in the next paragraph. Important to this effort are the approaches and techniques we have developed to sequence hantaviruses and map genetic diversity. These techniques represent our studies of the "population" structure of viruses within host. In our current efforts these techniques have been replaced by Nexgen approaches. We have now applied our approaches, not only hantaviruses, but to New World alphaviruses as part of a drug discovery effort.

As mentioned above, a third area of research in the lab is in the ecology and evolution of hantaviruses using a combination of field- and lab-based research approaches. My R01 lab-based efforts seeks to further the understanding of the evolution and host restriction mechanisms of hantaviruses in their natural rodent reservoir and spillover rodents. Secondly, we are studying the epidemiology and phylodynamics of hantaviruses in their natural hosts within populations in their natural rodent reservoir that are endemic in the Interior Atlantic Forest of Paraguay. As these are longitudinal collection studies, we are only just beginning to write manuscripts based on three years of collection efforts and several years of screening of rodent tissues for hantaviruses. Additionally, we have developed tiling techniques to obtain full length genomes by nexgen sequencing. Lastly, we have funding from NSF to model these relationships in collaboration with Dr. Linda Allen to understand the relationships of these viruses with their rodent reservoir. My current funding presents a valuable opportunity for understanding standing genetic diversity and plasticity of RNA viruses in wildlife in rapidly changing environments and genetic determinants driving its epidemiology.

Finally, I have a unique blend of professional experience and leadership skills gained from my positions over 30 years in industry, academics and not-for-profit institutes that would benefit the goals of the US-Brazil collaboration as the PI. I have led three major cross-institutional efforts that demonstrate my scientific and administrative leadership experience. In each of the major efforts in which I have engaged, I have built collaborative programs with other research institutions and developed cooperative programs with industry. My role as a leader in these programs has been to actively establish and communicate policy, mission, goals, and accomplishments, and foster collaborative networks among leadership, faculty, students and staff. I have been successful in fostering interdisciplinary research relationships and leading scientific studies focused on virology questions that bridge expertise across mathematics, ecology, medicinal chemistry and/or new technologies.

B. Positions and Honors

1981-1983 Monsanto- Summer Research Intern with Drs. Kishore, Castanho, Yoshikawa
08/83-08/85 Research Biologist, Monsanto- St. Louis, Mo. Molecular Biology Division
09/85-09/90 USDA Predoctoral Fellow with Dr. David Kuhn, Purdue University, Department of Biochemistry.
09/90-08/93 NRSA (F32) Postdoctoral Fellow with Dr. Monica Roth, UMDNJ, Department of Biochemistry
08/93-06/99 Assistant Professor, Department of Chemistry and Biochemistry
New Mexico State University (NMSU), Las Cruces, NM
7/99-6/2000 ORISE Sabbatical Fellow, United States Army Medical Institute of Infectious Disease, Virology Division with Dr. Connie Schmaljohn
08/99-08/03 Associate Professor (tenured), Department of Chemistry and Biochemistry, NMSU
08/03-10/04 Senior Research Scientist, Department of Biochemistry and Molecular Biology, Drug Discovery Division, Southern Research Institute (SRI), Birmingham, AL
08/03-08/08 Associate Professor, Department of Biochemistry and Molecular Genetics, University of Alabama, Birmingham, secondary appointment
08/03-08/08 Member, Graduate Program in Biochemistry and Molecular Genetics, UAB
10/04-01/06 Director, Emerging Pathogens, Drug Development Division, SRI
01/06-01/11 Program Leader, Emerging Infectious Disease Research, SRI
09/08-12/14 Professor, Department of Microbiology and Immunology, University of Louisville (UofL), KY
09/08-12/14 Director, Center for Predictive Medicine for Biodefense and Emerging Infectious Diseases, UofL, KY
08/11—12/14 Associate Faculty Member, Department of Pharmacology and Toxicology, University of Louisville, KY

12/15—	To present: Adjunct Professor, Department of Microbiology and Immunology, UofL, KY
12/14—6/17	Professor, Department of Microbiology, University of Tennessee, Knoxville, TN
12/14—6/17	Director, National Institute for Mathematical and Biological Synthesis (NIMBioS), University of Tennessee, Knoxville, TN
7/17-	To present: Van Vleet Chair of Excellence in Virology, Professor, Department of Microbiology, University of Tennessee Health Science Center (UTHSC), Memphis, TN
7/17	To present: Director, UTHSC Regional Biocontainment Laboratory, Memphis, TN

Other Experience and Professional Memberships (Selected) Study Sections: 1997-8, NIH, Structural AIDS Special Emphasis Panel; NSF Graduate Fellowship Panel; 2002-6, NIH, RCMI Study Section; 1998-2001,03, National Institutes of Health, Biodefense, Vaccine; 2003-4, NIH, Biodefense, Bioterrorism & Emerging Infectious Diseases; 2006, *Chair,* NIH, National Biocontainment Laboratories- BSL3 and BSL4; 2010-14: NIH, Drug Discovery and Resistance Study Section; Consultant: Pan American Health Organization in Tegucigulpa, Honduras, San Salvador, El Salvador, Mexico City, Mexico, Panama City, Panama; *Antiviral Research,* Editorial Board

Honors and Awards1985-1988, USDA National Needs Predoctoral Fellowship in Plant Biotechnology; 1992-93, Individual National Research Service Award, National Institutes of Health; 1992-93, University of Medicine and Dentistry, NJ Postdoctoral Fellowship; 1994, New Mexico State University Summer Research Award; 1996, McArthur Foundation Training Fellowship – Vector Borne Disease Workshop; 1997/1998, Battelle Summer Research Fellowship in the Division of Virology, United States Army Research Institute of Infectious Disease; 1997, Certificate of Recognition and Appreciation by the State of New Mexico for Service to the Community and New Mexico State University; 1999/2000, ORISE Sabbatical Fellow at USAMRIID; 2000, American Society of Microbiology International Professorship to Honduras; 2007, Distinguished Alumni Award, Purdue University College of Agriculture

B. Contributions to Science

Topic 1: Mapping the progression of inflammation and influenza virus infection in ferret lung. During the H1N1 2009 pandemic, I began a collaboration with Dr. Daniel Mollura at NIH to determine if we could use a commonly used clinical PET imaging probe, FDG, to follow the progression of inflammation in real-time in ferret. Building on our prior NIH funded work with the ferret models of influenza infection, we evaluated the virology, pathogenesis, immune/local gene responses of clinical isolates of H1N1pdm09 with radiological imaging. These studies taught us a great deal about the progression of inflammation in the lung. Surprisingly, and counter to our hypothesis, the FDG probe detected cellular regeneration during infection, and not immune infiltration as shown in cancer studies (Camp et al).

1. Bruder, C.E., Yao, S., Larson, F. Camp, J., Tap, J. McBrayer, A., Powers, N., Valdavia-Granada, W., and C.B. Jonsson. (2010) Development of molecular genetic analysis tools for the domestic ferret (*Mustela putorius furo*). BMC Genomics 11:251 PMID: 20403183
2. Jonsson, C.B, Camp, J.V., Wu, A., Zheng, H., Kraenzle, J., Biller A., Vanover, C.D., Chu, Y-K, Ng, C., Proctor, M., Sherwood, L., Steffen, M., Mollura, D.J. (2012) Molecular Imaging Reveals a Progressive Pulmonary Inflammation in Lower Airways in Ferrets Infected with 2009 H1N1 Pandemic Influenza Virus PLoS ONE. 7: e40094
3. Camp, J.V., Chu, Y-K, Chung, D., McAllister, R., Gerlach, R.L., Adcock, R.S., Wiemken, T.L., Peyrani, P., Ramirez, J., Summersgill, J.T., Jonsson, C.B. (2013) Phenotypic Differences in Virulence and Immune Response in Closely Related Clinical Isolates of Influenza A 2009 H1N1 Pandemic Viruses in Mice. PLoS ONE. 8: e56602. PMID: 23441208
4. Camp JV, Bagci U, Chu YK, Squier B, Fraig M, Uriarte SM, Guo H, Mollura DJ, Jonsson CB. (2015) Lower Respiratory Tract Infection of the Ferret by 2009 H1N1 Pandemic Influenza A Virus Triggers Biphasic, Systemic and Local Neutrophil Recruitment. J Virol. Jun 10. pii: JVI.00817-15.

Topic 2: High Throughput Screening (HTS) to Accelerate the Discovery and Translation of Potential Antivirals for RNA Viruses. During the SARS CoV outbreak in 2003, I was working to improve the technology and processes to accelerate small molecule screening in BSL3 containment. I led the successful implementation of this for a number of RNA viruses. In 2008, I was awarded a U54 grant to lead a screening center focused on BSL3 pathogens from the NIH Molecular Libraries Screening Program. This program, and my other collaborative research programs over the years, have led to patents for hantaviruses, influenza virus, and respiratory syncytial virus as well as interesting hits for SARS CoV and West Nile virus. One of the most exciting small molecules that has emerged from my HTS collaborations is with Drs. Chung and Golden that is focused on Venezuelen equine encephalitis. My role in this effort is the testing of the molecules in small animal models of VEEV and to lead the way toward translation in preclinical testing.

5. Severson, W.E., Shindo, N., Sosa, M., Fletcher, T., White, L. and C. Jonsson. (2007) Development, validation and optimization of a luminescence-based high throughput screen for inhibitors of Severe Acute Respiratory Syndrome. J. Biomol. Scr. 12:33-40.
6. Severson, W., Rasmussen, L., White, E. L. and C. B. Jonsson (2008) High-Throughput Screening of a 100,000 Compound Library for Inhibitors of Influenza A virus (H3N2). J. Biomol. Scr. 13:879-387
7. Jia, F., Maddox, C., Gao, A., Tran L., Severson, W., White, E.L., Rasmussen, L., Dang, A., Jonsson, C.B. (2010) A novel cell-based 384-well, label-free assay for discovery of inhibitors of influenza virus. Inter. J. High Throughput Screening 1:57-67.
8. Maddry, J.A., Chen, X., Jonsson, C.B., Ananthan, S., Hobrath, J., Smee, D.E., Noah, J.W., Noah, D., Xu, X., Jia, F., Maddox, C., Sosa , M.I., White, E.L. and Severson W. (2011) Discovery of Novel Benzoquinazolinones and Thiazoloimidazoles, Inhibitors of Influenza H5N1 and H1N1 viruses, from a Cell-Based High-throughput Screen. J. Biomol. Scr. 16:73-81. PMID: 21059874

Topic 3: Structure-function, intracellular trafficking and intracellular signaling of the hantaviral N protein. My lab showed the N protein preferentially recognizes its viral RNA with fairly high affinity and we mapped this to a central conserved domain. Subsequent research focused on cellular trafficking on N and we were the first to show the virus trafficked to the ERGIC and required microtubules, specifically dynein. Our studies also show that hantaviruses differ in the cellular components required for cellular entry/trafficking.

9. Severson, W.E., Partin, L., Schmaljohn, C. S. and C.B. Jonsson. (1999) Characterization of the Hantaan N protein-ribonucleic acid interaction. J. Biol. Chem. 274:33732-33739. PMID:10559265
10. Severson, W.E., Xu, X., and C.B. Jonsson. (2001) *Cis*-acting signals in the encapsidation of the Hantaan Virus S-segment vRNA by its N Protein. J. Virol. 75:2646-2652. PMID:11222687
11. Ramanathan, H.N. and Jonsson, C.B. (2008) New and Old World Hantaviruses Differentially Utilize Host Cytoskeletal Components During Their Life Cycles. Virology 374:138-50. PMID:18234268
12. Ontiveros, S.J. Li, Q., and Jonsson, C.B. (2010) Modulation of Apoptosis and Immune Signaling Pathways by the Hantaan Virus Nucleocapsid Protein. Virology 401:165-178. PMID: 20227103

Topic 4: Mechanism of action of ribavirin against hantaviruses. We found that ribavirin increased the mutation frequency (Mf) of HTNV *in vitro* that resulted in error catastrophe/extinction of the virus. Given this result, we asked whether Mf would similarly increase *in vivo* in the mouse model of lethal HTNV-infection, treated with ribavirin, which it did. Our mechanistic studies yielded insight into the genetic robustness and evolution of the virus. We have learned that HTNV has a window of Mf as well as a lethal threshold, past which it no longer can survive *in vitro*. We observed that the increased Mf actually correlates with persistence in the host, and an increase in positively-selected amino acids. In contrast, the untreated, HTNV-infected mice, showed a decrease in Mf (as compared to preexisting standing genetic variation suggesting negative selection of the virus. We have also shown that ribavirin is effective in clearing Andes virus in the hamster model in collaboration with Dr. Jay Hooper (USAMRIID).

13. Severson, W.E., Schmaljohn, C. S., Javadian, M.A. and C.B. Jonsson. (2003) Ribavirin causes error catastrophe during Hantaan virus replication. J. Virol. 77:481-488. PMID:12477853
14. Chung D., Sun, Y., Parker, W.B., Arterburn, J.A., and Jonsson, C.B. (2007) Ribavirin reveals a lethal threshold of allowed mutation frequency for Hantaan virus. J. Virol. 81:11722-9. PMID:17699579
15. Sun, Y., Chung D., Chu, Y.K., Jonsson, C.B. and W.B. Parker. (2007) Antiviral activity of ribavirin against Hantaan virus correlates with production of ribavirin-5'-triphosphate, not with inhibition of inosine monophosphate dehydrogenase. Antimicrobial Agents and Chemotherapy. 51:84-88. PMID:17060520
16. Chung, D.H.C., Västermark, A., Camp, J.V., McAllister, R.C., Remold, S., Chu, Y., and Jonsson, C.B. (2013) The Murine Model for Hantaan Virus-Induced Lethal Disease Shows Two Distinct Paths in Viral Evolutionary Trajectory with or without Ribavirin Treatment. J. Virol. 87:10997-1007. PMID: 23903835

Topic 5: Modeling the ecology, evolution and immune responses of hantaviruses. My current R01 seeks to further the understanding of the epidemiology and evolution of hantaviruses within populations in their natural rodent reservoir that are endemic in the Interior Atlantic Forest of Paraguay. These studies build upon our efforts (with Robert Owen) and the research of others, that suggest that host-virus relationships may not be exclusive, and that host-switching and adaptation to new hosts may account for much of the observed geographic diversity of hantaviruses. Our current funding presents a valuable opportunity for understanding standing genetic diversity and plasticity of RNA viruses in wildlife in rapidly changing environments and genetic determinants driving its epidemiology. Dr. Owen and I have endeavored to mathematically model these relationships in collaboration with Dr. Linda Allen. The modeling revealed many aspects in the ecology of the rodent-virus relationship that are not presently understood and led us to develop a theoretical biological model of these relationships based on the immune response of the rodent (reservoir versus nonreservoir). Our recent efforts funded by NSF seek to model immune regulatory mechanisms in reservoir, nonreservoir and humans which is important to interpretation of systemic and localized immune responses in human disease. Finally my prior NIH R01

hosted an R03 to build BSL3 capacity and discovery of viruses in rodents with Dr. L. Figueiredo in Brazil. This has resulted in the discovery of hantaviruses in bats.

17. Wesley, C.L., Allen, L.J., Jonsson, C.B., Chu, Y-K., Owen, R.D. (2009). A discrete-time rodent-hantavirus model structured by infection and developmental stages. Advanced Studies in Pure Mathematics, 53, 1-12.
18. Allen, L.J.S., Wesley, C.L., Owen, R.D., Goodin, D.G., Koch, D., Jonsson, C.B., Chu, Y-K., Hutchinson, S., Paige R.L. (2009) A habitat-based model for the spread of hantavirus between reservoir and spillover species. J. Theoretical Biol. 260:510-522.
19. Owen, R.D., D.G. Goodin, D.E. Koch, Y-K. Chu, and C.B. Jonsson. (2010) Spatiotemporal variation in *Akodon montensis* (Cricetidae: Sigmodontinae) populations and hantaviral seroprevalence in a subtropical forest ecosystem. Journal of Mammalogy. 91:467-481.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

NIH 1R01AI103053 - 01 Jonsson (PI) 03/31/14-03/30/18 NCE
Title: Evolutionary mechanisms of RNA virus host switching
Scope: To define the ecology and evolution of hantaviruses in their reservoir and nonreservoir hosts in wildlife populations in Paraguay and in in vitro cell culture models.

NIH 1 R01 AI118814-01 Jonsson (Multi-PI with Chung and Golden) 04/01/15-03/31/20
Title: Lead Optimization of ML336, a Potent VEEV Inhibitor
Scope: Drs. Hoon Chung, Jennifer Golden, and Jonsson have teamed together for the proposed drug discovery efforts in the evaluation of the antiviral candidates in efficacy, pharmaco -kinetic and -dynamic studies for VEEV.

NSF Mathematical Biology PD 12-7334 Jonsson (Co-PI, Dr. Linda Allen) 09/01/15-08/31/18 (NCE8/31/19)
Title: Collaborative Research: Modeling Immune Dynamics of RNA Viruses In Reservoir and Nonreservoir Species
Scope: In support of the mathematical modeling by Dr. Allen (Texas Tech U), the dynamics of the viral RNA levels, infectious virus and immune responses will be measured for Sin Nombre virus (SNV) in its host rodent reservoir, the deer mouse, (HR) in vitro. All viruses will be compared to infection in human cells. 4

Metabiota (DoD BTRP). Jonsson(PI) 10/02/17-10/01/18 (Year 1) and 2/18/19-2/17/20 (Year 2)
Title: Prevalence of Crimean Congo hemorrhagic fever virus and hantaviruses in Ukraine and the potential requirement for differential diagnosis of suspect leptospirosis patients
Scope: Training and surveillance of hantaviruses and CCHFV in environmental and human populations.

U19 AI142762-01 (PI: Jonsson) 03/2019-02/2024
Title: Center of Excellence for Encephalitic Alphavirus Therapeutics
Scope: This proposed research efforts of the Center aim to develop broad spectrum, medical countermeasures (MCM) against multiple pathogens (VEEV, EEEV, and WEEV) thereby enabling a "rapid response" capability to an outbreak or an intentional exposure scenario. The proposed Center of Excellence will facilitate all aspects that enable the progress toward safe and effective therapeutics for encephalitic alphaviruses and will advance the development of a broad-spectrum approach that has the capacity to address many of the performance attributes desired in the field of biodefense, namely a readily manufactured, safe antiviral with sufficient potency to provide protective efficacy against multiple pathogens once exposure is identified.

BUDGET JUSTIFICATION – University of Tennessee Health Science Center

Key Personnel

Colleen Jonsson, Ph.D. (5% effort, Year 1) – Dr. Jonsson from the UTHSC Department of Microbiology, Immunology and Biochemistry will provide scientific guidance of Briana Spruill-Harrell for the proposed studies. She will provide support for compliance of all recombinant DNA and the animal studies by obtaining the appropriate approvals. She will work with Briana each week in their one on one meeting to review the progress toward the proposed research and engage in the research as needed. She will provide oversight of the manuscript resulting from this research.

Other Personnel

Briana Spruill-Harrell (graduate student; 12 CMs Y1). Ms. Spruill-Harrell will oversee all of the lab work. She will lead the mouse studies and in vitro studies. Briana has been working with hantaviruses for over two years and has mastered all of the pertinent virology for this project. She has been trained for the mouse studies and has approval to work in ABSL3 in the Regional Biocontainment Lab. Dr. Jonsson will provide mentors from the RBL to provide specific instruction and mentoring unique to her studies. Briana will lead the writing of research resulting from her efforts.

Equipment

None

Supplies

The consumables are based on these estimates for standard virology, histology, and molecular biology supplies. Supplies include culture flasks and plates for growing and assaying virus, materials for collection of lung and kidney for downstream pathology and IHC, and molecular reagents for detection of virus, host genes (RNASeq) specific genes. We also include costs for housing of the mice at ABSL-3.

Travel (Domestic)

Scientific Meetings: Travel is budgeted for the graduate student to attend the annual American Society of Virology Meeting or similar in the USA to present research findings in summer 2021.

Hotel, airfare and ground transportation are calculated using rates from previous travel records. Per diem rates are calculated using UTHSC guidelines and the State of TN Accounting Manual.

Publication Costs $2,500/year

We request support for publications estimated at $2500. This is based on prior publication costs with color figures which will be an essential output of the work.

I. SPECIFIC AIMS

Hantaan virus (HTNV) is an emerging RNA virus belonging to the family *Hantaviridae*, genus *Orthohantavirus*. that causes hemorrhagic fever with renal syndrome (HFRS) in humans throughout Europe and Asia [1]. The global incidence of reported HFRS cases can be as high as 100,000 per year with a majority of cases occurring in geographically focused outbreaks that can results in hundreds to thousands of cases [1]. Hallmark features of HFRS include fever, hemorrhage, thrombocytopenia, and kidney dysfunction. Disease severity differs individually, as infection can range from mild to lethal with a case fatality reaching up to 15% in some outbreaks [4,5]. There are no FDA-approved vaccines or antivirals for treatment. In Europe and Asia, two closely-related hantaviruses, HTNV and Dobrava-Belgrade virus (DOBV) are the primary causative agents of severe HFRS. HTNV is carried by the rodent species *Apodemus agrarius*, belonging to the family *Muridae*, and is transmitted to humans through inhalation of virus contained in excrements [1-3]. Remarkably, no disease has been shown to be present in the rodent reservoir, which may persist over the lifetime of the rodent.

The current mouse models used to study HFRS have been developed on single inbred backgrounds and are predominantly models of infection or arguably irrelevant models of lethality. Mouse models of infection have been primarily conducted in adult mice which become infected but do not cause serious disease or lethality [6]. The primary lethal model has been achieved by intracranial injection of the virus into the brain of suckling mice [7-9]. Neither of these models recapitulates the pathophysiology of the disease in humans. Moreover, these models are not appropriate for preclinical testing of antivirals or vaccines or the study of pathogenesis. Therefore, we propose to identify and then develop a translationally relevant mouse model system of hantaviral infection and disease using the Collaborative Cross (CC) R1 mouse strains. Upon development of this model, we plan to investigate the underlying mechanisms of pathogenesis.

There are a few reports in the published literature that suggest the Collaborative Cross could be used to identify a relevant model of HFRS [10-11]. Wichmann et al. demonstrated that several adult laboratory mice strains including C57BL/6, BALB/c, AKR/J, and SJL/J mice, are susceptible to intraperitoneal (IP) infection of 10^5 pfu of HTNV (strain 76-118), but phenotypically differ in clinical course (i.e. time to death) [12]. Although these mice did not develop hallmarks of HFRS, this study suggests that host genetic variation likely influences infection outcome. The lack the genetic diversity seen in current mouse models make it difficult to recapitulate HFRS disease in humans. Therefore, we propose to use the Collaborative Cross which captures over 90% of diversity across three *Mus musculus* subspecies (*M. m. musculus, M. m. domesticus,* and *M. m. castaneus*), to test the hypothesis that host immune gene variation influences infection outcome [10-11].

The primary goals of the proposed project are to 1) Develop a translationally relevant mouse model system to study HTNV infection and disease, and 2) Identify genes that influence HTNV pathogenicity. Our strategy to accomplish these two goals are:

Aim 1. Evaluate susceptibility of the Collaborative Cross to HTNV virus infection. In this aim, we plan to test the hypothesis that inherent genetic variation in the Collaborative Cross will influence susceptibility to HTNV infection. To test this hypothesis, we propose to infect up to 80 strains of the CC that are readily available with HTNV 76-118 and we will monitor weight loss, clinical signs and survival over 14 days. We will screen the CC panel in groups of five across 20 strains. From this screen, we will select two mouse strains that show a greater level of symptoms of disease relevant to HFRS and two that show resistance to infection (for future follow on studies). For the two pairs of mouse strains selected, we will perform a serial sacrifice to obtain a preliminary understanding of the dynamics of infection and pathology with a focus on the kidney and lung; the two primary sites of viral replication. From this second study, we will choose one lethal mouse strain for the studies in Aim 2.

Aim 2. Identify host transcriptional responses associated with HTNV disease outcome. In this aim, we plan to test the hypothesis that the susceptibility in strains of mice with higher lethality is due to genes regulating innate and/or adaptive immunity. While we cannot predict apriori what genes may influence outcome, we hypothesize that an uncontrolled immune response to infection (in humans) will result in a greater degree of HTNV pathogenesis. We propose to test this hypothesis by infecting one of the two mouse strains showing greater pathogenesis with HTNV 76-118 and examining transcriptional response of the lungs and kidneys at 1, 3, 5, and 7 days post-infection and examining the gene expression profiles by RNASeq.

The proposed one-year pilot will provide the basis for future studies follow-on studies in collaboration with Dr. Klaus Schughart to use F2 crosses of the lethal and resistant mice strains to define what genes are critical for disease severity and the underlying biological mechanisms of pathogenesis.

II. RESEARCH STRATEGY

A. Significance

The proposed Collaborative Cross studies will advance the field of hantavirology by providing a novel, *in vivo* model to characterize virus-host interactions of an important human pathogen, HTNV, which is responsible for up to 50,000 cases of HFRS each year in Asia [14]. Development of the HFRS rodent model will set the foundation for follow-up studies to examine the underlying mechanisms of pathogenesis which will also be important for other Old World hantaviruses that cause disease in Europe. Further, a relevant model of HFRS will advance the identification and characterization of host factors contributing to hantavirus infection and disease outcome that may serve as targets for future drug and vaccine discovery. Laslty, the development of a relevant model for HFRS would be a tremendous resource to those involved in testing of drugs and vaccines for Old World hantaviruses.

B. Innovation

The innovation of the proposed research is two-fold. First, our research will result in a translationally relevant rodent model system of HFRS. Secondly, this model, once realized, will reveal genes that influence pathogenicity. Several groups have used the Collaborative Cross to model human variability to viral infections including studies with Ebola virus (EBOV), Influenza virus, SARS-Coronavirus, and West Nile virus [10-11]. Our studies will complement these efforts and may also provide additional insights into hemorrhagic viruses like EBOV.

C. Approach

Aim 1. Evaluate susceptibility of Collaborative Cross Mouse (CC) Strains to HTNV virus infection.

Rationale. Wichmann et al. showed that intraperitoneal (IP) injection of 10^5 pfu of HTNV 76-118 in 8-week-old C57BL/6 resulted in uniform lethality [12]. C57BL/6J mice are one of several founder strains of the Collaborative Cross therefore, we will use this age, route, and dose in the proposed experiments. Hence, we will use this dose and route to infect mice in the UTHSC Regional Biocontainment Laboratory ABSL-3 facilities. We will use male mice in the Aim 1 since male mice show a greater susceptibility than females. However in Aim 2, we will use males and females and include sex as a variable in our hypothesis. Dr. Jonsson has 24 years of experience in working in biocontainment with hantaviruses *in vitro* and *in vivo*; she has approved protocols in place from the IBC and IACUC for *in vitro* and *in vivo* study with HTNV. We hypothesize that inherent genetic variation in the CC strains will influence susceptibility to HTNV infection.

Experimental Design and Methods.

We propose two experiments; (Aim 1A) a survival study of the CC panel using up to 80 strains, and (Aim 1B) a serial sacrifice of the two CC strains that show the greatest signs of disease. **Aim 1A**: We will infect each 8-week old CC strain (n=4) by IP with 10^5 pfu of HTNV 76-118. We will screen in groups of 20 strains. We will monitor weight each day and clinical signs. Differences in survival will be compared using the Log-Rank (Mantel-Cox) Test in GraphPad Prism 8 (Graph Pad Software, Inc). P values generated by the Log-Rank test will be evaluated by comparison to a Bonferroni corrected threshold of 0.0125 (p=0.05) to determine statistical significance. **Aim 1B**: We will conduct a serial sacrifice of the two strains that show the most disease; we will include mock-infected controls for all groups. Using groups sizes of four, we will sacrifice mice on days 1, 3, 5 and 7. Weight loss and clinical signs will be monitored twice daily for 14 days. On 1 ,3, 5, and 7, tissues (i.e. brain, kidneys, heart, liver, lungs, and spleen) will be harvested following perfusion with PBS. Tissues will be divided into two equally sized portions. One portion will be fixed in 4% paraformaldehyde for histopathology. One portion will be homogenized in 0.5 mL of PBS for virus infectivity by plaque assay.

Anticipated Results, Potential Pitfalls and Alternative Approaches. Several studies suggest that genetic variation influences host susceptibility to HTNV infection. For example, in China, human leukocyte antigen (HLA) haplotypes such as HLA-DRB1*09 and HLA-B*46-DRB1*09 are common among HFRS patients compared to healthy controls and are correlated with disease severity [20]. If our hypothesis is correct, we expect that susceptibility measures (i.e. survival, weight loss, viral load, and pathology) will differ in the Collaborative Cross. We predict that viral load will be associated with weight loss, clinical signs, and pathology score. Adult males (20-60 years old) have a higher risk of HTNV infection [4, 25]. Therefore, we predict that there may be sex-dependent differences in infection outcome. The overall goal of this study is to identify a mouse model of HFRS with renal involvement. Particularly, we anticipate observing acute tubulointerstitial nephritis with mononuclear

cells and CD8+ T cell infiltration in the kidneys which is characteristic of HFRS [2,15]. If we get these results, we will characterize this model in future studies. If we do not observe renal pathology, this would suggest that other target sites are involved in HTNV-induced disease in the Collaborative Cross. Wichmann et al. demonstrated that IP infection in 8-week-old laboratory mice strains resulted in encephalitis [12]. If this happens, we will optimize viral dose and infection route to improve our model.

Aim 2. Identify host transcriptional responses associated with HTNV disease outcome.

Rationale. HFRS is a systemic inflammatory disease that cause vascular leakage and coagulation disorders. Kidney involvement occurs in up to 40% of cases and the most prominent pathological finding is acute tubulointerstitial nephritis with immune cell infiltration [15]. HTNV is non-cytopathic therefore, pathogenesis is suggested to involve an overwhelming inflammatory response. It is been demonstrated that the magnitude of the inflammatory response and HTNV load correlates with disease severity [16-19]. To begin identifying the immune genes and associated pathways that shape anti-HTNV immune responses and/or disease, we propose to examine lung and kidney transcriptional responses using RNA sequencing. We hypothesize that genetic variation in the Collaborative Cross at loci regulating innate and/or adaptive immunity influence HTNV pathogenesis.

Methods. Using the CC mouse strain with the greatest degree of HFRS relevant pathology and clinical signs, we will challenge groups of 8-week-old mice of both sexes by IP with 10^5 pfu of HTNV 76-118. Mock-infected mice will receive PBS. Weight loss and clinical signs will be monitored twice daily for 14 days. Mice will serially be sacrificed at 1, 3, 5, and 7 days post-infection at which time the lungs and kidneys will be harvested following perfusion with PBS. Tissues will be divided into two equally sized portions as described in Aim 1. We will perform TRIzol RNA isolation from homogenized lungs or kidneys collected from infected and mock-infected mice according to the manufacture's protocol (Thermo Fisher Scientific). RNASeq libraries will be prepared for paired-end (150 bp) sequencing on Illumina HiSeq. Differential expression analysis will be performed using the *Mus musculus* reference genome making use of nf-core's RNA seq pipeline and DESeq2 [26, 27]. Differentially expressed genes will be based upon a fold change > |2| and FDR corrected p-value <0.05. Gene Ontology Enrichment Analysis and KEGG Pathway Enrichment Analysis will be used to determine the biological functions and associated pathways of these genes.

Anticipated Results, Potential Pitfalls and Alternative Approaches. HTNV evades the early host immune response by delaying induction of the antiviral gene expression *in vitro* to establish infection [21-23]. Our preliminary results and other published *in vitro* studies show than HTNV infection results in elevated, prolonged expression of tumor necrosis factor alpha (TNF- α), interferon-γ (IFN-γ), interleukin-1β (IL-1β), interleukin-6 (IL-6), interleukin-8 (IL-8), interferon regulatory factor 7 (IRF7), chemokine (C-C motif) ligand-5 (CCL-5), and C-X-C motif ligand-10 (CXCL-10) in human endothelial cells [21-23]. These inflammatory mediators are also elevated in the serum and/or kidneys of HFRS patients [17-19]. In contrast, early induction of antiviral gene expression is observed with hantaviruses that do not cause human disease [21]. Based upon these findings, we expect to observe delayed induction but elevated, prolonged immune gene expression in the lungs and/or kidneys of mice susceptible to HTNV infection in a time-dependent manner compared to resistant mice. We anticipate that peak gene expression will correlate with viral load and replication [23]. If we do not detect any significant differences in gene expression between males and females, we will search for other potential factors such as age. We will also examine gene expression in other organs such as the brain and spleen in future efforts. Neurological complications have been reported in HFRS patient although, viral antigen has not been detected in the brain [1-2; 24]. Moreover, infection of several different laboratory mice strains with HTNV results in encephalitis [6-9;12]. We do not anticipate any potential problems in screening of the CC strains as Dr. Jonsson has over 15 years of experience in working with HTNV in mouse models.

Conclusions. At the end of the first year, we expect to identify at least two CC strains with relevant clinical signs. Our future efforts will endeavor to leverage our findings to develop a translationally relevant rodent model system of HFRS and to identify genes that influence pathogenicity. In the first year, we only proposed to examine one of the CC mice strains with the greatest clinical signs. If there are more strains that show clinical signs, these will be useful for identifying gene-phenotype relationships of disease severity in future efforts. Long term, these studies could be used to understand the underlying mechanisms of pathogenicity of other hantaviruses and help identify novel therapeutic targets to treat HFRS. We hold that our findings will complement and contribute to the overall understanding of host-pathogen interactions in the context of the other studies on-going within The Center for Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross at the University of North Carolina.

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SCOPE OF WORK

We propose to use the Collaborative Cross which captures over 90% of diversity across three Mus musculus subspecies (M. m. musculus, M. m. domesticus, and M. m. castaneus), to test the hypothesis that host immune gene variation influences infection outcome of the Old World hantavirus, Hantaan virus.

The primary goals of the proposed project are to 1) Develop a translationally relevant mouse model system to study HTNV infection and disease, and 2) Identify genes that influence HTNV pathogenicity.

Our strategy to accomplish these two goals are to:

(1) screen available collaborative cross strains with HTNV across the available strains in groups of 20. We will monitor weight loss, clinical signs and survival over 14 days.
(2) From this screen, we will select two mouse strains that show a greater level of symptoms of disease relevant to HFRS and two that show resistance to infection (for future follow on studies).
(3) For the two pairs of mouse strains selected, we will perform a serial sacrifice to obtain a preliminary understanding of the dynamics of infection and pathology with a focus on the kidney and lung; the two primary sites of viral replication.
(4) From the serial sacrifice study, we will choose one lethal mouse stain with both sexes in advance molecular studies.
(5) In the advanced molecular studies, we will infect one of the two mouse strains showing greater pathogenesis with HTNV 76-118 and examining transcriptional response of the lungs and kidneys at 1, 3, 5, and 7 days post-infection and examining the gene expression profiles by RNASeq.

Perform an unbiased screen of the Collaborative Cross resource to identify new loci influencing the immune response to malaria

Overall hypothesis: Identifying the genetic variants that link to improved immune responses to blood-stage malarial parasites will inform novel therapeutic designs.

Despite remarkable efforts toward eradicating malaria, this infectious disease remains a major global health problem. In 2018, there were 228 million cases worldwide and an estimated 405,000 deaths with >90% of the mortalities occurring in sub-Saharan Africa[1]. Malaria is caused by *Plasmodium* parasites. *P. falciparum* is the most virulent and deadly of the 5 human plasmodia species and accounts for close to 100% of malaria cases in sub-Saharan Africa[1]. In this region, children under the age of 5 years and pregnant women are the most vulnerable, developing serious and often deadly complications, namely, severe malarial anemia and cerebral malaria. Drug resistance in the malaria parasite, insecticide resistance in the mosquito vector, and climate change contribute to the lack of progress in malaria control. Liver stage infection is asymptomatic while the blood-stage causes disease[2]. Yet, the protective host immune response to blood-stage infection remains poorly understood and an effective vaccine that provides long-term protection is still not available. Although hemoglobinopathies have long been associated with resistance to malaria, there is growing evidence that variability in immune response genes contribute to susceptibility in individuals residing in endemic areas[3-5].

Identification of genetic variants that contribute to malarial susceptibility in humans presents considerable challenges[6]. *P. chabaudi* AS (PcAS) infection in mice mirrors many of the immunological and pathological features of *P. falciparum* infection making this parasite an important experimental tool to study the immunology of human malaria and to identify new targets for vaccine development and therapeutic intervention[7,8]. Similar to genetic variation among humans in susceptibility to *P. falciparum*, genetically-determined differences to PcAS infection occur among inbred mouse strains[7,9-12]. Using various classical genetic approaches, namely backcross mice, recombinant inbred strains, recombinant congenic strains, and ENU strains, we and our colleagues have shown that susceptibility to PcAS is a complex trait[9,11,13-15]. In addition to sex differences[9-11,16], eleven loci termed *Char* for chabaudi resistance have been identified[17]. Notably, these loci were identified based on peak parasitemia level and survival, with little to no investigation of the immune response. Consequently, most of these loci are linked to erythroid-specific traits that limit parasite replication in red blood cells (RBC). To design an effective vaccine or immune-based therapeutic approach, it would be most informative to identify the genetic variants linked to the immune response to PcAS.

Hypothesis: The CC strains will provide an unbiased means to identify new candidate genes regulating the immune response to blood-stage malaria.

Specific Aim 1 To determine the intra-strain variation and quantify the experimental variability for detecting immune responses to blood-stage PcAS infection in the eight CC founder strains.

Specific Aim 2 To identify genetic variants linked to the immune parameters for response to PcAS in the CC strains.

This research program builds on a budding collaboration between Dr. Mary Stevenson, expert on mouse models of malaria, and Dr. Sylvie Lesage, an immunogeneticist. It harbours outstanding potential to uncover novel genetic variants contributing to the immune response to blood-stage malaria. Identification of these genetic variants will inform us on the molecular pathways that have been naturally selected to modulate these immune traits, which may help to design better vaccines to prevent malaria or identify novel immunotherapy to treat malaria.

Perform an unbiased screen of the Collaborative Cross resource to identify new loci influencing the immune response to malaria

RESEARCH APPROACH

Rationale: Genetic studies in mice typically exploit two parental inbred strains with limited genetic diversity. To circumvent this limitation, hundreds of recombinant inbred mouse strains derived from eight diverse founder strains were produced[18,19]. This project was termed the Collaborative Cross (CC) and has emerged as a powerful genetic resource[18,19]. In our most recent work[20], we took advantage of the Australian CC cohort to characterize basal immunological traits in non-infected mice. Building on our expertise, we now wish to exploit the North American CC strains to study the immune response to blood-stage malaria using the mouse model of PcAS infection.

Specific Aim 1 To determine the intra-strain variation and quantify the experimental variability for detecting immune responses to blood-stage PcAS infection in the eight CC founder strains.

Prior to testing the CC strains, we will assess the intra-strain variation and quantify the experimental variability for detecting immune responses to PcAS in the 8 founder inbred strains, namely, A/J, B6, 129S, NOD, NZO, CAST, PWK, and WSB mice. We will infect 5-6 male and female mice per strain intraperitoneally with 10^6 PcAS-parasitized RBC (pRBC) and quantify peak blood parasitemia and survival. Blood smears will be prepared from individual mice, and the percentage of pRBC determined by microscopy every day beginning on day 4 post infection (p.i.) until resolution of infection, which is usually around day 28 p.i. in resistant B6 mice. Body weight and survival will be monitored daily. Separate groups of male and female mice of the founder strains will be infected with PcAS. Blood samples will be collected from individual mice to determine the total number of RBC and percentage of reticulocytes as a measure of anemia and erythropoietic response, respectively.

More importantly, a detailed characterization of parameters that correlate with immunity to PcAS will be performed on days 0, 2, 5, 10, 14, 21, and 28 p.i. in surviving mice. Blood samples will be collected. Sera will be used to quantify multiple cytokines, including but not limited to IL-1β, IL-2, IL-4, IL-6, IL-10, IL-12, IL-17A, IL-23, IFN-γ, MCP-1, GM-CSF and TNF-α, by multiplex ELISAs and to monitor PcAS-specific antibodies by ELISA. Blood cells will be prepared, total cell numbers determined, and flow cytometry used to phenotype the immune cell populations during infection. Specifically, we will quantify the proportion and activation status of various subsets of dendritic cells, macrophages, natural killer cells, T cells, and B cells, at the different time points during infection. At sacrifice (day 28 p.i. or earlier), spleens will be harvested, and size and weights determined as a measure of splenomegaly. Complete immune characterization of spleen cells will be performed by flow cytometry. PcAS-specific antibody ELISAs, multiplex ELISAs, and polychromatic flow cytometry are standard methods well established in our laboratories. A strength of this approach is to quantify intra-strain variability that is greater than experimental variability among the founder strains, allowing to select for the relevant parameters to investigate within the CC strains. Together, the detailed immune characterization along with the monitoring of blood parasitemia will provide a framework to reveal new traits as well as a complete picture of the immune response to PcAS in the founder strains.

Specific Aim 2 To identify genetic variants linked to the immune parameters for response to PcAS in the CC strains.

Once we have established the extent of intra-strain variation and quantified the experimental variability for detecting immune parameters indicative of a response to malaria in the eight

founder strains, we will investigate the responses in all CC strains available at the University of North Carolina at Chapel Hill (> 60 strains; analysis of 30 strains are budgeted in this pilot grant). Again, we will include 5-6 male and female mice per strain to account for biological and experimental variability inherent to *in vivo* and *ex vivo* experiments. At least three PcAS resistant B6 and susceptible A/J mice (founder strains) will be included as controls for each new infection cohort. This will allow data standardization over time. If the data from the B6 and A/J mice fall outside of the pre-established experimental range, the data from the CC strains tested on the same day will be discarded and additional mice from these CC strains will be re-tested. CC strains will first be examined for resistance/susceptibility to PcAS infection based on peak blood parasitemia and survival as described above. Separate groups of CC strain mice will be infected with PcAS and peripheral blood counts, splenomegaly, serum cytokine and antibody levels, and the number and proportion of immune cells will be determined as described in Aim 1.

After data collection, genetic associations will be plotted as logarithm of the odds (LOD) scores[20-25]. Sets of 1,000 permutations will be applied. Candidate genes contributing to the immune response to malaria will be extracted from the combined analyses of the founder coefficients at the loci linked to immune response to malaria together with analysis of the founder gene sequences at these loci. The degree of heritability of immune responses to malaria will also be quantified by taking into account genetic, phenotypic and environmental variance[20].

Expected results and interpretations: As we previously showed susceptibility to PcAS is a complex trait[10,12-14], we expect the eight founder strains will exhibit different levels of immune responses that influence disease outcomes to malaria. Based on our previous study examining 18 different basal immunological traits in CC strains[20], we expect that immune phenotypes in the CC strains will fall well outside of the variation range established by the founder strains. For example, we expect that most of the CC strains will exhibit either higher or lower phenotypes related to the response to malaria of any of the eight founder strains. This observation would agree with transgressive segregation suggesting the immune response to malaria results from interaction among multiple genetic variants that have been inherited independently by the CC strains. We also expect that the detailed characterization of the immune response to malaria will reveal distinct, associated genetic loci. As the CC has already proven useful in identifying genetic variants mediating different phenotypes[26-45], we fully expect that this approach will reveal novel genetic variants contributing to different aspects of the immune response to malaria.

Timeline and Personnel: In our recent work, we immunophenotyped 60 strains in 6 weeks[20]. The current proposed protocol is admittedly more time-consuming than our past immunophenotyping design. Still, we expect to complete the characterization of the eight founder strains within four months. We also expect that we will complete the typing for resistance/susceptibility to PcAS in thirty of CC strain mice, within the remaining eight months. An experienced research technician will maintain the mice, carry out the infection studies and immunophenotyping of the founder strains. An MSc student currently studying immune phenotypes in the eight founders, will also participate in the phenotypic analysis of the CC strains.

Future directions and impact: Following from this pilot study, the remainder of the CC strains will need to be analyzed. To improve mapping resolution, additional CC strains from the European and Australian cohorts will also be included. Subsequently, the impact of genetic variants linked to immune response to malaria will be validated by using knock-out or floxed-mice for key candidate genes. The information gained will identify loci linked to protective immune responses to blood-stage malaria, which will guide the design of novel therapies.

Perform an unbiased screen of the Collaborative Cross resource to identify new loci influencing the immune response to malaria

References

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3. Arama, C., *et al.* Ethnic differences in susceptibility to malaria: what have we learned from immuno-epidemiological studies in West Africa? *Acta Trop* **146**, 152-156 (2015).
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15. Caignard, G., *et al.* Mouse ENU Mutagenesis to Understand Immunity to Infection: Methods, Selected Examples, and Perspectives. *Genes* **5**, 887-925 (2014).
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27. Phillippi, J., *et al.* Using the emerging Collaborative Cross to probe the immune system. *Genes Immun* **15**, 38-46 (2014).
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29. Durrant, C., *et al.* Collaborative Cross mice and their power to map host susceptibility to Aspergillus fumigatus infection. *Genome Res* **21**, 1239-1248 (2011).
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33. Mao, J.H., *et al.* Identification of genetic factors that modify motor performance and body weight using Collaborative Cross mice. *Sci Rep* **5**, 16247 (2015).
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41. Boutilier, J.K., *et al.* Variable cardiac alpha-actin (Actc1) expression in early adult skeletal muscle correlates with promoter methylation. *Biochim Biophys Acta* **1860**, 1025-1036 (2017).
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44. Kristic, J., *et al.* Profiling and genetic control of the murine immunoglobulin G glycome. *Nat Chem Biol* **14**, 516-524 (2018).
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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Sylvie LESAGE, PhD

eRA COMMONS USER NAME (credential, e.g., agency login): SYLVIE_LESAGE

POSITION TITLE: Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
McGill University, Canada	BSc	04/1995	Immunology
McGill University, Canada	PhD	10/1999	Immunology
Australian National University, Australia	Post-doc	10/2002	Immunogenetics
Université de Montréal, Canada	Post-doc	09/2005	Immunology

A. Personal Statement

The immune system is comprised of many cell types that work together to fight cancer and infection. In some circumstances, immune cells can also turn against self and cause autoimmune diseases. Each individual's potential to combat infections, fight cancer and develop autoimmune diseases is in part controlled by genetic factors that impose variations in the composition and function of their immune system. I have established an original research program that aims to characterize these variations in immune homeostasis by taking advantage of various genetic mouse models. Specifically, we characterize dysregulation in immune cell types linked to disease development. The data acquired from the study of both the immunological function and the immunogenetic regulation of these cell types, feeds into our translational platform, wherein we aim to develop means to effectively restore immune function and prevent the onset of immunopathologies.

B. Positions and honors

Professional Experience:

2005-present Head, Cellular Immunogenetics Unit, Maisonneuve-Rosemont Hopsital
2005-2010 Assistant Professor, Dept. Microbiologie, infectiologie et immunologie, Université de Montréal
2010-2016 Associate Professor, Dept. Microbiologie, infectiologie et immunologie, Université de Montréal
2016-2017 Full Research Professor, Dept. Microbiologie, infectiologie et immunologie, Université de Montréal
2013-present Adjunct Professor, Dept. Microbiology and Immunology, McGill University
2017-present Full Professor, Dept. Microbiologie, infectiologie et immunologie, Université de Montréal

Selected Professional Services and Memberships

2006-Present Member, Canadian Society for Immunology
2006-Present Member, Conseil Professionnel de Diabète Québec
2008-2011 Member, MSc scholarship selection committee, Fonds de recherche Québec – Santé
2009-2013 Research Grant External Reviewer, Natural Sciences and Engineering Research Council
2009-Present Member, American Association of Immunologists
2009-Present Research Grant Review Panel, Canadian Diabetes Association (Co-Chair since 2013)

2010-2013	Board Member, Immunology Montreal
2010-Present	Review editor, Frontiers in Immunology
2011-Present	Member, ThéCell FRQS network
2012	Research Grant External Reviewer, Association Française contre les Myopathies
2012	Member, Post-doc scholarship selection committee, MITACS Elevate
2012-2013	Research Grant Review Panel, Arthritis Society
2012-2016	Associate Editor, Journal of Immunology
2013-2016	Member, MSc scholarship selection committee, Canadian Institutes of Health Research
2013-Present	Member, Montreal Diabetes Research Center
2013-Present	Member, National Research Council, Canadian Diabetes Association/Diabetes Canada
2014-Present	Member, McGill Center of Complex Traits
2014-2015	Research Grant Review Panel, Fondation des pompiers du Québec
2014-Present	Co-Chair, Montreal Immunology Meetings
2015	Research Grant External Reviewer, KU Leuven grant program, Belgium
2015	Member, Post-doc scholarship selection committee, Fonds Wetenschappelijk Onderzoek
2015-2019	Council member, Canadian Society for Immunology
2016	Research Grant Review Panel, NIH/NIDDK-JDRF
2016-2019	Member, Mid-career Investigator Salary Award selection committee, Fonds de recherche Québec - Santé
2016-Present	Review editor, Frontiers in Oncology
2017	Research Grant External Reviewer, European Research Council
2017	Research Grant External Reviewer, Agence National de la recherche, France
2017-2019	Research Grant Reviewer, Cancer Research Society
2017-Present	Scholarship Reviewer, Fondation le Grand Défi Pierre Lavoie
2018	Research Grant Reviewer, Canadian Institutes for Health Research – DOL committee
2018-2019	Research Grant Reviewer, Canadian Institutes for Health Research – IT committee
2019	Research Grant Reviewer, Canadian Institutes for Health Research – CIB committee
2019	Research Grant Reviewer, NIH/NIAID, Collaborative Cross R21
2019-Present	Chair, Scholarship and Grant Reviews, Diabète Québec
2020	Research Grant Reviewer, Fonds de recherche Québec – Santé, FCI-FLJE
2020	Local Organizing Committee, Canadian Society for Immunology Annual Conference
2020-Present	Scientific Officer, Canadian Institutes for Health Research – IT committee

Honors and Awards

1995	Excellence scholarship, Dean's Honours list, BSc
1995-1997	Fonds de recherche en santé du Québec, MSc scholarship
1997-1999	Fonds de recherche en santé du Québec, PhD scholarship
1999-2002	Canadian Institutes for Health Research, Postdoctoral fellowship
2002-2007	Canadian Institutes for Health Research, Senior Research Fellowship
2006	ThymOz, New Investigator Award
2007-2011	Fonds de recherche Québec - Santé, Junior Investigator Level 1
2010	AAI Junior Faculty Award
2010-2015	Canadian Institutes for Health Research, New Investigator Award
2015-2018	Fonds de recherche Québec - Santé, Senior
2019-2023	Fonds de recherche Québec - Santé, Research Scholars Emeritus

C. Contribution to Science

1. A key publication of relevance to this application presents our expertise in immunophenotyping mice of the CC strains. We examined 18 phenotypes in more than 60 CC strains.

   - Collin, R., Balmer, L., Morahan, G., Lesage, S. Common heritable immunological variations revealed in genetically diverse inbred mouse strains of the Collaborative Cross. 2019. J. Immunol. 202: 777-786.

2. In the past ten years, we focused our attention towards $CD4^{-}CD8^{-}$ (double negative, DN) T cells, as DN T cells had been shown to inhibit immune responses in a unique antigen-specific manner. We demonstrated

that DN T cells decrease serum auto-antibody levels, likely through the elimination of activated B cells. We also find that DN T cells are found in lower proportion in autoimmune prone mice and that a single intravenous injection of DN T cells is sufficient to protect from autoimmune disease progression. We performed phenotypic, functional and immunogenetic studies to characterize immunoregulatory DN T cells. Together, these findings highlight the biological relevance of defining the homeostatic regulation of DN T cell and the role of this cell subset in conferring immune tolerance of autoimmune diseases. Listed here, are a few selected articles on the topic of DN T cells, in both mice and humans.

- Dugas, V., Beauchamp, C., Chabot-Roy, G., Hillhouse, E.E., Lesage, S. Implication of the CD47 pathway in autoimmune diabetes. 2010. J Autoimmun. 35: 23-32.
- Hillhouse, E.E., Beauchamp, C., Chabot-Roy, G., Dugas, V., Lesage S. IL-10 limits the expansion of immunoregulatory CD4-CD8- T cells in autoimmune-prone NOD mice. 2010. Immuno Cell Biol. 88:771-780. **Highlighted as "Outstanding Observation"**. See also: News and Commentary, Pierson, W. & Liston, A. Immunol Cell Biol 88, 769-770 (2010).
- Hillhouse, E.E., Lesage, S. A comprehensive review of the phenotype and function of antigen-specific immunoregulatory double negative T cells. 2013. J Autoimmun. 40, 58-65.
- Dugas, V., Liston, A., Hillhouse, E.E., Collin, R., Chabot-Roy, G., Pelletier, A.N., Beauchamp, C., Hardy, K., Lesage, S. Idd13 is involved in determining immunoregulatory DN T cell number in NOD mice. 2014. Genes and Immunity. 15(2):82-7.
- Collin, R., Dugas, V., Pelletier, A.N., Chabot-Roy, G., Lesage, S. The mouse Idd2 locus is linked to the proportion of immunoregulatory DN T cells, a trait associated with autoimmune diabetes resistance. 2014. J. Immunol. 193(7): 3503-3512. **Selected by Faculty of 1000**.
- Collin, R., Doyon, K., Mullins-Dansereault, V., Karam, M., Chabot-Roy, G., Hillhouse, E.E., Orthwein, A., Lesage, S. Genetic interaction between two insulin-dependent diabetes susceptibility loci, Idd2 and Idd13, in determining immunoregulatory DN T cell proportion. 2018. Immunogenetics. 70: 495-509.
- Hillhouse, E.E., Thiant, S., Moutuou, M.M., Lombard-Vadnais, F., Parat, R., Delisle, J.S., Ahmad, I., Roy, D.C., Guimond, M., Roy, J., Lesage, S. Double negative T cells levels predict chronic graft-versus-host disease severity. 2019. Biol. Blood Marrow Transplant. 25: 19-25.

3. Dendritic cells play a key role in maintaining immune tolerance. In addition to studying immunoregulatory DN T cells, we thus investigated the immunogenetic regulation of DC subset and their link in various pathologies. Our work supports a strong role for non-conventional DC subsets in type 1 diabetes.

   - Pelletier, A.N., Guimont-Desrochers, F., Ashton, M.P., Brodnicki, T. Lesage, S. The size of the plasmacytoid dendritic cell compartment is a multigenic trait dominated by a locus on mouse chromosome 7. 2012. J Immunol. 188, 5561-5570. **Selected by Faculty of 1000**.
   - Pelletier, A.N., Lesage, S. The Idd13 congenic interval defines the number of merocytic dendritic cells, a novel trait associated with autoimmune diabetes susceptibility. 2013. J Autoimmun, 43, 70-77.
   - Audiger, C., Rahman, M.J., Yun, T.J., Tarbell, K., Lesage, S. The importance of dendritic cells in maintaining immune tolerance. 2017. J Immunol. 198 (6) 2223-2231.
   - Audiger, C., Lesage, S. BIM determines the number of merocytic dendritic cells, a cell type that breaks immune tolerance. 2018. Immunol Cell Biol. 96:1008-1017.
   - Boulet, S., Daudelin, J.F., Odagiu, L., Yun, T.J., Pelletier, A.N., Lesage, S., Cheong, C., Labrecque, N. NR4A3 plays a pivotal role in the differentiation of monocyte-derived dendritic cells. 2019. PNAS. 116:15150-15159.
   - Pham, T., Meziane., O., Miah, M., Volodina, O., Colas, C., Béland, K., Li. Y., Dallaire, F., Keler, T., Guimond, J., Lesage, S., Cheong, C., Haddad, E., Cohen, E. Flt3L-mediated expansion of plasmacytoid dendritic cells controls HIV infection in humanized mice. 2019. Cell Reports. 29: 2770-2782.
   - Audiger, C., Fois, A., Lesage, S. Merocytic dendritic cells compose a conventional dendritic cell subset with low glucose uptake potential. 2019. J Immunol. Revisions requested.

4. While characterizing variations in immune cell subsets in mice predisposed to type 1 diabetes, we found that a novel cell type, namely Interferon-producing killer dendritic cells (IKDC), was linked to diabetes susceptibility. In line with recent work by others, we demonstrate that the both the proportion and number of IKDC is strongly defined by genetic polymorphism. We importantly demonstrated that IKDC are immediate precursors to mature NK cells, closing the debate on their lineage origin. As such, we have proposed to

rename IKDC as pre-mNK cells. Our work contributed to defining a new cell type linked to diabetes and cancer susceptibility, and our ongoing work continues to define the immunogenetics of NK cell subsets.

- Guimont-Desrochers, F., Cappello, Z.J., Chagnon, M., McDuffie, M.J., Lesage, S. Genetic characterization of interferon-producing killer dendritic cells. 2009. J. Immunol. 182: 5193-5197
- Guimont-Desrochers, F., Boucher, G., Dong, Z., Dupuis, M., Veillette, A., Lesage, S. Redefining interferon-producing killer dendritic cells as a novel intermediate in NK cell differentiation. 2012. Blood 119, 4349-4357.Guimont-Desrochers, F., Lesage, S. Revisiting the prominent anti-tumoural potential of pre-mNK cells. 2013. Frontiers in Immunology. doi: 10.3389/fimmu.2013.00446. **Highlighted as "Plenary Paper"**. See also: Inside Blood, Zitvogel, L. & Housseau, F. Blood 119, 4345-4346 (2012).
- Pelletier, A.N., Guilbault, L., Guimont-Desrochers, F., Hillhouse, E.E., Lesage, S. NK cell proportion and number is influenced by genetic loci on chromosomes 8, 9 and 17. 2016. J.Immunol. 196: 2627-2636.
- Collin R, St-Pierre C, Guilbault L, Mullins-Dansereau V, Policheni A, Guimont-Desrochers F, Pelletier AN, Gray DH, Drobetsky, E, Perreault C, Hillhouse EE, Lesage S. An unbiased linkage approach reveals that the p53 pathway is intimately coupled to NK cell functional maturation. 2017. J Immunol. 199 (4) :1490-1504.
- Choi, J., Rudack, P.T., Lesage, S., Haeryfar, S.M.M. Glycolipid stimulation of iNKT cells expands a unique population of pre-mNK cells endowed with oncolytic and anti-metastatic properties. 2019. J. Immunol. 203:1808-1819.

5. Through various collaborations, our group has significantly contributed to defining immunogenetic aspects of type 1 diabetes, thyroiditis, inflammatory bowel diseases, sudden cardiac death, among others.

- Chognard, G., Bellemare, L., Pelletier, A.N., Dominguez-Punaro, M.C., Beauchamp, C., Guyon, M.J., Charron, G., Morin, N., Sivanesan, D., Kuchroo, V., Xavier, R., Michnick, S.W., Chemtob, S., Rioux, J.D., Lesage, S. The dichotomous pattern of IL-12R and IL-23R expression elucidates the role of IL-12 and IL-23 in inflammation. 2014. Plos One. 9(2):e89092. doi: 10.1371/journal.pone.0089092.
- Bourdin, B., Shakeri, B., Tétreault, M.P., Sauvé, R., Lesage, S., Parent, L. Functional characterization of CaVα2 mutations associated with sudden cardiac death. 2015. J. Biol. Chem. 290(5):2854-69.
- Tétreault, M.P., Bourdin, B., Briot, J., Segura, E., Lesage, S., Fiset, C., Parent, L. Identification of Glycosylation Sites Essential for Surface Expression of the CaVα2δ1 Subunit and Modulation of the Cardiac CaV1.2 Channel Activity. 2016. J. Biol. Chem. 291:4826-43.
- Dooley, J., Tian, L., Schonefeldt, S., Delghingaro-Augusto, V., Garcia-Perez, J.E., Pasciuto, E., Di Marino, D. Carr, E.J., Oskolkov, N., Lyssenko, V., Franckaert, D., Lagou, V., Overbergh, L., Vandenbussche, J., Allemeersch, J., Chabot-Roy, G., Dahlstrom, J., Socha, L., Gevaert, K., Jetten, A.M., Lambrechts, D., Linterman, M.A., Goodnow, C.C., Nolan, C.J., Lesage, S., Schlenner, S.M., Liston, A. Genetic predisposition for beta cell fragility underlies type 1 and type 2 diabetes. 2016. Nat Genet. 48: 519-527.
- Sivanesan, D., Talapatra, D., Beauchamp, C., Quinou, C., Lee, J., Lesage, S., Chemtob, S., Rioux, J.D., Michnick, S. IL23R protective variants display loss of function due to impaired protein stability and intracellular trafficking. 2016. J. Biol. Chem. 291: 4826-4843. **Selected by Faculty of 1000**.
- McLachlan, S.M., Lesage, S., Collin, R., Banuelos, B., Aliesky, H.A., Rapoport, B. Genes outside the major histocompatibility complex (MHC) locus are linked to the development of thyroid autoantibodies and thyroiditis in NOD.H2h4 mice. 2017. Endocrinology. 158(4):702-713. doi: 10.1210/en.2016-1875.
- Ivison, S., Des Rosiers, C., Lesage, S., Rioux, J.D., Levings, M.K. Biomarker-guided stratification of autoimmune patients for biologic therapy. 2017. Current Opinion in Immunology. 49: 56-63.
- Heremans, J., Garcia-Perez, J.E., Turro, E., Schlenner, S.M., Casteels, I., Collin, R., De Zegher, F., Greene, D., Humblet-Baron, S., Lesage, S., Matthys, P., Penkett, C.J., Put, K., Stirrups, K., Thys, C., Van Geet, C., van Nieuwenhove, E., NIHR BioResource, Wouters, C., Meyts, I., Freson, K., Liston A. Abnormal differentiation of B cells and megakaryocytes in Roifman syndrome. 2018. JACI. 142:630-646.

Complete List of Published Work in *My Bibliography*:
https://www.ncbi.nlm.nih.gov/myncbi/1BqirRCgIw-kE/bibliography/public/

D. Research Support

Ongoing Peer-Reviewed Research Support (**Amounts are in CAD; 1$ CAD is approximately 0.75$ USD**)

April 2017 – April 2022 Canadian Institutes of Health Research – 841 500$
Title: A subset-based model for defining NK cell differentiation and function: focus on pre-mNK cells
PI: Sylvie Lesage
Description: To study murine NK cell differentiation and subset function.

July 2018 – July 2021 Fonds québécois de la recherche sur la nature et les technologies (FQRNT) – 162 000$
Title : Novel parameter for optimized, fast, and precise cell characterization: definition and implementation
PI : Yves-Alain Peter, Co-PI : Sylvie Lesage, Jean-Sébastien Delisle
Description: To develop and integrate a device in flow cytometers that quantifies the cellular refractive index

July 2018 – July 2023 Canadian Institutes of Health Research – 1 500 000$
Title: Canadian Autoimmunity Standardization Core (CAN-ASC)
PI: Megan Levings, Co-PI: J Bramson, C Des Rosiers, J Dutz, E Haddad, S Ivison, J Kimmelman, S Lesage, A Prat, JD Rioux, S Ritz, S Turvey, S Vercauteren, J Wither
Description: To design and implement standardized protocols for nationwide analysis of human samples.

October 2018 – October 2023 Canadian Institutes of Health Research – 960 076$
Title: Thymic differentiation of immunoregulatory DN T cells
PI: Sylvie Lesage
Description: To study DN T cell differentiation in mouse models

October 2018 – October 2023 Canadian Institutes of Health Research – 749 700$
Title: Roles of CLCF1 and CRLF1 in IL-23-driven autoimmune pathologies
PI: Jean-François Gauchat, Co-PI: Sylvie Lesage
Description: To investigate the role of new cytokine complexes in mouse models of autoimmunity

Sept 2018 – Sept 2020 Cancer Research Society – 120 000$
Title: Evaluating the impact of immunosuppressive drugs on the therapeutic efficacy of human DN T cells
PI: Sylvie Lesage, Co-PI: Jean-Sébastien Delisle
Description: A preclinical study for the use of DN T cells in graft-vs-host disease

Sept 2018 – Sept 2020 Cancer Research Society – 120 000$
Title: p53 mutations in NK cells impede the anti-tumour immune response
PI: Sylvie Lesage
Description: To define the NK cell immune response in Li-Fraumeni patients

April 2019 – April 2024 Natural Sciences and Engineering Research Council of Canada – 210 000$
Title: Immunogenetics of antibody affinity
PI: Sylvie Lesage
Description: To identify genetic loci linked to antibody affinity maturation using the CC strains.

January 2019 – January 2022 EuroNanoMed III, Joint Transnational Competition – 900 000$
Title: A liquid corneal glue-filler as an alternative to transplantation in high-risk patients; LIQD-CORNEA
PI: May Griffith, Illimar Altosaar, Olivier Zelphati, Virginiija Bukelskiene, Co-PI: Sylvie Lesage, Rimvydas Asoklis, Evelin Loit.
Description: To design a safe, cost-effective, therapeutic approach for healing corneal lesions.

April 2020 – April 2025 Canadian Institutes of Health Research – 851 290$
Title: Control of metabolic inflammaging by traffic of B lymphocytes in adipose tissues
PI: Frédéric Picard, Co-PI: Sylvie Lesage, Mathieu Ferron
Description: To study the impact of B cells on adipose tissue biology during aging in mice.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Mary M. Stevenson PhD

eRA COMMONS USER NAME (credential, e.g., agency login): x44507

POSITION TITLE: Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Hood College, Frederick, MD, USA	B.A.	1973	Biology (Honors)
The Catholic University of America Washington, DC, USA	M.Sc.	1977	Microbiology
The Catholic University of America Washington, DC, USA	Ph.D.	1979	Microbiology
Division of Clinical Immunology, Montreal General Hospital Research Institute, Montreal, QC, Canada	Post-doctoral Fellow	1979-1981	Immunology
Division of Clinical Immunology, Montreal General Hospital Research Institute, Montreal, QC, Canada	Research Associate	1981-1982	Immunology

A. Personal Statement

A shared evolutionary history between parasites and their hosts has shaped a unique relationship reflected in their interactions at the immunologic and genetic interfaces. Malaria parasites especially *Plasmodium falciparum* has dramatically shaped the human genome, most notably human red cell traits. Pathogens have also shaped the human genome to favor their survival by their effects on immune response genes. My research focuses on defining the cellular mechanisms essential for protective immunity to blood-stage malaria and identifying the underlying causes of severe malarial anemia (SMA) responsible for high morbidity and mortality in vulnerable populations. In collaboration with McGill colleagues with expertise in genetic analysis of complex traits, my laboratory has contributed significantly to identifying previously unrecognized erythroid-specific traits regulating susceptibility to blood-stage malaria. Altogether, our findings provide important evidence directly translatable to the development of novel and effective therapeutic and vaccine strategies against blood-stage malaria.

B. Positions and Honors

Professional Experience

1982-1988	Assistant Professor, Department of Medicine, McGill University, Montreal, QC
1984-Present	Associate Member, Department of Physiology, McGill University, Montreal, QC
1988-1996	Associate Professor, Department of Medicine, McGill University, Montreal, QC
1988-Present	Associate Member, Institute of Parasitology, McGill University, Ste-Anne-de-Bellevue, QC
1996-2015	Professor, Department of Medicine, McGill University, Montreal, QC
2015-Present	Professor, Department of Microbiology and Immunology and Department of Medicine (Joint Appointment), McGill University, Montreal, QC

Selected Contributions to the Scientific Community

1998-Present	Founding Member and Canadian Representative, International Board, Malaria Foundation International, Inc., Atlanta, GA
1998-2000	Editorial Board, Infection and Immunity
2000-2004	Associate Editor, Journal of Immunology

2000	Special Study Section, NIAID/NIH, Tropical Medicine Research Center Program
2001	Special Study Section, NIAID/NIH, Malarial Anemia Research and Training Program
2001-2004	Panel Member, CIHR Operating Grants, Experimental Medicine Committee
2005	Special Study Section, NHLBI/NIH/Program Project Review, Malaria Anemia
2007-2009	Member, Post Doctoral Fellowship Review Committee, Fonds de recherche du Québec-Santé (FRQ-S)
2010	Member, FRQ-S-INSERM Exchange Program Review Committee, FRQ-S
2010-Present	Member, American Society of Tropical Medicine and Hygiene, Travel Awards Committee
2016	NSERC Studentship Selection Committee, Faculty of Medicine, McGill University
2017	Member, Vanier-CIHR Studentship Selection Committee, Faculty of Medicine, McGill University
2017	Member, Pathogens Program Review Panel, Francis Crick Institute, London, UK
2019-Present	Member, Research Scholars Emeritus Selection Committee, FRQ-S

Honors and Awards

1979-80	Post-Doctoral Fellowship	Cancer Research Society (Montreal)
1980	Travel Award, International Congress of Immunology, Paris, France	Canadian Society for Immunology and International Union of Immunological Societies
1981-82	New Investigator Award	The Montreal General Hospital Foundation
1982-87	New Investigator Award	Medical Research Council of Canada
1982-87	New Investigator Award (Declined)	Fonds de la Recherche en Santé du Québec
1985	Outstanding Young Alumnae Award	Hood College, Frederick, MD
1990	Visiting Lecturer, University of Alberta	Alberta Heritage Foundation for Medical Research (AHFMR)
1998-2002	New Initiatives in Malaria Research Award	Burroughs-Wellcome Fund
2002	Jay Keystone International Lectureship	University of Toronto, Toronto, ON
2003	International Travel Lectureship	Australian Society for Parasitology
2006	Visiting Lecturer, University of Calgary	AHFMR
2016	Fellow of the American Society of Tropical Medicine and Hygiene	American Society of Tropical Medicine and Hygiene

C. Contribution to Science (For a complete list of my publications, please see https://www.ncbi.nlm.nih.gov/myncbi/1H1aayuecivcyq/bibliography/public/)

1. The mouse model of *P. chabaudi* AS (PcAS) in resistant C57BL/6 (B6) and susceptible A/J mice is well established in my laboratory. I am recognized internationally for my expertise in this model and other mouse malaria models. We previously phenotyped a panel of inbred mouse strains and B6- and A/J-derived F1, backcross, recombinant inbred and recombinant congenic inbred (RCI) mice as well as B6-derived ENU strains as resistant or susceptible to PcAS based on peak blood parasitemia level and survival. The publications below demonstrate susceptibility to PcAS is a complex trait and that female mice are more resistant than male mice. This body of work is directly relevant to the studies to identify genetically-regulated immune responses to malaria in the Collaborative Cross mice proposed in the present application.
   - Stevenson, M.M., Lyanga, J.J. and Skamene, E. Murine malaria: genetic control of resistance to *Plasmodium chabaudi*. Infect. Immun. 38:80-88, 1982.
   - Skamene, E., Stevenson, M.M. and Lemieux, S. Murine malaria: dissociation of NK cell activity and resistance to *Plasmodium chabaudi*. Parasite Immunol. 5:557-565, 1983.
   - Stevenson, M.M., Lemieux, S. and Skamene, E. Genetic control of resistance to murine malaria. J. Cell. Biochem. 24:91-102, 1984.
   - Stevenson, M.M. and Skamene, E. Murine malaria: resistance of AXB/BXA recombinant inbred mice to *Plasmodium chabaudi*. Infect. Immun. 47:452-456, 1985.
   - Fortin, A., Belouchi, A., Tam, M.F., Cardon, L., Skamene, E., Stevenson, M.M. and Gros, P. Differential susceptibility to malaria in mice maps to chromosome 8. Nature Genet. 17:382-383, 1997.
   - Fortin, A., Cardon, L., Tam, M., Skamene, E., Stevenson, M.M. and Gros, P. Identification of a new locus controlling susceptibility to malaria infection in mice. PNAS (USA) 98:10793-10798, 2001.
   - Fortin, A., Stevenson, M.M. and Gros, P. Complex genetic control of susceptibility to malaria in mice. Genes Immun. 3:177-186, 2002.

- Fortin, A., Stevenson, M.M. and Gros, P. Susceptibility to malaria as a complex trait: huge pressure from a tiny creature. Hum. Mol. Genet. 11:2469-2478, 2002.
- Min-Oo, G., Fortin, A., Tam, M.-F., Nantel, A., Stevenson, M.M. and Gros, P. Pyruvate kinase deficiency in mice protects against malaria. Nature Genet. 35:357-362, 2003.
- Min-Oo, G., Fortin, A., Tam, M.-F., Gros, P. and Stevenson, M.M. Phenotypic expression of pyruvate kinase deficiency and protection against malaria in a mouse model. Genes Immun. 5: 68-175, 2004.
- Min-Oo, G., Fortin, A., Stevenson, M.M. and Gros, P. Complex genetic control of malaria: positional cloning of the *Char9* locus. J. Exp. Med. 204:511-524, 2007.
- Min-Oo, G., Tam, M.F., Stevenson, M.M. and Gros, P. Pyruvate kinase deficiency and hemolytic anemia in CBA-Pk^{slc} ($Pklr^{G338D}$) mice protect against malaria. Blood Cells Mole. Dis. 39:63-69, 2007.
- Min-Oo, G., Canonne-Hergaux, F., Tam, M., Stevenson, M.M. and Gros, P. Mapping of *Char10*, a novel malaria susceptibility locus on mouse chromosome 9. Genes Immun. 11:113-123, 2010.
- Laroque, A., Min-Oo, G., Tam, M., Stevenson, M.M. and Gros, P. Genetic control of susceptibility to infection with *Plasmodium chabaudi* in inbred mouse strains. Genes Immun. 13:155-165, 2012.
- Laroque, A., Min-Oo, G., Tam, M., Ponka, P., Stevenson, M.M. and Gros, P. The mouse *Char10* locus regulates severity of pyruvate kinase deficiency and susceptibility to malaria. PLoS One 12(5):e0177818, 2017.
- Xu, G., Fodil, N., van Bruggen, R., Gualtieri, C.O., Moradin, N., Bassenden, A., Lu, W., Tam, M., Stevenson, M., Berghuis, A., Muir, T., Rabinowitz, J., Vidal, S., and Gros, P. Bisphosphoglycerate mutase deficiency protects against cerebral malaria and severe malaria-induced anemia. Sci. Reports, *Revisions in progress.*

2. Efforts to develop a protective vaccine against blood-stage malaria are hampered by the lack of a clear understanding of the immune response to the Plasmodium parasite. Earlier studies identified candidate antigens based on their ability to stimulate high titers of antibodies. Yet, recombinant vaccines based on these antigens are not protective. My work to understand the immune response to malaria is focused on identifying the cellular mechanisms involved, in particular, the contributions of cells and cytokines important in innate and adaptive immunity. Based on this approach, we have identified critical roles for dendritic cells, NK cells, macrophages, $CD4^+$ Th1 cells, regulatory $Foxp3^+$ T cells, and the cytokines IL-12, IFN-γ and TNF-α in protective immunity to PcAS. These cells and cytokines have been confirmed to be essential for protective immunity to *P. falciparum* in humans supporting the validity of the PcAS model in mice as a robust experimental tool.
   - Stevenson, M.M. and Kraal, G. Histological changes in the spleen and liver during *Plasmodium chabaudi* infection in resistant and susceptible inbred mice. Exp. Mol. Pathol. 51:80-95, 1989.
   - Stevenson, M.M., Ghadirian, E., Phillips, N.C., Podoba, J.E. and Rae, D. Role of mononuclear phagocytes in elimination of *Plasmodium chabaudi* AS infection. Parasite Immunol. 11:529-544, 1989.
   - Stevenson, M.M. and Ghadirian, E. Human recombinant tumor necrosis factor alpha protects susceptible A/J mice against lethal *Plasmodium chabaudi* AS infection. Infect. Immun. 57:3936-3939, 1989.
   - Stevenson, M.M., Tam, M.F. and Nowotarski, M. Role of interferon-γ and tumor necrosis factor in host resistance to *Plasmodium chabaudi* AS. Immunol. Lett. 25:115-121, 1990.
   - Stevenson, M.M., Tam, M.F., Belosevic, M., van der Meide, P.H. and Podoba, J.E. Role of endogenous IFN-γ in host response to infection with blood-stage *Plasmodium chabaudi* AS. Infect. Immun. 58:3225-3232, 1990.
   - Podoba, J.E. and Stevenson, M.M. Both $CD4^+$ and $CD8^+$ T lymphocytes contribute to acquired immunity to blood-stage *Plasmodium chabaudi* AS. Infect. Immun. 59:51-58, 1991.
   - Stevenson, M.M., Huang, D.Y., Podoba, J. and Nowotarski, M.E. Macrophage activation during *Plasmodium chabaudi* AS infection in resistant and susceptible mice. Infect. Immun. 60:1193-1201, 1992.
   - Stevenson, M.M. and Tam, M.F. Differential induction of helper T cell subsets during blood-stage *Plasmodium chabaudi* AS infection in resistant and susceptible mice. Clin. Exp. Immunol. 92:77-83, 1993.
   - Yap, G.S. and Stevenson, M.M. Differential requirements for an intact spleen in the induction and expression of B cell-dependent immunity to *Plasmodium chabaudi* AS. Infect. Immun. 62:4219-4225, 1994.

- Stevenson, M.M., Tam, M.F., Wolf, S.F. and Sher, F. A. IL-12 induced protection against blood-stage *Plasmodium chabaudi* AS requires IFN-γ and TNF-α and occurs via an NO-dependent mechanism. J. Immunol. 155:2545-2556, 1995.
- Jacobs, P., Radzioch, D. and Stevenson, M.M. Resistance to *Plasmodium chabaudi* AS correlates with high nitric oxide synthase expression in the spleen, but not in the liver. J. Immunol. 155:5306-5313, 1995.
- Jacobs, P., Radzioch, D. and Stevenson, M.M. In vivo regulation of nitric oxide production by TNF-α and IFN-γ, but not IL-4, during blood-stage malaria in mice. Infect. Immun. 64:44-49, 1996.
- Jacobs, P., Radzioch, D. and Stevenson, M.M. A Th1 associated increase in TNF-α expression in the spleen correlates with resistance to blood-stage malaria in mice. Infect. Immun. 64:535-541, 1996.
- Mohan, K., Moulin, P. and Stevenson, M.M. NK cell cytokine production not cytotoxicity contributes to resistance against blood-stage *Plasmodium chabaudi* AS infection. J. Immunol. 159:4990-5004, 1997.
- Sam, H. and Stevenson, M.M. In vivo IL-12 production and IL-12Rβ1 and β2 mRNA expression in the spleen are differentially up-regulated in resistant C57BL/6 and susceptible A/J mice during early blood-stage *Plasmodium chabaudi* AS malaria. J. Immunol. 162:1582-1589, 1999.
- Sam. H. and Stevenson, M.M. Early IL-12 production by splenic macrophages correlates with host resistance to blood-stage *Plasmodium chabaudi* AS malaria. Clin. Exp. Immunol. 117:343-349, 1999.
- Su, Z. and Stevenson, M.M. The central role of endogenous IFN-γ in protective immunity against acute blood-stage *Plasmodium chabaudi* AS infection. Infect. Immun. 68:4399-4406, 2000.
- Su, Z. and Stevenson, M.M. IL-12 is required for antibody-mediated protective immunity against blood-stage *Plasmodium chabaudi* AS malaria infection in mice. J. Immunol. 168:1348-1355, 2002.
- Stevenson, M.M. and Riley, E.M. Innate immunity to malaria. Nature Rev. Immunol. 4:169-180, 2004.
- Ing, R., Gros, P. and Stevenson, M.M. Interleukin-15 enhances innate and adaptive immune responses to blood-stage malaria infection in mice. Infect. Immun. 73:3172-3177, 2005.
- Ing, R., Segura, M., Thawani, N., Tam, M. and Stevenson, M.M. Interaction of mouse dendritic cells and malaria-parasitized erythrocytes: uptake, maturation and antigen presentation. J. Immunol. 176:441-450, 2006.
- Turcotte, K., Gauthier, S., Malo, D., Tam, M., Stevenson, M.M. and Gros, P. *Icsbp1*/IRF-8 is required for innate and adaptive immune responses against intracellular pathogens. J. Immunol. 179:2467-2476, 2007.
- Ing, R. and Stevenson, M.M. Dendritic cell and NK cell reciprocal cross talk promotes gamma interferon-dependent immunity to blood-stage *Plasmodium chabaudi* AS infection in mice. Infect. Immun. 77:770-782, 2009.
- Berretta, F., St. Pierre, J., Piccirillo, C.A. and Stevenson, M.M. Interleukin 2 contributes to maintaining a balance between $CD4^+Foxp3^+$ regulatory T cells and effector $CD4^+$ T cells required for immune control of blood-stage malaria infection. J. Immunol. 186:4862-4871, 2011.
- Berretta, F., Piccirillo, C. and Stevenson, M.M. *Plasmodium chabaudi* AS infection induces $CD4^+$ Th1 cells and $Foxp3^+Tbet^+$ regulatory T cells that express CXCR3 and migrate to CXCR3 ligands. Front. Immunol. 10:e425, 2019.

3. Malarial anemia is complex and multifactorial and ranges from mild to severe in *P. falciparum*-infected children. Both host- and parasite-derived molecules contribute but their exact roles are unclear. During PcAS infection in mice, anemia occurs and like varies from mild to severe among inbred strains. We investigated erythropoiesis, reticulocytosis, erythropoietin (Epo) production, and the role of cytokines in regulating erythropoiesis in PcAS-infected mice. We provided the first evidence that late-stage erythropoiesis is suppressed during malaria despite adequate increases in Epo. Importantly, our findings were confirmed in vivo and in vitro in *P. falciparum*-infected children with SMA. We also demonstrated that *Plasmodium*-derived products directly contribute to suppression of erythropoiesis during malaria.
   - Yap, G.S. and Stevenson, M.M. *Plasmodium chabaudi* AS: erythropoietic responses during infection in resistant and susceptible mice. Exp. Parasitol. 75:340-352, 1992.
   - Mohan, K. and Stevenson, M.M. Interleukin 12 corrects severe anemia during blood-stage *Plasmodium chabaudi* AS in susceptible A/J mice. Exp. Hematol. 26:45-52, 1998.
   - Mohan, K. and Stevenson, M.M. Dyserythropoiesis and severe anemia associated with malaria correlate with deficient interleukin 12 production. Br. J. Haematol. 103:942-949, 1998.

- Chang, K.-H. and Stevenson, M.M. Comparison of murine Epo ELISA and EPO bioassay in detecting serum Epo levels during anemia associated with malaria infection. J. Immunol. Methods 262:129-136, 2002.
- Chang, K.-H., Tam, M.F. and Stevenson, M.M. Modulation of the course and outcome of blood-stage malaria by erythropoietin-induced reticulocytosis. J. Infect. Dis. 189:735-743, 2004.
- Chang, K.-H. and Stevenson, M.M. Effect of anemia and renal cytokine production on erythropoietin production during blood-stage malaria. Kidney Int. 65:1640-1646, 2004.
- Chang, K.-H., Tam, M.F. and Stevenson, M.M. Inappropriately low reticulocytosis in severe malarial anemia correlates with suppression in the development of late erythroid precursors. Blood 103:3727-3735, 2004.
- Chang, K.-H. and Stevenson, M.M. Malarial anemia: mechanisms and implications of insufficient erythropoiesis during blood-stage malarial. Int. J. Parasitol. 34:1501-1516, 2004.
- Thawani, N., Tam, M., Chang, K.-H. and Stevenson, M.M. Cytokine-mediated mechanisms of CpG-ODN-induced anemia: roles of suppressed erythropoiesis and decreased erythrocyte survival. Exp. Hematol. 34:1451-1461, 2006.
- Thawani, N., Tam, M. and Stevenson, M.M. STAT6-mediated suppression of erythropoiesis in an experimental model of malarial anemia. Haematologica 94:195-204, 2009.
- Thawani, N., Tam, M., Bellemare, M.-J., Bohle, D.S., Olivier, M., de Souza, J.B. and Stevenson, M.M. *Plasmodium* products contribute to severe malarial anemia by inhibiting erythropoietin-induced proliferation of erythroid precursors. J. Infect. Dis. 209:140-149, 2014.

4. Based on findings of our studies on the immune response to malaria, we developed novel immunotherapy and a protective vaccine against blood-stage malaria using IL-12. The findings of our previous genetic analyses in RCI mice derived from PcAS-resistant B6 and susceptible A/J mice that identified loci associated with erythroid-specific traits provided the rationale to test cysteamine, a drug used to treat nephropathic cystinosis, alone or in combination with artemisinin as chemotherapy against malaria.
   - Mohan, K., Sam, H. and Stevenson, M.M. Therapy with a combination of low dose IL-12 and chloroquine completely cures primary blood-stage malaria, prevents severe anemia and induces immunity to reinfection. Infect. Immun. 67: 513-519, 1999.
   - Stevenson, M.M., Su, Z., Sam, H., and Mohan, K. Modulation of host responses to blood-stage malaria by interleukin-12: from therapy to adjuvant activity. Microbes Infect. 3: 49-59, 2001.
   - Su, Z., Tam, M.-F., Jankovic, D, and Stevenson, M.M. Vaccination against blood-stage malaria in mice using novel immunostimulatory adjuvants. Infect. Immun. 71: 5178-5187, 2003.
   - Min-Oo, G., Ayi, K., Tam, M., Radovanovic, I., Gauthier, S., Santiago, H., Rothfuchs, A.G., Roffe, E., Sher, A., Mullick, A., Fortin, A., Stevenson, M.M., Kain, K.C., and Gros, P. Cysteamine, a natural reaction metabolite of pantheteinase, shows potent anti-malarial activity. Exp. Parasitol. 125: 315-324, 2010.
   - Min-Oo, G., Fortin, A., Poulin, J.F., Stevenson, M.M., and Gros, P. Cysteamine potentiates the efficacy of artemisinin against the malarial parasite. Antimicrobial. Agents Chemother. 54: 3262-3270, 2010.

D. Research Support as Principal Investigator/Team Leader

Iron homeostasis and the pathogenesis of malarial anemia
Canadian Institutes of Health Research Operating Grant
$565,505
2015-2020

Exploiting immunotherapeutic approaches to define protective immune mechanisms to chronic GI nematode infections
NSERC (Canada) Discovery Grant
$160,000
2018-2023

Metabolomic dissection of immunomodulatory molecules released by intestinal worms
Fonds de recherche du Québec-Nature et Technologies Team Grant
$205,740
2018-2021

Perform an unbiased screen of the Collaborative Cross resource to identify new loci influencing the immune response to malaria

SCOPE: Malaria continues to be a major global health problem despite efforts to eradicate this disease. Mosquito-borne *Plasmodium* parasites cause high morbidity and mortality in sub-Saharan Africa. In this region, *P. falciparum*, the deadliest species of human malaria, is endemic. Replication of the parasite in host red blood cells during blood-stage infection is responsible for severe malarial anemia and cerebral malaria which frequently result in death in children under the age of 5 and pregnant women. Yet, the protective immune response to blood-stage infection remains poorly understood and an effective vaccine that provides long-term protection is still not available. Although there is growing evidence that variability in immune response genes contributes to susceptibility in individuals residing in endemic areas, identification of genetic variants that contribute to malarial susceptibility in humans presents considerable challenges. A more viable approach is to perform genetic analyses in a robust experimental model in mice. To this end, we propose to perform an unbiased screen of the Collaborative Cross (CC) resource available from the University of North Carolina in Chapel Hill to identify new loci influencing the immune response to malaria using the mouse model of blood-stage *P. chabaudi* AS (PcAS). PcAS infection in mice mirrors many of the immunological and pathological features of *P. falciparum* infection making this parasite an important experimental tool to study the immunology of human malaria and identify new targets for vaccine development and immunotherapeutic interventions. We hypothesize that the CC strains will provide an unbiased means to identify new candidate genes regulating the immune response to blood-stage malaria. Parasitological and immunological approaches well established in our laboratories will be used in **Aim 1** to determine the intra-strain variation and quantify the experimental variability for detecting immune responses to PcAS infection in the eight CC founder strains and identify parameters that correlate with immunity to blood-stage malaria. Studies in **Aim 2** will identify genetic variants linked to the immune parameters identified for response to PcAS in the CC strains. This research program builds on a budding collaboration between Dr. Mary Stevenson, expert on mouse models of malaria, and Dr. Sylvie Lesage, an immunogeneticist. It harbours outstanding potential to uncover novel genetic variants contributing to the immune response to malaria. Identification of these genetic variants will inform us on the molecular pathways that have been naturally selected to modulate these immune traits, which may help design better vaccines to prevent malaria or to identify novel immunotherapy to treat malaria.

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

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Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
Unbiased CC mouse genetic screen for the immune response to blood-stage malaria

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☒ YES
(If "Yes," state number and title)
Number: Title: Systems Immunogenetics Project

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Lesage, Sylvie	BSc PhD	SYLVIE_LESAGE

3c. POSITION TITLE
Professor

3d. MAILING ADDRESS *(Street, city, state, zip code)*
Hôpital Maisonneuve-Rosemont
Centre de Recherche
5415, boul. de l'Assomption
Montréal (Québec) H1T 2M4
CANADA

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Maisonneuve-Rosemont Hospital Research Centre (CRHMR)

3f. MAJOR SUBDIVISION

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: 514-252-3400 x 4649 FAX:

E-MAIL ADDRESS:
sylvie.lesage@umontreal.ca

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☒ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☒ No ☐ Yes	☒ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No. 2020-1912

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
09/01/20	08/31/21			$115,000	$115,000

9. APPLICANT ORGANIZATION
Name: CIUSSS de l'EST-de-L'Ile-de-Montreal
Address: Hôpital Maisonneuve-Rosemont
Centre de Recherche (CRHMR)
5415, boul. de l'Assomption
Montréal (Québec) H1T 2M4
CANADA

10. TYPE OF ORGANIZATION
Public: → ☒ Federal ☐ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
DUNS NO. 2076299990000 Cong. District

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name: Pierre Fontaine
Title: Associate director
Address: 5415, de l'Assomption Blvd
Montreal, Qc, Canada, H1T 2M4
Tel: 514-252-3400x4642 FAX: 514-251-3047
E-Mail: pierre.fontaine.cemtl@ssss.gouv.qc.ca

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name: Denis Claude Roy
Title: Research Director
Address: 5415, de l'Assomption Blvd
Montreal, Qc, Canada, H1T 2M4
Tel: 514-252-3400x3331 FAX: 514-251-3047
E-Mail: denis-claude.roy@umontreal.ca

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.

SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)* DATE

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

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Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
Identifying polymorphic mobile element insertions as immune regulatory variants

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☐ YES
(If "Yes," state number and title)
Number: Title:

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Parrish, Nicholas, Fredric	M.D. Ph.D.	NICHOLAS.PARRISH

3c. POSITION TITLE
Hakubi Team leader (principal investigator)

3d. MAILING ADDRESS *(Street, city, state, zip code)*
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Genome Immunobiology RIKEN Hakubi Research Team

3f. MAJOR SUBDIVISION

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: +81 045-503-9589 FAX: +81 045-503-9566

E-MAIL ADDRESS:
Nicholas.parrish@riken.jp

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☐ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☐ No ☐ Yes	☐ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No.

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
09/01/20	08/31/21	37,000	39,960	37,000	39,960

9. APPLICANT ORGANIZATION
Name RIKEN
Address 2-1 Hirosawa, Wako, Saitama 351-0198, Japan

10. TYPE OF ORGANIZATION
Public: → ☒ Federal ☐ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
DUNS NO. 697034585 Cong. District

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name Yoichiro MATSUO
Title Deputy Manager, External Funds Office
Address 2-1 Hirosawa, Wako, Saitama 351-0198, Japan
Tel: +81-48-647-9299 FAX:
E-Mail: yoichiro.matsuo@riken.jp

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name Hiroshi TAKAYAMA
Title Director, External Funds Office
Address 2-1 Hirosawa, Wako, Saitama 351-0198, Japan
Tel: +81-48-647-9299 FAX:
E-Mail: grants@riken.jp

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.	SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)*	DATE

Specific Aims

Mammalian immune systems often effectively control exogenous mobile genetic elements (MGEs) i.e. viruses, preventing them from causing mortality or significant morbidity. Similarly, endogenous MGEs—including transposons and endogenous retroviruses (ERVs)—comprise ~50% of mammalian genomes and are generally controlled via diverse silencing mechanisms. The mechanisms controlling endogenous and exogenous MGEs are intertwined (e.g. 1-7). Moreover, control of both exogenous and endogenous MGEs is incomplete. Whereas incomplete viral control results in disease, incomplete silencing of endogenous MGEs in the germline results in mutation.

In humans, several classes of MGEs have been documented to cause mutations by *de novo* insertion, often discovered in the context of genetic disorders (8). Moreover, some human ERVs have been active in the recent past, as can be inferred based on population-specific insertions of these elements (9). Throughout evolution, mutations caused by MGEs have led to phenotypic changes important for organismal function, which is referred to as exaptation. For example, some human ERVs contain transcription factor (TF) binding sites which enable them to act as interferon-responsive enhancers, and these ERVs are critical for transcriptional regulation of the interferon pathway (4).

MGEs are even more active as mutagens of mouse genomes than in human (10). A high number of spontaneously-arising mutations on the B6J background are due to ERV insertions (11). In humans, large population cohorts have now been sequenced, allowing comprehensive genotyping of the polymorphic MGE insertions (12). Initial attempts to understand the phenotypic correlates, at the level of gene transcription, of polymorphic MGE genotypes in the human population have been undertaken (13). However, it remains unknown how polymorphic MGE insertions drive variation in physiologically-relevant immune phenotypes in humans and mice. In this proposal, we will use a newly-developed computational pipeline to genotype MGE insertions in collaborative cross (CC) mouse strains, then perform association testing between these insertions and phenotypes collected by other projects in the Center for Systems Immunogenetics of Biodefense Pathogens. This will allow us to map new immune regulatory genes and genetic variants important for defense against pathogens.

Aim 1. Map MGE insertion genotypes in CC recombinant inbred (CC-RI) F1 cross strains used in SARS-CoV, IAV, and WNV infection screens. A) We will first apply our MGE insertion detection pipeline to short-read datasets from the 8 founder strains, then will use existing haplotype data for CC-RI strains to partition MGE insertion genotypes to each strain based on the known recombination breakpoints and genetic contributions from the founder strains. B) We will also obtain long-read sequencing of select CC-RI strains in order to confirm genotypes and identify *de novo* MGE insertions arising during CC breeding.

Aim 2. Associate MGE insertion genotypes with immune system phenotypes to identify novel immune regulatory genes and new mechanisms of immune gene regulation. A) We will first perform genome-wide association studies of MGE insertion genotypes with immune phenotypes. B) To understand the transcriptional impact of polymorphic MGEs on the genes they regulate, we will perform RNAseq of immune cells from selected CC lines with MGE-dependent differences in viral outcomes.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Nicholas Fredric Parrish

eRA COMMONS USER NAME (credential, e.g., agency login): Nicholas.Parrish

POSITION TITLE: Hakubi Team Leader

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Emory University, Atlanta, GA	B.S.	05/2007	Neuroscience
University of Pennsylvania, Philadelphia, PA	Ph.D.	05/2013	Cell and Molecular Biology
Kyoto University, Kyoto, JP	Postdoctoral	10/2014	Virology
University of Pennsylvania, Philadelphia, PA	M.D.	05/2015	Medicine
Vanderbilt University, Nashville, TN	Residency	07/2018	General Surgery

A. Personal Statement

My research focuses on virus-host symbioses established upon integration of viral sequence information into the genome of the host. As over 50% of the human genome is derived from endogenous retroviruses and other retro-transposable elements, this has been a significant driver of human genome evolution. My team is currently studying host-integrated viral sequences derived from two human pathogens which do not encode integration enzymes; thus host, rather than viral, machinery was necessary for integration of these viral sequences into our genome: Borna disease virus, a recently emerging cause of human encephalitis, human herpesvirus 6, a ubiquitous human pathogen responsible for roseola in infants. The goal of this research is to understand and harness existing mechanisms of “natural” human genome editing to enable human resistance to disease. I am also a medical doctor with specialty training in general surgery and interest in translating basic science advances to surgical care, especially in the field of transplantation. I have been focusing exclusively on basic science research since 2018, when I started an independent research group at RIKEN in Japan.

1. Liu, X., Kosugi, S., Koide, R., Kawamura, Y., Ito, J., Miura, H., Matoba, N., Matsuzaki, M., Fujita, M., Kamada, A.J., Nakagawa, H., Tamiya, G., Matsuda, K., Murakami, Y., Kubo, M., Sato, K., Momozawa, Y., Ohashi, J., Terao, C., Yoshikawa, T., **Parrish, N.F.**, Kamatani, Y. Endogenization and excision of human herpesvirus 6 in human genomes. *bioRxiv*. doi: https://doi.org/10.1101/2019.12.19.882522. 2019.
2. **Parrish, N.F.**, Tomonaga, K. A Viral (Arc)hive for Metazoan Memory. *Cell.* 172(1):8-10, 2018.
3. **1000 Genomes Project Consortium**, Auton, A., Brooks, L.D., Durbin, R.M., Garrison, E.P., Kang, H.M., Korbel, J.O., Marchini, J.L., McCarthy, S., McVean, G.A., Abecasis, G.R. A global reference for human genetic variation. *Nature* 526(7571):68-74, 2015.
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5. **Parrish, N.F.**, Gao, F., Li, H., Giorgi, E.E., Barbian, H.J. Parrish, E.H., Zajic, L., Iyer, S.S., Decker, J.M., Kumar, A., Hora, B., Berg, A., Cai, F., Hopper, J., Denny, T.N., Ding, H., Ochsenbauer, C., Kappes, J.C., Galimidi, R., West A.P., Bjorkman, P.J., Wilen C.B., Doms, R.W., O’Brien M., Bhardwaj, N., Borrow, P., Haynes, B.F., Korber, B.T., Shaw, G.M., and Hahn, B.H. Phenotypic properties of transmitted founder HIV-1. *Proc Natl Acad Sci U S A* 110:6626-33, 2013.

B. Positions and Honors

Positions and Employment

2014	Japan Society for the Promotion of Science Postdoctoral Fellow, Kyoto University Institute for Virus Research
2015-2018	Resident Physician, Vanderbilt University Medical Center, Section of Surgical Sciences, General Surgery
2018-present	Hakubi Team Leader, RIKEN Center for Integrative Medical Sciences, Genome Immunobiology RIKEN Hakubi Research Team

Other Experience and Professional Memberships

2014-	Candidate Member, Association for Academic Surgery
2015-	Junior Fellow, International College of Surgeons
2015-	Resident Member, American College of Surgeons
2015-	Member, American Society for Transplantation Trainee and Young Faculty Community of Practice
2015-	Member, The RNA Society
2018-	Member, The Japanese Society for Virology
2019-	Member, The Molecular Biology Society of Japan

Honors

2007	Phi Beta Kappa, Gamma of Georgia
2009	Conference on Retrovirology and Opportunistic Infections (CROI) Young Investigator Award
2011	CROI Young Investigator Award
2011	Centers for HIV-1/AIDS Vaccine Immunology (CHAVI) Young Investigator Award
2012	CHAVI Immunogen Design Pre-Doctoral Student Award
2014	Richard K. Root Prize, Perelman School of Medicine
2018	American College of Surgeons International Exchange Scholarship
2018	J. Kenneth Jacobs Research Scholarship Award, Vanderbilt University
2019	Outstanding Abstract, 11th International Conference on Human Herpesvirus 6 & 7

C. Contributions to Science

Complete list of publications available on orcid: https://orcid.org/0000-0002-6971-8016
Citations: 7,966 (7,072 since 2015); i10-index: 19 (based on Google Scholar, Jan 2020)

1. I am currently studying the role of genomic sequences derived from non-retrotranscribing viruses on host immune function. I reported the first example of production of piRNAs, a class of interfering small RNA, from nonretroviral endogenous viral elements, specifically from endogenous bornavirus-like Nucleoprotein elements (EBLNs) in the mouse and human genome. I proposed that these piRNAs could be involved in sequence-specific antiviral immunity, a concept that has subsequently been demonstrated in chickens, mosquitos, and koalas. Currently, a major effort of my group is to test this concept using genome-engineered mice. This research highlights the remarkable ability of the host genome to integrate virus-specific nucleic acid information, potentially as immune memory.

1. Ophinni, Y., Palatini, U., Hayashi, Y., **Parrish, N.F.** piRNA-Guided CRISPR-like Immunity in Eukaryotes. *Trends in Immunology* 40(11):998-1010, 2019.

2. Parrish, N.F., Fujino, K., Honda, T., Shiromoto, Y., Iwasaki, K., Kuramochi-Miyagawa S., Nakano, T., Siomi, H., Tomonaga, K. piRNAs derived from ancient viral processed pseudogenes as transgenerational sequence-specific immune memory in mammals. *RNA* 21(10):1691-703, 2015.

3. Sofuku K., **Parrish, N.F.**, Honda T., Tomonaga, K. Transcription profiling demonstrates epigenetic control of non-retroviral RNA virus-derived elements in the human genome. *Cell Reports* 12(10):1548-54, 2015.

4. Parrish, N.F., Tomonaga, K. Endogenized viral sequences in mammals. *Current Opinion in Microbiology* 31:176-83, 2016.

5. Makino, A., Fujino, K., **Parrish, N.F.**, Honda, T., Tomonaga, K. Borna disease virus possesses an NF-κB inhibitory peptide sequence in the nucleoprotein gene. *Scientific Reports* 5:8696. doi: 10.1038/srep08696, 2015.

2. I have used whole genome sequencing to study virus genome-human genome interactions and the evolution of genomic novelty in general. As a member of the 1,000 Genome Structural Variation working group, I characterized the contribution of a novel RNA-templated DNA insertion mutation mechanism to genetic differences across individuals and human populations. I have continued this work to analyze the human "integrated virome" in non-reference genome-mapping reads from whole genome sequencing projects. In doing so, we have found evidence of relatively frequent integration of HHV-6 into certain telomeres. The existence of common HHV-6 integrations events which are identical by descent and linked to human haplotypes is an unexpected new finding. We consider it a scientific imperative to test the possibility that these integrated viruses act as a reservoir to generate infectious viruses or are otherwise capable of influencing human health.

1. Liu, X., Kosugi, S., Koide, R., Kawamura, Y., Ito, J., Miura, H., Matoba, N., Matsuzaki, M., Fujita, M., Kamada, A.J., Nakagawa, H., Tamiya, G., Matsuda, K., Murakami, Y., Kubo, M., Sato, K., Momozawa, Y., Ohashi, J., Terao, C., Yoshikawa, T., **Parrish, N.F.**, Kamatani, Y. Endogenization and excision of human herpesvirus 6 in human genomes. *bioRxiv*. doi: https://doi.org/10.1101/2019.12.19.882522, 2019.
2. 1000 Genomes Project Consortium, Auton, A., Brooks, L.D., Durbin, R.M., Garrison, E.P., Kang, H.M., Korbel, J.O., Marchini, J.L., McCarthy, S., McVean, G.A., Abecasis, G.R. A global reference for human genetic variation. *Nature* 526(7571):68-74, 2015.
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4. Abyzov, A., Li, S., Kim, D.R., Mohiyuddin, M., Stuetz, A., **Parrish, N.F.**, Mu, X.J., Clark, W., Harmanci, A., Chen, K., Hurles, M., Korbel, J. Lam, H.K.Y., Lee, C., Gerstein, M. Analysis of structural variation breakpoints from 1,092 humans reveals details of mutation mechanisms. *Nature Communications* 6:7256. doi: 10.1038/ncomms8256, 2015.

3. My graduate work focused on HIV-1 molecular virology in the laboratory of Dr. Beatrice Hahn. I was able to connect viral genotypes of interest, across the entire viral genome, to medically relevant phenotypes. This was made possible using chemically-synthesized molecular clones of large panels of HIV-1. We were able to, for the first time, define the virus phenotypes that are associated with mucosal transmission, and link these phenotypes back to the diverse genotypes responsible for the HIV-1 pandemic.

1. Parrish, N.F., Gao, F., Li, H., Giorgi, E.E., Barbian, H.J. Parrish, E.H., Zajic, L., Iyer, S.S., Decker, J.M., Kumar, A., Hora, B., Berg, A., Cai, F., Hopper, J., Denny, T.N., Ding, H., Ochsenbauer, C., Kappes, J.C., Galimidi, R., West A.P., Bjorkman, P.J., Wilen C.B., Doms, R.W., O'Brien M., Bhardwaj, N., Borrow, P., Haynes, B.F., Korber, B.T., Shaw, G.M., and Hahn, B.H. Phenotypic properties of transmitted founder HIV-1. *Proc Natl Acad Sci U S A* 110:6626-33, 2013.
2. Parrish, N.F.*, Wilen, C.B.*, Banks, L.B., Iyer, S.S., Pfaff, J.M., Salazar-Gonzalez, J.F., Salazar, M.G., Decker, J.M., Parrish, E.H., Berg, A., Henning, Hopper, J., Hora, B., Kumar, A., Mahlokozera, T., Yuan, S., Coleman, C., Vermeulen, M., Ding, H., Ochsenbauer, C., Tilton, J.C., Permar, S. R., Kappes, J.C., Betts, M.R., Busch, M.P., Gao, F., Montefiori, D.C., Haynes, B.F., Shaw, G.M., Hahn, B.H., and Doms, R.W. Transmitted founder and chronic subtype C HIV-1 use CD4 and CCR5 receptors with equal efficiency and are not inhibited by blocking the integrin α4β7. *PLoS Pathog* 8(5): e1002686, 2012. ***authors contributed equally**
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Gao, F. Primary Infection by a human immunodeficiency virus with atypical coreceptor tropism. *J Virol* 85:10669-10681, 2011. ***authors contributed equally**

4. Wilen, C.B.*, **Parrish, N.F.***, Pfaff, J.M., Decker, J.M., Henning, E.A., Haim, H., Petersen, J.E., Wojcechowskyj, J.A., Sodroski, J., Haynes, B.F., Montefiori, D.C., Tilton, J.C., Shaw, G.M., Hahn, B.H., and Doms, R.W. Phenotypic and immunologic comparison of clade B transmitted founder and chronic HIV-1 envelope glycoproteins. *J Virol* 85: 8514-8527, 2011. ***authors contributed equally**

D. Additional Information: Research Support and/or Scholastic Performance

Current Support: My laboratory is funded by an internal RIKEN program, the "Hakubi" program which aims to recruit exceptionally talented individuals to develop the next generation of leading researchers with a global outlook. My team's budget is ~40 million JPY (~360,000 USD) annually for 5-7 years. I am fully eligible for additional external funds and internal funds, of which I was able to compete for 6.8 million JPY in the previous fiscal year.

Previous Support:

Long Term Fellowship award number LT001020 Award declined
Human Frontiers Science Program Organization
Co-mentors Keizo Tomonaga, Kyoto University and Haruhiko Siomi, Keio University
Investigating the Function of piRNA Derived from Endogenous Bornaviral Elements

Postdoctoral Fellowship award number PE13075 03/02/2014 – 09/28/2014
Japan Society for the Promotion of Science Postdoctoral Fellowship
Human Tumor Virus Laboratory, Institute for Virus Research, Kyoto University
A Novel Mechanism of Antiviral Immunity Mediated by Endogenous Viral Elements

Penn/Tulane CFAR Non-human Primate Pilot Grant 11/16/2011 – 11/16/2012
(P.I. Hahn, co-P.I. **Parrish**)
University of Pennsylvania Center for AIDS Research
Transmissibility of a SIVmac239 Mutant with Increased Env Content

T32 AI0007632 (P.I. Doms) 09/04/2011 – 09/04/2012
National Institutes of Health (NIH)
University of Pennsylvania Microbiology Training Grant

UAB SDRC Pilot and Feasibility Grant #17 (P.I. Hahn) 08/01/2010 – 08/01/2011
University of Alabama at Birmingham Skin Diseases Research Center
Developing and Validating a Skin Explant Model of HIV Transmission

T32 GM008361 (P.I. Lorenz) 08/15/2007 – 08/15/2011
National Institutes of Health (NIH)
University of Alabama at Birmingham Medical Scientist Training Program Training Grant

Research Approach

The goals of this pilot project are to identify MGE insertions that are polymorphic in different CC lines and characterize them as novel immune regulatory genes. To this end, we will use a new computational method to discover MGE insertions using short-read sequencing data. We developed a new pipeline that uses the BLAST homology search algorithm to "explain" unmapped reads or reads that map partially to a reference genome with non-reference MGE insertions. BLAST has previously been too computationally costly for this purpose, however we have implemented our pipeline using supercomputing resources available at RIKEN and the University of Tokyo. This pipeline outperforms "Mobile Element Locator Tool," the pipeline used to genotype mobile element insertions in the 1000 Genomes Project (14 and unpublished data). Critically, it is also applicable to mouse, not only human, genomes and allows detection of polymorphic ERVs, not only transposons. To demonstrate the feasibility of our pipeline to achieve this aim, we have already applied it to sequencing data from *Mus musculus castaneus* (CAST/EiJ, Cast). In this preliminary work, we identified over 15,000 MGE insertions present in either the Cast or mouse reference (C57BL/6J, B6J) genome, but not both, including over 5,000 ERVs. If funded, we will implement this pipeline using publically-available short-read whole-genome sequencing (WGS) data from 8 CC founder strains. Next, we will use the available haplotype data from the CC-RI strains, as well as WGS data available for 75 CC strains, to generate inferred MGE insertion genotypes, genome-wide, for all CC-RI strains used in the infection screens performed by the Center for Systems Immunogenetics of Biodefense Pathogens (15).

MGE can quickly generate genetic novelty, potentially influencing immune regulation. However the rapid evolution of MGEs complicates their genotyping based on reference datasets, because new insertions can arise in the generations that separate the individual(s) sequenced to produce a reference dataset and the actual individuals of interest (in this case, the CC-RI cross lines that were actually experimented on). In humans, *de novo* MGE insertions have been detected in 6% of live births (16), and the MGE insertion rate in mice is higher than that of humans (10). Moreover, because human data addressing this point is based only on short-read sequencing from pedigrees, which has limited sensitivity for detecting *de novo* MGE insertions, it is likely an underestimation. To address this point, we will obtain approximately 30x coverage long-read WGS data of six selected CC-RI lines. We will coordinate this with the University of Washington PacBio Sequencing Service in consultation with members of the Center for Systems Immunogenetics of Biodefense Pathogens. This dataset will allow us to genotype *de novo* MGE insertions arising during the CC breeding process, and will also generate a "ground truth" MGE insertion dataset to validate our genotyping pipeline in mice, as we have previously done using human long-read sequencing results (unpublished data).

Next, we will perform association studies using the new genotypes obtained above with the rich phenotypic data collected during the previously-performed infection screens, in collaboration with current investigators in this project. To demonstrate the feasibility of MGE insertions to act as immune regulatory variants and influence viral infection outcomes, we analyzed the location of MGE insertions in the Cast genome, relative to the B6J genome, in relation to Ensembl gene transcriptional start sites (TSS). We found 1220 MGE insertions within 10 kilobases upstream of all genes' TSS, which represents a significant enrichment relative to random distribution throughout the mouse genome ($p<0.0001$). There were 402 MGE insertions absent in Cast, but present in B6J, which also represents a statistical enrichment ($p=0.01$). Downstream insertions were not enriched. Considering only TSS of immune genes, we detected 50 MGEs polymorphic between B6J and Cast; there are reasonable candidate loci to be involved in regulating immune responses differently between these

lines. The diverse CC strains used in the infection studies will be a powerful resource to allow us to discover which, if any, of these genetic variants associate with viral infection phenotypes of interest. It is important to note that these MGE insertions are not genotyped using existing approaches, so these MGE insertions may explain "missing heritability" of already-studied phenotypes, or may represent the "hidden" causative variants at loci already known to be associated with traits of interest. This subaim adresses a major open question in the genomics of immune regulation. While we thus cannot guarantee that MGEs will indeed be revealed as immune regulatory variants, there are a number known overlaps between the immune genes and mechanisms that control ERVs and other MGEs with those that control exogenous viruses (e.g. 3, 17,18). Thus it is reasonable to anticipate that some of the genetic variation contributed by the activity of MGEs in recent mouse diversification evolved under selective pressure from viruses and ERVs, and will thus influence variation in immune phenotype.

In the final aspect of this pilot project, we will perform RNA sequencing of immune cells sorted from different CC-RI lines. This will be performed in collaboration with Dr. Hideyuki Yoshida, an expert in single cell sequencing and immune transcriptomics (19, 20). We will choose 6 CC-RI lines which have highly divergent responses to SARS-CoV, IAV, and WNV, as well as candidate MGE insertions which may influence these responses. In the event that we cannot find suitable lines that differ based on MGE insertions putatively influencing antiviral immune function, we will choose any six diverse CC-RI lines for this purpose. We will first use flow sorting to quantify and separate immune cells into the 11 basic cell types characterized in the Immgen consortium (20). In all lines, we will minimally sequence bulk splenic native CD4 T cells, CD8 T cells, and natural killer T cells. To limit cost, we will employ a pooled single cell RNAseq approach followed by de-multiplexing of single cells based on the known genotypes of the CC-RI lines (21). Based on the MGE insertions we identify, we will tailor additional sequenced populations (e.g. if MGEs are identified near TFs known to regulate development of immune cell types) and whether or not they are sequenced after stimulus (e.g. if MGEs are identified near interferon-stimulated genes). To preliminarily validate that this approach can identify MGE insertions as immune regulatory variants, we used single cell RNA sequencing data from B6J and Cast naive CD4 T cells (22). 51 genes with a MGE insertion within 10kb of the TSS were differentially expressed in naive CD4 T cells from these two lines. Notably, one of these genes is a known antiviral gene which is highly upregulated (>20 fold) in CD4 T cells from Cast relative to B6J (Figure 1). In the Cast genome, but not the B6J genome, an ERV has inserted 1.8 kilobases downstream of the gene's TSS (Figure 2). We thus anticipate that the deep genetic resource of the CC, along with existing phenotypic datasets from viral infections, coupled with unique genotypic and transcriptomic data we will generate on a pilot scale if funded, will enable us to identify MGE insertion as a genetic mechanism underlying variation in immune responses and their regulation.

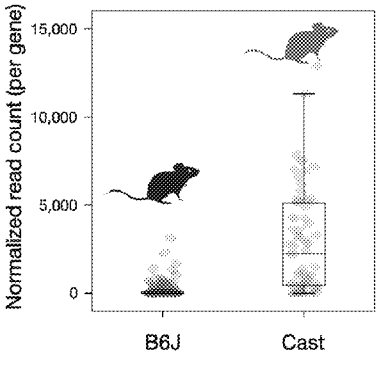

Figure 1. Expression of an antiviral gene in single cell RNA-seq of CD4 T cells

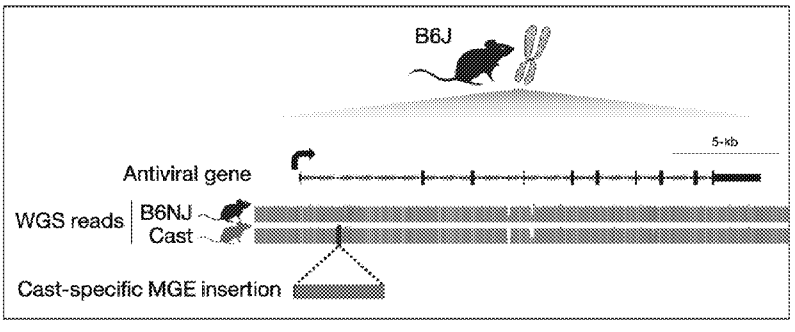

Figure 2. Cast-specific MGE insertion in an antiviral gene

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20. Mostafavi, S., Yoshida, H., et al., Parsing the Interferon Transcriptional Network and Its Disease Associations. Cell, 2016. 164(3): p. 564-578.

21. Kang, H.M., et al., Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol, 2018. 36(1): p. 89-94.

22. Martinez-Jimenez, C.P., et al., Aging increases cell-to-cell transcriptional variability upon immune stimulation. Science, 2017. 355(6332): p. 1433-1436.

Scope of Work

Nicholas Parrish, MD PhD, will oversee this project. He will spend approximately 15% of his time on this pilot project during the grant period. He will direct the implementation of the described mobile genetic element genotyping pipeline. Funds are requested to support supercomputer usage time in order to implement genotyping. He will coordinate a service agreement with the University of Washington PacBio sequencing service (https://pacbio.gs.washington.edu/) or another service provider to perform long-read resequencing of 6 CC-RI lines. Dr. Parrish will act as liaison with other Systems Immunogenetics Project members. He will oversee association testing between mobile genetic element insertions as genotyped by his group and existing and future phenotypic data collected by Systems Immunogenetics Project members.

Dr. KOJIMA Shohei (postdoctoral researcher, RIKEN IMS) will assist with implementation of the pipeline and will perform association testing. GWAS implementation and statistical genetics is available through our laboratories existing collaboration with the RIKEN IMS Laboratory for Statistical and Translational Genetics (PI Dr. TERAO Chikashi). Dr, KOJIMA will analyze PacBio sequencing data.

Ms. Erica Parrish will perform animal care for the requested CC-RI lines.

Dr. YOSHIDA Hideyuki will perform FACS sorting of various immune cell subsets from CC-RI lines. He will generate RNA sequencing libraries from these cells. We will contract with Macrogen Japan company (https://www.macrogen-japan.co.jp/) to sequence the resulting libraries. Dr. Yoshida will collaborate with Dr. Parrish and Dr. KOJIMA to perform association testing between gene expression levels, polymorphic mobile genetic element genotypes, and phenotype data collected by Systems Immunogenetics Project members.

Indirect costs are calculated at 8%

Budget Justification:

Personnel: No personnel costs are requested. Dr. PARRISH, Dr. YOSHIDA and one postdoctoral researcher (KOJIMA Shohei) will be the personnel involved, however salary support for the grant period is already covered.

Equipment/Travel/Participant fees: Dr. Parrish requests funds to travel once to UNC from Japan to present the outcome of the pilot project: $5,400

Direct costs:

Materials and supplies:

Animal costs and embryo/sperm frozen shipping fees: $2,500

RIKEN animal facility fees for mouse clean-up: $76 x 6 strains: $460

Animal care costs: 24 cages x 180 days x $0.65: $2,800

Antibodies for flow sorting: $5,240

RNA sequencing library preparation reagents: $12,000

Hard drives for data transfer and shipping: $1,000

ADP/ computer services:

"D4" course with 1024 cores x 12 months at Shirokane supercomputer, University of Tokyo: $3,600

Contract costs:

University of Washington PacBio sequencing service (four 30-hour sequel II runs, with 3 samples multiplexed per run, each sample in duplicate): $19,600

Macrogen HiSeqX sequencing service, 18 lanes total: $23,400

Facility User fees:

RIKEN IMS FACS core user fees: $2,000

Indirect costs: RIKEN indirect costs at 8%

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

LEAVE BLANK—FOR PHS USE ONLY.		
Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*

New models to dissect the genetic determinants of disease tolerance

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☒ NO ☐ YES
(If "Yes," state number and title)
Number: Title:

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Smith, Clare M.		

3c. POSITION TITLE
Assistant Professor of Molecul

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Molecular Genetics & Microbiology

3f. MAJOR SUBDIVISION
School of Medicine

3d. MAILING ADDRESS *(Street, city, state, zip code)*
271 Jones BOX3054
250 Jones
Box 3054
Durham, NC 27710

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: (919) 613-6378 FAX:

E-MAIL ADDRESS:
clare.m.smith@duke.edu

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☐ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☐ No ☐ Yes	☒ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No A3195-01

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
09/01/20	08/31/21	$71,428	$115,000	$71,428	$115,000

9. APPLICANT ORGANIZATION
Name Duke University
Address
2200 West Main St.
Suite 820 Erwin Square Plaza
Durham, NC 27705

10. TYPE OF ORGANIZATION
Public: → ☐ Federal ☐ State ☐ Local
Private: → ☒ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
56-0532129
DUNS NO.044387793 Cong. District 01

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name John M. Michnowicz
Title Director, Off of Research Admn
Address 2200 West Main St.
Suite 820 Erwin Square Plaza
Durham, NC 27705
Tel: (919) 684-5175 FAX: (919) 684-6278
E-Mail: gcmail@mc.duke.edu

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name John M. Michnowicz
Title Director, Off of Research Admn
Address 2200 West Main St.
Suite 820 Erwin Square Plaza
Durham, NC 27705
Tel: (919) 684-5175 FAX: (919) 684-6278
E-Mail: jae.furman@duke.edu

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.

SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)*

DATE 02/27/20

SPECIFIC AIMS

The survival of a host infected with a chronic pathogen is ultimately determined by the host response that must include both resistance and disease tolerance mechanisms. "Resistance" involves antimicrobial pathways that directly control bacterial burden, while disease "tolerance" comprises of mechanisms to withstand the cumulative damage of tissue damage that chronic infection entails. In the context of tuberculosis (TB), resistance pathways eventually breakdown and *Mycobacterium tuberculosis (Mtb)* is able to persist in tissues long-term. At that point, disease tolerance is vital for regulating the immune response to prevent overt damage and ensure ultimate survival of the host. With the failure of current therapies that focus on directly targeting microbial pathways, **this proposal instead focuses on identifying the mediators of host tolerance** that may be leveraged to design new host-directed strategies.

From preliminary studies, we found that the Collaborative Cross panel models the broad phenotypic spectrum of TB disease traits observed in human cohorts. We identified resistant CC genotypes able to control bacterial burden through to highly susceptible CC genotypes that succumbed to disease within one month of infection. While we found many disease traits were generally correlated, we also identified several "outlier" genotypes where typical disease metrics were broken. For example, bacterial burden and weight loss are correlated in the standard C57BL/6J model of infection, however among CC strains harboring 10_7 CFU in their lungs, we identified genotypes with a wide variation in weight loss and survival. Several genotypes showed limited pathology and could tolerate disease at that burden, while other CC genotypes exhibited weight loss and succumbed to disease at the same CFU. These data suggest that distinct genetic mechanisms underlie disease tolerance. In the current proposal we will **leverage these CC "outlier" strains as new models of disease tolerance to define the immunological and genetic mechanisms** underpinning this essential and understudied component of protective immunity to pathogens.

We will pursue the following aims:

Aim 1: Define the immunological hallmarks and kinetics of disease tolerance in outlier CC genotypes. In our previous study, we identified disease tolerant and non-tolerant CC genotypes, however the cellular players and timing mediating this protective state is yet unknown. We hypothesize that specific immunological profiles can distinguish tolerant and non-tolerant responses. Here, we will profile the innate and adaptive immune responses in two tolerant and two non-tolerant CC genotypes during the course of infection with *Mtb*. Overall, this aim will Identify the immunological biomarkers that distinguish disease tolerance from non-tolerance in diverse hosts.

Aim 2: Elucidate the genetic determinants that underlie disease tolerance. The identification of outlier CC strains that maintain the same bacterial burden, yet show vastly different disease outcomes implies that these traits are under distinct genetic control. In this aim, we will identify the genetic loci underlying disease tolerance in an F2 mapping population created between the two most extreme tolerant and non-tolerant CC strains that we identified in the initial CC infection study. F2 mice will be genotyped, infected with *Mtb* and phenotyped for bacterial burden and disease tolerance traits. QTL mapping will identify novel host loci that underlie disease tolerance in these CC outlier strains.

Impact: Overall, this work will provide new insights into disease tolerance that is relevant to genetically diverse hosts. Understanding the immunological and genetic mediators of disease tolerance will allow the rationale design of novel host-directed strategies that may be applied to tuberculosis and other chronic infections.

A. SIGNIFICANCE

Infection with *Mycobacterium tuberculosis* (*Mtb*) results in highly variable disease progression and clinical outcomes. Most individuals exposed to *Mtb* have latent infection and remain asymptomatic for a lifetime. However, about 10% of those infected develop active tuberculosis (TB), and even amongst these patients the timing, location and presentation of pathology is remarkably diverse. Two major questions facing the field include: predicting which people are most at risk for disease, and determining the optimal immune response a vaccine or intervention should elicit. Thus, **understanding the cellular and genetic determinants of the host response to infection** is a fundamental challenge in developing more effective strategies in TB prevention, diagnosis and treatment.

A challenge in understanding the mechanisms underpinning protective immunity is the lack of adequate diverse animal model systems. In contrast to the genetic and phenotypic diversity observed in natural outbred populations, the vast majority of small animal models for TB utilize single strains of genetically identical animals. *The lack of a tractable small animal model that incorporates relevant genetic diversity limits our ability to rationally design interventions that are likely to be effective in natural outbred and variable populations (*Smith *et al. 2018;* https://doi.org/10.1016/j.tim.2018.08.002). The Collaborative Cross (CC) mouse panel is unique in its genetic diversity that allows for the generation of new models that replicate diverse disease states. Importantly, this variability can be generated reproducibly, creating tractable models in which to interrogate mechanisms of protection (Smith *et al.* 2016; https://mbio.asm.org/content/7/5/e01516-16).

From preliminary studies in the 8 parental strains and ~55 recombinant inbred Collaborative Cross (CC) lines, we found that the CC panel encompassed a broad response to infection with *Mtb*. In particular, we identified several CC genotypes that maintained relatively high bacterial burden (10_6 to 10_7 CFU), yet showed no typical disease traits including weight loss or pathological sequelae. This ability to withstand inflammation and disease at high bacterial burden is known as "disease tolerance", and may be an important arm of the host response needed to survive chronic infections. We also identified "non-tolerant" strains that at that same bacterial burden succumbed to infection, reminiscent of the classical "wasting" disease associated with TB in susceptible human cohorts. In this project, **we will leverage outlier CC strains to define the immunological and genetic basis of disease tolerance**. This work will provide new models and genetic loci underlying disease tolerance that will inform novel host-directed strategies to augment host tolerance to infection.

B. INNOVATION

This proposal is conceptually innovative in 3 main ways:

(i) Incorporating genetic variability in a reproducible manner using the CC is critical to produce a more accurate model of **diverse TB disease**. Here, we will identify immune responses associated with disease tolerance in the genetically diverse but reproducible CC strains.

(ii) **Disease tolerance** is a critical, yet understudied aspect of protective immunity to chronic infections. Thus, our identification of new models of disease tolerance within the CC panel will enable mechanistic studies to dissect disease tolerance that may also be applicable to other chronic infections

(iii) The F2 intercross approach between two phenotypic outlier CC strains is an effective method to **map and identify casual variants** underlying distinct disease states. We have successfully leveraged this approach to identify a causal variant underlying susceptibility to TB (Smith *et al.* 2019; https://doi.org/10.1128/mBio.02791-19) and will now leverage the extreme phenotypic difference between a CC tolerant strain and non-tolerant strain to map the genetic loci and associated pathways underlying disease tolerance. These pathways and mechanisms may be widely applicable to other chronic infections.

C. APPROACH

In this project, we will select strains from the CC panel that demonstrate the extremes of disease tolerance to TB (Fig1). We will leverage the tractable CC model to functionally characterize these responses at the immunological and genetic level, to discover new pathways of protective immunity and disease tolerance that can be leveraged for new host-directed interventions. We will do this by 1) Defining the characteristics and kinetics of immunity and pathology in tolerant and non-tolerant CC lines and 2) Identifying the genetic loci that underly disease tolerance to *Mtb* infection.

Overall approach: We will profile the adaptive immune responses and histopathological progression during infection with *Mtb* in two tolerant CC strains and two non-tolerant CC strains. Profiling several independent CC strains of each category enables the identification of multiple tolerance pathways. After defining the traits and timepoint that distinguish disease tolerance between these extreme tolerance outliers, we will map the genetic loci driving the divergent disease tolerance response, as described:

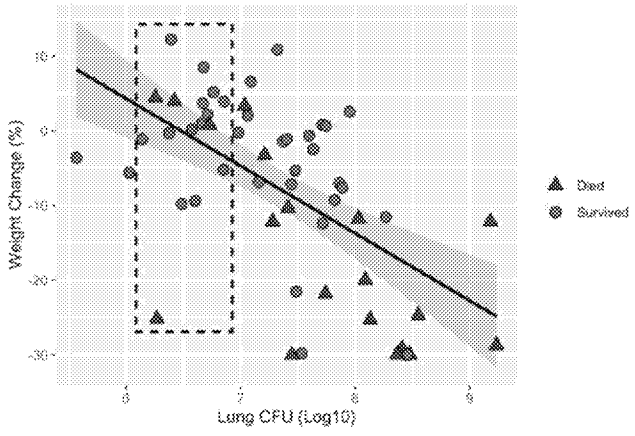

Fig1. Identifying disease tolerant vs non-tolerant CC strains. Bacterial burden (CFU) vs weight loss across ~55 CC strains. Strains within the box have similar burden but vastly different disease, based on weight loss. Each point represents a CC genotype (the average of n=3-5 mice/genotype). Triangles indicate genotypes that were moribund at 4wks post-Mtb infection.

Aim 1: Determine the immune and histopathological characteristics of tolerance to tuberculosis in tolerant and non-tolerant CC lines.

Choice of tolerance outlier lines: Based on our ongoing studies, we have chosen to focus on 4 CC strains; 2 tolerant lines (high bacterial burden but do not lose weight) and 2 non-tolerant strains (that at the same bacterial burden, succumb to disease after four weeks of *Mtb* infection) (Fig1). These genotypes represent the phenotypic extremes of TB tolerance.
Infection: Mice will be infected by the aerosol route with *Mtb* reference strain H37Rv. Groups of 5 mice per genotype will be sacrificed at 2 weeks (prior to the onset of adaptive immunity), 3 weeks (onset of adaptive immunity) and 4 weeks (plateau of bacterial burden and adaptive immunity) after *Mtb* challenge. Lungs and spleen will be collected for i) immune profiling by flow cytometry and ii) fixation for histopathological analysis of cellular infiltrate location and lesion formation. Mice will be monitored for weight loss, and one anatomic lung lobe homogenized / plated for bacterial counts.

We will perform the following set of functional assays and unbiased immune profiling strategies by flow cytometry:
T-cell subsets: We will enumerate the proportion of $CD4_+$, $CD8_+$, $TCR\gamma\partial_+$, and invariant (iNKT and MAIT) T cells.
T helper subtypes: We will compare transcription factor expression (t-bet, RORγT, Foxp3, and GATA-3), surface receptor expression (CXCR3, CCR6, CCR4, and CD25), and intracellular cytokine production (IFNγ, IL-17, IL-22, IL-10, and IL-4) after stimulation with Mtb purified protein derivative (PPD) to evaluate the contribution of each T helper (Th) subset (Th1, Th17, Treg, and Th2, respectively) of Mtb-specific T helper cells.
T cell function: Without ex vivo stimulation, we will directly estimate the proportion of cells secreting several effector cytokines that contribute to antimicrobial function during TB by direct intracellular cytokine staining / flow cytometry of T cell subsets, including: IFNγ, TNF, IL-2, IL-17, IL-21, and GM-CSF. CTL function will be estimated by measuring intracellular granzyme B and perforin by antibody staining and flow cytometry. Surface receptors associated with T cell exhaustion (PD-1, 2B4, Tim-3, CTLA-4, Lag-3), terminal effector differentiation (KLRG1), and T cell activation (CD69 and CD25 expression, intracellular Nur-77, IRF-4 expression, and CD27 and CD127 down-regulation) will also be compared. Each assay has been already tested in the parental strains of the CCs to ensure validity of antibodies.
Total organ cytokines will also be measured by multiplex ELISA assays, to correlate inflammatory profiles that separate tolerant from non-tolerant CC responses to *Mtb*.

Together, this data will distinguish the cellular and histopathological changes that ***separate disease tolerance and non-tolerance in the selected CC outlier strains*** during the innate and adaptive host response to TB. The deep profiling of these CC strains will ensure their implementation as new models in which future studies can test host-directed strategies to augment tolerance to TB and other chronic infections.

Aim 2: Elucidate underlying genetic drivers of disease tolerance to TB.

The identification of outlier lines that at the same bacterial burden have vastly different inflammatory sequalae, implies that bacterial burden and pathological disease traits are under independent genetic control. We aim to *identify the underlying host loci driving the extreme disease tolerance responses by a genetic mapping approach*.

In collaboration with Dr Martin Ferris and Dr Fernando Pardo-Manuel de Villena at UNC Chapel Hill, the two most extreme disease tolerance CC genotypes will be intercrossed to make F1s; F1 progeny will then be intercrossed to create an F2 mapping cohort. Tail snips will be taken and genomic DNA extracted for genotyping on the miniMUGA array (~10,000 markers), developed by our UNC collaborators and that we have extensively used. We will infect ~200 F2 mice with *Mtb*, collect lungs and spleen for bacterial counts and multi-immunological phenotyping (determined by the informative phenotypes that distinguish tolerance from non-tolerance as determined in aim 1 above). The QTL associated with disease tolerance traits will be mapped using RQTL2. Additionally, analysis in RQTL2 can explicitly identify sex-specific genetic effects and 2-gene epistatic interactions.

This extreme CCxCC F2 approach will identify **host loci that underlie disease tolerance.** Future studies can verify candidate loci through further crosses (congenics) and swapping of alleles between tolerant/non-tolerant strains and/or knock-out strians using Crispr/Cas9 technology.

Future directions:

This proposal will identify and define new models of disease tolerance and is the first step in identifying the genetic determinants that underly this vital arm of protective immunity to pathogens. Findings from this work will form the preliminary data to setup an R01 application, that will aim to identify the causal drivers of disease tolerance and how these pathways may be targeted as novel host-directed therapeutic interventions.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Clare M. Smith, PhD

eRA COMMONS USER NAME (credential, e.g., agency login): CLAREMSMITH

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Tasmania, Australia	BBiotech (Hons)	2007	Molecular Biology and Biochemistry
Menzies Research Institute, Australia	PhD	2012	Genetics
University of Massachusetts Medical School, MA	Postdoctoral	2019	Genetics, Microbiology

A. Personal Statement. Throughout my scientific career I have focused on understanding the genetic determinants underlying infectious disease, successfully translating these insights into human clinical settings. My honors thesis and PhD work in the laboratory of Dr. Simon Foote focused on understanding the contribution of host and *Plasmodium* enzymes to malarial infection in the red blood cell. I discovered that several host heme enzymes are required for parasite growth in the red cell and I validated these enzymes as novel host-directed therapeutic targets using a range of *in vitro*, *in vivo* mouse and *ex vivo* human studies. I stayed in the Foote laboratory immediately after my PhD defense to test the target and compound I discovered during my PhD in a human malarial challenge phase IIb trial. My PhD training under a renowned mouse and human geneticist gave me the skills to tackle host aspects of the longstanding evolutionary battle between host and pathogen but left me with the feeling that this was truly only half of the answer. To truly understand the genetic basis of susceptibility to infection, we needed a way to incorporate pathogen diversity.

The quest to understand the host-pathogen interaction at a genome-wide level subsequently led me to postdoc with Dr. Chris Sassetti at UMASS, who developed tools to understand bacterial genetic requirements during tuberculosis infection. This was a productive collaboration, where I mastered new bacterial genetic technologies and applied my background in mammalian genetics to **create a tractable new model to understand the contribution of both host and pathogen variation underlying infection**. This "dual-genome" model leverages genetically diverse mice (including Collaborative Cross (CC) and Diversity Outbred mouse panels) and libraries of bacterial mutants to define the host-pathogen genetic interactions that allow *Mycobacterium tuberculosis* to survive in diverse environments. I have also leveraged the CC to understand protective immunity and vaccine protection across genetically diverse hosts. My postdoctoral work has established the use of the CC in the tuberculosis and pathogenesis fields as a way to incorporate genetically diverse but tractable models to understand mechanisms of protective immunity observed in human cohorts.

Having established novel Systems Genetics approaches to define the host-pathogen interactions underlying tuberculosis disease and treatment, I am now poised to launch my own group in the Molecular Genetics and Microbiology (MGM) Department as Duke University. Here, I am in a unique position to lead the effort to incorporate genetically diverse models including the CC into the broader pathogenesis field. As a leader in Mammalian Genetics and an expert in the CC and wild-derived mouse resources, I have established collaborations within Duke, the NC research triangle and to the broader pathogenesis and tuberculosis research fields. Here, my lab's "dual genome" systems genetics approaches can be broadly applied to understand disease pathogenesis in the context of genetically diverse hosts.

a. **Smith CM.**, Jerkovic A, Puy H, Winship I, Deybach JC, Gouya L, van Dooren G, Goodman CD, Sturm A, Manceau H, McFadden GI, David P, Mercereau-Puijalon O, Burgio G, McMorran BJ, Foote SJ (2015) "Red cells from ferrochelatase-deficient erythropoietic protoporphyria patients are resistant to growth of malarial parasites," *Blood;* **125**(3):534-41. doi.org/10.1182/blood-2014-04-567149

b. **Smith CM***, Proulx MK*, Lai R*, Kiritsy MC, Bell TA, Hock P, Pardo-Manuel de Villena F, Ferris MT, Baker RE, Behar SM, Sassetti CM. 2019. Functionally overlapping variants control tuberculosis susceptibility in Collaborative Cross mice. *mBio* **10**:e02791-19. doi.org/10.1128/mBio.02791-19. bioRxiv: doi.org/10.1101/785725. *denotes equal contributions.

c. **Smith CM,** Proulx MK, Olive AJ, Laddy D, Mishra BB, Moss C, Gutierrez NM, Bellerose MM, Barreira-Silva P, Phuah JY, Baker RE, Behar SM, Kornfeld H, Evans TG, Beamer G and Sassetti CM. 2016. Tuberculosis susceptibility and vaccine protection are independently controlled by host genotype. *mBio* 7(5):e01516-16. doi:10.1128/mBio.

d. **Smith CM** and Sassetti CM. "Modeling diversity: do homogenous lab strains limit discovery?" 2018. *Trends in Genetics*. doi.org/10.1016/j.tim.2018.08.002.

B. Positions and Honors

Positions and employment

2006	Undergraduate thesis research. Advisor: Dr John Ross, University of Tasmania, Australia. "Genetic regulators of gibberellin synthesis and root growth in *Pisum sativum*"
2007	Honors thesis research. Advisor: Dr Simon Foote, University of Tasmania, Australia. "A bioinformatic approach to dissecting host vs parasite metabolic genes"
2008-2012	Graduate student, Laboratory of Dr. Simon Foote, Menzies Research Institute, Australia. "An investigation of novel host-directed antimalarial therapeutics"
2009	Summer research fellow, Laboratory of Dr. Odile Puijalon, The Pasteur Institute, Paris.
2012	Visiting research fellow, Laboratory of Dr. Maria Mota, Institute of Molecular Medicine, Lisbon, Portugal
2013-2019	Postdoctoral Research Fellow. University of Massachusetts Medical School, MA. Advisor: Professor Christopher Sassetti. "Systems Genetics of Tuberculosis"
12/2019-	Assistant Professor, Molecular Genetics and Microbiology Department; Member of Duke Human Vaccine Institute, Duke University, NC.

Honors and awards:

2008 – Awarded GlaxoSmithKline Postgraduate Fellowship

2009 – Awarded best talk at the Australian Society for Parasitology National Conference, Sydney, Australia

2010 – Awarded best poster at Lorne Genome National Conference, Lorne, Australia

2011 – Awarded Bede Morris Fellowship from the Australian Academy of Science

2012 – Awarded OzEMalaR (Australia-Europe Malaria Cooperation) Fellowship for researcher exchange

2013 – Young Australian of the Year award; Tasmanian State winner and National finalist

2014 - Awarded Verne Chapman Young Investigator for best talk at the International Mammalian Genome Conference, Bar Harbor, ME. This award resulted in election to the Secretariat of the International Mammalian Genome Society

2014 – Lorraine Flaherty Award, International Mammalian Genome Conference, Bar Harbor, ME

2015 – Judged Best Overall Talk at the Complex Traits Consortium Meeting, Portland, OR

2016 – University of Tasmania Foundation Award, awarded in recognition of professional achievement

2016 – Session chair for plenary session on human disease models, TAGC, Orlando, FL

2017 – Charles A. King Postdoctoral Fellowship

2020 – Whitehead Research Scholar, Duke University

Editorial and Review Activities

Ad hoc reviewer for eLife, Trends in Genetics, Trends in Microbiology and Mammalian Genome
Editor of Mammalian Genome Journal Special Edition on genetics of Infectious Disease

C. Contributions to Science

1. Identified new host resistance genes in response to malarial infection and successfully translated these insights into human clinical settings. During my honor's year in the Foote lab, I took a bioinformatics approach to identify biochemical pathways in the both the host and the malarial parasite *Plasmodium falciparum* during red blood cell infection. I identified enzymes present in the mature red cell that were lacking in the parasite, and hypothesized that these would be scavenged from the host cell and thereby offer a point of interference in the host-parasite interaction. I discovered that many enzymes from the heme pathway were absent in the parasite during this stage of their life-cycle. I functionally demonstrated that each of these enzymes was required for parasite growth, as parasites were unable to grow in blood from individuals with genetic mutations in the uroporphyrinogen-III synthase or ferrochelatase genes (ie. blood from patients with porphyria). This was also the case in mice with ENU-induced mutations in these same enzymes. I subsequently showed that chemical inhibition of these red blood cell enzymes also blocked the growth of the parasite *in vitro*. As one of these compounds was FDA approved for human use as an antifungal, I subsequently showed the compound had *ex vivo* anti-parasitic activity in human patients taking the drug. My honors and PhD work hence identified an Achilles heel of the malarial parasite and my results led to an experimental human infection clinical study, a patent application, two accepted first-author manuscripts, a funded NHMRC project grant and a funded Gates grant.

a. **Smith CM.**, Jerkovic A, Puy H, Winship I, Deybach JC, Gouya L, van Dooren G, Goodman CD, Sturm A, Manceau H, McFadden GI, David P, Mercereau-Puijalon O, Burgio G, McMorran BJ, Foote SJ (2015) "Red cells from ferrochelatase-deficient erythropoietic protoporphyria patients are resistant to growth of malarial parasites," *Blood;* **125**(3):534-41. doi.org/10.1182/blood-2014-04-567149
b. **Smith CM**, Jerkovic A, Truong TT, Foote SJ, McCarthy JS and McMorran BJ (2017) "Griseofulvin impairs intraerythrocytic growth of *Plasmodium falciparum* through ferrochelatase inhibition but lacks activity in an experimental human infection study", *Scientific Reports* **7,** 41975. doi.org/10.1038/srep41975
c. International (PCT) application for letters patent: PCT/AU2012/001422. Registered in the names of (inventors): **Clare M Smith**, Brendan J McMorran and Simon J Foote. Description of patent: "A method of treatment and prophylaxis and compositions useful therfor".
d. McMorran BJ, Wieczorski L, Drysdale K, Chan J, Huang H, **Smith CM**, Mitiku C, Beeson JB, Burgio G, Foote SJ. (212) Platelet Factor 4 and Duffy Antigen Required for Platelet Killing of Plasmodium falciparum. *Science*; 338(6112):1348-1351. doi: science.sciencemag.org/content/338/6112/1348

2. Created a new model system to understand the contribution of host and pathogen to outcome of tuberculosis (TB). The outcome to TB is remarkably diverse and current models are insufficient to dissect the roles of host genetics, bacterial variation and environment factors that contribute to the progression and outcome of disease. I have addressed the shortcomings of existing animal models by leveraging new mammalian and bacterial genetic resources to create a novel, tractable model to understand host and bacterial determinants of susceptibility to TB. Host diversity is modeled using diverse mice (including wild-derived, single-gene knockout and the BXD and Collaborative Cross recombinant inbred panels) and bacterial variation is incorporated using *Mtb* clinical isolates and large-scale bacterial genetic techniques including transposon mutagenesis (TnSeq). Here I have I have demonstrated that the CCs have wide phenotypic diversity in susceptibility and resistance traits that are relevant to human disease. Through the coordinated use of mammalian and bacterial genetics, I have associated different underlying disease states with more than 10 distinct host loci that influence disease progression and outcome to TB (host-interacting with pathogen QTL; hipQTL). I have additionally leveraged F2 crosses between phenodeviant CC strains to further resolve and map new TB susceptibility loci. Individual genetic variants I have identified from these studies are being tested in human clinical cohorts.

a. **Smith CM***, Proulx MK*, Lai R*, Kiritsy MC, Bell TA, Hock P, Pardo-Manuel de Villena F, Ferris MT, Baker RE, Behar SM, Sassetti CM. 2019. Functionally overlapping variants control tuberculosis susceptibility in Collaborative Cross mice. *mBio* **10**:e02791-19. doi.org/10.1128/mBio.02791-19. bioRxiv:

doi.org/10.1101/785725. *denotes equal contributions.

b. **Smith CM**, Long J, Mishra B, Proulx M, Williams R, de Villena FP, Ferris MT, Baker R and Sassetti CM, "The genetic landscape of host-pathogen interactions underlies *Mtb* pathogenesis". Expected submission March 2020

3. Dissected host resistance from vaccine protection in genetically diverse mice. The efficacy of the currently used TB vaccine, *M. bovis* BCG, is highly variable. The design of more broadly-efficacious vaccines depends on understanding the factors that limit the protection imparted by BCG. While these complex factors are difficult to disentangle in natural populations, I leveraged the CC parental strains and several CC RI lines to understand the basis of vaccine efficacy in protection against tuberculosis. Using this new preclinical model, I discovered that natural host genetic diversity is a major determinant of TB vaccine efficacy. I am now using this system to identify immunological correlates of effective vaccination and screen new vaccines that may protect host backgrounds that are unresponsive to standard intervention.

a. **Smith CM,** Proulx MK, Olive AJ, Laddy D, Mishra BB, Moss C, Gutierrez NM, Bellerose MM, Barreira-Silva P, Phuah JY, Baker RE, Behar SM, Kornfeld H, Evans TG, Beamer G and Sassetti CM. 2016. Tuberculosis susceptibility and vaccine protection are independently controlled by host genotype. *mBio* 7(5):e01516-16. doi:10.1128/mBio.

For full list of accepted works, see ORCID profile: http://orcid.org/0000-0003-2601-0955

D. Additional Information: Research Support and/or Scholastic Performance

Completed

Systems Genetics of Tuberculosis
Charles A. King Trust Postdoctoral Fellowship 09/01/2017 – 08/30/2019
Role: Principal Investigator
This postdoctoral fellowship was to investigate the molecular and biological basis of TB-associated host polymorphisms that underly susceptibility to disease.

Investigating immunological outliers to understand protective adaptive immunity during tuberculosis
Innovation grant from the Broad Institute 09/01/2017 – 12/01/2018
Role: Principal Investigator
The major goal of this gift grant from the Broad Institute was to identify and characterize new host models of non-canonical immunity to tuberculosis.

Understanding the contribution of host genetics to BCG efficacy
AERAS Biotechnology 09/01/2015-05/31/2016
Role: Co-Principal Investigator with Dr Christopher Sassetti.
In this project, we leveraged strains from the Collaborative Cross to define the contribution of host genetics in vaccine protection against infection with Mycobacterium tuberculosis.

New models to dissect the genetic determinants of disease tolerance

9/1/2020 – 8/31/21

Dr. Clare M Smith

In this project, we will leverage the genetic diversity of the Collaborative Cross (CC) in conjunction with immunophenotyping and genetic mapping approaches to examine disease tolerance to tuberculosis. In order to understand the immunological hallmarks of disease tolerance during infection with *Mycobacterium tuberculosis*, we will define the cellular players and kinetics of disease tolerance in several tolerant vs. non-tolerant CC strains. Concurrently, we will take a CCxCC intercross approach between a tolerant and non-tolerant CC line to generate an F2 mapping population to identify the genetic loci underlying disease tolerance during the chronic infection of tuberculosis. Overall, this work will define new models of disease tolerance and map novel genetic loci driving protective immunity that may be directly applied to other chronic infectious diseases.

Determination of the Host Genetic Determinants of Cytomegalovirus Infection and Immunity

Specific Aims

Human cytomegalovirus (HCMV) is a ubiquitous β-herpes virus that continues to be an important human health concern. Although HCMV infection is largely asymptomatic in individuals with intact immune systems, HCMV has been implicated in the development of a number of diseases including: vascular disease, solid organ and bone marrow transplant rejection, pneumonia, retinitis and certain cancers. In addition, HCMV is transmitted vertically and is the leading viral cause of congenital disease in neonates where it causes a syndrome of sequelae that include neurological malformations, deafness, blindness, and mental retardation. However, the viral and cellular mechanisms involved in these diseases are still largely unknown.

CMV infections are life-long, and the virus alters host immunity through the induction of chronic inflammation, infection and persistence in myeloid lineage antigen presenting cells, escaping T and B cell responses to a large extent, while altering T cell phenotypes and frequencies [1]. However, the latter ability of the virus has ignited a recent area of vaccine development through the use of CMV as a vaccine platform to elicit long lasting, broadly active T cell responses against genome-incorporated foreign antigens. The Streblow lab recently used murine CMV (MCMV)-based vaccines against Chikungunya virus (CHIKV) to induce protective CD8 T cell immunity that reshaped the inflammatory environment following CHIKV footpad challenge. Similarly, our RhCMV vaccine vectors containing Simian immunodeficiency virus (SIV) antigens have been used to vaccinate rhesus macaques. Data from these studies have also challenged dogma by uncovering unique aspects of T cell biology. While the RhCMV vaccine vectors elicit broadly reactive, potent, antigen-specific effector T cells in all vaccinated animals, an important caveat that has emerged is the finding that only approximately half of the vaccinated animals are protected against SIV acquisition upon repeated challenge [2]. Because the induction of T cell responses is fairly uniform across these vaccinated animals, this finding is highly suggestive that host genetics play an important role in how a host responds to CMV infection and to the induction of protective vaccine efficacy, which we feel are most likely functionally linked.

Host genetics dictate responses to CMV infections and may predispose some individuals to CMV infection and disease. This effect has been shown for MCMV in different mouse strains wherein BALB/C mice are more sensitive to virus infection whereas C57BL/6 are more resistant. This difference has been partially linked to the Ly49H gene [3, 4]. The important point is that the inability to clear virus in BALB/C mice also enhances and prolongs immune activation [5]. Thus, genetic susceptibility to HCMV infections may also manifest through: 1) higher tissue viral loads due to an increased viral replication; 2) a decreased ability to control the virus through modified immune mechanisms; as well as 3) an increased susceptibility to heightened inflammation, change in inflammatory profiles or the lack of controls that limit inflammatory processes. Deciphering the host genetic networks that control CMV infection and disease may impact whether we can identify susceptible patients, how we monitor their CMV infection and potential disease manifestations and when to intervene. In addition, if CMV-vectored vaccines become FDA approved, host genetics could be used to predict genetic susceptibility to vaccine failure. Most mouse studies are performed in highly inbred mice with limited genetic diversity, which hampers the ability to identify traits associated with CMV infection. Human studies or those performed in outbred nonhuman primates are limited by feasibility and resources. Therefore, we intend to use the genetically diverse Collaborative Cross (CC) mouse population to determine the genetic networks involved in MCMV infection and disease. We propose the following aims:

SA1. Determine host gene networks control MCMV *in vivo* replication and tissue distribution.
We will quantify viral loads and tissue distribution during acute and persistent infection times to identify QTL associated with MCMV replication *in vivo*.

SA2. Identify host immunological gene networks that regulate anti-MCMV induced immunity
We will quantify and characterize antiviral adaptive immune responses following MCMV infection and correlate these data with viral loads/distribution (SA1) to QTL that affect antiviral immunity.

SA3. Determine host gene networks involved in CMV-induced inflammation
We will quantify inflammatory cytokine levels as well as lung and spleen immunopathogenesis to identify QTL that predict acute and chronic inflammatory disease following MCMV infection.

Translation of our findings could be applied to identify populations of humans that are susceptible to CMV infection and disease, which would be especially important in newborns and patients undergoing immune suppression.

Determination of the Host Genetic Determinants of Cytomegalovirus Infection and Immunity

Significance: Infection with HCMV is linked to the development of a number of human diseases including vascular disease, pneumonia, fetal neurological syndrome, solid organ and bone marrow transplant rejection, as well as, cancer. Studies have indicated that there exists a genetic predisposition to CMV infection and disease, but the susceptibility or resistance gene networks that govern CMV infection are not known. Mice and MCMV are the most commonly used *in vivo* models of CMV infection and disease. We propose to identify the gene networks associated with *in vivo* MCMV replication, anti-viral immunity and virus-mediated inflammation.

Innovation: The Collaborative Cross (CC) is a genetic reference population of mice specifically designed to support Systems-wide Genetics Studies to identify complex phenotypes governed by diverse gene networks. Our pilot project is highly innovative because we do not yet understand the host genetic networks that control increased host susceptibility to CMV infection and disease. We anticipate to identify gene networks associated with susceptibility to infection, antiviral immunity and inflammation. Our CC analysis of MCMV infection could lead to the identification of additional unique mouse models of CMV infection and disease, a process that would benefit the entire MCMV field. Our results could be applied to the analysis of the herpes simplex viruses and MHV-68, prototypic α and γ herpesviruses. Our genetic data could be used to modify CMV treatments.

Research Team: This proposal represents an ongoing collaboration between Drs. Nathaniel Moorman (UNC) and Daniel Streblow (OHSU). Dr. Moorman provides expertise in CMV biology and using the CC to map and study polymorphic immune response genes. Dr. Streblow has expertise in CMV pathogenesis, immunity and inflammation as well as the development of rat, mouse, and rhesus animal models of CMV. The Team will be assisted by the Center for Systems Immunogenetics CC Animal Core and Genetics Analysis Team (UNC). The team will have monthly videoconferences to share and interpret data and plan experiments, with additional calls as needed to discuss new results or experimental issues.

Overall Study Design: Sets of 10 mice (4-6 weeks of age) from each of the 65 currently available CC lines will be infected with $1x10^5$ pfu of wild type MCMV Smith strain by intraperitoneal injection. The virus establishes local infection that becomes distributed throughout the body by trafficking myeloid lineage cells (e.g. macrophages and dendritic cells). During the acute phase (day 0-7 post infection), MCMV rapidly spreads and infects nearly all tissues. The acute phase is followed by lifelong salivary gland persistence and latency in myeloid lineage precursors. We plan to perform our analysis at two different times post infection. One cohort (n=5) will be harvested at 5 days post infection (dpi) due to the high tissue distribution of virus and activation of host innate immunity. The second cohort (n=5) will be harvested at 14 dpi because this is the beginning of viral persistence and the adaptive immune responses will be fully activated at this time. The dysregulation of inflammation will be assessed for both acute (d5) and persistence (d14) times post infection as we would predict that gene networks modify control of these pathways and this could be associated with disease. All animals will be bled prior to infection to assess baseline levels of antibodies, cytokines, and immune cell profiles. At the time of harvest, the animals will be bled by heart puncture and bone marrow, brain, heart, kidneys, lungs, liver, intestines, spleen, salivary glands, and mesenteric lymph nodes will be collected from each animal. A portion of each tissue will be bead beaten in 1ml of PBS, which will be used to detect infectious virus by plaque assay and DNA isolation for viral load determination by Taqman. This sample can also be used to quantify tissue cytokines levels. A second portion of tissue will be collected in RNA later for future host & viral transcriptomics analyses. A third portion of spleen, lung, and salivary gland tissues will be collected in formalin for histological analyses to assess inflammation. Blood will be separated into plasma and cell fractions. The plasma will be analyzed by: 1) cytokine multiplex assays to quantify cytokine and chemokine levels; 2) virus-specific ELISA to identify antibody binding titers and Ig isotypes; and 3) $PRNT_{50}$ to quantify the presence of neutralizing antibodies against MCMV. A phenotypic analysis of mouse T and B cell markers will be performed on the PBMC fraction to characterize perturbations in T cells profiles. The specific methods for each SA are listed below:

SA1. Determine host gene networks control MCMV *in vivo* replication and tissue distribution

Viral loads and tissue distribution will be determined using plaque assays and vDNA Taqman. The results represent a quantitative amount per tissue and the number of positive tissues per animal can be calculated.

Plaque assay. Tissue homogenates will be serially diluted in culture medium and added to confluent monolayers of NIH3T3 cells in 48-well dishes. After 2 hours incubation, the cells will be overlaid with medium containing carboxymethylcellulose. At 5 dpi, the plates will be fixed with 3% formalin and then stained with methylene blue dye, and washed. Plaques will be visualized by microscopy and titers will be calculated.

vDNA Taqman. Total DNA will be isolated from 100µl of the tissue homogenates using our modified DNAzol method that contains extra wash steps. A total of 1µg of DNA will be analyzed by quantitative real-time PCR (Taqman) utilizing a MCMV-specific primers and probe set targeting the viral polymerase M54 and Taqman reagents from ABI. Samples will be analyzed using an ABI QuantStudio7. A stock of BAC derived DNA containing

the entire MCMV genome will be used as a standard to calculate relative copy numbers of viral genome using ABI software.

SA2. Identify host immunological gene networks that regulate anti-MCMV induced immunity

Binding and neutralizing antibody titers will be calculated per ml of plasma. Flow cytometry results are can be quantitative and the level of activated cells or those expressing specific sub-type markers can be used to identify phenotypes driving QTL.

Analysis of Ab responses: (a) ELISA. Purified MCMV virions or infected cell lysates will be bound onto high binding ELISA plates. Plates will be blocked and then serially diluted heat-inactivated serum (day 0, 5, and 14) will be added. Anti-MCMV Ab isotypes will be determined using anti-mouse IgM, IgG, IgG1, IgG2b, IgG2a/c, or IgG3 secondary Abs. Ab levels will be determined by calculating a variety of metrics, including area under the curve, last positive dilution, or saturation dilutions. **(b) Neutralization assays.** $PRNT_{50}$ analysis will be used to quantify neutralization capacity of the serum samples.

PBMC Immunophenotyping. Two panels of antibodies directed against PBMC cell surface markers and cytokines will help determine the frequency, phenotype, and activation status of immune cells. Panel 1: Innate Immune Cell: CD3, CD8a, CD45, CD11b, CD11c, Ly6G/C, I-A/I-E, NK1.1, CD80, CD83, CD19, and CD138; Panel 2: T cell and B cell: CD3, CD4, CD8, CD44, CD62L, CD25, CD223, GITR, IL-17a and Ki67.

SA3. Determine host gene networks involved in CMV-induced inflammation

We will quantify host cytokines and chemokines associated with inflammation and the generation of specific immune responses. The results from this analysis are typically expressed in pg/ml. Histological evaluation will be performed to assess immune infiltration in the lungs and rearrangement of splenic architecture (these results might be best expressed as a binary factor, although a grading scale could be applied).

Analysis of cytokines: Serum cytokines will be evaluated by multiplex assays for the following mouse cytokines: Eotaxin, G-CSF, GM-CSF, IFN-γ, IL-1α, IL-1β, IL-2, IL-4, IL-5, IL-6, IL-7, IL-9, IL-10, IL-12p70, IL-15, IL-17, IP-10, KC/GRO, LIF, LIX, MCP-1, M-CSF, MIG, MIP-1α, MIP-1β, MIP-2, RANTES, TNF-α, and VEGF.

Histology: Lung, spleen and salivary gland tissues will be analyzed by histology for the presence of inflammation. We will stain tissue sections with H&E for microscopic analysis and grading of tissues using our inflammation scoring system.

Evaluation of Correlations Between Phenotypes. We can take advantage of the diversity in the CC population to test the relationship between different virus replication and immune phenotypes. Therefore, we will perform correlation testing to determine whether the viral loads or tissue distribution correlate with the magnitude of specific immune phenotypes (e.g., specific cytokines), Ab response over time, composition (Ab subtype composition), or neutralizing activity Ab response, the frequency and activation status of immune cells, or markers of inflammation.

QTL Mapping. We will identify QTL for all phenotypes assessed within the CC RI screen by linkage disequilibrium mapping. We will conduct *de novo* QTL mapping of all collected traits within the CC population. Phenotypes at both time points will be mapped as continuous traits (viral loads, tissue distribution, antibody levels, cytokines, etc.) although some of the results (such as histology) may need to be mapped as binary traits. However, we have utilized a histology grading scale in the past and this could be applied to our analysis, which would allow for the QTL to be mapped as continuous traits as well. We will perform genome-wide linkage analysis using an additive haplotype model, with parametric bootstrapping for significance. QTL intervals will be defined as the region associated with a 1.5 LOD drop from the peak LOD score. For QTL that reach genome wide significance ($p<0.05$) we will determine both the effect size (percent of heritable and total variation in the trait explained by the QTL) and the haplotype effects associated with high, low, or intermediate QTL effects using our established methods available through the consortium.

Expected Results: We would predict that we will be able to identify QTL for multiple phenotypes. We would expect that there could be traits that limit virus replication in all or specific subsets of tissues. These effects on replication could be validated using *in vitro* cultures of cells (fibroblasts, SMC, EC, DC, Macs, Epithelial cells) derived from specific mouse strains. We would also predict to identify unique QTL that determine adaptive immunity and inflammatory responses. Depending on the specific phenotype these QTL could also be validated in cells isolated from individual mouse strains from the CC.

**The results from this CC mouse screen will be a springboard for the identification of host factors that determine susceptibility to CMV infection and immunity against the virus. Our results will be *directly compared* to the genetic factors that govern infection susceptibility and disease manifestations that have been identified using the CC mouse resource following challenge with other viruses. Future R01-type funding will be made possible to validate specific QTL involved in MCMV infection and to identify specific genes and mechanisms that drive the phenotype.

References Cited

1. Cicin-Sain L, Brien JD, Uhrlaub JL, Drabig A, Marandu TF, Nikolich-Zugich J. Cytomegalovirus infection impairs immune responses and accentuates T-cell pool changes observed in mice with aging. PLoS Pathog. 2012;8(8):e1002849. Epub 2012/08/24. doi: 10.1371/journal.ppat.1002849. PMCID: PMC3420928.
2. Hansen SG, Marshall EE, Malouli D, Ventura AB, Hughes CM, Ainslie E, et al. A live-attenuated RhCMV/SIV vaccine shows long-term efficacy against heterologous SIV challenge. Sci Transl Med. 2019;11(501). Epub 2019/07/19. doi: 10.1126/scitranslmed.aaw2607. PMCID: PMC6788755.
3. Corbett AJ, Coudert JD, Forbes CA, Scalzo AA. Functional consequences of natural sequence variation of murine cytomegalovirus m157 for Ly49 receptor specificity and NK cell activation. J Immunol. 2011;186(3):1713-22. Epub 2010/12/29. doi: 10.4049/jimmunol.1003308. PubMed PMID: 21187440.
4. Krmpotic A, Bubic I, Polic B, Lucin P, Jonjic S. Pathogenesis of murine cytomegalovirus infection. Microbes Infect. 2003;5(13):1263-77. Epub 2003/11/19. doi: 10.1016/j.micinf.2003.09.007. PubMed PMID: 14623023.
5. Brisse E, Imbrechts M, Put K, Avau A, Mitera T, Berghmans N, et al. Mouse Cytomegalovirus Infection in BALB/c Mice Resembles Virus-Associated Secondary Hemophagocytic Lymphohistiocytosis and Shows a Pathogenesis Distinct from Primary Hemophagocytic Lymphohistiocytosis. J Immunol. 2016; 196(7):3124-34. Epub 2016/02/24. PMID: 26903481.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Streblow, Daniel N., Ph.D.

eRA COMMONS USER NAME (credential, e.g., agency login): streblowd

POSITION TITLE: Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Wisconsin, Madison, WI	BS	05/92	Pharmacology
University of Wisconsin, Madison, WI	PhD	08/97	Viral Pathogenesis
Oregon Health & Science University, Portland, OR	Postdoc	12/01	

A. Personal Statement

My graduate and post-doctoral training have made me well suited to conduct research and mentor graduate students. My graduate training at the University of Wisconsin-Madison was in the field of HIV pathogenesis and involved work at both the molecular and whole animal (rhesus macaque) levels. During my post-doctoral training I shifted my focus to the large DNA virus, human cytomegalovirus (CMV). We developed a model of MCMV-accelerated atherosclerosis and worked to define chemokines and chemokine receptors across CMV species including MCMV, RCMV and HCMV. Since then my lab has developed a number of *in vitro* and *in vivo* models to determine the mechanisms of CMV-accelerated allograft rejection. In addition, we have been involved in the development of CMV vaccine vectors in rhesus-CMV wherein we are identifying viral and host factors involved CMV infection and vaccine efficacy. My laboratory, generated both mouse and rhesus macaque chikungunya virus (CHIKV) infection animal models to identify age-related defects in the response to CHIKV infection. We have utilized these models to characterize CHIKV infection and define the immune responses to the virus infection and efficacy test therapeutic antibodies, small molecule inhibitors, and vaccines against CHIKV. We have developed protocols and reagents for the identification and quantification of virus as well as to characterize both innate and adaptive (T and B cell) responses directed against CHIKV. Utilizing MCMV- and Adenovirus-vectored vaccines we discovered that CD8 T cell specific vaccines against CHIKV modulate inflammation following challenge in mice, which acts to prevent CHIKV-mediated joint disease (Broeckel et al. 2019). We have applied these virological and immunological assays to develop an NHP model of Zika virus infection and pathogenesis and assess anti-Zika virus immunity in adult and neonatal NHP (Hirsch et al. 2017, PLOS Pathogens & Dudley et al. 2018, Nature Medicine). We have found that ZIKV infection during pregnancy causes placental damage and inflammation which affects placental function having important ramifications on fetal development, viral transmission and disease (Hirsch et al. 2018, Nature Communications). Overall, we have utilized animal models and to identify key host and viral factors that are involved viral pathogenesis in order to develop novel therapeutics to prevent and treat viral disease.

B. Positions and Honors

Positions and Employment

1997-2001 Postdoctoral Fellow, Oregon Health Sciences University, Portland, OR
2001-2003 Research Assistant Professor, Department of Molecular Microbiology & Immunology, Oregon Health Sciences University, Portland, OR
2003-2013 Assistant Professor, Vaccine & Gene Therapy Institute, Oregon Health & Science University, Portland, OR
2006-Present Instructor, Oregon Health & Science University, Portland, OR
2007-Current Adjunct Faculty Member, Department of Medical Microbiology and Immunology, OHSU

2007-2019 Faculty Member, Division of Pathobiology & Immunology, ONPRC, OHSU
2013-Present Associate Professor, Vaccine & Gene Therapy Institute, OHSU, Portland, OR
2019-Current Professor, VGTI and Division of Pathobiology and Immunology, ONPRC, OHSU. Joint Appointment

Professional Activities

2007-Present Editorial Board Member, Journal of Virology
2010-Present NIH Peer Review Committee, NIAID, ad hoc reviewer
2010-Present Welcome Trust-Intermediate Level Biology Grants, ad hoc reviewer
2009-2015 PNWRCE National Small Molecule Screening Library for the Biodefense RCEs, review board

Honors

1991-1992 'Hilldale Fellowship' at the University of Wisconsin, Madison, WI
1995-1996 'Cremer Scholar Award,' Dept. of Pathology, University of Wisconsin, Madison, WI
1997-2001 Postdoctoral Fellowship, Oregon Health Sciences University, Portland, OR
2000 Oregon Health & Science University Postdoctoral Paper of the Year

C. Contribution to Science

1. Development of a Non-human Primate Model of Zika Virus Infection and Disease.

Zika virus (ZIKV) is an emerging Flavivirus that spread explosively through the Western hemisphere in 2014-2016. Infection has been associated with dengue-like symptoms, including fever, rash, arthralgia, and conjunctivitis, and also Guillain-Barré syndrome. The most significant finding to date is that ZIKV infection of pregnant women has been associated microcephaly, other developmental abnormalities or death of the fetus. We have developed a rhesus macaque model of ZIKV infection in pregnant and non-pregnant rhesus macaques and characterized clinical features, viral replication, tropism, and immune response. We are currently characterizing the impact of ZIKV on placental biology and the developing fetus in order to identify novel therapeutics and assess the efficacy of antivirals and vaccines directed against the virus.

1. Hirsch AJ, Smith JL, Haese NN, Broeckel RM, Parkins CJ, Kreklywich C, DeFilippis VR, Denton M, Smith PP, Messer WB, Colgin LM, Ducore RM, Grigsby PL, Hennebold JD, Swanson T, Legasse AW, Axthelm MK, MacAllister R, Wiley CA, Nelson JA, and **Streblow DN**. Zika Virus infection of rhesus macaques leads to viral persistence in multiple tissues. *PLoS Pathog*. 2017 Mar 9;13(3):e1006219. PMCID: PMC5344528
2. Zika virus infection in pregnant rhesus macaques causes placental dysfunction and immunopathology. Hirsch AJ, Roberts VHJ, Grigsby PL, Haese N, Schabel MC, Wang X, Lo JO, Liu Z, Kroenke CD, Smith JL, Kelleher M, Broeckel R, Kreklywich CN, Parkins CJ, Denton M, Smith P, DeFilippis V, Messer W, Nelson JA, Hennebold JD, Grafe M, Colgin L, Lewis A, Ducore R, Swanson T, Legasse AW, Axthelm MK, MacAllister R, Moses AV, Morgan TK, Frias AE, **Streblow DN**. *Nature Commun*. 2018 Jan 17;9(1):263. doi: 10.1038/s41467-017-02499-9. PMID: 29343712, PMCID: PMC5772047
3. Miscarriage and stillbirth following maternal Zika virus infection in nonhuman primates. Dudley DM, Van Rompay KK, Coffey LL, Ardeshir A, Keesler RI, Bliss-Moreau E, Grigsby PL, Steinbach RJ, Hirsch AJ, MacAllister RP, Pecoraro HL, Colgin LM, Hodge T, **Streblow DN**, Tardif S, Patterson JL, Tamhankar M, Simmons HA, Mejia A, Friedrich TC, Golos TG, O'Connor DH. *Nature Med*. 2018 Jul 2. PMCID: PMC6082723
4. Risk of Zika Microcephaly Correlates With Features of Maternal Antibodies. Robbiani DF, Olsen PC, Costa F, Haese N, Smith J, Lewis A, Colgin L, Roberts V, Frias A, Kelleher M, Hirsch A, **Streblow DN**, Rice CM, MacDonald MR, de Almeida ARP, Van Rompay KKA, Ko AI, Nussenzweig MC. *Journal of Experimental Medicine*. 2019 Aug 14. PMCID: PMC6781003

2. Development of a Non-human Primate Model of CHIKV Infection and Disease.

CHIKV is a NIAID Category C Biodefense priority mosquito-transmitted Alphavirus that causes a febrile, sometimes-fatal disease that involves incapacitating myalgia and arthralgia that can persist for years. FDA approved anti-CHIKV therapeutics and vaccines are currently not available. Therefore, in order to reduce the impact of this virus and devastating arthralgia that it causes, we must develop new therapies and vaccines to treat persistent CHIKV infections. We have developed a non-human primate model that parallels CHIKV infection and disease in humans; and we are characterizing CHIKV infection and antiviral immunity in this model using both adult and aged Rhesus monkeys. Using our NHP-CHIKV infection model, we have demonstrated that aged animals exhibit higher susceptibility to persistent CHIKV infection as a result of defects in the development of T cell responses directed against the virus. A safe and effective vaccine that can protect

vulnerable populations from CHIKV infection is clearly warranted. In addition, we are currently determining whether there exist differences in joint disease, viral load, distribution and/or immune infiltrates between CHIKV infected adult and aged animals at early times post infection in an effort to lay the foundation for the design of successful vaccine strategies to prevent CHIKV-associated morbidities in vulnerable populations. Lastly, we have tested the efficacy of neutralizing antibody therapy has on pre-existing CHIKV infection of NHP joint tissues. This model will be extremely useful for the pre-clinical efficacy testing of antiviral therapies and vaccines directed against CHIKV. I served as primary or co-investigator for these studies:

1. Chikungunya virus infection results in higher and persistent viral replication in aged rhesus macaques due to defects in anti-viral immunity.Messaoudi I, Vomaske J, Totonchy T, Kreklywich CN, Haberthur K, Springgay L, Brien JD, Diamond MS, Defilippis VR, and **Streblow DN**. PLoS Negl Trop Dis. 2013 Jul 25;7(7):e2343. PMCID: PMC3723534
2. Chikungunya viruses that escape monoclonal antibody therapy are clinically attenuated, stable, and not purified in mosquitoes. P Pal, Hawman DW, Huang YJ, Messaoudi I, Kreklywich C, Denton M, Legasse AW, Smith PP, Johnson S, Axthelm MK, Vanlandingham DL, **Streblow DN**, Higgs S, Morrison TE and Diamond MS. Journal of Virology. 2014 Aug:88(15)8213-26. PMCID: PMC4135940
3. Therapeutic administration of a recombinant human monoclonal antibody reduces the severity of chikungunya virus disease in rhesus macaques. Broeckel R, Fox JM, Haese N, Kreklywich CN, Sukulpovi-Petty S, Legasse A, Smith PP, Denton M, Corvey C, Krishnan S, Colgin LMA, Ducore RM, Lewis AD, Axthelm MK, Mandron M, Cortez P, Rothblatt J, Rao E, Focken I, Carter K, Sapparapau G, Crowe JE Jr, Diamond MS, **Streblow** DN *PLoS NTD*. 2017 Jun 19;11(6):e0005637. PMCID: PMC5491320

3. Characterization of the Role of Cytomegalovirus in the Development of Vascular Disease and Chronic Allograft Rejection.

We are studying the role of human cytomegalovirus (HCMV) in the development of chronic diseases including vascular disease and chronic rejection (CR) of solid organ transplants. The precise role of CMV in these diseases is still uncharacterized, and as such my lab has been studying the mechanisms of HCMV-accelerated vascular disease through: 1) identification of viral and cellular genes expressed during these diseases and determining their function using *in vitro* and *in vivo* models of CMV-accelerated vascular disease; 2) determination of the immunological mechanisms of viral acceleration of chronic allograft rejection from latently infected donors, which is the most common cause of HCMV-associated disease in transplant patients; 3) determination of the function of CMV-encoded chemokines and chemokine receptors; and 4) generation of vaccine strategies to prevent CMV reactivation and disease in transplant patients.

1. Cytomegalovirus Latency Promotes Cardiac Lymphoid Neogenesis and Accelerated Allograft Rejection in CMV Naïve Recipients. Orloff SL, Hwee YK, Kreklywich CN, Andoh TF, Hart E, Smith P, Messaoudi I and **Streblow DN**. Amer Journal of Transpl. 2011 Jan;11(1):45-55. PMCID: PMC3454525
2. Rat cytomegalovirus vaccine prevents acclerated chronic rejection in CMV-naïve recipients of infected donor allograft hearts. **DN Streblow**, Hwee YK, Kreklywich CN, Ando T, Denton M, Smith P, Hart E, Broekel R, Pallett C, Rogers K, Streblow AD, Chuop M, Perry A, Slifka M, Messaoudi I, and Orloff SL. *Amer J Transplant*. 2015 July:15(7):1805-16. PMCID: PMC5006870
3. Rat cytomegalovirus gene expression in cardiac allograft recipients is tissue specific and does not parallel the profiles detected *in vitro*. **DN Streblow**, KW van Cleef, CN Kreklywich, C Meyer, P Smith, V Defilippis, F Grey, K Fruh, R Searles, C Bruggeman, C Vink, JA Nelson, SL Orloff. 2007 *Journal of Virology*. Apr;81(8):3816-26. PMCID: PMC1866122.
4. Cytomegalovirus miRNA expression is tissue specific and associated with persistence. Meyer C, Grey F, Kreklywich CN, Andoh TF, Tirabassi RS, Orloff SL and **Streblow DN**. *Journal of Virology*. 2011 Jan;85(1):378-89. PMCID: PMC3014154

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/daniel.streblow.1/bibliography/41163876/public/?sort=date&direction=ascending

D. Research Support

Ongoing Research Support

5 R01 AI116633-03 Streblow (PI) 03/01/2016 – 02/28/2021
NIH/NIAID
Characterizing the Role of CMV Latency in Solid Organ Transplant Rejection
The main goal of this project is to determine the mechanisms of cytomegalovirus-mediated solid organ transplant rejection. Role: PI

1 U19 AI142759-01 Whitley (PI) 03/01/2019 – 02/29/2024
NIH/NIAID
Antiviral Drug Discovery and Development Center: Project 2: Novel Therapeutics for Emerging Alphavirus
The major goal of this project is to develop novel small molecule therapeutics targeting emerging Alphaviruses
Role: Project 2 Leader

Global Health Proposal OPP1107409 Picker (PI) 07/28/2014 – 08/31/2020
Bill & Melinda Gates Foundation
Development of Attenuated CMV Vectors for an HIV/AIDS Vaccine
The overall goal of this project is the development of an HCMV vector-based HIV/AIDS vaccine (composed of one or more HIV insert-expressing HCMV vectors) that is optimized for safety, efficacy and manufacturability.
Role: Project Leader, Activity 2.3

1 U19 AI128741-03 (Picker) 03/02/2017 – 02/28/2022
NIH/NIAID
Development of Immunogenicity- and Efficacy-Optimized CMV Vectors for an HIV/AIDS Vaccine: Project 4: Optimization of CMV Vector CD8+ T Cell Response Programming by Modification of CMV-Encoded Molecular Mechanisms That Interfere with Unconventional CD8+ T Cell Response Priming
In Project 4 we first seek to identify the specific motifs in the UL128 and UL130 proteins which block MHC-E-restricted CD8+ T cell priming with the goal of mutating these regions to abrogate their MHC-E-response inhibition while retaining PRC function. Utilizing a deletion strategy we will ascertain whether any non-essential HCMV genes have this activity. Finally, utilizing the data from Projects 2-4, Project 4 will construct the 2nd generation "response and safety" optimized HCMV/HIV vector for manufacture and clinical testing in Project 5.
Role: PI, Project 4

1 P01 AI127335-02 (Nelson/Yurochko) 08/15/2017 – 07/31/2022
NIH/NIAID
Human Cytomegalovirus Dysregulation of Host Hematopoietic Progenitor Cell Signaling Pathways to Modulate Latency, Reactivation and Hematopoiesis during Transplantation: Project 3: HCMV US28 regulation of host cell signaling in viral latency and hematopoiesis
In this project we will examine UL7 signaling in CD34+ HPCs and identify the cellular pathways necessary for viral reactivation and hematopoiesis in the context of infection. We will also determine whether these UL7 pathways cross-talk with pathways modulated by UL133/8 (Project 1), HCMV miRNAs (Project 2), US28 (Project 3) and wild-type HCMV infection (Project 5).
Role: Project Leader, Project 3

1 R01 AI143660-02 (DeFilippis) 01/23/2019 – 12/31/2023
NIH/NIAID
Mechanistic Exploration of cGAS-STING-Mediated Vaccine Enhancement
The major goals of this project are to characterize the molecular, cellular, and immunological bases of adaptive immune responses augmented by the innate protein STING.
Role: Co-Investigator

Completed Research Support
Global Health Proposal OPP1108533 Picker (PI) 09/22/2014 – 09/30/2017
Bill & Melinda Gates Foundation
MHC II- and MHC E-restricted CD8+ T Cells and Control of HIV
The goal of this project is to provide fundamental research on a new type of vaccine-elicited CD8+ T cell immunity with the potential to control and clear HIV. Role: Project Manager; Outcome 8 Activity 4.3

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Moorman, Nathaniel J.

eRA COMMONS USER NAME (credential, e.g., agency login): nmoorman

POSITION TITLE: Associate Professor of Microbiology & Immunology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Illinois, Urbana-Champaign	B.S.	1991-1995	Microbiology
Washington University, St. Louis, MO	Ph.D.	1998-2004	Molecular Virology
Princeton University	Postdoctoral	2004-2010	Molecular Virology

A. Personal Statement

My research is focused on understanding the complex interaction between pathogens and their hosts at the molecular level. My research expertise lies in the broad area of viral pathogenesis. Throughout my career, I have studied how viruses manipulate host cell biology to maximize their replication. My work uses a combination of cell biology, biochemistry and viral genetics to reveal novel interactions between viral proteins and the host, and how these interactions contribute to viral disease. In addition I have extensive experience studying viral determinants of herpesvirus pathogenesis in mice. Together these experiences provide me with the necessary expertise to study mechanisms driving herpesvirus disease in the complex genetic backgrounds of Collaborative Cross mice.

My prior research experiences have also provided me with extensive experience with collaborative studies, such as the multi-group effort proposed herein. An important aspect of collaborative science is the ability of the investigators to work together effectively. Throughout my career I have been a strong proponent of integrating new techniques and approaches into my research, as demonstrated by my track record of successful collaborative science. As a postdoc I worked closely with two other fellows as part of a multi-disciplinary program project grant, providing me with the ability to communicate effectively and approach problems from unique perspectives. My lab currently has funding as part of a U19 grant that involves 6 investigators from 3 different institutions, an additional funded multi-PI R01 proposal, and several multi-PI R21 awards. These experiences have taught me to effectively shared resources toward common group goals. Thus my current and previous experiences with collaborative studies and my firm commitment to collaborative science provide me with the needed experience to work productively in multi-group projects.

B. Positions and Honors

Positions and Employment

1995-1998 Lead Research Technician, lab of Dr. David Leib, Washington University
1998-2004 Graduate Student, Drs. Sam Speck & Skip Virgin, co-mentors, Washington University

2004-2010 Postdoctoral Fellow, lab of Dr. Tom Shenk, Princeton University
2010-2017 Assistant Professor, University of North Carolina at Chapel Hill
2017-present Associate Professor, University of North Carolina at Chapel Hill

Other Experience and Professional Memberships

2006-2009 American Cancer Society Postdoctoral Fellow
2009 American Cancer Society Postdoctoral Conference Organizer
2010-present Member, American Society for Microbiology
2014 Organizing Committee, NIH workshop "Roseoloviruses: Clinical Impact, Interventions & Research Needs"
2015-17 MRC Research grant reviewer, ad hoc
2017-18 NIH Peer Review Committee; ZRG1 IDM S (02), ad hoc
2017-present Editorial Board, Journal of Virology

C. Contribution to Science

1. Understanding manipulation of the AMPK/mTOR signaling during HCMV infection. Viruses manipulate host signaling pathways to facilitate their replication. I have used multiple approaches to decipher how viruses manipulate the AMPK and mTORC1 kinases to promote their replication. Using a proteomics approach, I found that HCMV pUL38 maintains mTORC1 signaling by inhibiting the tumor suppressor TSC2, an mTORC1 antagonist (a). Building on this work I found that potent and specific mTOR inhibitors inhibit the replication of representative α, β and γ-herpesviruses (b). We found that elevated mTORC1 signaling is necessary to promote the synthesis of fatty acids needed for infectious virion production (c). However we also found that virus infection activates AMPK, which inhibits mTORC1 by activating TSC2, and that AMPK activity is also required for virus replication (d). Together this work uncovers a novel strategy used by HCMV to manipulate the host AMPK/mTOR pathway to its advantage. While active AMPK typically inhibits mTORC1, HCMV uses the UL38 protein to "short circuit" this pathway, allowing for simultaneous AMPK and mTORC1 activity. Dysregulation of the AMPK/mTORC1 signaling axis allows the virus to harness the increased metabolites arising from both AMPK and mTORC1 activation, while also maintaining mTORC1-dependent expression of host proteins needed for virus replication.

    a. **Moorman NJ**, Cristea IM, Terhune SS, Rout MP, Chait BT, Shenk T. (2008) Human cytomegalovirus protein UL38 inhibits host cell stress responses by antagonizing the tuberous sclerosis protein complex. *Cell Host Microbe*. 3(4):253-262. PMC2759192.
    b. **Moorman NJ**, Shenk T. (2010) Rapamycin-resistant mTORC1 kinase activity is required for herpesvirus replication. *J Virol*. 84(10):5260-5269. PMC2863801.
    c. Spencer CM, Schafer XL, **Moorman NJ**, Munger J. (2011) Human cytomegalovirus induces the activity and expression of acetyl-coenzyme A carboxylase, a fatty acid biosynthetic enzyme whose inhibition attenuates viral replication. *J Virol*. 85(12):5814-5824. PMC3126312.
    d. McArdle J, **Moorman NJ**, Munger J. (2012) HCMV targets the metabolic stress response through activation of AMPK whose activity is important for viral replication. *PLoS Pathog*. 8(1):e1002502. PMC3266935.

2. Defining HCMV strategies to regulate mRNA translation. Like host mRNAs, all viral mRNAs must associate with host ribosomes for their translation, as no virus encodes its own ribosome. As a result all viruses must co-opt the host translation machinery for their replication. My group has developed a number of approaches to determine how viruses regulate the translation of host and viral mRNAs during infection. We recently demonstrated that HCMV stimulates the translation of host pro-survival factors to prolong the survival of HCMV-infected monocytes (a). By measuring the association of host and viral mRNAs with polysomes, we found that inhibiting or disrupting the host eIF4F translation initiation complex limits the translation of host mRNAs without impacting the translation of HCMV mRNAs (b). Thus host and viral mRNAs differ in their requirement for key translation initiation factors. To define host or viral factors that might facilitate ribosome recruitment to viral mRNAs, we used a proteomic analysis to identify proteins that bind the mRNA cap in HCMV-infected cells. We identified a novel role for the HCMV TRS1 protein as an mRNA cap-binding protein that was independent of the eIF4F complex, and that TRS1 expression alone was sufficient to increase the rate of protein synthesis

(c). The TRS1 protein also regulates the antiviral kinase PKR, which potently limits protein synthesis when activated by viral RNA ligands. We identified TRS1 binding to PKR as a critical step in maintaining protein synthesis during HCMV infection (d). However we also found that TRS1 increased protein synthesis in cells lacking PKR. Thus our work uncovers a new role for an HCMV protein in the regulation of protein synthesis during infection. The TRS1 protein both suppresses the host antiviral response, and also stimulating protein synthesis in a PKR-independent manner.

a. Peppenelli, M., Arend, K., Cojohari, O., **Moorman, NJ**., Chan, G. Human cytomegalovirus stimulates the synthesis of select Akt-dependent antiapoptotic proteins during viral entry to promote survival of infected monocytes. *J Virol*. 2016 Jan 6. pii: JVI.02879-15 PMID:26739047
b. Lenarcic E, Ziehr B, De Leon G, Mitchell D, **Moorman NJ**. (2014) Differential role for host translation factors in host and viral protein synthesis during HCMV infection. *J Virol.* 88(3):1473-1483. PMC3911597.
c. Ziehr, B., Lenarcic, E., Cecil, C. Garcia, B., Shenk, T., **Moorman, NJ**. HCMV pTRS1 is a novel viral translation factor. *Proteomics*. 2015 Apr 20. PMID 25894605
d. Ziehr, B., Vincent, HA**., Moorman, NJ**. Human cytomegalovirus pTRS1 antagonizes PKR to promote virus replication. *J Virol*. 2016 Jan 27. pii: JVI.02714-15 PMID:26819306

3. Development of proteomic approaches to identify critical virus:host interactions during viral infection. The identification of protein binding partners for viral proteins is often used to identify new functions for viral proteins. Until recently this strategy relied on genetic approaches such as yeast two hybrid assays, or multi-step biochemical purification of viral proteins and their binding partners. While informative, these approaches limited in their usefulness for identifying interactions in the context of HCMV infection. In collaboration with two other postdoctoral fellows, I helped devise an improved strategy for the rapid proteomic identification of binding partners for HCMV proteins in the context of viral infection. We developed a system to epitope-tag specific viral proteins in their native location in the viral genome under the control of their normal promoter, resulting in endogenous levels of expression. The tagged viral protein and its binding partners captured by immunoaffinity purification, and identified by mass spectrometry. We systematized the mutagenesis, virus production and mass spectrometry steps to generate a collection of over 100 viral mutants. Using this collection I helped define novel activities for multiple HCMV proteins including interactions that: regulate the innate immune response to infection (a), novel interactions between a viral protein and a host histone deacteylase complex that facilitates transcription of viral genes (b) and systematically defined interactions driving the assembly and egress of HCMV particles (c). Most relevant for this application, we also recently developed methods to identify host and viral proteins that associate with the mRNA cap (d) and mRNAs in general (e) in virally infected cells. Together these approaches provide a significant advance in our ability to define virus:host interactions that regulate virus replication.

a. Terhune SS*, **Moorman NJ***, Cristea IM*, Savaryn JP, Cuevas-Bennett C, Rout MP, Chait BT, Shenk T. (2010) Human cytomegalovirus UL29/28 protein interacts with components of the NuRD complex which promote accumulation of immediate-early RNA. *PLoS Pathog.* 6(6):e1000965. PMC2891856.
b. **Moorman NJ**, Sharon-Friling R, Shenk T, Cristea I. (2010) A targeted spatial-temporal proteomic approach implicates multiple cellular trafficking pathways in human cytomegalovirus virion maturation. *Mol Cell Proteomics*. 9(5):851-860. PMC2871419.
c. Ziehr, B., Lenarcic, E., Cecil, C. Garcia, B., Shenk, T., **Moorman, NJ**. Human cytomegalovirus TRS1 protein associates with the 7-methylguanosine mRNA cap and facilitates translation. *Proteomics*. 2015 Apr 20. PMID 25894605
d. Lenarcic, E. Ziehr, B., **Moorman, NJ**. An unbiased proteomics approach to identify viral RNA binding proteins. *Virology*. 2015 Mar 9; 481:13-23. PMID 25765003

Complete List of Published Work in MyBibliography:

http://www.ncbi.nlm.nih.gov/sites/myncbi/nathaniel.moorman.1/bibliography/46829675/public/?sort=date&direction=ascending.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

R01AI103311-06 (PI: Moorman) 07/01/18-06/30/23
NIH/NIAID
The role of host and viral translation factors during HCMV infection
In this proposal we explore the role of host and human cytomegalovirus protein in the control of viral mRNA translation.

R01 AI143191-01 (MPI:Goodrum/Moorman/Kamil) 09/24/18 – 08/31/23
NIH/NIAID
Molecular Switch Regulating Human Cytomegalovirus Replicative & Latent States. This proposal explores novel transcriptional units controlling the reactivation of latent HCMV infections.

R21 AI138056-01 (MPI: Moorman/Heise) 06/01/18-05/31/20
NIH/NIAID
Defining Functional RNA Structures in an Arthritic Alphavirus Genome
In this proposal we use structure-function studies to determine how secondary RNA structures in the Chikungunya virus genome regulate virus replication in human and mosquito cells.

R21 AI137887-01 (MPI:Moorman/Heise) 02/05/18-01/31/20
NIH/NIAID
Molecular Characterization of Functional RNA Structures in the ZIKV genome
This proposal will identify novel RNA structures in the ZIKV genome, and determine how they contribute to virus pathogenesis.

R21 AI144548-01 (MPI: Wolfgang/Moorman) 04/01/19- 03/31/21
NIH/NIAID
Pseudomonas avoids immune clearance by dysregulating host AMPK/mTOR signaling
This proposal determines how small molecules secreted by Pseudomonas affect host immune cell signaling and function.

U19 AI107810-05 (PI: Baric; co-investigator Moorman) 06/01/2013-05/31/19NCE
NIH/NIAID
Characterization of Novel Genes Encoded by RNA and DNA Viruses
In this supplement we will identify known and putative viral genes that regulate protein synthesis and mTOR signaling. Role: Co-Investigator

Completed

R21 AI123811 (MPI: Moorman/Prins) 02/01/16-01/3119 NCE
NIH/NIAID
Hybrid Sequencing to Define the Full-Length Transcriptome of Double Stranded DNA Viruses
This proposal seeks to develop a hybrid sequencing approach to unravel the complex transcriptomes of DNA viruses.

R01AI103311-05 (PI: Moorman) 12/01/12-04/05/18
NIH/NIAID
The role of host and viral translation factors during HCMV infection
In this proposal we explore the role of host and human cytomegalovirus protein in the control of viral mRNA translation.

RESEARCH & RELATED BUDGET - Budget Period 1

OMB Number: 4040-0001
Expiration Date: 10/31/2019

ORGANIZATIONAL DUNS: 0969975150000 **Enter name of Organization:** Oregon Health & Science University

Budget Type: ☐ Project ☒ Subaward/Consortium **Budget Period: 1** **Start Date:** 09/01/2020 **End Date:** 08/31/2021

A. Senior/Key Person

Prefix	First	Middle	Last	Suffix	Base Salary ($)	Months Cal.	Months Acad.	Months Sum.	Requested Salary ($)	Fringe Benefits ($)	Funds Requested ($)
	Daniel		Streblow	PhD	197,300.00	0.12			1,973.00	691.00	2,664.00

Project Role: PD/PI

Additional Senior Key Persons: Add Attachment | Delete Attachment | View Attachment

Total Funds requested for all Senior Key Persons in the attached file

Total Senior/Key Person 2,664.00

B. Other Personnel

Number of Personnel	Project Role	Months Cal.	Months Acad.	Months Sum.	Requested Salary ($)	Fringe Benefits ($)	Funds Requested ($)
1	Post Doctoral Associates	1.20			5,626.00	1,575.00	7,201.00
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						

1 **Total Number Other Personnel**

Total Other Personnel 7,201.00

Total Salary, Wages and Fringe Benefits (A+B) 9,865.00

C. Equipment Description

List items and dollar amount for each item exceeding $5,000

Equipment item	Funds Requested ($)

Additional Equipment: Add Attachment | Delete Attachment | View Attachment

Total funds requested for all equipment listed in the attached file

Total Equipment

D. Travel

	Funds Requested ($)
1. Domestic Travel Costs (Incl. Canada, Mexico and U.S. Possessions)	
2. Foreign Travel Costs	
Total Travel Cost	

E. Participant/Trainee Support Costs

	Funds Requested ($)
1. Tuition/Fees/Health Insurance	
2. Stipends	
3. Travel	
4. Subsistence	
5. Other	
Number of Participants/Trainees — **Total Participant/Trainee Support Costs**	

F. Other Direct Costs

		Funds Requested ($)
1.	Materials and Supplies	10,830.00
2.	Publication Costs	
3.	Consultant Services	
4.	ADP/Computer Services	
5.	Subawards/Consortium/Contractual Costs	19,293.00
6.	Equipment or Facility Rental/User Fees	
7.	Alterations and Renovations	
8.	Fee For Service: UNC Genomic Core Mice Screening	34,500.00
9.		
10.		
	Total Other Direct Costs	64,623.00

G. Direct Costs

	Funds Requested ($)
Total Direct Costs (A thru F)	74,488.00

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)
MTDC - OHSU	54.00	55,195.00	29,805.00
MTDC - UNC	55.50	19,293.00	10,707.00

Total Indirect Costs	40,512.00

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number)

DHHS, Arif M. Karim, (415)-437-7820 - OHSU
DHHS, Darryl W. Mayes, (301) 492-4855- UNC

I. Total Direct and Indirect Costs

	Funds Requested ($)
Total Direct and Indirect Institutional Costs (G + H)	115,000.00

J. Fee

Funds Requested ($)

K. Total Costs and Fee

	Funds Requested ($)
Total Costs and Fee (I + J)	115,000.00

L. Budget Justification

(Only attach one file.) Add Attachment | Delete Attachment | View Attachment

RESEARCH & RELATED BUDGET - Cumulative Budget

		Totals ($)
Section A, Senior/Key Person		2,664.00
Section B, Other Personnel		7,201.00
Total Number Other Personnel	1	
Total Salary, Wages and Fringe Benefits (A+B)		9,865.00
Section C, Equipment		
Section D, Travel		
1. Domestic		
2. Foreign		
Section E, Participant/Trainee Support Costs		
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other		
6. Number of Participants/Trainees		
Section F, Other Direct Costs		64,623.00
1. Materials and Supplies	10,830.00	
2. Publication Costs		
3. Consultant Services		
4. ADP/Computer Services		
5. Subawards/Consortium/Contractual Costs	19,293.00	
6. Equipment or Facility Rental/User Fees		
7. Alterations and Renovations		
8. Other 1	34,500.00	
9. Other 2		
10. Other 3		
Section G, Direct Costs (A thru F)		74,488.00
Section H, Indirect Costs		40,512.00
Section I, Total Direct and Indirect Costs (G + H)		115,000.00
Section J, Fee		
Section K, Total Costs and Fee (I + J)		115,000.00

BUDGET JUSTIFICATION – OREGON HEALTH & SCIENCE UNIVERSITY / UNC

KEY PERSONNEL:
Daniel N. Streblow, Ph.D., PI, (0.12 calendar months). Dr. Streblow is a Professor in the Vaccine and Gene Therapy Institute (VGTI) at OHSU, with an adjunct position in the Division of Pathobiology and Immunology at the ONPRC. Dr. Streblow will be the PI and provide the oversight and organizational structure to ensure clear lines of authority and oversight of research activities, including those of all key personnel and technical staff. Dr. Streblow will have responsibility for planning and maintaining communication with UNC. Dr. Streblow will be responsible for helping to ensure compliance with all federal and NIH regulations as well as the safety and security of data, materials, facilities and resources of the program. Dr. Streblow has extensive experience with *in vitro* and *in vivo* animal models of CMV infection and disease. Dr. Streblow will be responsible for data analysis and preparation of reports and publications derived from the project.

NON-KEY PERSONNEL:
Nicole Haese, Ph.D., Postdoctoral Scholar (1.2 calendar months). Dr. Haese is a postdoctoral scientist in the Streblow lab. Dr. Haese was trained in viral pathogenesis and immunology, and she has a strong background in immunology. She will devote much of her time to characterizing the immune responses in the infected animals. Dr. Haese's previous work experience makes her an important addition to the group for completion of the proposed experiments.

OTHER COSTS (Fee for service)
The UNC Genomics Core will perform mouse experiments as a fee for service. A total of $34,500 direct costs is budgeted to perform the screen in 65 currently available CC mouse strains.

MATERIALS AND SUPPLIES
Tissue Culture Supplies: These will be required for all cell growth and maintenance as well as virus growth and titration and isolation from tissues. This includes cell culture growth media, animal serum, PBS, trypsin, sucrose, sorbitol, disposable sterilizing filters, antibiotics, and syringes. This also includes Disposable plasticware required for cell and virus culture, virus titration and virus isolation, and molecular biological work. ($830)

Antibodies: Antibodies will be required for numerous assays including flow cytometry to monitor changes in host lymphocyte phenotype and activation status. ($2,000)

Luminex Cytokine Assays: For quantitative analysis of cytokine and chemokine levels, we are requesting $7,000 for the purchase of Luminex assay kits.

Flow Cytometry Core Services: T cell and B cell and innate/adaptive immune cell phenotypic characterization and activation will be assessed using flow cytometry in the VGTI core facilities, which employs a fee-for-service operational model. ($1,000)

BUDGET JUSTIFICATION – UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL
KEY PERSONNEL:
Nathaniel Moorman, PhD, Principal Investigator, (2% effort, 0.24 cal. months). Dr. Moorman will design and lead all aspects of the proposed studies. He will supervise Mr. Sanders during the completion of the proposed work. Dr. Moorman will supervise all aspects of the proposed studies, including analyzing the data, designing experiments, and overseeing the publication of manuscripts describing the results.

NON-KEY PERSONNEL:
Wes Sander, M.S., Research Technician, (10% effort, 1.2 cal. months). Mr. Sanders will perform experiments to measure virus replication in tissues of Collaborative Cross mice under the direct supervision of Dr. Moorman.

SUPPLIES:
Tissue culture: ($8,847) These funds will be used to purchase plasticware, consumables, growth media and supplements needed to culture cells and virus, and measure virus load in tissues of Collaborative Cross mice.

SCOPE OF WORK

Cytomegalovirus infections are lifelong and associated with a number of diseases. However, the impact of host genetics on viral replication, host immunity and inflammation are relatively unknown. Mouse cytomegalovirus is an important animal model of human infections and has been used to identify a number of key features of host immunity following CMV infection and immune evasion. There is a pressing need to identify the host gene networks that are involved in CMV infection and disease. However, the reliance on the limited genetic diversity present in inbred mouse strains has restricted a genome-wide identification of these disease gene networks. In collaboration with Dr. Nathaniel Moorman (UNC), we will utilize the genetically diverse mouse collaborative cross line to identify host genes involved in MCMV replication and immunity. For this pilot project proposal, we will characterize antibody and T cell immunity and our collaborator at UNC will quantify viral loads and tissue distribution following MCMV infection of the CC. Our labs have considerable experience with all facets of the proposed studies, including MCMV infections in mice, processing of samples for viral load and dissemination, and characterization of the host innate and adaptive immune responses to virus challenge.

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

LEAVE BLANK—FOR PHS USE ONLY.		
Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
Determination of the Host Genetic Determinants of Cytomegalovirus Infection and Immunity

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☒ YES
(If "Yes," state number and title)
Number: Title: Pilot Project: CSBIO

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Daniel Streblow	PhD	

3c. POSITION TITLE
Professor

3d. MAILING ADDRESS *(Street, city, state, zip code)*
505 NW 185th Ave. Mail Code: VGTI
Beaverton, Oregon 97006-3448

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Vaccine and Gene Therapy Institute

3f. MAJOR SUBDIVISION

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL 503-418-2772 FAX: 503-481-2719

E-MAIL ADDRESS: streblowd@ohsu.edu

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☐ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☐ No ☐ Yes	☐ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No. A3304-01

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
9/1/2020	8/31/2021	74,488	115,000	74,488	115,000

9. APPLICANT ORGANIZATION
Name: Oregon Health & Science University
Address: 3181 SW Sam Jackson Park Road
Portland, Oregon 97239-3098

10. TYPE OF ORGANIZATION
Public: → ☐ Federal ☒ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
1931176109A1
DUNS NO. 09-699-7515 Cong. District OR-001

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name: Elizabeth Salvatierra
Title: Grants & Contracts Administrator
Address: 3181 SW Sam Jackson Park Road L106OPAM
Portland, Oregon 97239-3098
Tel: 503-494-0627 FAX: 503-494-
E-Mail: salvatie@ohsu.edu

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name: Kellie Guentert
Title: Director
Address: 3181 SW Sam Jackson Park Road L106OPAM
Portland, Oregon 97239-3098
Tel: 503-494-7784 FAX: 503-494-7787
E-Mail: orserv@ohsu.edu

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.	SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)*	DATE

Department of Health and Human Services
Public Health Services

Grant Application

Do not exceed character length restrictions indicated.

LEAVE BLANK—FOR PHS USE ONLY.		
Type	Activity	Number
Review Group		Formerly
Council/Board (Month, Year)		Date Received

1. TITLE OF PROJECT *(Do not exceed 81 characters, including spaces and punctuation.)*
Genetic Regulation of Host Proteomein Response to Influenza A in Collaborative Cross Mice

2. RESPONSE TO SPECIFIC REQUEST FOR APPLICATIONS OR PROGRAM ANNOUNCEMENT OR SOLICITATION ☐ NO ☐ YES
(If "Yes," state number and title)
Number: Title:

3. PROGRAM DIRECTOR/PRINCIPAL INVESTIGATOR

3a. NAME (Last, first, middle)	3b. DEGREE(S)	3h. eRA Commons User Name
Wang, Xusheng	Ph.D.	XWANG39

3c. POSITION TITLE
Assistant Professor

3d. MAILING ADDRESS *(Street, city, state, zip code)*
10 Cornell St. 9019, Grand Forks, ND 58202-9019

3e. DEPARTMENT, SERVICE, LABORATORY, OR EQUIVALENT
Biology

3f. MAJOR SUBDIVISION
Bioinformatics

3g. TELEPHONE AND FAX *(Area code, number and extension)*
TEL: 7017774673 FAX: 7017772623

E-MAIL ADDRESS:
xusheng.wang@und.edu

4. HUMAN SUBJECTS RESEARCH	4a. Research Exempt	If "Yes," Exemption No.
☒ No ☐ Yes	☒ No ☐ Yes	

4b. Federal-Wide Assurance No.	4c. Clinical Trial	4d. NIH-defined Phase III Clinical Trial
	☒ No ☐ Yes	☒ No ☐ Yes

5. VERTEBRATE ANIMALS ☐ No ☒ Yes — 5a. Animal Welfare Assurance No. D16-00584 (A4091-01) from IU

6. DATES OF PROPOSED PERIOD OF SUPPORT *(month, day, year—MM/DD/YY)*		7. COSTS REQUESTED FOR INITIAL BUDGET PERIOD		8. COSTS REQUESTED FOR PROPOSED PERIOD OF SUPPORT	
From	Through	7a. Direct Costs ($)	7b. Total Costs ($)	8a. Direct Costs ($)	8b. Total Costs ($)
9/1/2020	8/31/21	$81,122	$114,382	$81,122	$114,382

9. APPLICANT ORGANIZATION
Name UNIVERSITY OF NORTH DAKOTA
Address 264 Centennial Dr, Stop 7306
GRAND FORKS, North Dakota, 582027306

10. TYPE OF ORGANIZATION
Public: → ☐ Federal ☒ State ☐ Local
Private: → ☐ Private Nonprofit
For-profit: → ☐ General ☐ Small Business
☐ Woman-owned ☐ Socially and Economically Disadvantaged

11. ENTITY IDENTIFICATION NUMBER
456002491
DUNS NO. 1022807810000 Cong. District ND-001

12. ADMINISTRATIVE OFFICIAL TO BE NOTIFIED IF AWARD IS MADE
Name Jamie Mitzel
Title Sr. Pre-Award officer
Address 4201 James Ray Drive, Stop 8367
GRAND FORKS, North Dakota, 582027306
Tel: 701-777-4146 FAX:
E-Mail: jamie.mitzel@UND.edu

13. OFFICIAL SIGNING FOR APPLICANT ORGANIZATION
Name Jamie Mitzel
Title Sr. Pre-Award officer
Address 4201 James Ray Drive, Stop 8367
GRAND FORKS, North Dakota, 582027306
Tel: 701-777-4146 FAX:
E-Mail: jamie.mitzel@UND.edu

14. APPLICANT ORGANIZATION CERTIFICATION AND ACCEPTANCE: I certify that the statements herein are true, complete and accurate to the best of my knowledge, and accept the obligation to comply with Public Health Services terms and conditions if a grant is awarded as a result of this application. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties.

SIGNATURE OF OFFICIAL NAMED IN 13. *(In ink. "Per" signature not acceptable.)* DATE

Title

Genetic Regulation of Host Proteome in Response to Influenza A in Collaborative Cross (CC) Mice

Specific Aims

The overarching goal of the proposal is to understand genetic regulation of host protein expression in response to influenza A in collaborative cross (CC) mice. The CC mice for genetic regulation studies are greatly enhanced by the availability of complete genome sequences and massive transcriptomic profiling. A comprehensive dissection of the regulation of molecular composition (e.g. DNAs, RNAs, proteins, and metabolites) in CC mice is critical for understanding molecular mechanisms underlying complex diseases (e.g., infectious diseases). Genetic regulation at transcript level from 44 influenza-infected pre-CC lines has identified putative regulatory regions potentially controlling their expression in response to influenza A infection. However, transcripts are usually not a direct proxy for proteins and genetic regulation at the protein level has not yet been defined in response to influenza A infection in CC mice.

Recently, liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) has proven to be a powerful technology for large-scale identification of peptides and quantification of protein abundance. Both PI groups (i.e., Wang and Yang) have profiled proteomics data for immune systems (e.g., molecular and metabolic regulation of T cell activation) and human diseases (e.g., Alzheimer's disease). The Wang Lab has been working on the development of computational algorithms and tools for MS-based proteomics, and on the application of systems genetics approaches to study genetic regulation of expression at transcript and protein levels. The Yang Lab focuses on understanding fundamental mechanisms involved in the regulation of T cell metabolism and function in autoimmune and infectious diseases. In this proposal, we will combine our expertise in proteomics, systems genetics, and immunology, to systematically understand the genetic architecture of the regulation of protein expression in host response to influenza A in CC mice. Two specific aims are:

Aim 1. Generate and analyze lung T cell proteome of 69 CC lines after influenza A infection using 16-plex tandem mass tag (TMT) LC/LC-MS/MS.

Aim 1a. We will first generate CC lines with influenza A infection. Female mice (8−16 weeks of age) from the 69 CC lines will be obtained from the UNC CC consortium. At 14 days post infection, mice will be euthanized, and the lung for subsequent proteome profiling. **Aim 1b.** We will profile deep lung proteome of 69 CC lines after influenza A infection using 16-plex TMT LC-MS/MS technology. In this pilot proposal, we will use 69 CC lines whose genome sequences are available. **Aim 1c.** We will identify peptides and quantify proteins using JUMP, a comprehensive proteomic analysis pipeline developed by the PI. Our goal is to identify and quantify ~10,000 proteins at false discovery rate (FDR) of 1% from all 69 CC lines. The generated raw MS data will be submitted to the PRIDE database (https://www.ebi.ac.uk/pride/), and protein quantification and mapping results will be released to the research community via the UNC Systems Genetics portal (https://csbio.unc.edu/CCstatus/index.py).

Aim 2. Integrate multi-omics data to understand the genetic regulation of protein expression.

Aim 2a. We will identify variant peptides from the mouse lung T cell proteome using the proteogenomics approach, which combines genomic and proteomic data. The whole genome sequences of 69 CC lines will be obtained from the UNC Systems Genetics portal. Variants from the genome of 69 CC lines will be used to curate a customized proteomic database for the identification of variant peptides. **Aim 2b.** We will determine quantitative trait loci for protein expression (pQTLs) in response to influenza A infection using genotype and acquired lung proteome of the 69 CC lines. We will also compare commonality and differences in genetic loci that are defined at transcript (i.e. eQTLs) and protein (i.e. pQTLs) levels. The goal of this aim is to detect ~500 variant peptides that are confirmed at both transcript and protein levels and to detect ~800 genetic loci for protein expression including *cis*- and *trans*-regulations.

The successful outcome of the project will produce a deep lung T cell proteome dataset for CC mice, which will be a valuable resource for the research community. The project will also address a fundamental question essential to genetic regulation of protein expression influenza A infection and characterize commonalities and differences in genetic regulation at transcript and protein levels.

Background and Significance

Recombinant inbred (RI) strains are a useful resource for identifying genetic variation in phenotype [1]. The Collaborative Cross (CC) panel of multi-parental RI mice, derived from eight founder strains, exhibits high and uniform levels of genetic and phenotypic variation than other currently available animal models [2], especially in response to virus infection, such as Ebola [3], SARS-CoV [4], and influenza A [5]. In recent years, expression quantitative trait locus (eQTL) mapping has emerged as an important approach to understand genetic modulation of gene expression and to facilitate the identification of causal variants and/or genes for traits in the CC RI strains. For example, genetic regulation at transcript level from 44 influenza-infected pre-CC lines has identified putative regulatory regions potentially controlling their expression in host response to influenza A infection [6]. However, the transcript level is often not accurate indicators of the protein abundance [7, 8] and the regulation of protein expression is not well defined in response to influenza A infection in CC mice.

Dr. Wang has extensive experience in developing computational algorithms and tools for MS-based proteomics [9-11] and applying the tools to understanding biological systems and human diseases [12-14]. I also have long interest in studying genetic regulation of gene expression [15-17]. With the combination of molecular, genetics, and systems biology approaches, Dr. Yang has been to investigate regulatory mechanisms coordinating immune signals and cellular metabolism to control T cell immune responses in the context of autoimmune [18, 19], inflammatory [20, 21], and infectious diseases [14, 19, 22]. In addition, he has extensive experience in studying molecular mechanisms governing the innate response to viral infection [23-25]. In this pilot grant, we propose: (1) to generate and analyze lung proteome of 69 CC lines in response to influenza A infection using 16-plex tandem mass tag (TMT) LC/LC-MS/MS; (2) to integrate multi-omics data to understand the genetic regulation of protein expression in response to influenza A infection.

Research Strategy

Aim 1. Generate and analyze spleen proteome of 69 CC lines in response to influenza A infection using 16-plex tandem mass tag (TMT) LC/LC-MS/MS

Aim 1a. Generate CC lines with influenza A infection. Female mice (8−16 weeks of age) from the 69 CC lines will be obtained from the UNC CC consortium. Influenza A strain A/PR/8/34 (H1N1)(ATCC® VR-95) used for all infection experiments will be grown in allantoic cavities from 10-11-day old embryonated chicken eggs for 2 days at 37°C. The viral titer will be determined by a standard plaque assay using Madin-Darby canine kidney (MDCK) cells grown in high glucose Dulbecco's minimal eagle's medium (10% fetal bovine serum, 1% penicillin/streptomycin). For intranasal infection, mice will be fully anesthetized via inhalation with Attane Isoflurane (Minrad Inc, Orchard Park, NY), and then injected by intranasal application of 20 μL of virus suspension (10 PFU in PBS). Mice will be assayed daily for morbidity (determined as % weight loss), mortality, and clinical disease scores. At 14 days post infection, we will collect lungs, serum, and bronchoalveolar lavage (BALF) for various assays. To obtain single lung cell suspensions, lungs will be perfused with 10 ml PBS through the right ventricle, minced using razor blades, and incubated in RPMI containing 5% FBS, 1 mM $CaCl_2$, 1mM $MgCl_2$, 2.5 mM HEPES, and 0.5 mg/ml collagenase D 37°C for 60 min. Twenty percent of single-cell suspension will be stained with anti-B220, anti-CD3, anti-CD4, anti-CD8a, anti-MHC class II, anti-CD19, anti-F4/80, anti-DX5, anti-CD11c, anti-Siglec-F, anti-CD11b, or anti-CD45.2 antibodie to examine immune cell subsets. The remaining single-cell suspension will be used to purify $CD4^+$ and $CD8^+$ T cells. Serum and BALF will be used for measurement of virus titers and production of the cytokines IL-1β and IFNγ.

Aim 1b. Profile deep lung proteome of 69 CC lines using TMT LC-MS/MS technology. We will profile lung $CD4^+$ and $CD8^+$ T cell proteome of 69 CC strains. By using 16-plex tandem mass tag (TMT)-based LC/LC-MS/MS, we will perform proteome profiling for 69 CC strains with 5 TMT batches. Each batch includes 15 biological samples and two internal standards (i.e., a mixed 69 samples). The internal standards will be used for batch normalization. For each batch, 14 CC samples are lysed. The samples are weighed and homogenized in lysis buffer, and protein concentration is measured by the BCA assay (Thermo Fisher) and confirmed by Coomassie-stained short SDS gels. Quantified protein samples (~1 mg in the lysis

buffer with 8 M urea) for each TMT channel are proteolyzed with Lys-C (Wako, 1:100 w/w) at 21° C for 2 h, diluted 4-fold to reduce urea to 2 M, and digest by trypsin (Promega, 1:50 w/w) at 21°C overnight. The digestion is terminated by the addition of 1% trifluoroacetic acid, followed by centrifugation. Each sample is resuspended in 50 mM HEPES, pH 8.5, labels with TMT reagents, mix equally, and desalt again. The TMT labeled samples are fractionated by offline basic pH reverse phase LC followed by acidic pH reverse phase LC-MS/MS analysis. We performed two offline LC runs (~2-3 h gradient, ~40-120 concatenated fractions) on an XBridge C18 column. In the acidic pH LC-MS/MS analysis, each fraction is run sequentially on a column interfaced with Q Exactive HF Orbitrap MS (Thermo Fisher). Peptides are eluted by a 2-3 h gradient. MS settings include MS1 scans (60,000 resolution, 1 x 10^6 AGC and 100 ms maximal ion time) and 20 data-dependent MS2 scans.

Aim 1c. Perform in-depth identification and quantification of peptides and proteins

Data analysis and interpretation are crucial in proteomic studies. We developed JUMP software for better peptide identification, a novel tag-based database search engine [11]. JUMP shows a significant improvement compared to SEQUEST or MASCOT, two widely used commercial peptide identification tools (~30% increase in identification). We propose to use JUMP to process the proteomic data generated in **Aim 1a**. Below are detailed steps for protein identification and quantification:

- **Perform database search using JUMP program** [11]. To increase the sensitivity, our developed TMT spectral library will be used for low-quality spectra [9].
- **Evaluate false discovery rate (FDR) of peptide identification**. We will use the concatenated target-decoy strategy [26, 27] to filter the PSMs to achieve ~1% FDR.
- **Quantify protein using JUMPq** [28]. We recently developed JUMPq program to remove the effects of ion suppression.
- **Control batch effect.** We control the batch effect by two methods: (1) the control channel, which is a mixed sample; (2) the function of "Remove Batch Effect" in the LIMMA software, which employs a linear correction to account for the batch effect.

Aim 2. Integration of multi-omics data to understand genetic regulation of protein expression

Aim 2a. Identify variant peptides using proteogenomics approach

We will download the whole genome sequences of 69 CC mice from the UNC Systems Genetics portal and use JUMPg [29], a proteogenomics program that we developed for variant peptides detection.

- **Call variants from BAM files.** We will use GATK-HC and SAMtools to call genetic variants from the genomic data. In this pilot study, we will only use single nucleotide variants.
- **Extract 100bp flanking sequences** (50 bp each side) for each genetic variant, and translate the nucleotide sequences into protein sequences and serve as potential variant peptides.
- **Combine all potential variant peptides with a mouse reference protein database**. The mouse reference protein database will be downloaded from the UniProt database. The reference protein database will be combined with all potential variant peptides.
- **Detect and annotate coding genetic variants** using our recently developed JUMPg, which is a proteogenomic program to detect variant peptides from MS data.

Aim 2b. Determine pQTL in response to influenza A infection

We will perform pQTL mapping for proteomic data. Although our preliminary data consist of a small number of (i.e. n = 69) CC strains, the result will provide insights into the genetic regulation of protein expression and genetic regulatory difference at transcript and protein levels in response to influenza A infection in CC mice.

- **Genotype of CC lines** will be downloaded from the UNC Systems Genetics portal.
- **Composite interval QTL map for protein expression** will be performed with the Bagpipe package [30]. We will categorize all *cis*-pQTLs and *trans*-pQTL.
- **Genome-wide significance** will be defined using the permutation method. A significance level of 0.05 will be applied.
- **Comparison of eQTLs and pQTLs.** Previous published eQTL results will be compared with our pQTL to determine the commonalities and differences of the regulation at transcript and protein levels.

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Wang, Xusheng

eRA COMMONS USER NAME (credential, e.g., agency login): XWANG39

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Zhejiang University, Hangzhou, China	BS	07/2000	Biology
Zhejiang University, Hangzhou, China / International Rice Research Institute, Manila, Philippines	MS	09/2003	Genetics
Zhejiang University, Hangzhou, China / University of California, Davis, CA	PhD	12/2006	Bioinformatics
University of Tennessee Health Science Center, Memphis, TN	Postdoctoral Fellow	09/2008	Systems Genetics

A. Personal Statement

I am currently working as an Assistant Professor in the Department of Biology at the University of North Dakota (UND) and I will serve as a principal investigator on this project. I received my PhD training in Bioinformatics from Zhejiang University under a joined program with University of California, Davis. Following my postdoctoral training in Dr. Williams lab at the University of Tennessee Health Science Center (UTHSC), and I became a Bioinformatics Group Leader in the Center for Proteomics and Metabolomics at St. Jude Children's Research Hospital until I move to UND this August. My research focuses on developing computational algorithms and tools for integrating large-scale omics data and applying developed tools for understanding molecular mechanisms underlying human complex diseases. Recently, I have been collaborating locally and regionally with several research groups to discover the molecular mechanisms involved in various diseases, such as cancer. I have unique and extensive interdisciplinary expertise in fields, including Bioinformatics, Genomics, Proteomics, and Metabolomics. Over the past ten years, my research has led to 60 scholarly publications in academic journals. I have developed several computational algorithms and tools, including JUMP for peptide identification, JUMPg for proteogenomic analysis, tandem mass tag (TMT) spectral library, and a target-decoy strategy for metabolomics. I have been collaborating locally and regionally with several research groups to apply these developed MS-based computational tools to discover molecular mechanisms involved in various diseases, including rhabdomyosarcoma and Alzheimer disease. During the four-year research at the University of Tennessee Health Science Center (UTHSC), my research focused on systems genetics that are closely relevant to the study of genetic regulations using BXD recombinant inbred (RI) mice. I had implemented many advanced bioinformatics approaches to assembly the genome of DBA/2J, performed transcriptome and genome linkage analyses, and developed novel phenome-wide association study (PheWAS) in mouse. The goal of this proposal is to understand genetic regulation of host proteins in response to influenza A by profiling proteome of the collaborative cross (CC) mice. I believe that my academic training and research experience have prepared me to be an effective investigator in this proposed project.

1. Bai B, **Wang X** (**co-first and co-corresponding author**), Li Y, Chen PC, Yu K, Dey KK, Yarbro JM, Han X, Lutz BM, Rao S, Jiao Y, Sifford JM, Han J, Wang M, Tan H, Shaw TI, Cho JH, Zhou S, Wang H, Niu M, Mancieri A, Messler KA, Sun X, Wu Z, Pagala V, High AA, Bi W, Zhang H, Chi H, Haroutunian V, Zhang B, Beach TG, Yu G, Peng J. Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. Neuron. 2020. doi: 10.1016/j.neuron.2019.12.015. PMID: 31926610

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B. Positions and Honors

Positions and Employment

2008–2011	Research Associate, University of Tennessee Health Science Center, Memphis, TN
2011–2012	Bioinformatics Research Associate, St. Jude Children's Research Hospital, Memphis, TN
2011–2014	Bioinformatics Scientist, St. Jude Children's Research Hospital, Memphis, TN
2014–2015	Sr. Bioinformatics Research Scientist, St. Jude Children's Research Hospital, Memphis, TN
2015–2019	Bioinformatics Group Leader, St. Jude Children's Research Hospital, Memphis, TN
2019–present	Assistant Professor, University of North Dakota

Other Experience and Professional Memberships

2008–present	Member, International Complex Trait Consortium
2011–present	Member, American Society for Mass Spectrometry
2013–present	Editor, Frontiers in Genetics, Genetic Disorders
2014–present	Associate Editor, Frontiers in Evolutionary and Population Genetics
2018–present	Editor, PLoS One

Honors

2002–2003	Rockefeller scholarship, International Rice Research Institute

C. Contribution to Science

1. **Development of novel computational frameworks for mass spectrometry–based proteomics and metabolomics.** One of the cornerstones of mass spectrometry–based proteomics is peptide identification. As a group leader in the Center for Proteomics and Metabolomics at St. Jude Children's Research Hospital since 2011, I have developed several computational algorithms and tools for mass spectrometry–based proteomics and metabolomics to increase the sensitivity and specificity of peptide identification. These tools include the JUMP program for peptide identification, the JUMPg program for proteogenomics, and a tandem mass tag (TMT) spectral library. JUMP, for example, increases the sensitivity of the identification at the peptide-spectrum match level by 30% when compared to other commercially available tools, and the sensitivity for TMT data can be further improved by 30% with our recently developed TMT spectral library.

    a. Shen J, Pagala VR, Breuer AM, Peng J, Bin Ma, **Wang X** (**Corresponding author**). Spectral library search improves assignment of TMT labeled MS/MS spectra. J Proteome Res. 2018; 17(9):3325–3331. PubMed PMID: 30096983.

b. **Wang X**, Jones DR, Shaw TI, Cho JH, Wang Y, Tan H, Xie B, Zhou S, Li Y, Peng J. Target-decoy–based false discovery rate estimation for large-scale metabolite identification. J Proteome Res. 2018; 17(7):2328–2334. PubMed PMID: 29790753.

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d. **Wang X**, Li Y, Wu Z, Wang H, Tan H, Peng J. JUMP: a tag-based database search tool for peptide identification with high sensitivity and accuracy. Mol Cell Proteomics. 2014; 13(12):3663–3673. PubMed PMID: 25202125; PubMed Central PMCID: PMC4256513.

2. **Understanding the genetic basis of complex diseases.** As a postdoctoral and research associate at the University of Tennessee Health Science Center (UTHSC), my research was focused on elucidating genetic mechanisms of complex diseases using a systems genetics approach, linking genetic variants to phenotype traits. One of my major projects was to characterize sequence variants in two parental strains of the BXD family and to analyze genome-to-phenome relations in mice and humans using the PheWAS approach. Other projects included studies of genetic regulation of the variation in gene expression and linking it to classic phenotypes, such as alcohol and stress responses.

a. **Wang X**, Pandey AK, Mulligan MK, Williams EG, Mozhui K, Li Z, Jovaisaite V, Quarles LD, Xiao Z, Huang J, Capra JA, Chen Z, Taylor WL, Bastarache L, Niu X, Pollard KS, Ciobanu DC, Reznik AO, Tishkov AV, Zhulin IB, Peng J, Nelson SF, Denny JC, Auwerx J, Lu L, Williams RW. Joint mouse-human phenome-wide association to test gene function and disease risk. Nat Commun. 2016;7:10464. PubMed PMID: 26833085; PubMed Central PMCID: PMC4740880.

b. **Wang X**, Mozhui K, Li Z, Mulligan MK, Ingels JF, Zhou X, Hori RT, Chen H, Cook MN, Williams RW, Lu L. A promoter polymorphism in the *Per3* gene is associated with alcohol and stress response. Transl Psychiatry. 2012;2:e73. PubMed PMID: 22832735; PubMed Central PMCID: PMC3309544.

c. **Wang X**, Chen Y, Wang X, Lu L. Genetic regulatory network analysis for app based on genetical genomics approach. Exp Aging Res. 2010;36(1):79–93. PubMed PMID: 20054728.

d. Dai J, **Wang X** (co-first author), Chen Y, Wang X, Zhu J, Lu L. Expression quantitative trait loci and genetic regulatory network analysis reveals that *Gabra2* is involved in stress responses in the mouse. Stress. 2009;12(6):499–506. PubMed PMID: 19212922.

3. **Application of our proteomics tools to understanding human diseases.** I have been collaborating locally and regionally with several research groups to apply our novel MS-based proteomics tools to discovering molecular mechanisms involved in various diseases, including rhabdomyosarcoma and Alzheimer disease, as well as mechanisms of T-cell activation.

a. Stewart E, McEvoy J, Wang H, Chen X, Honnell V, Ocarz M, Gordon B, Dapper J, Blankenship K, Yang Y, Li Y, Shaw TI, Cho JH, **Wang X**, Xu B, Gupta P, Fan Y, Liu Y, Rusch M, Griffiths L, Jeon J, Freeman BB 3rd, Clay MR, Pappo A, Easton J, Shurtleff S, Shelat A, Zhou X, Boggs K, Mulder H, Yergeau D, Bahrami A, Mardis ER, Wilson RK, Zhang J, Peng J, Downing JR, Dyer MA. Identification of therapeutic targets in rhabdomyosarcoma through integrated genomic, epigenomic, and proteomic analyses. Cancer Cell. 2018;34(3):411–426.e19. PubMed PMID: 30146332.

b. Scott DC, Hammill JT, Min J, Rhee DY, Connelly M, Sviderskiy VO, Bhasin D, Chen Y, Ong SS, Chai SC, Goktug AN, Huang G, Monda JK, Low J, Kim HS, Paulo JA, Cannon JR, Shelat AA, Chen T, Kelsall IR, Alpi AF, Pagala V, **Wang X**, Peng J, Singh B, Harper JW, Schulman BA, Guy RK. Blocking an N-terminal acetylation–dependent protein interaction inhibits an E3 ligase. Nat Chem Biol. 2017;13(8):850–857. PubMed PMID: 28581483; PubMed Central PMCID: PMC5577376.

c. Tan H, Yang K, Li Y, Shaw TI, Wang Y, Blanco DB, **Wang X**, Cho JH, Wang H, Rankin S, Guy C, Peng J, Chi H. Integrative proteomics and phosphoproteomics profiling reveals dynamic signaling networks and bioenergetics pathways underlying T cell activation. Immunity. 2017;46(3):488–503. PubMed PMID: 28285833; PubMed Central PMCID: PMC5466820.

d. Bai B, Hales CM, Chen PC, Gozal Y, Dammer EB, Fritz JJ, **Wang X**, Xia Q, Duong DM, Street C, Cantero G, Cheng D, Jones DR, Wu Z, Li Y, Diner I, Heilman CJ, Rees HD, Wu H, Lin L, Szulwach KE, Gearing M, Mufson EJ, Bennett DA, Montine TJ, Seyfried NT, Wingo TS, Sun YE, Jin P, Hanfelt J, Willcock DM, Levey A, Lah JJ, Peng J. U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. Proc Natl Acad Sci U S A. 2013;110(41):16562–16567. PubMed PMID: 24023061; PubMed Central PMCID: PMC3799305.

4. **Development of genetic markers in plants.** During my graduate studies, I developed a novel type of genetic marker—intron length polymorphisms (ILPs)—in rice (Wang et al., 2006; DNA Res). Owing to its ease of use, this new type of marker has been widely adopted for other plant species, such as maize, millet, and *Brassica* species, and has become a powerful resource for genetic linkage analysis and evolutionary studies. Because of this innovative development, I received an award from the National Natural Science Foundation of China (Project No. 30700517). In addition, I developed several new algorithms and computational tools. For example, I developed a deep learning (i.e., artificial neural network) method to predict infections in tomatoes.

   a. **Wang X**, Zhao X, Zhu J, Wu W. Genome-wide investigation of intron length polymorphisms and their potential as molecular markers in rice (*Oryza sativa L.*). DNA Res. 2005;12(6):417–427. PubMed PMID: 16769698.
   b. **Wang X**, Zhu J, Mansueto L, Bruskiewich R. Identification of candidate genes for drought stress tolerance in rice by the integration of a genetic (QTL) map with the rice genome physical map. J Zhejiang Univ Sci B. 2005;6(5):382–388. PubMed PMID: 15822152; PubMed Central PMCID: PMC1389755.
   c. Bruskiewich RM, Cosico AB, Eusebio W, Portugal AM, Ramos LM, Reyes MT, Sallan MA, Ulat VJ, **Wang X**, McNally KL, Sackville Hamilton R, McLaren CG. Linking genotype to phenotype: the International Rice Information System (IRIS). Bioinformatics. 2003;19 Suppl 1:i63–i65. PubMed PMID: 12855438.

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/xusheng.wang.1/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

Pilot Project Award
Title: "Genetic Regulation of the Rat Brain Proteome" Awarded as Subcontract of Pilot Research Project Core NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome. National Institute of Drug Abuse (1P30DA044223-01).
Xusheng Wang (PI)
01/01/20-12/30/22

UND COBRE pilot grant
Title: Allele-Specific and Imprinted Expression of Mouse Brain Proteome
Xusheng Wang (PI)
07/01/20–06/30/21

UND startup funding
08/16/19–08/15/24

Completed Research Support

30700517, National Natural Science Foundation of China
Xusheng Wang (PI)
01/01/08–12/31/10
Title: Large-scale exploitation of conserved species span polymorphism (CSSP) markers
Role: PI

U01AA0016662, NIH Office of the Director
Robert W. Williams (PI) and Xusheng Wang (Co-investigator)
02/01/12–01/31/17
Title: INIA: Bioinformatics Core
Role: Co-investigator

GM114260, NIH Office of the Director
Junmin Peng (PI) and Xusheng Wang (Co-investigator)
01/01/16–12/01/19
Title: Proteomics approaches to protein turnover
Role: Co-investigator

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Kai Yang

eRA COMMONS USER NAME (credential, e.g., agency login): YANGKAI

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Southwest University, Chongqing, China	BA	07/2001	Biology
Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Shanghai, China	PhD	07/2008	Molecular Biology, Biochemistry
St. Jude Children's Research Hospital, Memphis, TN	Postdoc	08/2014	Immunology

A. Personal Statement

My doctoral studies focused on understanding regulatory mechanisms involved in the control of the IRF3 signaling pathway that induces innate immune responses to viral infection. To investigate physiological relevance of immune signaling in T cell immunity, I received postdoctoral training with Dr. Hongbo Chi at St. Jude Children's Research Hospital. Using various genetic and disease models, I have been to elucidate fundamental mechanisms by which T cells coordinate immune signals and reprogramming of cellular metabolism in the regulation of T cell homeostasis, differentiation and function at steady state and during immune responses. I have demonstrated that LKB1- and PTEN-dependent signaling networks in Tregs orchestrate functional specification and metabolic fitness to enforce their suppressive function in maintaining immune tolerance and preventing the pathogenesis of immune-mediated diseases. In addition, I have demonstrated that mTOR signaling and cellular metabolism play pivotal roles in dictating T cell activation and differentiation. The intimate interplay of mTOR signaling and metabolic programs not only contributes to T cell survival and expansion, but also shapes T cell differentiation and function. By integrative analyses of proteome and phosphoproteome profiling in naïve and activated T cells, I have shown that the temporal interactions of signaling networks and bioenergetics pathways underpin T cell activation and differentiation via mTOR-dependent and –independent mechanisms. Better understanding the interaction of immune signaling and metabolic pathways in the physiologic setting could provide significant insights into the development of new therapeutic strategies for the treatment of immune-mediated diseases.

B. Positions and Honors

Positions and Employment

2008-2009	Research Associate, Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Shanghai, China
2014-2017	Staff Scientist, Department of Immunology, St. Jude Children's Research Hospital, Memphis, TN
2017-present	Assistant Professor, Wells Center for Pediatric Research, Department of Pediatrics, Indiana University School of Medicine, Indianapolis, IN

Honors

2011-2014	Postdoctoral Fellowship, the Arthritis Foundation
2016-2017	ANRF Scholar, Arthritis National Research Foundation
2018-2019	Showalter Young Investigator Award

C. Contributions to Science

My research has been to understand fundamental mechanisms coordinating immune signals and reprogramming of cellular metabolism in T cell immunity. With a combination of various genetic and disease models and systems biology approaches, I have highlighted that regulation of mTOR signaling and metabolic programs plays a central role in regulating T cell homeostasis, differentiation and function. In addition, I also investigated the regulatory mechanism governing the activation of the IRF3 signaling pathway in response to viral infection. My major scientific contributions have included:

1) *Demonstration of functions of mTOR signaling and cellular metabolism in T cell differentiation and development.* mTOR signaling regulates cell growth and metabolism. Our studies indicate that mTOR signaling integrates distinct microenvironmental cues and cellular metabolism in dictating T cell fate decisions. We have uncovered that sphingosine-1–phosphate receptor 1 (S1PR1) reciprocally regulates the differentiation of T_H1 and T_{reg} cells and the outcome of immune responses through control of mTOR activation. We went on to understand the functions of distinct mTOR complexes in the development of thymocytes, including αβ T cells, γδ T cells and invariant natural killer T (iNKT) cells. Key publications included: *Identification of new regulators of IRF3 signaling pathway in response to viral infection.* Viruses can activate IRF3 signaling pathway that induces innate immune responses to suppress viral replication. I identified various regulators that control virus-induced activation of IRF3 signaling pathway through distinct mechanisms. Key publications included:
    a. Liu G*, **Yang K***, Burns S, Shrestha S, Huang G and Chi H (* equal contribution). The S1P1-mTOR axis directs the reciprocal differentiation of T_H1 and T_{reg} cells. ***Nat Immunol.*** 11: 1047-56, 2010.
    b. Wei J*, **Yang K*** and Chi H (* equal contribution). Cutting edge: Discrete functions of mTOR signaling in invariant NKT cell development and NKT17 fate decision. ***J Immunol.*** 193: 4297-301, 2014.
    c. **Yang K** and Chi H. Metabolic control of Th17 cell generation and CNS inflammation. ***J Neurol Neurophysiol.*** S12: 004, 2014.
    d. **Yang K***, Blanco DB*, Chen X*, Dash P, Neale G, Rosencrance C, Easton J, Chen W, Dhungana Y, KC A, Awad W, Guo X, Thomas P and Chi H (* equal contribution). Metabolic signaling directs the reciprocal lineage decisions of αβ and γδ T cells. ***Sci Immunol.*** 565: 101-105, 2018.

2) *Elucidation of molecular and metabolic mechanisms involved in the control of T cell quiescence.* Before our studies there was lack of information about central regulatory mechanisms in maintaining quiescence of naïve T cells. Using various genetic models, we have provided evidence that mTOR signaling and cellular metabolism are key players that coordinate immune signals and transcriptional programs to control quiescence status of naïve and memory T cells. By integrative analysis of proteomics and phosphoproteomics profiling in T cells, we have recently revealed that the temporal interactions of signaling networks and bioenergetics pathways underpin T cell quiescence exit and differentiation. Key publications included:
    a. **Yang K**, Neale G, Green DR, He W and Chi H. The tumor suppressor Tsc1 enforces quiescence of naive T cells to promote immune homeostasis and function. ***Nat Immunol.*** 12: 888-97, 2011.
    b. **Yang K**, Shrestha S, Zeng H, Karmaus PW, Neale G, Vogel P, Guertin DA, Lamb RF and Chi H. T cell exit from quiescence and differentiation into T_H2 cells depend on Raptor-mTORC1-mediated metabolic reprogramming. ***Immunity.*** 39: 1043-56, 2013.
    c. Shrestha S*, **Yang K***, Wei J, Karmaus PW, Neale G, and Chi H (* equal contribution). Tsc1 promotes the differentiation of memory $CD8^+$ T cells via orchestrating the transcriptional and metabolic programs. ***Proc Natl Acad Sci U S A.*** 111: 14858-63, 2014.
    d. Tan H*, **Yang K***, Li Y*, Shaw T*, Wang Y, Blanco DB, Wang X, Cho J, Wang H, Rankin S, Guy C, Peng J, and Chi H (* equal contribution). Integrative proteomics and phosphoproteomics profiling reveals dynamic signaling networks and bioenergetics pathways underlying T cell activation. ***Immunity*** 46: 488-503, 2017.

3) *Elucidation of regulatory mechanisms governing cellular metabolism and functional integrity of T_{reg} cells.* Before our studies there was lack of evidence about the interaction of immune signaling and cellular metabolism in regulating T_{reg} cell homeostasis and function. In trying to understand physiological functions of immune signaling in T_{reg} cells, we unexpectedly found mTORC1 signaling and metabolic reprogramming are essential for T_{reg} cell activation and function. We went on to examine the roles of various regulators of mTOR

signaling, demonstrating that these regulators enforce functional fitness of T_{reg} cells through coordinating distinct immune signals and metabolic programs. Key publications included:

a. Zeng H, **Yang K**, Cloer C, Neale G, Vogel P, and Chi H. (2013). mTORC1 couples immune signals and metabolic programming to establish Treg-cell function. ***Nature***. 499: 485-90, 2013.
b. Shrestha S*, **Yang K***, Guy C, Neale G, Vogel P, and Chi H (* equal contribution). Treg cells require the phosphatase PTEN to restrain TH1 and TFH cell responses. ***Nat Immunol.*** 16: 178-87, 2015.
c. Wei J, Long L, **Yang K**, Guy C, Shrestha S, Chen Z, Wu C, Vogel P, Neale G, Green DR, and Chi H. Autophagy enforces functional integrity of regulatory T cells by coupling environmental cues and metabolic homeostasis. ***Nat Immunol.*** 17: 277-85, 2016.
d. **Yang K**, Blanco DB, Neale G, Vogel P, Avila J, Clish CB, Wu C, Shrestha S, and Chi H. Homeostatic control of metabolic and functional fitness of T_{reg} cells by LKB1 signaling. ***Nature*** 548: 602-606, 2017.

4) *Identification of new regulators of IRF3 signaling pathway in response to viral infection.* Viruses can activate IRF3 signaling pathway that induces innate immune responses to suppress viral replication. I identified various regulators that control virus-induced activation of IRF3 signaling pathway through distinct mechanisms. Key publications included:

a. **Yang K**, Shi HX, Qi R, Sun SG, Tang YJ, Zhang BH and Wang C. Hsp90 Regulates Activation of Interferon Regulatory Factor 3 and TBK-1 Stabilization in Sendai Virus-infected Cells. ***Mol Biol Cell.*** 17:1461-71, 2006.
b. **Yang K**, Shi HX, Liu XY, Shan YF, Wei B, Chen S and Wang C. TRIM21 is essential to sustain IRF3 activation during antiviral response. ***J Immunol.*** 182: 3782-92, 2009.
c. Shi HX*, **Yang K***, Liu X, Liu XY, Wei B, Shan YF, Zhu LH and Wang C (* equal contribution). Positive regulation of interferon regulatory factor 3 activation by Herc5 via ISG15 modification. ***Mol Cell Biol.*** 30: 2424-36, 2010.

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1-m1TAgh4cgA3/bibliography/49530288/public/?sort=date&direction=descending

D. Additional Information: Research Support and/or Scholastic Performance

Completed Research Support
Completed

Kai Yang (PI) 07/2018-06/2019

Showalter Young Investigator Award

Title: Treg cell signaling and metabolism in the pathogenesis of allergic diseases

Kai Yang (PI) 04/2018-03/2019

Biomedical Research Grant

Title: Regulation of Treg cell metabolism and stability in autoimmunity

Kai Yang (PI) 07/2016-07/2017

National Arthritis Research Foundation

Title: Regulation of Treg metabolism and stability by PTEN in autoimmune diseases

Kai Yang (PI) 07/2011-07/2014

Postdoctoral fellowship grant from Arthritis Foundation

Title: Modulation of S1P/S1P1 signaling in autoimmune diseases

BUDGET JUSTIFICATION

A. PERSONNEL

Xusheng Wang, Ph.D., Principal Investigator (effort = 0.5 calendar months). Dr. Wang will be responsible for the overall coordination and supervision of all aspects of the project. This includes hiring, training, and supervising staff/students; recruiting study participants; scheduling and staff assignments; and data management. In addition, He will conduct proteomics data collection and analyses, and be responsible for reporting the study's findings. His time is not budgeted in the grant and will be covered by his department as part of the research allocation for his 9-month academic year contract.

Kai Yang, Ph.D., Co-Investigator (effort = 0.5 calendar months). Dr. Yang will be responsible for performing influenza A infection in CC mice and tissue collection. He will also assist in manuscript preparation. His time is not budgeted in the grant and will be covered by his department as part of the research allocation for his 9-month academic year contract.

B. OTHER PERSONNEL

TBA Graduate Student (effort = 12 Calendar Months effort). One graduate student will work with Dr. Wang to perform proteomics data collection and analyses. His/her 12-month base salary is $26,040, with a 1% fringe benefit rate.

C. Equipment

None.

D. TRAVEL - $1,950 is requested for travel to professional conferences (i.e., 18th Annual Meeting of the Complex Trait Community in collaboration with the Rat Genomics Community. Manchester UK. September 2-4, 2020) to present findings associated with the investigation.

F. OTHER DIRECT COSTS

F.1 Materials and Supplies
General research supplies - We request for $6,000 for TMT reagent and mass spectrometry proteome profiling, and office supplies ($1,000).

PUBLICATION COSTS: An amount of $1,000 is budget for publications.

F.2 Subawards/Consortium/Contractual Costs
One subaward for $52,000 will be made to the Indiana University (Dr. Kai Yang), including $19,192 (58.5%) indirect costs.

Saogang Sun; Technician (effort = 3 Calendar Months effort). He will work with Dr. Yang to perform influenza A infection in CC mice and tissue collection. His/her 12-month base salary is $38,000, with a 40% fringe benefit rate. Thus, a total of $15,985 is requested.

A total of $9,822 is requested for lab supplies and $7,000 for mouse work.

Applicant Principal Investigator(s):

OVERALL IMPACT

Reviewers will provide an overall impact score to reflect their assessment of the likelihood for the project to exert a sustained, powerful influence on the research field(s) involved, in consideration of the following five scored review criteria, and additional review criteria. An application does not need to be strong in all categories to be judged likely to have major scientific impact.

Overall Impact *Write a paragraph summarizing the factors that informed your Overall Impact score.*
OVERALL IMPACT SCORE:

SCORED REVIEW CRITERIA

Reviewers will consider each of the five review criteria below in the determination of scientific and technical merit and give a separate score for each.

1. Significance Score:
Strengths • **Weaknesses** •

2. Investigator(s) Score:
Strengths • **Weaknesses** •

3. Innovation Score:
Strengths • **Weaknesses** •

4. Approach Score:
Strengths

-

Weaknesses

-

5. Potential for Fit/Collaboration with SIG-U19 Program Score:
Strengths • **Weaknesses** •

From: Wei, Guowei <weig@msu.edu>
Sent: Saturday, February 8, 2020 9:40 AM
To: shiyi@im.ac.cn;cyh-birm@263.net;dschui@cuhk.edu.hk;tanwj@ivdc.chinacdc.cn;gaof@im.ac.cn;wugz@ivdc.chinacdc.cn;jonathan.read@lancaster.ac.uk;christian.drosten@charite.de;christian.drosten@charite.de;rothe@lrz.uni-muenchen.de;caobin_ben@163.com;Menachery, Vineet;mawj@dgiph.org.cn;neil.ferguson@imperial.ac.uk;joewu@hku.hk;kyyuen@hku.hk;zhaoshi.cmsa@gmail.com;maggiew@cuhk.edu.hk;christian.althaus@alumni.ethz.ch;shechen@cityu.edu.hk;qixiaolong@vip.163.com;jhyoo@catholic.ac.kr;tanwj@ivdc.chinacdc.cn;zhangli080806@163.com;christian.drosten@charite.de;xjwang@genetics.ac.cn;zuow@tongji.edu.cn;nishiurah@med.hokudai.ac.jp;Shengjie.Lai@soton.ac.uk;A.J.Tatem@soton.ac.uk;mhoffmann@dpz.eu;spoehlmann@dpz.eu;zhaoshi.cmsa@gmail.com
Subject: Potentially highly potent drugs for 2019-nCoV
Attachments: 2019-nCoV-Reposition_13.pdf; Anti-2019-nCoV.docx

Dear Researchers,
There is a pressing need to find effective medications for 2019-nCoV. Therefore, I would like to bring your attention to a class of potentially highly potent drugs for 2019-nCoV. Sorry for disturbing your weekend!

We use deep learning to screen 1465 drugs in the DrugBank that have been approved by the U.S. Food and Drug Administration (FDA), based on the inhibition of 2019-nCoV 3CL protease. We found a few market drugs that might be effective for curing 2019-nCoV, ranked by their binding affinities in inhibiting the 2019-nCoV 3CL protease.

Table 1: A summary of potentially highly potent anti2019-nCoV drugs with predicted binding free energies (unit: kcal/mol) and
corresponding trade names.

Drug ID	Type	Trade Name	Predicted Binding Affinity
DB00188	Bortezomib	Velcade, Chemobort, Bortecad	-12.15
DB00690	Flurazepam	Dalmane, Dalmadorm, Fluzepam	-10.38
DB08901	Ponatinib	Iclusig	-10.25
DB00398	Sorafenib	Nexavar	-10.01
DB01254	Dasatinib	Sprycel, Dasanix	-9.87
DB01384	Paramethasone	Cortidene Depot, Dilar, Dilarmine	-9.71
DB00838	Clocortolone	Victrelis	-9.58
DB00301	Flucloxacillin	Flora, Flox, Floxapen	-9.57
DB06144	Sertindole	Serdolect and Serlect	-9.54
DB04920	Clevidipine	Cleviprex	-9.52
DB00673	Aprepitant	Emend	-9.49
DB01076	Atorvastatin	Lipitor, Sortis	-9.49
DB01594	Cinolazepam	Gerodorm	-9.47
DB00845	Clofazimine	Lamprene	-9.43
DB06717	Fosaprepitant	Emend, Ivemend	-9.39

Among FDA approved protease-based antiviral drugs, the most possible one is Boceprevir (binding affinity -9.36 kcal/mol), see Table of the attached manuscript. A brief summary is also given in Chinese.

Best regards,

Guowei Wei
Professor
Mathematics
Electrical and Computer Engineering
Biochemistry and Molecular Biology
Michigan State University
http://users.math.msu.edu/users/wei/

Potentially highly potent drugs for 2019-nCoV

Duc Duy Nguyen[1], Kaifu Gao[1], Jiahui Chen[1], Rui Wang[1], and Guo-Wei Wei[1,2,3] *
[1] Department of Mathematics, Michigan State University, MI 48824, USA
[2] Department of Biochemistry and Molecular Biology
Michigan State University, MI 48824, USA
[3] Department of Electrical and Computer Engineering
Michigan State University, MI 48824, USA

February 5, 2020

Abstract

The World Health Organization (WHO) has declared the 2019 novel coronavirus (2019-nCoV) infection outbreak a global health emergency. Currently, there is no effective anti-2019-nCoV medication. The sequence identity of the 3CL proteases of 2019-nCoV and SARS is 96%, which provides a sound foundation for structural-based drug repositioning (SBDR). Based on a SARS 3CL protease X-ray crystal structure, we construct a 3D homology structure of 2019-nCoV 3CL protease. Based on this structure and existing experimental datasets for SARS 3CL protease inhibitors, we develop an SBDR model based on machine learning and mathematics to screen 1465 drugs in the DrugBank that have been approved by the U.S. Food and Drug Administration (FDA). We found that many FDA approved drugs are potentially highly potent to 2019-nCoV.

Key words: 2019-nCoV, Drug repositioning, DrugBank, deep learning, algebraic topology.

*Address correspondences to Guo-Wei Wei. E-mail:wei@math.msu.edu

1 Introduction

The 2019 novel coronavirus (2019-nCoV) caused the pneumonia outbreak in Wuhan, China, in late December 2019 and has rapidly spread around the world. By Feb 5, 2020, more than 24000 individuals were infected and more than 490 fatalities had been reported. The World Health Organization (WHO) has declared this novel coronavirus outbreak a global health emergency. Currently, there is no specific antiviral drug for this epidemic. Considering the severity of this widespread dissemination and health threats, panic patients misled by media flocked to the pharmacies for Chinese Medicine herbs which were reported to "inhibit" the 2019-nCoV, despite no clinical evidence supporting the claim. Many researchers are engaged in developing anti-2019-nCoV drug s [1, 2]. However, new drug discovery and development is a long, costly and rigorous scientific process. A more effective approach is to search for anti-2019-nCoV therapies from the existing FDA-approved drug database.

Drug repositioning (also known as drug repurposing), which concerns the investigation of existing drugs for new therapeutic target indications, has emerged as a successful strategy for drug discovery due to the reduced costs and expedited approval procedures [3–5]. Several successful examples unveil its great values in practice: Nelfinavir, initially developed to treat the human immunodeficiency virus (HIV), is now being used for cancer treatments. Amantadine was firstly designed to treat influenza caused by type A influenza viral infection and is being used for Parkinson's disease later on [6]. In recent years, the rapid growth of drug-related datasets, as well as open data initiatives, has led to new developments for computational drug repositioning, particularly, structural-based drug repositioning (SBDR). Machine learning, network analysis, and text mining and semantic inference are three major computational approaches commonly applied in drug repositioning [7]. The rapid accumulation of genetic and structural databases [8], the development of low-dimensional mathematical representations of complex biomolecular structures [9, 10], and the availability of advanced deep learning algorithms have made machine learning-based drug reposition a promising approach [7]. Considering the urgent need for anti-2019-nCoV drugs, a computational drug repositioning is one of the most feasible strategies for discovering 2019-nCoV drugs.

In SBDR, one needs to select one or a few effective targets. Study shows that 2019-nCoV genome is very close to that of the severe acute respiratory syndrome (SARS)-CoV [11]. The sequence identities of 2019-nCoV 3CL protease, RNA polymerase, and the spike protein with corresponding SARS-CoV proteins are 96.08%, 96%, and 76%, respectively [12]. We, therefore, hypothesize that a potent SARS 3CL protease inhibitor is also a potent 2019-nCoV 3CL protease inhibitor. Unfortunately, there is no effective SARS therapy at present. Nevertheless, the X-ray crystal structure of SARS 3CL protease has been reported [13] and the binding affinities of 115 potential SARS 3CL protease inhibitors are available in ChEMBL database [14]. Additionally, there are 15,843 protein-ligand complexes in PDBbind 2018 general set with binding affinities and X-ray crystal structures [15]. Moreover, the DrugBank contains about 1600 drugs approved by the U.S. Food and Drug Administration (FDA) [16]. The aforementioned information provides a sound foundation to develop an SBDR machine learning model for 2019-nCoV 3CL protease inhibition.

Recently, we have developed low-dimensional mathematical representations [9, 10] to reduce the structural complexity of macromolecules based on abstract mathematics, such as algebraic topology [17–20], differential geometry, and spectral graph theory [10, 21]. We exploit these representations to extract critical chemical and biological information for protein-ligand pose selection, binding affinity ranking, prediction, ranking, scoring, and screening [9, 10]. Paired with various machine learning, including deep algorithms, these approaches are the top competitor for D3R Grand Challenges, a worldwide competition series in computer-aided drug design in the past few years [22, 23].

In responding to the pressing need for anti-2019-nCoV medications, we develop mathematics-based deep learning models to systematically eventuate FDA approved drugs in the DrugBank for 2019-nCoV 3CL protease inhibition. With the consensus of two deep learning models based on convolutional neural

networks and multitask deep learning, we report the top 15 potentially highly potent anti-2019-nCoV 3CL inhibitors, which provide timely guidance for the further development of anti-2019nCoV drugs.

2 Results

2.1 Sequence identity analysis

The sequence identity is defined as the percentage of characters that match exactly between two different sequences. The sequence identities between 2019-nCoV protease and the protease of SARS-CoV, MERS-CoV, HKU-1, OC43, HCoVNL63, 229E, and HIV are 96.1%, 52.0%, 49.0%, 48.4%, 45.2%, 41.9%, and 23.7%, respectively. It is seen that 2019-nCoV protease is very close to SARS-CoV protease, but is distinguished from other proteases. Clearly, 2019-nCoV has a strong genetic relationship with SARS-CoV, the sequence alignment in Figure 1 further confirms their relationship. Additionally, the available experimental data of SARS-CoV protease inhibitors can be used as the training set to generate new inhibitors of 2019-nCoV protease.

2.2 Structure similarity analysis

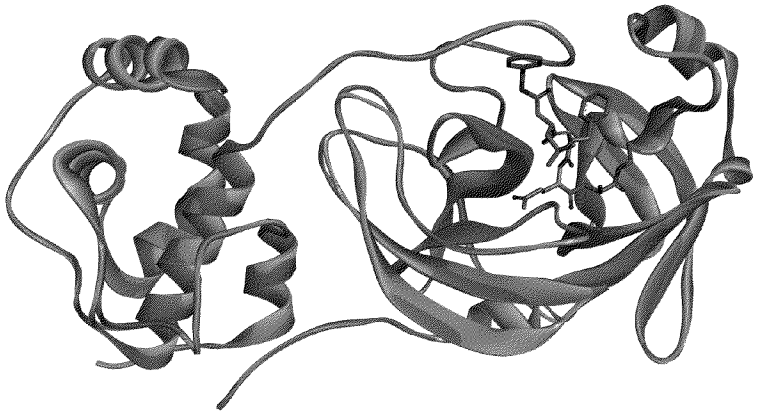


Figure 2: Illustration of the similarity and difference between protease structures of 2019-nCoV 3CL protease (in gold) and SARS-CoV 3CL protease (PDB ID: 2A5I, in green). The anti-SARS inhibitor in dark color indicates the binding site.

Since the sequences are highly identical, the 2019-nCoV protease structure can be built by homology modeling with the SARS-CoV 3CL protease (PDB ID: 2A5I) [13] as a template. It turns out, as shown in Fig. 2, the homology structure of the 2019-nCoV protease is essentially identical to the X-ray structure of SARS-CoV 3CL protease. Particularly, the RMSD of two structures at the binding site is 0.21 Å. The high structural similarity between the two proteases suggests that anti-SARS-CoV chemicals can be equally effective for the treatment of 2019-nCoV.

2.3 Binding analysis

We predict the binding affinities of 1465 3D FDA-approved drugs and 2019-nCoV protease complexes using two models, 3DALL and 3DMT. 3DALL is built with deep convolutional neural networks (CNNs) using the algebraic topology-based representation of protein-ligand complexes, with 84 SARS-CoV protease inhibitors and 15843 complexes from the PDBbind 2018 general set as the training set. 3DMT, a deep

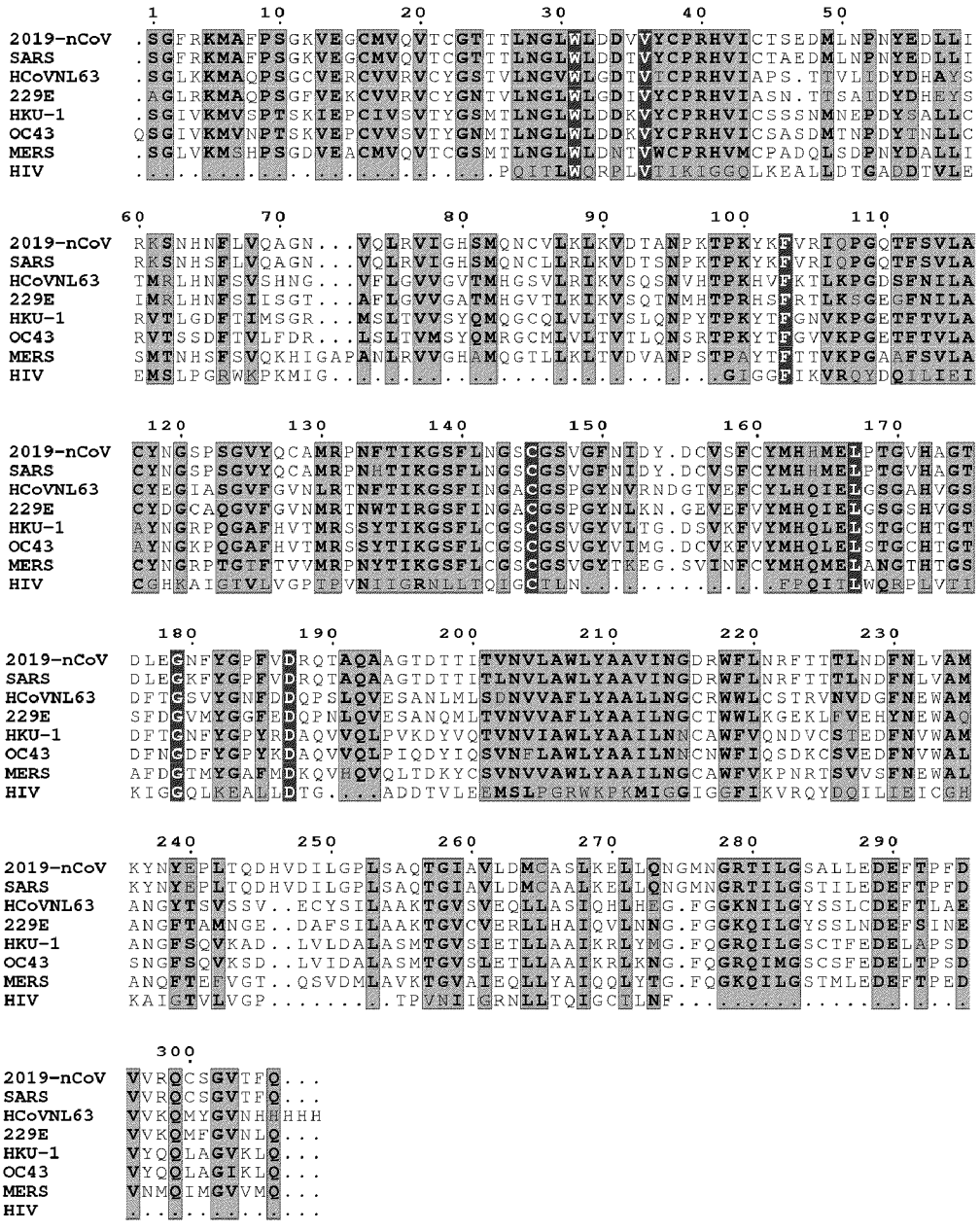


Figure 1: The protease sequence alignment between 2019-nCoV, SARS, MERS, OC43, HCoVNL63, HKU-1, 229E, and HIV.

multitask CNN model based on the algebraic topology representation of protein-ligand complexes is the second model. In the current work, two tasks were developed in the 3DMT. The first task involves 1465 2019-nCoV protease complexes as the test set and 84 SARS-CoV protease inhibitors as the training set. The second task is trained with the PDBbind 2018 general set of 15843 protein-ligand complexes. Our top 15 potential 2019-nCoV inhibitors based on consensus binding affinities of the aforementioned two models are listed in Table 1. A complete list of predicted binding affinities of 1465 FDA-approved drugs is given in the Supplementary Material.

We briefly describe the predicted potentially highly potent anti-2019-nCoV drugs. The most potent one is Bortezomib, an anti-cancer medication, which is known as proteasome inhibitor and can be used to treat multiple myeloma and mantle cell lymphoma. The second drug is Flurazepam, which is a benzodiazepine derivative that possesses anxiolytic, anticonvulsant, hypnotic, sedative, and skeletal muscle

Table 1: A summary of potentially highly potent anti2019-nCoV drugs with predicted binding free energies (unit: kcal/mol) and corresponding trade names.

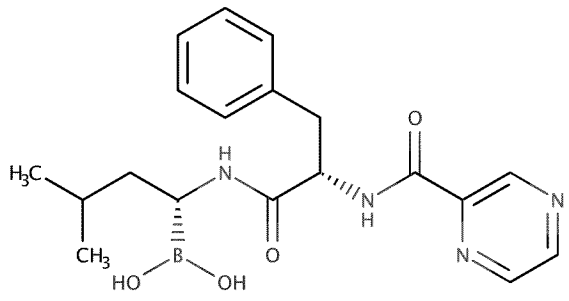
DrugID	Type	Trade Name	Predicted Binding Affinity
DB00188	Bortezomib	Velcade, Chemobort, Bortecad	-12.15
DB00690	Flurazepam	Dalmane, Dalmadorm, Fluzepam	-10.38
DB08901	Ponatinib	Iclusig	-10.25
DB00398	Sorafenib	Nexavar	-10.01
DB01254	Dasatinib	Sprycel, Dasanix	-9.87
DB01384	Paramethasone	Cortidene Depot, Dilar, Dilarmine	-9.71
DB00838	Clocortolone	Victrelis	-9.58
DB00301	Flucloxacillin	Flora, Flox, Floxapen	-9.57
DB06144	Sertindole	Serdolect and Serlect	-9.54
DB04920	Clevidipine	Cleviprex	-9.52
DB00673	Aprepitant	Emend	-9.49
DB01076	Atorvastatin	Lipitor, Sortis	-9.49
DB01594	Cinolazepam	Gerodorm	-9.47
DB00845	Clofazimine	Lamprene	-9.43
DB06717	Fosaprepitant	Emend, Ivemend	-9.39

relaxant properties. The third one, Ponatinib, an oral drug for the treatment of chronic myeloid leukemia and Philadelphia chromosome-positive acute lymphoblastic leukemia, which is a multi-targeted tyrosine kinase inhibitor. It is important to notice that this drug has the risk of life-threatening blood clots and severe narrowing of blood vessels. The next one is Sorafenib, a kinase inhibitor for the treatment of primary kidney cancer and liver cancer. The fifth drug, Dasatinib, is a therapy for treating certain cases of chronic myelogenous leukemia and acute lymphoblastic leukemia. The next one, Paramethasone, is a glucocorticoid with the general properties of corticosteroids. The seventh drug is Clocortolone, a topical steroid that is used in the form of an ester, clocortolone pivalate. It is interesting to note that this drug is always applied as a cream for the treatment of dermatitis. It is considered a medium-strength corticosteroid. Therefore, this drug might be used to clean 2019-nCoV contaminated materials, offering an extra layer of protection. The number eight drug, Flucloxacillin, is a narrow-spectrum beta-lactam antibiotic of the penicillin class. It is used to treat infections caused by susceptible Gram-positive bacteria. The next one, Sertindole, is an antipsychotic medication. The number ten drug, Clevidipine, is a dihydropyridine calcium channel blocker that used for the reduction of blood pressure when oral therapy is not feasible or not desirable. The eleventh drug, Aprepitant, is used to prevent chemotherapy-induced nausea and vomiting, as well as postoperative nausea and vomiting. The number twelve, Atorvastatin, is a statin drug used to prevent cardiovascular disease in those at high risk and treat abnormal lipid levels. The next drug is Cinolazepam, a benzodiazepine derivative. It possesses anxiolytic, anticonvulsant, sedative, and skeletal muscle relaxant properties. The number fourteen drug, Clofazimine, is used together with rifampicin and dapsone to treat leprosy. The fifteenth number drug, Fosaprepitant, is an antiemetic medication used in the prevention of acute and delayed nausea and vomiting associated with chemotherapy treatment.

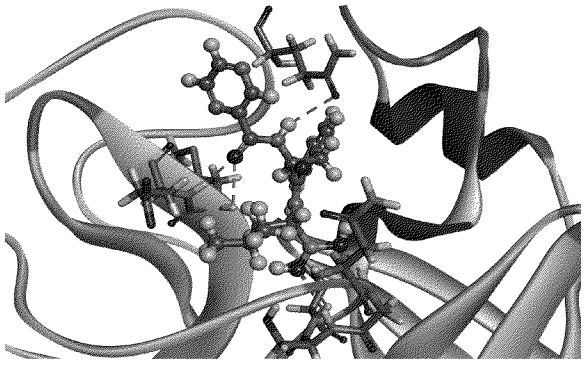
3 Discussion

3.1 The structural analysis of top 3 potent drug candidates

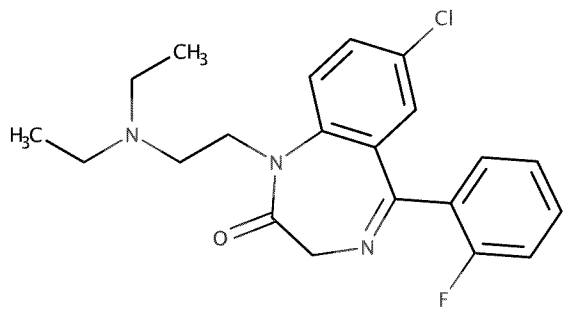
The top-ranking candidate of the existing drugs is Bortezomib (see Figure 3(b)). Its predicted binding affinity to the nCoV-2019 protease is -12.29 kcal/mol. The high binding affinity is due to the strong hydrogen bond network formed between the drug and the nCoV-2019 protease. For example, the strongest hydrogen



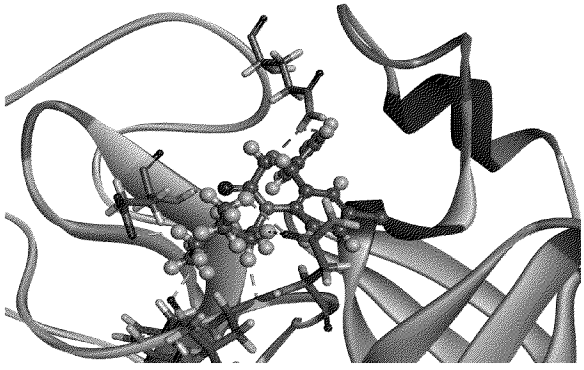
(a) Bortezomib, -12.15 kcal/mol



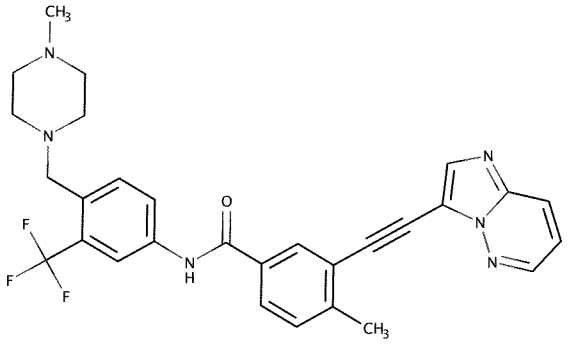
(b) 2019-nCoV protease and Bortezomib complex



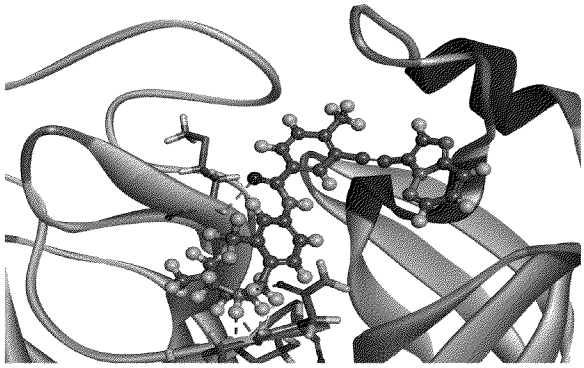
(c) Flurazepam, -10.38 kcal/mol



(d) 2019-nCoV protease and Flurazepam complex



(e) Ponatinib, -10.25 kcal/mol



(f) 2019-nCoV protease and Ponatinib complex

Figure 3: Bortezomib, Flurazepam, Ponatinib and their complexes with 2019-nCoV protease.

bonds are formed by two O atoms in two hydroxyls on the head of Bortezomib and three different aminos in the main chains of residues Gly143, Ser144, and Cys145 of nCoV-2019 protease. Therefore, the head bonds tightly with the side chains of the aforementioned residues. The other two important hydrogen bonds are located at the tail of the drug molecule. The first one is between the O atom in the Hydroxyl on the tail and the two H atoms in the amino acid of the main chain of Glu166 and the methyl of the main chain of Met165. The second one is the H atom in the amino on the tail and the O atom in the side chain of Gln189. As a result, the head, body, and tail of Bortezomib interact firmly with the protease binding site.

The second-best drug is Flurazepam (see Figure 3(d)) with a binding affinity of -10.37 kcal/mol. The strong hydrogen bonds between this molecule and the protease are formed by five different H atoms on the head of the drug with four different O atoms in the main chains of Phe140 , Leu141, as well as the side

chains of Asn142 and Glu166. Another important bond is formed by the H atom in the amino of the side chain of Gln189 with the F atom of the fluorobenzene and one N atom of the 1,4-diazepane in the drug. Additionally, the O atom in the drug adjacent to the 1,4-diazepane is bonded with the amino H atom of the side chain of Glu166. Therefore, the head, tail, and body of the molecule are firmly fixed to the binding site, which promises a strong binding to the 2019-nCoV protease.

The third one, Ponatinib (see Figure 3(f)), has a binding affinity -10.29 kcal/mol. The strong hydrogen bonds between this molecule and the protease are formed by two H atoms of the piperazine with the O atom in the side chain of Ser144 and the main chain of Leu141. Additionally, a bond exists between the O atom in the main chain of the drug and the H atom in the methyl of the main chain of Met165. These hydrogen bonds lead to a high binding affinity with 2019-nCoV protease.

The 3D complexes of 2019-nCoV protease and other 12 potential drugs are given in Supplementary Material.

3.2 Binding affinities of anti-virus protease drugs

It is interesting to analyze the predicted binding affinities of existing antiviral drugs developed as protease inhibitors. Their binding affinities are listed in Table 2. It is interesting to see that except for Boceprevir, which is a protease inhibitor used to treat hepatitis caused by the hepatitis C virus (HCV), the rest of protease inhibitors do not have a strong effect on 2019-nCoV. The predicted values by a recent study [24] are given in the parenthesis. It appears that these values are overestimated.

Table 2: A summary of predicted binding affinities (unit: kcal/mol) of antiviral protease inhibitors. Numbers in parenthesis are results from the literature [24].

DrugID	Predicted Binding Energy	DrugID	Predicted Binding Affinity
Boceprevir	-9.36	Atazanavir	-7.28 (-9.57)
Tipranavir	-8.87	Ritonavir	-7.19 (-8.47)
Fosamprenavir	-7.82	Lopinavir	-7.12
Saquinavir	-7.75	Darunavir	-7.05
Simeprevir	-7.52 (-8.29)	Nelfinavir	-6.74
Telaprevir	-7.50	Amprenavir	-6.73
Indinavir	-7.46		

4 Material and methods

Our deep learning-based drug repositioning models employ mathematical pose (MathPose) and mathematical deep learning (MathDL) to predict 3D poses and protein-ligand binding affinities. The latter is used as a major criterion for searching anti-2019-nCoV therapies from the existing FDA-approved drugs. We first build a 3D 2019-nCoV 3CL protease structure by using homology modeling. A set of SARS-CoV protease inhibitors are docked to the 3D 2019-nCoV 3CL protease structure using our MathPose. The resulting complexes are used as a set of machine learning training. Additionally, a set of protein-ligand complexes from the PDBBind database is collected as another machine learning training set. Our training accuracy in terms of the Pearson correlation coefficient is higher than 0.99 in all deep learning models.

4.1 3D 2019-nCoV protease structure

Homology modeling, a procedure that constructs an atomic-resolution model of a protein from its amino acid sequence and experimental 3D structure of the related homologous protein, i.e., the "template," is used to generate the 3D structure of 2019-nCoV 3CL protease. The SWISS model (https://swissmodel.expasy.org/) is employed with the protease structure of SARS-CoV (PDB ID: 2A5I [13]) as a template. The sequence identity between the 3CL proteases of SARS-CoV and 2019-nCoV is 96.08%.

4.2 SARS-CoV protease inhibitor dataset

ChEMBL [14], an open database that brings chemical, bioactivity, and genomic data together to translate genomic information into effective new drugs, is employed to construct our 2019-nCoV training set. Considering the high sequence identity between viral proteases of 2019-nCoV and SARS-CoV, we take the protease of SARS-CoV as the input target in ChEMBL and a total 115 ChEMBL IDs of the target can be found. The experimental ΔG values of 2019-nCoV 115 SARS-CoV protease inhibition compounds range from -10.0 kcal/mol to 7.5 kcal/mol. We exclude compounds with positive values, resulting in a total of 84 SARS-nCoV protease inhibition compounds for our machine learning training. A collection of these 84 compounds is given in the Supplementary Materials.

4.3 Binding affinity training set

The PDBbind database is a yearly updated collection of experimentally measured binding affinity data (Kd, Ki, and IC50) for the protein-ligand complexes deposited in the Protein Data Bank (PDB). The PDBbind general set, instead of the high-quality refined set, is chosen as our training set because of the FDA approved drugs involve a wide range of protein targets. In the current work, we use a set of 15,843 X-ray crystal structures of protein-ligand complexes and associated binding affinities from the PDBbind v2018 general set [15]. The information of these complexes is provided in the Supplementary Materials.

4.4 FDA approved drugs

DrugBank (www.drugbank.ca) is a richly annotated, freely accessible online database that integrates massive drug, drug target, drug action, and drug interaction information about FDA-approved drugs with the experimental drugs which are going through the FDA approval process [16]. Due to the high quality and sufficient information contained in, the DrugBank has become one of the most popular reference drug resources used all over the world. A total of 1553 FDA-approved drugs are contained in the DrugBank. However, in the present work, a number of FDA-approved drugs encountered difficulties in docking with the target molecule. Therefore, the MathPose successfully created 3D protein-ligand complex structures for 1465 FDA-approved drugs and 2019-nCoV protease.

4.5 MathDL

MathDL, designed for predicting various druggable properties of 3D molecules [23], is capable of efficiently and accurately encoding the high-dimensional biomolecular interactions into low-dimensional representations. Algebraic graph theory-based algorithms [25], differential geometry, and algebraic topology methods [23] are applied to generate three mathematical representations of data in MathDL. These data

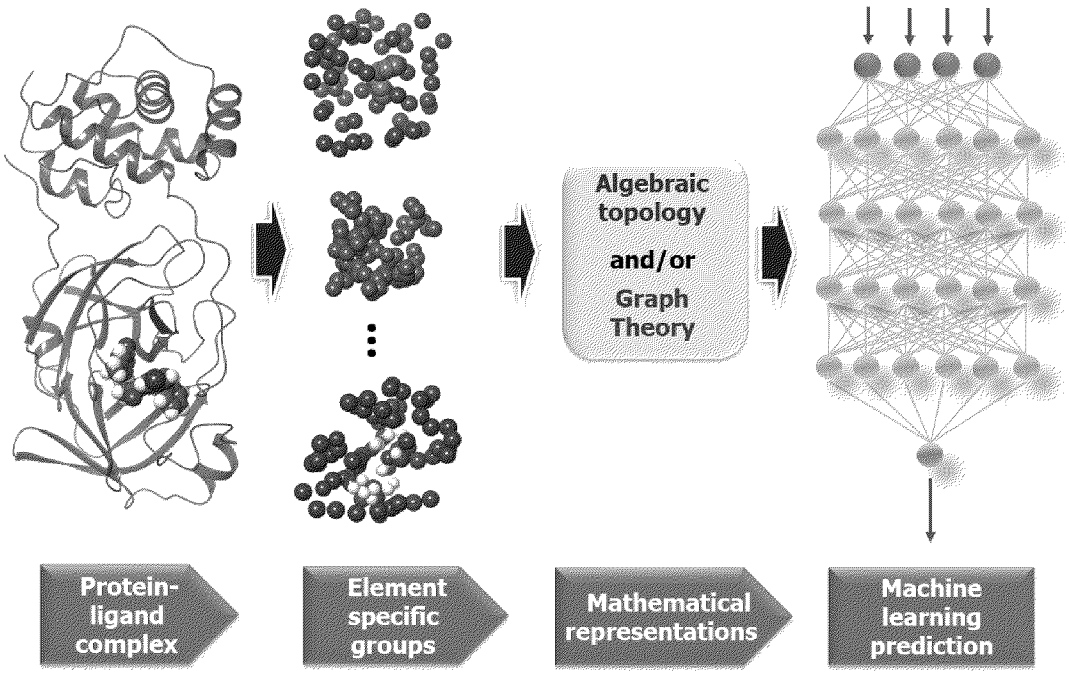


Figure 4: A framework of MathDL energy prediction model which integrates advanced mathematical representations with sophisticated CNN architectures

representations can be integrated with well-designed deep learning models, such as gradient-boosted trees (GBTs) and convolutional neural networks (CNNs), for pose ranking and binding affinity predictions. In D3R Grand Challenges (https://drugdesigndata.org/about/grand-challenge), a worldwide competition series in computer-aided drug design, MathDL had been proved as the top performer in free energy prediction and ranking [22, 23]. Figure 4 illustrates the framework of the MathDL model, which combined the aforementioned mathematical representations with the CNN architecture for druggable properties predictions. The PDBbind 2018 general set [15], along with the SARS 3CL protease related dataset is used in our training process. In this section, we briefly describe the algebraic topology representation used in the present work. Details can be found in the literature [23].

4.5.1 Algebraic topology-based representation

Even with a glimpse of topology, one can realize it dramatically simplifies geometric complexity [9, 17–20]. The study of topology reveals characterizes of different dimensions. As a type of algebraic topology, simplicial homology studies complexes on discrete datasets under various settings, such as the Vietoris-Rips (VR) complex, Čech complex or alpha complex, and identifies the topological invariants of a point-cloud dataset such as atomic coordinates in a protein [26]. Separated components, rings, and cavities can be classified for a given configuration and their numbers are referred to as Betti-0, Betti-1, and Betti-2, respectively. In this topological analysis process, the metrics or coordinates are fully abandoned. Instead, geometric and topological information is captured as data representation. Moreover, as a new development branch of algebraic topology, persistent homology which combines multiscale geometric information and topological invariants to achieve a geometry-enriched topological characteristic, e.g., barcodes. Therefore, the "birth" and "death" of separated components, circles, rings, voids or cavities can be indicated at all spatial scales by topological measurements. Key concepts are briefly shown as following.

In algebraic topology, simplices are the essential building blocks. Let $v_0, v_1, v_2, \cdots, v_k$ be $k+1$ affinely independent points. A (geometric) k-simplex σ^k is the linear combinations of these points in $\mathbb{R}^n$ ($n \geq k$),

whose coefficients are positive and satisfy that their summation equals to 1. For example, a 0, 1, 2, or 3-simplex is considered as a vertex, an edge, a triangle, or a tetrahedron, respectively. A simplicial complex K is a topological space composed of simplices which satisfies that every face of a simplex $\sigma_k \in K$ is also in K and the non-empty intersection of any two simplices is a face for both. To identify the homology group, a k-chain $[\sigma^k]$ is a summation $\sum_i \alpha_i \sigma_i^k$ of k-simplices σ_i^k, and the set of all k-chains of the simplicial complex K equipped with an algebraic field (typically, $\mathbb{Z}_2$) forms an abelian group $C_k(K, \mathbb{Z}_2)$. The homology defined on a series of abelian groups is used to analyze topological invariants which requires boundary operators to connect these chain spaces. The boundary operators $\partial_k : C_k \to C_{k-1}$ for a k-simplex $\sigma^k = \{v_0, v_1, v_2, \cdots, v_k\}$ are homomorphisms defined as $\partial_k \sigma^k = \sum_{i=0}^{k} (-1)^i \{v_0, v_1, \cdots, \hat{v_i}, \cdots, v_k\}$, where $\{v_0, v_1, \cdots, \hat{v_i}, \cdots, v_k\}$ is a $(k-1)$-simplex excluding v_i from the vertex set. Consequently, a important property of boundary operator, $\partial_{k-1}\partial_k = \emptyset$, follows from that boundaries are boundaryless. The algebraic construction to connect a sequence of complexes by boundary maps is called a chain complex

$$\cdots \xrightarrow{\partial_{i+1}} C_i(X) \xrightarrow{\partial_i} C_{i-1}(X) \xrightarrow{\partial_{i-1}} \cdots \xrightarrow{\partial_2} C_1(X) \xrightarrow{\partial_1} C_0(X) \xrightarrow{\partial_0} 0$$

and the kth homology group is the quotient group defined by

$$H_k = Z_k / B_k, \tag{1}$$

where the k-cycle group Z_k and the k-boundary group B_k are the subgroups of C_k defined as, $Z_k = \ker \partial_k = \{c \in C_k \mid \partial_k c = \emptyset\}$, $B_k = \text{im } \partial_{k+1} = \{\partial_{k+1} c \mid c \in C_{k+1}\}$. The aforementioned property implies $B_k \subseteq Z_k \subseteq C_k$. The Betti numbers are defined by the ranks of kth homology group H_k which counts k-dimensional holes, especially, $\beta_0 = \text{rank}(H_0)$ reflects the number of connected components, $\beta_1 = \text{rank}(H_1)$ reflects the number of loops, and $\beta_2 = \text{rank}(H_2)$ reveals the number of voids or cavities. Together, the set of Betti numbers $\{\beta_0, \beta_1, \beta_2, \cdots\}$ indicates the intrinsic topological property of a system.

Persistent homology [18] is devised to track the multiscale topological information over different scales along a filtration. A filtration of a topology space K is a nested sequence of subspaces $\{K^t\}_{t=0,\ldots,m}$ of K such that $\emptyset = K^0 \subseteq K^1 \subseteq K^2 \subseteq \cdots \subseteq K^m = K$. Moreover, on this complex sequence, we obtain a sequence of chain complexes by homomorphisms: $C_*(K^0) \to C_*(K^1) \to \cdots \to C_*(K^m)$ and a homology sequence: $H_*(K^0) \to H_*(K^1) \to \cdots \to H_*(K^m)$, correspondingly. The p-persistent kth homology group of K^t is defined as

$$H_k^{t,p} = Z_k^t / (B_k^{t+p} \bigcap Z_k^t), \tag{2}$$

where $B_k^{t+p} = \text{im}\partial_{k+1}(K^{t+p})$. Intuitively, this homology group records the homology classes of K^t that are persistent at least until K^{t+p}. Under the filtration process, the persistent homology barcodes can be generated. To make use of advanced deep learning algorithms, we vectorize persistent homology barcodes by dividing them into bins and calculating persistence, birth, and death incidents in each bin. Furthermore, the statistics of element-specific persistent homology barcodes are taken into consideration as well in fixed-length features.

4.6 MathPose

MathPose, a 3D pose predictor which converts SMILES strings into 3D poses with references of target molecules, was the top performer in D3R Grand Challenge 4 in predicting the poses of 24 beta-secretase 1 (BACE) binders [23]. For one SMILES string, around 1000 3D structures can be generated by a common docking software tool, i.e., GLIDE [27]. Moreover, a selected set of known complexes is re-docked by the three docking software packages mentioned above to generate at 100 decoy complexes per input ligand as a machine learning training set. The machine learning labels will be the calculated root mean squared deviations (RMSDs) between the decoy and native structures for this training set. Furthermore, MathDL models will be set up and applied to select the top-ranked pose for the given ligand. Additionally, the top poses will be fed into the MathDL for druggable proprieties evaluation.

5 Conclusion

The current pneumonia outbreak caused by a new coronavirus (CoV), called 2019-nCoV in China, has evolved into a global health emergency declared by the World Health Organization. Although there is no effective anti-viral medicine for the 2019-nCoV, the 3CL proteases of 2019-nCoV and SARS-CoV have a sequence identity of 96%, which provides a foundation for us to hypothesize that all potential anti-SARS-CoV chemotherapies are also effective anti-2019-CoV molecules. We build a three-dimensional (3D) 2019-nCoV 3CL protease structure using a SARS-CoV 3CL protease crystal structure as a template and collect a set of 84 SARS-CoV inhibition experimental data. The molecules of this set are docked to the 3D 2019-nCoV 3CL protease structure to form a machine learning training set. Additionally, the PDBbind 2018 general set of 15,843 protein-ligand complexes is also included as an additional machine learning training set. Using these training sets, we develop two deep learning models based on low-dimensional algebraic topology representations of macromolecular complexes. A total of 1465 FDA-approved drugs is evaluated by their binding affinities predicted by the consensus of two models built with 1) a combination of algebraic topology and deep convolutional neural networks (CNNs), and 2) a combination of algebraic topology and deep multitask CNNs. According to the predicted binding affinities, we recommend many FDA-approved drugs as potentially highly potent medications to 2019-nCoV, which serve as a crucial step for the development of anti-2019-nCoV drugs.

Supplementary Materials

Supplementary Materials are available online for 3D structure information and affinities of SARS-CoV inhibitors, FDA-approved drugs, and PDBbind data set.

Acknowledgments

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(A brief summary in Chinese)

潜在的高效抗新冠状病毒药

运用分子生物学, 结构生物学, 药物设计原理, 扑拓学, 大数据, 以及深度学习, 从联邦食品及药物管理局已经批准的1465种药物中筛选出了以下潜在的高效抗新冠病毒药 (按照预测的药物与病毒剪切酶的结合能, i.e, predicted drug-2019-nCoV 3CL protease binding affinity, 由强到弱排列):

1. Bortezomib 万珂, 在台湾的正式商品名为萬科（原用途: 延缓、停止及治疗多发性骨髓瘤和被套细胞淋巴瘤恶化的情况, 属于标靶治疗的新型抗癌药. 潜在抗新冠病毒效果极强. 预测结合能: -12.2 kcal/mol）

2. Flurazepam 盐酸氟西泮（原用途: 抗焦虑药、镇痉剂、镇静剂及肌肉松弛剂. 预测结合能: -10.4 kcal/mol）

3. Ponatinib 普纳替尼（原用途: 白血病治疗药物. 预测结合能: -10.3 kcal/mol）

4. Sorafenib 蕾莎瓦（原用途: 治疗肾细胞癌及肝癌. 预测结合能: -10.0 kcal/mol）

5. Dasatinib 达沙替尼（原用途: 慢性粒细胞性白血病，费城染色体呈阳性的急性髓性白血病该药，前列腺癌等. 预测结合能: -9.9 kcal/mol）

6. Paramethasone 帕拉米松（原用途: 严重的细菌感染和严重的过敏性疾病、各种各种血小板减少性紫癜、粒细胞减少症、严重皮肤病、器官移植的免疫排斥反应、肿瘤的治疗及对糖皮质激素敏感的眼部炎症等. 预测结合能: -9.7 kcal/mol）

7. Clocortolone 氯可托龙（原用途: 各种皮肤病, 例如，湿疹，皮炎，过敏，皮疹. 预测结合能: -9.6 kcal/mol）

8. Flucloxacillin 氟氯西林（原用途: 半合成的耐青霉素酶的青霉素. 预测结合能: -9.6 kcal/mol）

9. Sertindole 舍吲哚（原用途: 非典型抗精神病药物. 预测结合能: -9.5 kcal/mol）

10. Clevidipine 氯维地平（原用途: 治疗高血压. 预测结合能: -9.5 kcal/mol）

11. Aprepitant 阿瑞吡坦胶囊（原用途:止吐. 预测结合能: -9.5 kcal/mol）

12. Atorvastatin 立普妥（原用途: 降低血液胆固醇水平的常见药物. 预测结合能: -9.5 kcal/mol）

13. Cinolazepam 西诺西泮（原用途: 抗焦虑镇静催眠药. 预测结合能: -9.5 kcal/mol）

14. Clofazimine 氯法齐（原用途: 治疗结核病 (TB)、麻风病和其它相关传染病的抗生素. 预测结合能: -9.4 kcal/mol）

15. Fosaprepitant 福沙匹坦（原用途: 一种肿瘤辅助用药. 预测结合能: -9.4 kcal/mol）

另外, 联邦食品及药物管理局已经批准的抗病毒剪切酶的药物中, 分析表明唯有 Boceprevir 博赛泼维（原用途:丙型肝炎蛋白酶抑制剂）可能有一定的效果 (排名18. 预测结合能: -9.3 kcal/mol). 顺便提一下, 以前传的抗艾滋病药, 洛匹那韦/利托那韦片 (Lopinavir/ Ritonavir), 排名很靠后 (预测结合能: -7.1/-7.2 kcal/mol). 达芦那韦 (Darunavir) 排名也很靠后 (预测结合能: -7.1 kcal/mol).

参考文献:

MS ID#: BIORXIV/2020/936013
MS TITLE: Potentially highly potent drugs for 2019-nCoV

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Mark Denison[mark.denison@vumc.org]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; vincent.munster_nih.gov vincent.munster@nih.gov[vincent.munster@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Tue 3/17/2020 9:10:02 AM (UTC-05:00)
Subject: NASEM Standing Committee on EIDs and 21st Century Health Threats
Standing Committee on EIDs and 21st C Health Threats. Details.pdf
SC on EID and 21st Century Threats - One Pager.pdf

Alan, Erik

Here are some details on the NASEM "Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats" – the charge to the committee, and the agenda and membership details from the first call last week. There is a draft doc on research agenda being finalized and sent to OSTP Director also.

This Committee was set up at the request of the OSTP Director, who joined the first call as well as NSC staff, and I'm sure they'll be involved heavily in future calls/reports.

I hope NIH/NIAID can be involved and so you're aware, all of the above info is public domain, and there was a session open to the public for the first meeting.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474

Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>
Sent: Thursday, February 20, 2020 8:18 AM
To: Mark Denison <mark.denison@vumc.org>; aneesh.mehta@emory.edu; Johnson, Reed (NIH/NIAID) [E] <johnsonreed@niaid.nih.gov>; vincent.munster_nih.gov vincent.munster@nih.gov <vincent.munster@nih.gov>; Leo Poon <llmpoon@hku.hk>; Webby, Richard <Richard.Webby@STJUDE.ORG>; malik <malik@hku.hk>; Ghazi Kayali <ghazi@human-link.org>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@STJUDE.ORG>; 'david_topham@urmc.rochester.edu'; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>; Baric, Ralph <rbaric@email.unc.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; zhu huachen <zhuhch@hku.hk>; Aubree Gordon <gordonal@umich.edu>; PETERPALESE <peter.palese@mssm.edu>; 'Krammer, Florian' <florian.krammer@mssm.edu>; Ben Cowling <bcowling@hku.hk>; larry.anderson@emory.edu; jwramme@emory.edu; Baric, Toni C <antoinette_baric@med.unc.edu>; MASATO HATTA <masato.hatta@wisc.edu>; Gabriele Neumann (gabriele.neumann@wisc.edu) <gabriele.neumann@wisc.edu>; Subbarao, Kanta <kanta.subbarao@influenzacentre.org>; Mathur, Punam (NIH/NIAID) [E] <mathurpu@niaid.nih.gov>; jmclellan@austin.utexas.edu; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; gavin.smith@duke-nus.edu.sg
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID) <agf1@CDC.GOV>; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD) <map1@CDC.GOV>; Hall, Aron (CDC/DDID/NCIRD/DVD) <esg3@CDC.GOV>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Lampley, Rebecca (NIH/VRC) [F] <rebecca.lampley@nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Andy Pekosz <apekosz1@jhu.edu>; Topham, David <David_Topham@URMC.Rochester.edu>; Gerber, Susan I. (CDC/DDID/NCIRD/DVD) <bhx1@cdc.gov>; zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E] <brooke.bozick@nih.gov>; martin.linster@duke-nus.edu.sg
Subject: RE: nCoV weekly investigators meeting

Hello everyone,

As we discussed on the last call, it could be useful to share information certain experimental results, especially animal model work, in as close to real time as possible enable better planning of experiments by the entire group.

During the Zika response, the portal that was used for this was LabKey's Open Research Portal: https://openresearch.labkey.com/project/home/begin.view. This is a fully public portal.

Please consider if this platform might work, and we can discuss on our next call including any logistics and support needed for setting up accounts.

Thank you!

Marciela

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: Mark Denison; aneesh.mehta@emory.edu; Johnson, Reed (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E];

martin.linster@duke-nus.edu.sg
Subject: nCoV weekly investigators meeting
When: Tuesday, February 18, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

STANDING COMMITTEE ON EMERGING INFECTIOUS DISEASES AND 21ST CENTURY HEALTH THREATS

Health and Medicine Division

Board on Health Sciences Policy
Board on Global Health

Briefing Materials
Meeting 1
March 11, 2020

Virtual Meeting

For committee use only—Do not circulate

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

TAB 1

Agenda and Remote Participation Information

First Meeting of the Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats

Final Agenda

Wednesday, March 11, 2020, 12:00 p.m. – 5:30 p.m. ET
Virtual Zoom Meeting/Keck 201 for Local Participants

Background:
In response to a request from the Office of Science and Technology Policy (OSTP) and the Office of the Assistant Secretary for Preparedness and Response (ASPR), the National Academies of Sciences, Engineering, and Medicine will convene a standing committee of experts to help inform the federal government on critical science and policy issues related to emerging infectious diseases and other 21st century health threats. The standing committee will include members with expertise in emerging infectious diseases, public health, public health preparedness and response, biological sciences, clinical care and crisis standards of care, risk communication, epidemiology, and regulatory issues, as well as veterinary science, One Health, ethics, and community engagement. The standing committee will provide a venue for the exchange of ideas among federal government agencies, the private sector, and the academic community, as well as other relevant stakeholders.

Meeting Objectives

- Discuss the statement of task (SOT) and role of the standing committee
- Conduct the bias and conflict of interest discussion
- Discuss relevant context and key issues
- Explore potential research priorities arising as a result of the emergence of COVID-19 in the U.S. and globally
- Discuss next steps to move forward on key issues; plan second meeting and identify speakers and topics

Wednesday, March 11, 2020

CLOSED SESSION (COMMITTEE MEMBERS ONLY)

12:00 p.m. **Welcome and Introductions**

- Brief introductions
- Discussion of meeting objectives

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

Andrew Pope
Director, Board on Health Sciences Policy
Health and Medicine Division

Julie Pavlin
Director, Board on Global Health
Health and Medicine Division

12:10 p.m. **Role of National Academies Standing Committees**

Andrew Pope
Director, Board on Health Sciences Policy
Health and Medicine Division

12:15 p.m. **Discussion of Bias and Conflict of Interest**

Lauren Shern
Associate Executive Director
Health and Medicine Division

12:30 p.m. **Committee Discussion with Sponsor to Inform Open Session**

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

OPEN SESSION

SESSION I **Welcoming Remarks, Introductions, and Sponsors' Charge to the Committee**

1:30 p.m. **Welcome and Introductions**

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

Marcia McNutt
President
National Academy of Sciences

Victor Dzau
President
National Academy of Medicine

Gregory Symmes
Chief Program Officer
The National Academies of Sciences, Engineering, and Medicine

1:45 p.m. **Sponsors' Charge to the Committee**

- Discuss the context/purpose for the standing committee
- Review the statement of task

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy

David (Chris) Hassell
Senior Science Advisor
Assistant Secretary for Preparedness and Response
U.S. Department of Health and Human Services

2:00 p.m. **Committee Discussion with the Sponsor**

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

2:30 p.m. *BREAK*

SESSION II **Diagnostics and Viral Characterization**

2:45 p.m. **Presentation of the Issues**

Ian Watson
Assistant Director for Biotechnology & Biosecurity
Office of Science & Technology Policy

Paige Waterman
Assistant Director for Biological Threat Defense
Office of Science & Technology Policy

David (Chris) Hassell
Senior Science Advisor
Assistant Secretary for Preparedness and Response
U.S. Department of Health and Human Services

3:00 p.m. **Committee Discussion of the Issues**

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

SESSION III **Other Selected Topics and Issues**

4:00 p.m. **Discussion of Committee's Selected Topics and Issues**

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

CLOSED SESSION (COMMITTEE ONLY)

5:00 p.m. **Committee Debrief, Next Steps, and Potential Future Meeting Topics**

Harvey Fineberg, *Committee Chair*
President
Gordon and Betty Moore Foundation

5:30 p.m. ***ADJOURN MEETING***

The National Academies of
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TAB 2

Standing Committee Membership Information

The National Academies of

SCIENCES • ENGINEERING • MEDICINE

Health and Medicine Division

Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats

INTERNAL COMMITTEE ROSTER

Harvey Fineberg, M.D., M.P.H. ***(Chair)***
President
Gordon and Betty Moore Foundation
1661 Page Mill Road
Palo Alto, CA 94304-1226
Phone: 650-213-3100
Email: harvey.fineberg@gmail.com
harvey.fineberg@moore.org

Kristian Andersen, Ph.D.
Associate Professor and Director of Infectious Disease Genomics, Scripps Research Translational Institute
The Scripps Research Institute
Phone: 857-389-1742
Email: andersen@scripps.edu

Mary Bassett, M.D., M.P.H.
Director, François-Xavier Bagnoud Professor of the Practice and Human Rights
François-Xavier Bagnoud Center for Health
Department of Social and Behavioral Sciences
Harvard School of Public Health
651 Huntington Avenue
FXB Building, 7th Floor
Boston, MA 02215
Phone: 617-432-4750
Email: mbassett@hsph.harvard.edu
Assistant: Samuel Francis
Phone: 617-432-9239
Email: speisch@hsph.harvard.edu

Trevor Bedford, M.D. M.P.H.
Associate Faculty Member, Vaccine and Infectious Disease Division, Public Health Sciences Division, and Human Biology Division
Fred Hutchinson Cancer Research Center
Email: trevor@bedford.io

Georges Benjamin, M.D.
Executive Director
American Public Health Association
800 I Street, NW
Washington, DC 20001-3710
Phone: 202-777-2430
Email: georges.benjamin@apha.org

Richard Besser, M.D.
President and CEO
Robert Wood Johnson Foundation
50 College Road, East
Princeton, NJ 08540
Phone: 609-627-6614
Email: rbesser@rwjf.org
Assistant: Jill Faulknor
Email: jbaker@rwjf.org

Peter Daszak, Ph.D.
President and CEO
EcoHealth Alliance
460 West 34th St., Ste 1701
New York, NY 10001
Phone: 212-380-4474
Email: daszak@ecohealthalliance.org
Assistant: Allison Andre
Phone: 212-380-4462
Email: andre@ecohealthalliance.org

Ellen Embrey
Managing Partner
Stratitia, Inc.
7801 Huntsman Boulevard
Springfield, VA 22153-3921
Phone: (703) 801-9305
Email: eembrey@stratitia.com

Diane Griffin, M.D., Ph.D.
Distinguished University Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins School of Public Health
615 N. Wolfe Street
Suite E5636
Baltimore, MD 21205
Phone: 410-955-3459
Email: dgriffi6@jhu.edu

Margaret Hamburg, M.D.
Foreign Secretary
National Academy of Medicine
500 Fifth Street, NW, NAS-316
Washington, DC 20001
Phone: 202-334-3882
Email: peggy@hbfam.net

John Hick, M.D.
Associate Medical Director for EMS
Medical Director for EMS
Medical Director of Emergency Medicine
Hennepin County Medical Center
701 Park Ave.
Minneapolic, MN 55415
Phone: 612-873-3131
Email: hick.john@gmail.com

Kent E. Kester, M.D.
Vice President and Head, Translational Sciences and Biomarkers
Sanofi Pasteur
Discovery Dr.
Swiftwater, PA 18370
Phone: 570-957-1924
Email: kent.kester@sanokfi.com

Patricia King, J.D.
Professor Emerita
Georgetown University Law Center
600 New Jersey Avenue, N.W.
Washington, DC 20001-2075
Phone: 202-662-9085
Email: kingp@law.georgetown.edu

Jonna Mazet, D.V.M., M.P.V.M., Ph.D.
Professor of Epidemiology and Disease Ecology and Esecutive Director
One Health Institute
UC Davis School of Veterinary Medicine
Veterinary Medicine 3B Building
944 Garrod Dr.
Davis, CA 95616
Phone: 530-752-7526
Email: jkmazet@ucdavis.edu

Phyllis Meadows, Ph.D., M.S.N., R.N.
Senior Fellow, Health Programs
The Kresge Foundation
3215 W. Big Beaver Road.
Tory, MI 48084
Phone: 248-643-9630
Email: pmeadows@kresge.org

Tara O'Toole, M.D., M.P.H.
Executive Vice-President
In-Q-Tel
2107 Wilson Blvd.
Arlington, VA 22209
Phone: 703-248-3000
Email: totoole@oqt.org
Assistant: Maureen Navish
Phone: 571-206-0595
Email: mnavish@iqt.org

Alexandra Phelan, S.J.D., LL.M., LL.B.
Faculty Research Instructor
Center for Global Heatlh Sciend and Security
Georgetown University
Medical-Dental Building, NW306
3900 Reservoir Road NW
Washington, DC 20007
Email: alexandra.phelan@georgetown.edu

David Relman, M.D.
Thomas C. and Joan M. Merigan Professor of Medicine, and of Microbiology & Immunology
Stanford University
Chief of Infectious Diseases
Veterans Affairs Palo Alto Health Care System
3801 Miranda Ave.
Palo Alto, CA 94304
Phone: 650-852-3308
Email: relman@stanford.edu

Mark Smolinski, M.D. M.P.H.
President
Ending Pandemics
870 Market St.
San Francisco, CA 94102
Email: mark@endingpandemics.org

David Walt, Ph.D.
Hansjörg Wyss Professor of Biologically-Inspired Engineering
Harvard University
Department of Pathology
Brigham and Women's Hospital
60 Fernwood Road HBTM-8002
Boston, MA 02115
Phone: 857-307-1112
Email: dwalt@bwh.harvard.edu

Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats

COMMITTEE MEMBER BIOSKETCHES

Harvey Fineberg, M.D., Ph.D. ***(Chair)***
President
Gordon and Betty Moore Foundation

Harvey Fineberg is president of the Gordon and Betty Moore Foundation. He previously served as president of the Institute of Medicine from 2002 to 2014 and as provost of Harvard University from 1997 to 2001, following 13 years as dean of the Harvard School of Public Health. Fineberg devoted most of his academic career to the fields of health policy and medical decision-making. His past research has focused on the process of policy development and implementation, assessment of medical technology, evaluation and use of vaccines, and dissemination of medical innovations. Fineberg serves on the boards of the Carnegie Endowment for International Peace and the China Medical Board. He helped found and served as president of the Society for Medical Decision Making, previously served on and chaired the board of the William and Flora Hewlett Foundation, and chaired the committee to review the performance of the World Health Organization and the functioning of the International Health Regulations (2005) during the 2009 H1N1 influenza pandemic. Fineberg is co-author of the books *Clinical Decision Analysis*, *Innovators in Physician Education* and *The Epidemic That Never Was*, an analysis of the controversial federal immunization program against swine flu in 1976. He has co-edited several books on such diverse topics as AIDS prevention, vaccine safety, understanding risk in society and global health. He has also authored numerous articles published in professional journals. Fineberg chaired the National Academies committee that produced the 2019 report on *Reproducibility and Replicability in Science*. He earned his bachelor's and doctoral degrees at Harvard and is the recipient of several honorary degrees.

Kristian Andersen, Ph.D.
Associate Professor and Director of Infectious Disease Genomics, Scripps Research Translational Institute
The Scripps Research Institute

Kristian Andersen is an associate professor in the Department of Immunology and Microbiology at Scripps Research, with joint appointments in the Department of Integrative Structural and Computational Biology, and at the Scripps Research Translational Institute. Over the past decade, his research has focused on the complex relationship between host and pathogen. Using a combination of next-generation sequencing, field work, experimentation, and computational biology he has spearheaded large international collaborations investigating the emergence, spread and evolution of deadly pathogens, including SARS-CoV-2, Zika virus, Ebola virus, West Nile virus, and Lassa virus. His work is highly cross-disciplinary and exceptionally collaborative. Kristian earned his doctoral degree from the University of Cambridge and performed postdoctoral work in Pardis Sabeti's group at Harvard University and the Broad Institute.

Mary Bassett, M.D., M.P.H.
Director of the François-Xavier Bagnoud Center for Health and Human Rights
Harvard School of Public Health

Mary Bassett is the Director of the FXB Center for Health and Human Rights at Harvard University, as well as the FXB Professor of the Practice of Health and Human Rights at the Harvard School of Public Health. With more than 30 years of experience in public health, Dr. Mary Travis Bassett has dedicated her career to advancing health equity. Prior to her directorship at the FXB Center, Dr. Bassett served for four years as commissioner of Health for New York City. As commissioner, she worked to ensure that every New York City neighborhood supported the health of its residents, with the goal of closing gaps in population health across the city. Originally from New York City, Dr. Bassett lived in Zimbabwe for nearly 20 years. Previously, she was the Program Director for the African Health Initiative and the Child Well-being Program at the Doris Duke Charitable Foundation. She received her B.A. in History and Science from Harvard University and her M.D. from Columbia University's College of Physicians and Surgeons. She served her medical residency at Harlem Hospital Center, and has a master's degree in Public Health from the University of Washington, where she was a Robert Wood Johnson Clinical Scholar.

Trevor Bedford, Ph.D.
Associate Faculty Member, Vaccine and Infectious Disease Division, Public Health Sciences Division, and Human Biology Division
Fred Hutchinson Cancer Research Center

Trevor Bedford is currently Associate Member of the Vaccine and Infectious Disease Division, the Public Health Sciences Division, and the Human Biology Division at the Fred Hutchinson Cancer Research Center. Dr. Bedford uses powerful computers and complex statistical methods to study the rapid spread and evolution of viruses. Data gathered from these processes help researchers develop successful strategies for monitoring and controlling infectious diseases. His visual representations of viral family trees are used to show how the fate of dangerous outbreaks is often determined by the genetics of the infectious agent, human behavior and geography. Dr. Bedford has applied these techniques to document the worldwide spread of seasonal flu viruses. He is developing models to predict which strains of influenza are likely to be most challenging to humans — data that help inform the crucial early decisions about which strains to include in annual flu shots. He specializes in tracking the evolutionary changes of viruses such as HIV and influenza that use RNA, rather than DNA, to carry their genetic information. RNA viruses are much more prone to rapid mutation, which makes many of them particularly nimble at escaping the human immune system and difficult to stop with vaccines. He is a leading advocate for the immediate release of research analyzing viral evolution during epidemics, fresh information that could make a lifesaving difference. He received his Ph.D. in biology from Harvard University.

Georges Benjamin, M.D.
Executive Director
American Public Health Association

Georges Benjamin is well-known as a health leader, practitioner, and administrator. Dr. Benjamin has served as the executive director of the American Public Health Association, the nation's oldest and largest organization of public health professionals, since December 2002. He is a former secretary of Health for the state of Maryland. Dr. Benjamin is a graduate of the Illinois Institute of Technology and the University Of Illinois College Of Medicine. He is board-certified in internal medicine, a Master of the American College of Physicians, a fellow of the National Academy of Public Administration and a fellow emeritus of the American College of Emergency Physicians. He serves on several nonprofit boards such as Research!America, the University of Maryland Medical System and, the Reagan-Udall Foundation. He is a member of the National Academy of Medicine. In April 2016, President Obama appointed Benjamin

to the National Infrastructure Advisory Council, a council that advises the president on how best to assure the security of the nation's critical infrastructure.

Richard Besser, M.D.
President and CEO
Robert Wood Johnson Foundation

Richard Besser is president and CEO of the Robert Wood Johnson Foundation (RWJF), a position he assumed in April 2017. Dr. Besser is the former acting director for the Centers for Disease Control and Prevention (CDC), and ABC News' former chief health and medical editor. At RWJF, Dr. Besser leads the largest private foundation in the country devoted solely to improving the nation's health. RWJF's work is focused on building a comprehensive Culture of Health that provides everyone in America with a fair and just opportunity to live the healthiest life possible. In Dr. Besser's role at ABC News, he provided medical analysis and reports for all ABC News programs and platforms. His weekly health chats on social media reached millions. Before joining ABC News in 2009, Dr. Besser worked as director of the Coordinating Office for Terrorism Preparedness and Emergency Response at the CDC. In that role, he was responsible for all the CDC's public health emergency preparedness and emergency response activities. He also served as acting director of the CDC from January to June 2009, during which time he led the CDC's response to the H1N1 influenza pandemic. He is a member of the National Academy of Medicine. He received the Surgeon General's Medallion for his leadership during the H1N1 response, and in 2011 he accepted the Dean's Medal for his contributions to public health from the Johns Hopkins Bloomberg School of Public Health. Dr. Besser received his Bachelor of Arts degree in economics from Williams College and medical degree from the University of Pennsylvania. He completed a residency and chief residency in pediatrics at Johns Hopkins University Hospital in Baltimore.

Peter Daszak, Ph.D.
President and CEO
EcoHealth Alliance

Peter Daszak is President of EcoHealth Alliance, a US-based organization that conducts research and outreach programs on global health, conservation, and international development. Dr. Daszak's research has been instrumental in identifying and predicting the origins and impact of emerging diseases across the globe. He is one of the founders of the field of Conservation Medicine and has been instrumental in the growth of EcoHealth, One Health, and now Planetary Health. Dr. Daszak is a member of the National Academy of Medicine and Chair of the NASEM's Forum on Microbial Threats. He is a member of the NRC Advisory Committee to the US Global Change Research Program, the Supervisory Board of the One Health Platform, the One Health Commission Council of Advisors, the CEEZAD External Advisory Board, the Cosmos Club, and the Advisory Council of the Bridge Collaborative. He has served on the IOM Committee on global surveillance for emerging zoonoses, the NRC committee on the future of veterinary research, the International Standing Advisory Board of the Australian Biosecurity CRC; and has advised the Director for Medical Preparedness Policy on the White House National Security Staff on global health issues. Dr. Daszak is a regular advisor to WHO on pathogen prioritization for R&D. He received his Ph.D. in parasitic infectious disease from the University of East London.

Ellen Embrey
Managing Partner
Stratitia, Inc.

Ellen Embrey is Managing Partner of Stratitia, Inc., a consulting firm focused on developing meaningful and innovative strategies, and delivering supporting tools and partnerships to bring them successfully to life. Ms. Embrey brings deep expertise in health and medical issues, as well as a wealth of other experience gained during her extensive federal service. In her last federal role, she performed the duties of

the Assistant Secretary of Defense for Health Affairs and the Director, TRICARE Management Activity during the presidential transition period in 2009-2010. From 2002 to 2009, Ms. Embrey was the Deputy Assistant Secretary of Defense for Force Health Protection and Readiness, leading significant changes in Department of Defense policies and programs affecting deployment and combat casualty medicine, health promotion and preventive medicine, medical readiness and public health emergency preparedness and response. For 9 months in 2001, Ms. Embrey performed the duties of Assistant Secretary of Defense for Reserve Affairs, shaping policies affecting the readiness and use of the National Guard and Reserve in both federal and state status. From 2000 to 2001, she served as Chief of Staff of that office, and from 1998 to 2001, as Deputy Assistant Secretary of Defense for Military Assistance to Civil Authorities, developing policies that shaped the role of the National Guard and Reserve components in supporting homeland security, disaster preparedness, and national disaster response capabilities, including advising the president on such matters in the days and weeks following September 11, 2001. Between 1978 and 1997, Ms. Embrey served in senior-level policy analyst, budget analyst, program analyst, management analyst, and systems analyst positions in the Office of the Assistant Secretary of Defense for Reserve Affairs, the Defense Contract Audit Agency, and the Office of Personnel Management. Ms. Embrey was recognized with the Secretary of Defense's Distinguished Civilian Service Award in 2001 and 2004, and twice received the Meritorious Executive Presidential Rank Award in 2006 and 2009.

Diane Griffin, M.D., Ph.D.
Professor, Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health

Diane Griffin is University Distinguished Service Professor and Alfred and Jill Sommer Chair of the W. Harry Feinstone Department of Molecular Microbiology and Immunology at Johns Hopkins Bloomberg School of Public Health. Dr. Griffin is a virologist recognized for her work on the pathogenesis of viral infections. She is known particularly for her studies on measles and alphavirus encephalomyelitis that have delineated the role of the immune response in virus clearance, vaccine-induced protection from infection, tissue damage and immune suppression. Dr. Griffin was born in Iowa City, Iowa, and grew up in Oklahoma City. She graduated from Augustana College, Rock Island, Illinois with a degree in biology and from Stanford University School of Medicine in 1968 with a Ph.D. in immunology and M.D., followed by a residency in internal medicine. She was a postdoctoral fellow in virology and infectious diseases at Johns Hopkins University School of Medicine and joined the faculty in 1974. She has been president of the American Society for Virology and of the American Society for Microbiology and is a member of both the National Academy of Sciences and the National Academy of Medicine.

Margaret Hamburg, M.D.
Foreign Secretary
National Academy of Medicine

Margaret Hamburg is an internationally recognized leader in public health and medicine, and currently serves as foreign secretary of the National Academy of Medicine and chair of the NTI | bio Advisory Group. She is a former Commissioner of the U.S. Food and Drug Administration (FDA), having served for almost six years. As FDA Commissioner she was known for advancing regulatory science, streamlining and modernizing FDA's regulatory pathways, and globalization of the agency. Before joining FDA, Hamburg was founding vice president and senior scientist at the Nuclear Threat Initiative. Previous government positions include Assistant Secretary for Planning and Evaluation, U.S. Department of Health and Human Services, Health Commissioner for New York City, and Assistant Director of the National Institute of Allergy and Infectious Diseases, National Institutes of Health. She is President-elect of the American Association for the Advancement of Science (AAAS), as well as an elected member of the Council on Foreign Relations and the National Academy of Medicine. Hamburg currently sits on the boards of the Commonwealth Fund, the Simons Foundation, the Urban Institute, the Global Alliance for Vaccines and Immunization, the Parker Institute for Cancer Immunotherapy and the American Museum

of Natural History. She is chair of the Joint Coordinating Group for the Coalition for Epidemic Preparedness and Innovation, and a member of the Harvard University Global Advisory Council, the Global Health Scientific Advisory Committee for the Gates Foundation, the Harvard Medical School Board of Fellows, and the World Dementia Council. Dr. Hamburg earned her B.A. from Harvard College, her M.D. from Harvard Medical School and completed her medical residency at Weill Cornell Medical Center. She is the recipient of multiple honorary degrees and numerous awards.

John Hick, M.D.
Associate Medical Director for EMS
Medical Director of Emergency Medicine
Hennepin County Medical Center

John L. Hick is a faculty emergency physician at Hennepin Healthcare and a Professor of Emergency Medicine at the University of Minnesota. Dr. Hick serves as the deputy medical director for Hennepin County Emergency Medical Services and Medical Director for Emergency Preparedness at HCMC. He is also the Vice-Chair of the Clinical Council for Life Link III helicopter service and medical director for MN TF-1 state US&R team. He served the Minnesota Department of Health as the medical director for the Office of Emergency Preparedness until becoming an Advisor to the Director of OEM at ASPR/HHS where he is the lead editor for the TRACIE healthcare disaster preparedness website. He is the founder and past chair of the Minneapolis/St. Paul Metropolitan Hospital Compact, a 32-hospital mutual aid and planning group active since 2002. He is a national speaker on hospital preparedness issues and has published numerous papers dealing with hospital preparedness for contaminated casualties, personal protective equipment, crisis standards of care, and surge capacity and was honored to serve the Institute of Medicine on their Crisis Standards of Care projects as well as the Forum on Medical and Public Health Preparedness for Disasters and Emergencies. Dr. Hick holds an M.D. from the Mayo Medical School.

Kent E. Kester, M.D.
Vice President and Head, Translational Science and Biomarkers
Sanofi Pasteur

Kent Kester is currently Vice President and Head, Translational Science and Biomarkers at Sanofi Pasteur. In this capacity, Dr. Kester leads a team of over 200 research and clinical professionals in the US and France focused on the translational development of new vaccines. During a 24-year career in the US Army, he worked extensively in clinical vaccine development and led multiple research platforms at the Walter Reed Army Institute of Research, the U.S. Department of Defense's largest and most diverse biomedical research laboratory with a major emphasis on emerging infectious diseases, an institution he later led as its Commander/Director. His final military assignment was as the Associate Dean for Clinical Research in the School of Medicine at the Uniformed Services University of the Health Sciences (USUHS). During his military service, Dr. Kester was appointed as the lead policy advisor to the US Army Surgeon General in both Infectious Diseases and in Medical Research & Development. In these capacities, he worked extensively in the interagency environment and developed a variety of Army and DoD medical policies related to infectious diseases, both clinical and research aspects. Dr. Kester holds an undergraduate degree from Bucknell University and an M.D. from Jefferson Medical College, completing his internship and residency in internal medicine at the University of Maryland and a research fellowship in infectious diseases at the Walter Reed Army Medical Center. Currently a member of the US Government Presidential Advisory Council on Combating Antibiotic-Resistant Bacteria (PACCARB) and the Department of Veterans Affairs Health Services Research & Development Service Merit Review Board, he previously chaired the Steering Committee of the NIAID/USUHS Infectious Disease Clinical Research Program, and has served as a member of the FDA Vaccines & Related Biologics Products Advisory Committee (VRBPAC), the NIAID Advisory Council, and the CDC Office of Infectious Diseases Board of Scientific Counselors. He is the Vice Chair of the National Academy of Medicine Forum on Microbial Threats. Board-certified in both internal medicine and infectious diseases, Dr. Kester

holds faculty appointments at USUHS and the University of Maryland; and is a fellow of the American College of Physicians, the Royal College of Physicians of Edinburgh, the Infectious Disease Society of America, and the American Society of Tropical Medicine and Hygiene. He is a member of the clinical faculty at the University of Maryland Shock Trauma Center in Baltimore.

Patricia King, J.D.
Professor Emerita
Georgetown University Law Center

Patricia King is Professor of Law emeritus at Georgetown University Law Center and an Adjunct Professor in the Department of Health Policy and Management, School of Hygiene and Public Health at Johns Hopkins University. She is the co-author of Cases and Materials on Law, Science and Medicine. She is a member of the National Academy of Medicine, a member of the American Law Institute, a fellow of the Hastings Center and a faculty affiliate of Georgetown's Kennedy Institute of Ethics. Her scholarship focuses on race and genomics, racial disparities in health and reproductive health. Professor King has served on numerous national advisory bodies formed to address the ethical issues generated by developments in science and technology, including the National Commission for the Protection of Human Subjects of Biomedical and Behavioral Research (1974-78), which produced the seminal "Belmont Report," the President's Advisory Committee on Human Radiation Experiments (1994-95), the National Institutes of Health's Embryo Research Panel (co-chair for policy, 1994), the Ethics, Legal and Social Issues Working Group of the NIH's Human Genome Project (1989-95), and the NIH's Recombinant DNA Advisory Committee (1979-81). She has served on numerous boards and Institute of Medicine committees and is currently a member of the Board of Health Sciences Policy of the National Academies. She is also a Director of Mathematica an employee-owned company.She is a graduate of Wheaton College (Massachusetts) and has served as a Trustee and Chair of the Wheaton College Board of Trustees. In 2018 she was designated a Life Trustee by the Wheaton College Board. She graduated from Harvard Law School and is a past member of the Harvard Corporation the governing board of Harvard University. She has received honorary degrees from Wheaton College, Old Dominion University, and Harvard University.

Jonna Mazet, D.V.M., M.P.V.M., Ph.D.
Executive Director, One Health Institute
UC Davis School of Veterinary Medicine

Jonna Mazet is a Professor of Epidemiology and Disease Ecology and Executive Director of the One Health Institute in the UC Davis School of Veterinary Medicine, where she focuses on global health problem solving, especially for emerging infectious disease and conservation challenges. Dr. Mazet is active in international One Health research programs, most notably in relation to disease transmission among wildlife, domestic animals, and people and the ecological drivers of disease emergence. Currently, she is the Global Director of a $175 million viral emergence early warning project, named PREDICT, that has been developed with the US Agency for International Development's (USAID) Emerging Pandemic Threats Program. She was elected to the National Academy of Medicine in 2013 in recognition of her successful and innovative approach to emerging environmental and global health threats and serves on the National Academies' Forum on Microbial Threats, as well as chairs the Academies' One Health Work Group. Jonna joined the UC Global Health Institute Board of Directors as co-vice chair in April 2019. She holds a D.V.M., M.P.V.M., and Ph.D. from UC Davis.

Phyllis Meadows, Ph.D., M.S.N., R.N.
Senior Fellow, Health
The Kresge Foundation

Phyllis Meadows currently serves as the Senior Fellow and Program Advisor for the Kresge Foundation Health Team. In this role, she is responsible for supporting the health team in the development and implementation of investment opportunities within and across the Foundation's various programming areas. Her professional career includes leadership roles in philanthropy, academia, community health and governmental public health. She has previously served in the role of Associate Dean for Public Health Practice and Clinical Professor - Health, Management and Policy with the University of Michigan School of Public Health. She has led several initiatives to expand multi-disciplinary practice in communities, designing the University's first certification program on population health and health equity for medical residents. She is currently a Distinguished Towsley Policy Maker in Residence with the University of Michigan's Gerald Ford School of Public Policy. She has taught and developed graduate level and professional continuing education courses to address emerging health issues, including topics on health policy and public health leadership. Dr. Meadows has extensive experience in public health practice having served in various leadership roles in public health. She has held several official appointments in public health leadership at the state, county and local levels. In her most recent appointment, she served as the Chief Health Officer and Director of Health for the City of Detroit, providing leadership for the department of health, environmental health, infectious diseases, child health, clinical and dental services for the residents of Detroit. Her philanthropic experience includes positions as Program Director for the W.K. Kellogg Foundation - Youth, Education and Higher Education; and advisor for several national initiatives of the Robert Wood Johnson Foundation including the Nurse Executive Leadership Program, Partners in Nursing, and the County Roadmaps project. As a registered nurse, she has worked in both community-based health and hospitals. She currently serves as a Board Member and Advisor for several state level organizations and private foundations focusing on health.

Tara O'Toole, M.D., M.P.H.
Executive Vice President
In-Q-Tel

Tara O'Toole currently serves as Executive Vice President at In-Q-Tel. Dr. O'Toole was confirmed as the Under Secretary for Science and Technology (S&T) at the U.S. Department of Homeland Security (DHS) and served from November 4, 2009 to September 23, 2013. From 2003 to November 2009, Dr. O'Toole was the CEO and Director of the Center for Biosecurity at the University of Pittsburgh Medical Center (UPMC), and Professor of Medicine and of Public Health at the University of Pittsburgh. The Center for Biosecurity of UPMC is an independent organization dedicated to improving the country's resilience to major biological threats. Dr. O'Toole is internationally known for her work on biosecurity and on health and safety issues related to the U.S. nuclear weapons complex. Her publications in the biodefense field include articles on the response to anthrax, smallpox, and plague biological attacks; containment of contagious disease epidemics; biodefense research and development strategies; and hospital preparedness. She is the founding editor of the journal Biosecurity and Bioterrorism: Biodefense Strategy, Practice, and Science. She was a principal author and producer of Dark Winter, an influential exercise conducted in June 2001 to alert national leaders to the dangers of bioterrorist attacks. She was also a principal writer and producer of Atlantic Storm, an international ministerial-level biosecurity exercise held in January 2005. Prior to founding the UPMC in 2003, Dr. O'Toole was one of the original members of the Johns Hopkins Center for Civilian Biodefense Strategies and served as its director from 2001 to 2003. She has served on numerous government and expert advisory committees dealing with biodefense, including panels of the Defense Science Board; the National Academy of Engineering Committee on Combating Terrorism; and the National Academy of Sciences Working Group on Biological Weapons. She served as chair of the Board of the Federation of American Scientists from 2006 to 2007, and in 2006 she was appointed to the board of Google Foundation's International Networked System for Total Early Disease

Detection. From 1993 to 1997, Dr. O'Toole served as Assistant Secretary of Energy for Environment Safety and Health. In this position, she was the principal advisor to the Secretary of Energy on environmental protection and on the health and safety of the approximately 100,000 workers in the U.S. nuclear weapons complex and Department of Energy (DOE) laboratories. She developed the first overall management and safety plan for dealing with the highly enriched uranium, plutonium, spent fuel, and radioactive waste left in place when nuclear weapons production was stopped in the early 1990s. She ran the multi-agency, multimillion-dollar task force that oversaw the government's investigations into human radiation experiments conducted during the Cold War and led the U.S. delegation to Russia to establish the U.S./Russia cooperative effort to study radiationexposure and environmental hazards of the Russian nuclear weapons complex. Prior to her work at DOE, Dr. O'Toole was a senior analyst at the Congressional Office of Technology Assessment, where she directed several projects and studies, including the health impact of pollution resulting from nuclear weapons production. She also served as a consultant to industry and government in matters related to occupational and environmental health; worker participation in workplace safety protection; and organizational change. Dr. O'Toole practiced general internal medicine in community health centers in Baltimore from 1984 to 1988. She is board certified in internal medicine and occupational and environmental health. She has a bachelor's degree from Vassar College, an M.D. from the George Washington University, and a Master of Public Health degree from Johns Hopkins University. She completed internal medicine residency training at Yale University and a fellowship in Occupational and Environmental Medicine at Johns Hopkins University.

Alexandra Phelan, S.J.D., LL.M., LL.B.
Faculty Research Instructor
Center for Global Health Science and Security
Georgetown University

Alexandra Phelan is a member of the Center for Global Health Science and Security and a Faculty Research Instructor in the Department of Microbiology and Immunology at Georgetown University. Dr. Phelan also holds an appointment as Adjunct Professor of Law at Georgetown University Law Center. Dr. Phelan works on legal and policy issues related to infectious diseases, with a particular focus on emerging and reemerging infectious disease outbreaks and international law. She has worked as a consultant for the World Health Organization, the World Bank, and Gavi: the vaccine alliance, and has advised on matters including international law and pathogen sharing, human rights law and Zika, intellectual property law, and contract law. She previously worked for a number of years as a solicitor at a firm in Melbourne, Australia and was admitted to practice to the Supreme Court of Victoria and High Court of Australia in 2010. Dr. Phelan's doctorate examined how overlap between fields of international law – in particular, global health law, international human rights law, and international environmental law – can serve as the catalyst to progressively develop international law to prevent and respond to infectious diseases. She also holds a Master of Laws, specializing in international law, from the Australian National University and a Bachelor of Biomedical Science/Bachelor of Laws (Honours) double degree from Monash University. She also holds a Diploma of Languages (Mandarin Chinese). Dr. Phelan is a General Sir John Monash Scholar and was recognized as an Associate Fellow of the Royal Commonwealth Society in 2015 for her human rights advocacy during the 2013-16 Ebola outbreak.

David Relman, M.D.
Thomas C. and Joan M. Merigan Professor in Medicine, and Chief of Infectious Diseases
Stanford University; VA Palo Alto Health Care System

David Relman is the Thomas C. and Joan M. Merigan Professor in Medicine, and Microbiology and Immunology at Stanford University, and Chief of Infectious Diseases at the Veterans Affairs Palo Alto Health Care System. Dr. Relman is also Senior Fellow at the Freeman Spogli Institute for International Studies (FSI), and served as Science Co-Director at the Center for International Security and Cooperation (2013-2017), at Stanford. He is currently director of a new Biosecurity Initiative at FSI. Relman trained at

MIT and then Harvard Medical School, followed by clinical training in internal medicine and infectious diseases at the Massachusetts General Hospital in Boston, and then a postdoctoral fellowship in microbiology at Stanford. His early research focused on molecular methods for pathogen discovery and over the past 20 years, on the human microbiome. He was elected to the National Academy of Medicine in 2011. Dr. Relman served as vice-chair of the National Research Council Committee that reviewed the science performed for the FBI 2001 Anthrax Letters investigation, chair of the Forum on Microbial Threats (2007-2017), and is currently a member of the Intelligence Community Studies Board (2016-) as well as Chair of a Standing Committee tasked with examining the health-related problems of US embassy personnel stationed overseas, all at the U.S. National Academies of Science. He was a founding member of the National Science Advisory Board on Biosecurity (2005-2014), a member of the Working Group on Biodefense for the President's Council of Advisors on Science and Technology (The White House) (2016), and served as President of the Infectious Diseases Society of America (2012-2013). He holds an M.D. from Harvard Medical School.

Mark Smolinski, M.D., M.P.H.
President
Ending Pandemics

Mark Smolinski currently serves as President of Ending Pandemics. Dr. Smolinksi brings 25 years of experience in applying innovative solutions to improve disease prevention, response, and control across the globe. Mark is leading a well-knit team—bringing together technologists; human, animal, and environmental health experts; and key community stakeholders to co-create tools for early detection, advanced warning, and prevention of pandemic threats. Since 2009, Mark has served as the Chief Medical Officer and Director of Global Health at the Skoll Global Threats Fund (SGTF), where he developed the Ending Pandemics in Our Lifetime Initiative in 2012. His work at SGTF created a solid foundation for the work of Ending Pandemics, which branched out as an independent entity on January 1, 2018. Prior to SGTF, Mark developed the Predict and Prevent Initiative at Google.org, as part of the starting team at Google's philanthropic arm. Working with a team of engineers, Google Flu Trends (a project that had tremendous impact on the use of big data for disease surveillance) was created in partnership with the U.S. Centers for Disease Control. Mark has served as Vice President for Biological Programs at the Nuclear Threat Initiative, a public charity directed by CNN founder Ted Turner and former U.S. Senator Sam Nunn. Before NTI, he led an 18-member expert committee of the National Academy of Medicine on the 2003 landmark report "Microbial Threats to Health: Emergence, Detection, and Response." Mark served as the sixth Luther Terry Fellow in Washington, D.C., in the Office of the U.S. Surgeon General and as an Epidemic Intelligence Officer with the U.S. Centers for Disease Control and Prevention. Mark received his B.S. in Biology and M.D. from the University of Michigan in Ann Arbor. He is board-certified in preventive medicine and public health and holds an M.P.H. from the University of Arizona.

David Walt, Ph.D.
Hansjörg Wyss Professor of Biologically Inspired Engineering
Harvard Medical School

David Walt is a member of the faculty at Harvard Medical School in the Department of Pathology, and a Howard Hughes Medical Institute Professor. Dr. Walt pioneered the use of microwell arrays for single-molecule detection and analysis, which has revolutionized the process of genetic and proteomic sequencing, enabling the cost of DNA sequencing and genotyping to plummet nearly a millionfold in the last decade. His current research employs optical fiber microarrays for the detection and analysis of single enzyme molecules to provide mechanistic insight into enzyme mechanisms. In another project, hhe is also investigating the limits of creating high-density sensing arrays containing thousands of microsensors and nanosensors, and are preparing arrays to perform high-density nucleic acid and protein analysis. Dr. Walt is the Scientific Founder of Illumina, Inc. and Quanterix Corp, and has co-founded several other life sciences startups. Previously, he was a University Professor, Professor of Neuroscience, and Professor of

Oral Medicine at Tufts University. He is a member of the National Academy of Engineering, the National Academy of Medicine, a Fellow of the American Academy of Arts and Sciences, a Fellow of the American Institute for Medical and Biological Engineering, and a Fellow of the National Academy of Inventors. He has received numerous awards and honors, including the 2017 American Chemical Society Kathryn C. Hach Award for Entrepreneurial Success, the 2016 Ralph Adams Award in Bioanalytical Chemistry, the 2014 American Chemical Society Gustavus John Esselen Award, the 2013 Analytical Chemistry Spectrochemical Analysis Award, the 2013 Pittsburgh Analytical Chemistry Award, and the 2010 ACS National Award for Creative Invention. He received a B.S. in chemistry from the University of Michigan and a Ph.D. in chemical biology from SUNY at Stony Brook, and did postdoctoral studies at MIT.

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

TAB 3

Statement of Task

The National Academies of

SCIENCES • ENGINEERING • MEDICINE

Health and Medicine Division

Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats

In response to a request from the Office of Science and Technology Policy (OSTP) and the Office of the Assistant Secretary for Preparedness and Response (ASPR), the National Academies of Sciences, Engineering, and Medicine will convene a standing committee of experts to help inform the federal government on critical science and policy issues related to emerging infectious diseases and other 21st century health threats. The standing committee will include members with expertise in emerging infectious diseases, public health, public health preparedness and response, biological sciences, clinical care and crisis standards of care, risk communication, epidemiology, and regulatory issues, as well as veterinary science, One Health, ethics, and community engagement. The standing committee will provide a venue for the exchange of ideas among federal government agencies, the private sector, and the academic community, as well as other relevant stakeholders.

The standing committee will:

- Stand ready to respond on short notice to requests from the federal government to assess and consider the science and policy implications of an emerging infectious disease or significant public health threat;
- Provide a venue to enable science and policy discussions relevant to the federal government on emerging issues, research, and activities through in-depth knowledge of the sponsor's programs, goals, and objectives;
- Identify opportunities to integrate science into national preparedness and response decision making;
- Explore lessons learned and best practices from previous preparedness and response efforts, and identify opportunities to disseminate that information to a variety of stakeholders;
- Serve as a focal point for national policy discussions by experts and other leaders in the field;
- Consider, identify, and discuss strategies for addressing misinformation; and
- Respond to the federal government's needs for continuing dialog related to strategic planning and program development to address emerging infectious diseases, biosecurity, and public health and medical preparedness.

At the request of the sponsors, the standing committee will be involved in the planning, development, and oversight of related ad hoc activities undertaken by separately appointed committees operating under its auspices.

The standing committee will serve as a focal point for the discussion of scientific, technical, and policy issues relevant to emerging infectious diseases and public health preparedness and response that warrant detailed examination. Topics for discussion with the standing committee may include:

- Technical assistance and/or assessment of response to emerging infectious diseases;
- Availability of and access to information, samples, and other materials to determine the origin and evolution of emerging infectious diseases;
- International coordination and engagement;
- Technical assessment of ecological and evolutionary drivers of disease emergence;
- Approaches to proactive public messaging and strategies to address misinformation;
- Other science and policy issues relevant to emerging infectious diseases and 21st century health threats.

The committee will carry out its charge at its in-person and virtual meetings by gathering evidence from experts, deliberating, and, when necessary, by preparing short reports.

COMMITTEE SPONSORS

White House Office of Science and Technology Policy and HHS Office of Assistant Secretary for Preparedness and Response

PROVISIONAL COMMITTEE ROSTER

Harvey Fineberg, M.D., Ph.D. *(Chair)*
President
Gordon and Betty Moore Foundation

Kristian Andersen, Ph.D.
Associate Professor and Director of Infectious Disease Genomics, Scripps Research Translational Institute
The Scripps Research Institute

Mary Bassett, M.D., M.P.H.
Director of the François-Xavier Bagnoud Center for Health and Human Rights
Harvard School of Public Health

Trevor Bedford, Ph.D.
Associate Faculty Member, Vaccine and Infectious Disease Division, Public Health Sciences Division, and Human Biology Division
Fred Hutchinson Cancer Research Center

Georges Benjamin, M.D.
Executive Director
American Public Health Association

Richard Besser, M.D.
President and CEO
Robert Wood Johnson Foundation

Peter Daszak, Ph.D.
President and CEO
EcoHealth Alliance

Ellen Embrey
Managing Partner
Stratitia, Inc.

Diane Griffin, M.D., Ph.D.
Professor, Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health

Margaret Hamburg, M.D.
Foreign Secretary
National Academy of Medicine

John Hick, M.D.
Associate Medical Director for EMS
Medical Director of Emergency Medicine
Hennepin County Medical Center

Kent E. Kester, M.D.
Vice President and Head, Translational Science and Biomarkers
Sanofi Pasteur

Patricia King, J.D.
Professor Emerita
Georgetown University Law Center

Jonna Mazet, D.V.M., M.P.V.M., Ph.D.
Executive Director, One Health Institute
UC Davis School of Veterinary Medicine

Phyllis Meadows, Ph.D., M.S.N., R.N.
Senior Fellow, Health
The Kresge Foundation

Tara O'Toole, M.D., M.P.H.
Executive Vice President
In-Q-Tel

Alexandra Phelan, S.J.D., LL.M., LL.B.
Faculty Research Instructor
Center for Global Health Science and Security
Georgetown University

David Relman, M.D.
Thomas C. and Joan M. Merigan Professor of Medicine, and of Microbiology & Immunology; Chief of Infectious Diseases
Stanford University; VA Palo Alto Health Care System

Mark Smolinski, M.D., M.P.H.
President
Ending Pandemics

David Walt, Ph.D.
Hansjörg Wyss Professor of Biologically Inspired Engineering
Harvard Medical School

CONTACT INFORMATION

Andrew Pope
Director, Board on Health Sciences Policy
202-334-1739 (office)
apope@nas.edu

ADDITIONAL INFORMATION

For additional information, please visit http://nationalacademies.org/hmd/Activities/PublicHealth/EmergingInfectiousDiseasesand21stCenturyHealthThreats.aspx

The National Academies of
SCIENCES • ENGINEERING • MEDICINE

Health and Medicine Division

Standing Committees: What They Do

Standing committees provide sponsors with an ongoing mechanism to engage the National Academies of Sciences, Engineering, and Medicine, stakeholders, and committee members on specific issues in a variety of ways. They are designed to serve sponsors by helping them address their needs on a continuing basis for short and long-term strategic planning and program development.

Standing committees:

1) Stand ready to respond on short notice to requests and other needs from the sponsor(s);
2) Provide high-level strategic guidance to sponsor(s) on emerging issues, research, and activities through in-depth knowledge of the sponsor's programs, goals, and activities;
3) Serve as a focal point for national policy discussions by experts and other leaders in the field; and
4) Respond to sponsor(s) needs for continuing advice through planning, strategic thinking, and program development.

As part of the ongoing nature of the activity, the standing committee becomes very familiar with the sponsor(s) program/agency. This understanding and familiarity with the sponsor(s) programs facilitates the standing committee's ability to respond quickly and effectively with in-depth knowledge and insight about the sponsor(s) program.

Standing committee activities may include:

- Meeting periodically with the sponsor(s) and others in information-gathering sessions;
- Inviting experts/guests to provide input on the issues that will serve to inform the sponsor and the standing committee in its strategic planning and program development roles; and
- Conducting public outreach, such as through the development of websites and newsletters from the Academies that provides general information about the standing committee's activities or other related initiatives of the Academies.

Standing committee outputs may include:

Type	Product	Source/Origin	Recipient	Process
1	Immediate, **informal verbal feedback and guidance** provided to sponsors at public meetings	Individual Committee Members during meetings	Sponsors	Public meeting discussions

2	**Meeting "Recap,"** which is a high-level summary of issues discussed at a committee meeting	Staff prepares the recap/summary	Sponsors (and Committee Members)	Internal review by HMD staff
3	**Letter Report,** which is a formal report from the committee, based primarily on information presented and discussed at a committee meeting, that may include findings, conclusions, and recommendations on a specific topic	Committee (with Staff support)	Sponsors and the Public	Formal institutional review process
4	**Consensus Report,** which is a separate Academies report (or workshop) prepared by an ad hoc committee appointed specifically for the identified task	The Standing Committee can identify the need for, and recommend to the Academies that they conduct a study	Sponsors and the Public	Standing committees may also develop 'spin off' ideas for workshops and studies that are conducted via separate ad hoc committees (standing committee members may serve on the committees for these ad hoc workshops and studies along with additional members recruited to address the specific workshop or study charge).

EXECUTIVE OFFICE OF THE PRESIDENT
OFFICE OF SCIENCE AND TECHNOLOGY POLICY
WASHINGTON, D.C. 20502

February 3, 2020

Dr. Marcia McNutt
President, National Academy of Sciences
2101 Constitution Ave, N.W.
Washington, D.C., U.S. 20418

SUBJECT: Rapid Response Assessment of 2019-nCoV Data Needs

In support of the Office of Science and Technology's (OSTP) National Science and Technology Committee (NSTC) rapid research response work for the 2019-nCoV response, and the Administration's efforts to characterize and provide evidence-based assessments for outbreak response efforts, I am writing to ask the National Academies of Sciences, Engineering, and Medicine (NASEM) to rapidly examine information and identify data requirements that would help determine the origins of 2019-nCoV, specifically from an evolutionary/structural biology standpoint. I also ask NASEM to consider whether this should include more temporally and geographically diverse clinical isolates, sequences, etc.

Although a widely-disputed paper, "Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Hag," posted on the pre-print server bioRxiv last week has been withdrawn, the response to that manuscript highlights the need to determine information and data requirements as quickly as possible to better perform and validate such analyses of origin. These questions are important not only for this current situation, but to inform future outbreak preparation and better understand animal/human and environmental transmission aspects of coronaviruses. As part of a broader deliberative process, this review will aid preparedness for future events by establishing a process that quickly assembles subject matter experts for evaluating other potentially threatening organisms.

OSTP requests NASEM convene a meeting of experts, particularly world class geneticists, coronavirus experts, and evolutionary biologists, to assess what data, information, and samples are needed to address the unknowns, in order to understand the evolutionary origins of 2019-nCoV and more effectively respond to both the outbreak and any resulting misinformation. I request a letter statement from the National Academies be prepared and provided in response to this solicitation. A more in-depth examination of the issues will be established as a follow up as needed.

Sincerely,

Kelvin K. Droegemeier
Director

February 6, 2020

Kelvin Droegemeier
Director
White House Office of Science and Technology Policy
1650 Pennsylvania Avenue, NW
Washington, D.C. 20504

Dear Dr. Droegemeier:

Thank you for your letter regarding the current outbreak of a new respiratory virus, the 2019 Novel Coronavirus, or 2019-nCoV, which was first detected in Wuhan, China, and has now been reported in a growing number of locations worldwide, including the United States.[1] The request from OSTP is timely given the declaration of a public health emergency and potential for misinformation to confound the response.

In response to your request, we consulted leading experts[2] in the fields of virology, infectious disease genomics, genome sciences, epidemiology, microbiology, immunobiology, coronaviruses, emerging infections, biosecurity, and global health. We wanted their views about the data needs that could help elucidate the origin and evolution of 2019-nCoV.

Research studies to better understand the origin of 2019-nCoV and how it relates to viruses found in bats and other species are already underway.[3] The closest known relative of 2019-nCoV appears to be a coronavirus identified from bat-derived samples collected in China.[4] The experts informed us that additional genomic sequence data from geographically- and temporally-diverse viral samples are needed to determine the origin and evolution of the virus. Samples collected as early as possible in the outbreak in Wuhan and samples from wildlife would be particularly valuable. Understanding the driving forces behind viral evolution would help facilitate the development of more effective strategies for managing the 2019-nCoV outbreak and for preventing future outbreaks. In this regard, we understand from Chunli Bai, President, Chinese Academy of Sciences, and the Alliance of International Science Organizations (ANSO), that the Wuhan National Biosafety Laboratory of the Chinese Academy of Sciences is willing to share isolates of the 2019-nCoV with the international community and is working with the University of Texas Medical Branch and other international research institutions on the specifics for the sharing and distribution of the isolates. International collaboration of this kind is more important than ever to overcome these types of global challenges.

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[1] "2019 Novel Coronavirus (2019-nCoV) Situation Summary." *Centers for Disease Control and Prevention*, 3 Feb. 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html#anchor_1580079137454. Accessed 3 Feb. 2020.

[2] Experts consulted: Kristian G. Andersen (Scripps Research Institute), Ralph Baric (UNC School of Public Health), Trevor Bedford (Fred Hutchinson Cancer Institute), Aravinda Chakravarti (New York University School of Medicine), Peter Daszak (EcoHealth Alliance), Gigi K. Gronvall (Johns Hopkins Bloomberg School of Public Health), Tom Inglesby (Johns Hopkins Center for Health Security), and Stanley Perlman (University of Iowa).

[3] Latinne *et al.* "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications,* in review.

[4] Zhou *et. al.* "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 2020. https://doi.org/10.1038/s41586-020-2012-7 (2020).

The National Academies stand ready to assemble a committee of experts to examine these issues in more detail and provide evidence-based advice to you in an expedited manner if requested. We appreciate your trust in the National Academies and our efforts to advise the nation and inform public policy decisions.

Sincerely,

Marcia McNutt, President National Academy of Sciences	John L. Anderson., President National Academy of Engineering	Victor J. Dzau, President National Academy of Medicine

cc: Secretary Alex M. Azar, Department of Health and Human Services

EXECUTIVE OFFICE OF THE PRESIDENT

OFFICE OF SCIENCE AND TECHNOLOGY POLICY

WASHINGTON, D.C. 20502

February 26, 2020

Dr. Marcia McNutt
President, National Academy of Sciences
2101 Constitution Ave, N.W.
Washington, D.C., U.S. 20418

SUBJECT: National Academies Standing Committee for Emerging Infectious Disease and 21st Century Health Threats

Dear Dr. McNutt, Marcia

Given the complexities of assessing and responding to emerging infectious diseases and other 21st Century health threats, as demonstrated by the present situation with COVID-19, a need exists to establish an ongoing activity to facilitate rapid access to expert, independent perspectives and insights. A neutral venue is needed through which the U.S. Government can engage subject matter experts from the private sector, non-governmental organizations, the academic community, and other relevant stakeholders involved in topics of emerging infectious disease, biosecurity, and public health and medical preparedness. The purpose is to provide a means for examining critical issues in depth and providing strategic input and guidance, based on the best available information and expertise.

To address this need, and stemming from the offer you extended in your letter to me dated February 6, 2020, the Office of Science and Technology Policy (OSTP) and the Department of Health and Human Services (HHS) have been working with Dr. Andy Pope, and his colleagues from your organization, on a request for the National Academies of Sciences, Engineering, and Medicine (NASEM) to establish a Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats. This committee would:

- Stand ready to respond on short notice to requests from the Federal government to assess and consider the science and policy implications of an emerging infectious disease or other significant public health threat;
- Provide a venue to enable science and policy discussions relevant to the Federal government on emerging issues, research, and activities through in-depth knowledge of the sponsor's programs, goals, and objectives;
- Identify opportunities to integrate science into national preparedness and response decision making;
- Explore lessons learned and best practices from previous preparedness and response efforts, and identify opportunities to disseminate that information to a variety of stakeholders;
- Serve as a focal point for national policy discussions with experts and other leaders in the field;
- Consider, identify and discuss strategies for addressing misinformation; and

- Respond to the Federal government's needs for continuing dialog related to strategic planning and program development to address emerging infectious diseases, biosecurity, and public health and medical preparedness.

I would request that the standing committee serve as a focal point for the discussion of scientific, technical, and policy issues relevant to emerging infectious diseases and public health preparedness and response that warrant detailed examination.

The committee members should include experts in emerging infectious diseases, epidemiology, disease modeling and forecasting, genomics, public health, public health preparedness and response, clinical care and crisis standards of care, risk communication, and regulatory issues. The committee would provide a venue for the exchange of ideas among Federal government agencies, the private sector, and the academic community, as well as other relevant stakeholders such as non-profit/philanthropic organizations.

Topics for discussion with the Committee may include:

- Technical assistance and/or assessment of response to emerging infectious diseases;
- Availability of and access to information, samples, and other materials to determine the origin and evolution of emerging infectious diseases;
- International coordination and engagement;
- Technical assessment of ecological and evolutionary drivers of disease emergence
- Approaches to proactive public messaging and strategies to address misinformation;
- Other science and policy issues relevant to emerging infectious diseases and 21st century health threats.

Thank you for your partnership and willingness to bring scientific expertise to bear on this important issue.

Sincerely,

Kelvin K. Droegemeier
Director

Thank you, Marcia!

– Kelvin

The National Academies of

SCIENCES • ENGINEERING • MEDICINE

Health and Medicine Division

Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats

In response to a request from the Office of Science and Technology Policy (OSTP) and the Office of the Assistant Secretary for Preparedness and Response (ASPR), the National Academies of Sciences, Engineering, and Medicine will convene a standing committee of experts to help inform the federal government on critical science and policy issues related to emerging infectious diseases and other 21st century health threats. The standing committee will include approximately 15 members with expertise in emerging infectious diseases, public health, public health preparedness and response, biological sciences, clinical care and crisis standards of care, risk communication, epidemiology, and regulatory issues, as well as veterinary science, One Health, ethics, and community engagement. The standing committee will provide a venue for the exchange of ideas among federal government agencies, the private sector, and the academic community, as well as other relevant stakeholders.

The standing committee will:

- Stand ready to respond on short notice to requests from the federal government to assess and consider the science and policy implications of an emerging infectious disease or significant public health threat;
- Provide a venue to enable science and policy discussions relevant to the federal government on emerging issues, research, and activities through in-depth knowledge of the sponsor's programs, goals, and objectives;
- Identify opportunities to integrate science into national preparedness and response decision making;
- Explore lessons learned and best practices from previous preparedness and response efforts, and identify opportunities to disseminate that information to a variety of stakeholders;
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- Consider, identify, and discuss strategies for addressing misinformation; and
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At the request of the sponsors, the standing committee will be involved in the planning, development, and oversight of related ad hoc activities undertaken by separately appointed committees operating under its auspices.

The standing committee will serve as a focal point for the discussion of scientific, technical, and policy issues relevant to emerging infectious diseases and public health preparedness and response that warrant detailed examination. Topics for discussion with the standing committee may include:

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- Other science and policy issues relevant to emerging infectious diseases and 21st century health threats.

The committee will carry out its charge at its in-person and virtual meetings by gathering evidence from experts, deliberating, and, when necessary, by preparing short reports.

CONTACT INFORMATION

Andrew Pope
Director, Board on Health Sciences Policy
202-334-1739 (office)
apope@nas.edu

To: rbaric@email.unc.edu[rbaric@email.unc.edu]; vineet@email.unc.edu[vineet@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: X X[xuzhxu@hotmail.com]
Sent: Tue 2/4/2020 2:20:49 AM (UTC-06:00)
Subject: Nature publication on coronaviruses

Dear Professor Baric and Menachery,

You may have already received inquiries about your nature paper published in 2015
"A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence"

A "rumor" or "speculation" is being reported in the news, that the current novel coronaviruses outbreak in Wuhan China was originated from laboratory. Owing to the fact that hundreds of people have died and tens of thousands people are infected, I dare to ask the questions below.

1. Could you please kindly clarify where the in vitro and in vivo experiments were performed, Wuhan China or North Carolina, USA? Particularly, the generation/production and recovery of chimeric viruses, in vitro virus replication in primary human airway cells and mouse model.

2. At the end of your study, what has been done with the samples containing coronaviruses? Were those samples destroyed safely or stored away? If stored away, again, in China or USA?

3. At any point of time, were any of the coronaviruses, in vitro or in vivo experiment samples ever shipped to China, if the critical and bulk of experiments were done in North Carolina USA?

I'm looking forward to your clarification.

Many thanks for your help,

Mike

To: czq@wh.iov.cn[czq@wh.iov.cn]; xiaogf@wh.iov.cn[xiaogf@wh.iov.cn]; liud@wh.iov.cn[liud@wh.iov.cn]; Shi, Peiyong[peshi@UTMB.EDU]; infosci@uOttawa.ca[infosci@uOttawa.ca]; gradsci@uOttawa.ca[gradsci@uOttawa.ca]; alumni@uOttawa.ca[alumni@uOttawa.ca]; tdurst@science.uOttawa.ca[tdurst@science.uOttawa.ca]; jkrich@uottawa.ca[jkrich@uottawa.ca]; jlewis@uOttawa.ca[jlewis@uOttawa.ca]; rben@uOttawa.ca[rben@uOttawa.ca]; alison.flynn@uOttawa.ca[alison.flynn@uOttawa.ca]; sgambaro@uOttawa.ca[sgambaro@uOttawa.ca]; maria.musgaard@uOttawa.ca[maria.musgaard@uOttawa.ca]; wogilvie@science.uOttawa.ca[wogilvie@science.uOttawa.ca]; jscaiano@uOttawa.ca[jscaiano@uOttawa.ca]; astolow@uottawa.ca[astolow@uottawa.ca]; dete@uOttawa.ca[dete@uOttawa.ca]; twoo@uOttawa.ca[twoo@uOttawa.ca]
From: YURIY YAKUBTSOV[science-kyiv@ukr.net]
Sent: Tue 4/21/2020 10:17:36 AM (UTC-05:00)
Subject: Cooperation wanted

Dear Scientist,

I want to cooperate with you on "Selecting plants (grass, herbs) for Inhalated Theraputic Treatment of Coronovirus infected humans to stop the spread".

Goal of this online resarch : to find plants (grass, herbs) that will stop the demonic Virus spread.

Base and mechanism of action:

Lord Allah Sky Father planted herbs (or minerals like salt) that release bioprotectors to help humans in difficult times of demon attacks.We need to find the exatle plant mixture on the Planet to help people. We will work like bees, who select flowers and lets show like ants - how cooperative scientists can be worldwide.

How to join: send your email with idias to everybody and start applying.

Financing required: to pay all scientists for their work use Financial Department who can request officially for an additional emission of currency from local Central Banks in your country.

Equipment o be used: any inhalator can be loaded in your region.

Motivation videos and audios:
https://www.youtube.com/watch?v=SZakLr9bH2A
https://www.youtube.com/watch?v=aICW1JRpE5E&t=1883s
https://www.youtube.com/watch?v=WCX50GiR6QU
https://www.youtube.com/watch?v=WCX50GiR6QU
https://www.youtube.com/watch?v=C7vvPXz-Qes
https://www.youtube.com/watch?v=CBwh1OXw6uI
https://www.youtube.com/watch?v=x6UITRjhijI

Methodology Developer:

YURIY YAKUBTSOV,
Master of Biochemistry, Multidisciplinary Scientist

VIBER + 38-099-432-12-04

Location : Kiev, Ukraine
Graduated from: https://science.uottawa.ca/en and https://biology.univ.kiev.ua/
Publication: https://www.ncbi.nlm.nih.gov/pubmed/18525259

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Department of Global Communications
United Nations Headquarters
New York, NY 10017

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Suryanarayanan2_TPIA_0000000550

Expert Opin Drug Saf. Author manuscript; available in PMC 2015 Aug 7.
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Expert Opin Drug Saf. 2009 Jul; 8(4): 435–449.
doi: 10.1517/14740330903036083
PMCID: PMC4527977
NIHMSID: NIHMS710030
PMID: 19538104

Inhaled therapeutics for prevention and treatment of pneumonia

Amar Safdar, MD,† Samuel A. Shelburne, Scott E. Evans, and Burton F. Dickey

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Abstract

Go to:

The lungs are the most common site of serious infection owing to their large surface area exposed to the external environment and minimum barrier defense. However, this architecture makes the lungs readily available for topical therapy. Therapeutic aerosols include those directed towards improving mucociliary clearance of pathogens, stimulation of innate resistance to microbial infection, cytokine stimulation of immune function and delivery of antibiotics. In our opinion inhaled antimicrobials are underused, especially in patients with difficult-to-treat lung infections. The use of inhaled antimicrobial therapy has become an important part of the treatment of airway infection with *Pseudomonas aeruginosa* in cystic fibrosis and the prevention of invasive fungal infection in patients undergoing heart and lung transplantation. Cytokine inhaled therapy has also been explored in the treatment of neoplastic and infectious disease. The choice of pulmonary drug delivery systems remains critical as air-jet and ultrasonic nebulizer may deliver sub-optimum drug concentration if not used properly. In future development of this field, we recommend an emphasis on the study of the use of aerosolized hypertonic saline solution to reduce pathogen burden in the airways of subjects infected with microbes of low virulence, stimulation of innate resistance to prevent pneumonia in immunocompromised subjects using cytokines or synthetic pathogen-associated molecular pattern analogues and more opportunities for the use of inhaled antimicrobials. These therapeutics are still in their infancy but show great promise.

Keywords: amikacin, antifungal, antiviral, aspergillosis, cancer, colistin, cytokine, inhaled tobramycin, innate immunity, pneumonia, Pseudomonas, transplantation, vancomycin, ventilator-associated pneumonia, zygomycosis

1. Introduction

Go to:

тельных и хронических болезнях (туберкулез, нагноения, новообразования, системные болезни крови, алкоголизм и др.) или при длительном применении иммунодепрессивных препаратов.

Симптомы, течение. Выделяют 4 формы бронхолегочного аспергиллеза. Легкая форма протекает как быстропреходящий острый трахеобронхит. Для аллергического бронхиального аспергиллеза характерны транзиторные легочные инфильтраты, эозинофилия, лихорадка, бронхоспазм; мокрота может иметь коричневый оттенок, иногда откашливаются слепки бронхов; течение может быть длительным с повторными обострениями и развитием тяжелой бронхиальной астмы; в ряде случаев наступает выздоровление. Аспергиллома (колонии из мицелия гриба, свободно лежащие в туберкулезной каверне, в полости абсцесса, бронхоэктазах, участке медленно рассасывающейся пневмонии, инфаркта легкого, в области опухоли) может протекать бессимптомно, но чаще наблюдаются кашель с выделением мокроты без запаха, кровохарканье, потеря массы тела (вплоть до кахексии), высокая температура, боль в груди, прогрессирующее ухудшение состояния. Некротическая форма легочного аспергиллеза протекает с выраженной интоксикацией, лихорадкой.

В диагностике используют данные рентгенологического исследования, посевов мокроты, серологических методов.

Лечение. Эффективен амфотерицин В. Суточную дозу (250 ЕД/кг) вводят в 450 мл 5% раствора стерильной глюкозы в/в капельно в течение 4—6 ч через день или 2 раза в неделю в течение 4—8 нед; ингаляции 50 000 ЕД амфотерицина В в 10 мл воды для инъекций производят 1—2 раза в день в течение 10—14 дней. Противогрибковое действие препарата усиливается при сочетании с рифампицином. Амфотерицин В обладает способностью к кумулированию, нейро-нефро- и гепатотоксичен.

БРОНХИАЛЬНАЯ АСТМА — хроническое рецили-

мый по 300—500 мл 0,1% раствора [illegible] капельно в течение 3—4 ч ежедневно или через день.

Эффективность сульфаниламидов и антибиотиков при пневмониях, как правило, выявляется к концу первых суток лечения, но не позже 3 дней их применения; после этого срока при отсутствии терапевтического эффекта назначенный препарат следует заменить другим. Но и в случаях положительного эффекта желательна смена препарата (препаратов) через каждые 5—6 дней. Антибактериальная терапия контролируется клиническими и параклиническими методами как для оценки ее эффективности, так и для выявления непереносимости (особенно лекарственной аллергии и гемоцитодепрессивного действия).

При тяжелых вирусно-бактериальных пневмониях, нередко возникающих вследствие взаимодействия вируса гриппа и стафилококка, наряду с внутривенно вводимыми антибиотиками широкого спектра действия показано введение специфического донорского противогриппозного γ-глобулина по 3—6 мл, при необходимости повторно каждые 4—6 ч, в первые 2 дня болезни. Применяют также дезинтоксикационные средства (гемодез и др.).

При выраженной тахикардии, снижении систолического давления до 100 мм рт. ст. и ниже больным пневмониями назначают строфантин (0,05% раствор по 0,25—0,5 мл в/в 1 раз в день), кордиамин (по 2 мл в/м или в/в 3—4 раза в день), сульфокамфокаин (по 2 мл в/м 10% раствора 2—4 раза в день). При выраженной одышке и цианозе назначают длительные ингаляции увлажненного кислорода. При пневмонии, развившейся на фоне хронического обструктивного бронхита, эмфиземы легких, концентрации кислорода не должны превышать 30%, а ингаляции его контролируют исследованием кислотно-щелочного баланса. Используют безаппаратную физиотерапию (круговые банки, аппликации парафина, озокерита, лечебной грязи), после нормализации температуры тела можно назначить ко-

ротковолновую диатермию, электрическое поле УВЧ и др. При тяжелом течении острых и обострении хронических пневмоний, осложненных острой или хронической дыхательной недостаточностью, больных помещают в палаты интенсивной терапии; может быть проведен бронхоскопический дренаж, при артериальной гиперкапнии — вспомогательная искусственная вентиляция легких. При развитии отека легких, инфекционно-токсического шока и других тяжелых осложнений лечение больных пневмонией ведут совместно с реаниматологом.

Выписанные из стационара в период клинического выздоровления или ремиссии лица, перенесшие пневмонию, должны быть взяты под диспансерное наблюдение. Для проведения реабилитации их можно направлять в местные санатории. Больные хронической пневмонией без выраженного нагноительного процесса и легочно-сердечной недостаточности II — III стадии в фазе ремиссии могут быть направлены на лечение на курорты Южного берега Крыма, горные климатические курорты Кавказа, Алтая, в санатории Подмосковья, Приморья, Сибири и др.

Прогноз при пневмониях значительно улучшился с начала применения антибактериальных средств. Но он остается серьезным при стафилококковых и «фридлендеровских» пневмониях, при часто рецидивирующих хронических пневмониях, осложненных обструктивным процессом, дыхательной и легочно-сердечной недостаточностью, а также при возникновении пневмонии у лиц с тяжелыми болезнями сердечно-сосудистой и других систем. Летальность от пневмонии в этих случаях остается высокой.

ПНЕВМОСКЛЕРОЗ — развитие в легких соединительной ткани как исход неспецифического (пневмонии, бронхиты) или специфического (туберкулез, сифилис) воспалительного процесса, а также пневмокониозов, длительного застоя в малом круге кровообращения

To: LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Bente, Dennis A.[dabente@UTMB.EDU]; yzm@wh.iov.cn[yzm@wh.iov.cn]; hanxia@wh.iov.cn[hanxia@wh.iov.cn]
From: Shan, Chao[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=3306114A447E496CB9EBA019AE29AE6E-SHAN, CHAO]
Sent: Fri 5/3/2019 8:36:45 PM (UTC-05:00)
Subject: Re: Wuhan CCHFV application

Hi Dr. LeDuc,

Many thanks for your comments. I modified the proposal based on your comments.

Best,

Chao

From: LeDuc, James W.
Sent: Friday, May 3, 2019 1:56:10 PM
To: Shan, Chao; Shi, Pei yong; Bente, Dennis A.; yzm@wh.iov.cn; hanxia@wh.iov.cn
Subject: RE: Wuhan CCHFV application

Please see attached with some minor edits and questions in track change. Very nicely done! Good luck to us all!

Jim

James W. Le Duc, Ph.D.

Director

Galveston National Laboratory

University of Texas Medical Branch

Galveston, TX 77555-0610

(t) 409-266-6500

(f) 409-266-6810

(m) 409-789-2012

From: Shan, Chao <chshan@UTMB.EDU>
Sent: Friday, May 03, 2019 11:05 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; yzm@wh.iov.cn; hanxia@wh.iov.cn
Subject: Wuhan CCHFV application

Dear All,

Here is the application I wrote with help from Han for Wuhan collaboration. Please take a look and let me know if anything needs to be changed.

Thanks very much for all the supports from you.

Best,

Chao

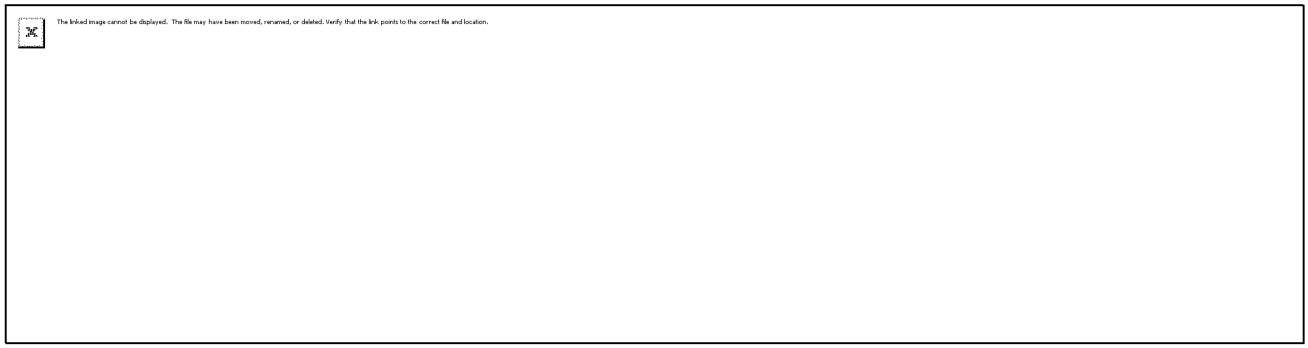
From: LeDuc, James W.
Sent: Friday, July 24, 2020 8:23 PM
To: zengli Shi; Yuan Zhiming; Shi, Pei yong
Subject: Fwd: Weekly Roundup of AJTMH COVID-19 Articles, 7/24

You May find the first two papers of special interest.

Best wishes. Jim
Sent from my iPhone

Begin forwarded message:

From: ASTMH <info@astmh.org>
Date: July 24, 2020 at 4:04:55 PM CDT
To: "LeDuc, James W." <jwleduc@UTMB.EDU>
Subject: Weekly Roundup of AJTMH COVID-19 Articles, 7/24
Reply-To: info@astmh.org



Weekly Roundup of COVID-19 Articles

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All COVID-19 articles are being made freely available on the *Journal* website. Click here for the most up-to-date list of what's been published.

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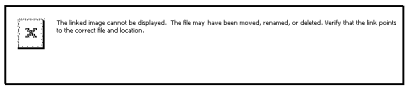

From: LeDuc, James W. [/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: 4/3/2020 12:48:26 PM
To: Shi, Pei yong [peshi@UTMB.EDU]; Yuan Zhiming [yzm@wh.iov.cn]; zlshi [zlshi@wh.iov.cn]
Subject: How did covid-19 begin? Its initial origin story is shaky. from The Washington Post

https://www.washingtonpost.com/opinions/global-opinions/how-did-covid-19-begin-its-initial-origin-story-is-shaky/2020/04/02/1475d488-7521-11ea-87da-77a8136c1a6d_story.html

Please see link to article that appeared today in the Washington Post. I've has inquiries already. Any information you might have to address the work done in the Wuhan CDC would be helpful. BSL2 work there on coronaviruses? True?

Thanks, and I hope you are all well. Things are heating up here but so far everyone is well.

Best wishes, Jim

From: LeDuc, James W.
Sent: Wednesday, February 12, 2020 8:42 AM
To: Shi, Pei yong; df@wh.iov.cn; zlshi
Cc: yzm; wangyy; Ksiazek, Thomas G.
Subject: RE: RE: sharing of isolates of 2019nCoV

I strongly agree. We need to show international scientific collaborations at this time of potentially global crisis.

Thank you Fei for your continued efforts.

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, February 12, 2020 7:10 AM
To: df@wh.iov.cn; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: RE: RE: sharing of isolates of 2019nCoV

Thanks, Fei
Although US CDC has already shared the virus isolate with a number of US institutions (including UTMB) last week, it is still important to successfully transfer and share the isolate(s) from China.
Best,

- Pei-Yong

From: df@wh.iov.cn <df@wh.iov.cn>
Sent: Wednesday, February 12, 2020 3:34 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: RE: sharing of isolates of 2019nCoV

No prompt reply from the Custom until today. President Bai is trying to push it in Beijing. Please wait for a while.

With best

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong
Date: 2020-02-05 20:41
To: df@wh.iov.cn; zlshi
CC: LeDuc, James W.; yzm; wangyy; Ksiazek, Thomas G.
Subject: RE: FW: sharing of isolates of 2019nCoV

Hi Fei,
Thanks for the update. We look forward to further progress.
Best,

- Pei-Yong

From: df@wh.iov.cn <df@wh.iov.cn>
Sent: Wednesday, February 5, 2020 5:57 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; zlshi <zlshi@wh.iov.cn>
Cc: LeDuc, James W. <jwleduc@UTMB.EDU>; yzm <yzm@wh.iov.cn>; wangyy <wangyy@wh.iov.cn>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: Re: FW: sharing of isolates of 2019nCoV

Thanks for your information.
We are trying to discuss this with the General Administration of Customs in Beijing directly.
I will keep on contacting with you.

Best wishes,
Fei

Dr. Fei Deng
Virus Resource and Bioinformation Center,
Wuhan Institute of Virology, Chinese Academy of Sciences.
Tel/Fax:0086-27-87198465
Email: df@wh.iov.cn

From: Shi, Pei yong

Date: 2020-02-04 22:52
To: df@wh.iov.cn; zlshi
CC: LeDuc, James W.; Yuan Zhiming; wangyy@wh.iov.cn; Ksiazek, Thomas G.
Subject: FW: sharing of isolates of 2019nCoV
Dear Fei and Zhengli,

Please see the response from President Bai. Zhiming and Yanyi were copied on the original email. Let us know anything we could help to facilitate the isolate transfer.

Best regards,

• Pei-Yong

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Tuesday, February 4, 2020 8:39 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: FW: sharing of isolates of 2019nCoV

From: "president-office@cas.cn" <president-office@cas.cn>
Date: February 3, 2020 at 11:20:56 PM EST
To: dgriffi6 <dgriffi6@jhmi.edu>, MHamburg <MHamburg@nas.edu>
Cc: mlowenth <mlowenth@nas.edu>, Peggy Hamburg <peggy@hbfam.net>, jwleduc <jwleduc@nas.edu>, jhilderbr <jhilderbr@arizona.edu>, BRsek <BRsek@nas.edu>, jboright <jboright@nas.edu>, clbai <clbai@cas.cn>, zhangyp <zhangyp@cashq.ac.cn>, gaof <gaof@im.ac.cn>, jh-cao <jh-cao@cashq.ac.cn>, liyin <liyin@cashq.ac.cn>, sunhui <sunhui@cashq.ac.cn>, wangyy <wangyy@wh.iov.cn>, yzm <yzm@wh.iov.cn>
Subject: sharing of isolates of 2019nCoV

Diane E. Griffin, Vice President, NAS,
Margaret Hamburg, Foreign Secretary, NAM

Dear Prof. Griffin and Prof. Hamburg,

Thank you for your concerns on the recent outbreak of the 2019 novo-coronavirus epidemic. Upon receiving your letter dated January 28, my colleagues have discussed with Dr. George Fu Gao and other experts and we are willing to share isolates of the 2019 nCoV with the international community. We believe this is critical to engaging joint international efforts to contain the spread of the virus.

The National Biosafety Laboratory Wuhan of the Chinese Academy of Sciences is prepared and willing to work with The University of Texas Medical Branch and

other international research institutions on the specifics for the sharing and distribution of the isolates. We are in the process of getting it ready.

I look forward to hearing your further advice on this matter.

With best regards,

Chunli Bai

Chunli Bai
President
Chinese Academy of Sciences
The Alliance of International Science Organizations (ANSO)

From: jwleduc@UTMB.EDU
Sent: Friday, July 24, 2020 8:23 PM
To: zengli Shi; Yuan Zhiming; Shi, Pei yong
Subject: Fwd: Weekly Roundup of AJTMH COVID-19 Articles, 7/24

You May find the first two papers of special interest.

Best wishes. Jim
Sent from my iPhone

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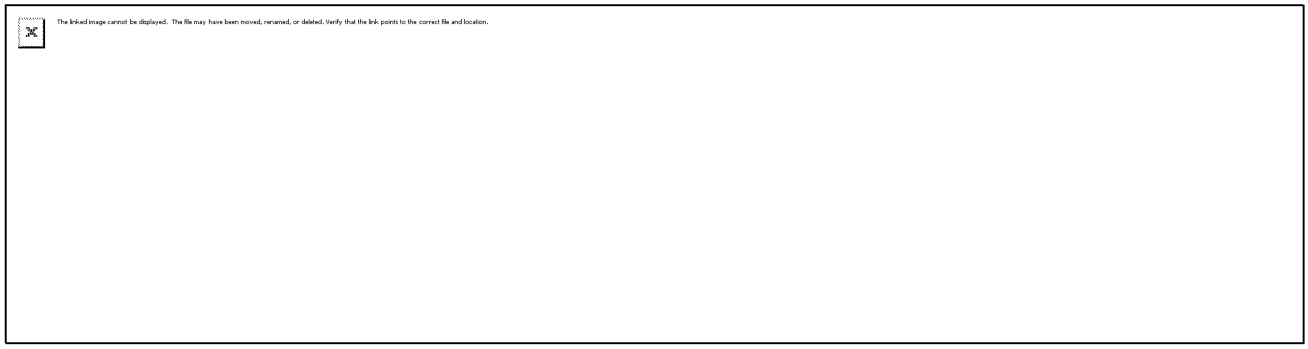
Subject: Weekly Roundup of AJTMH COVID-19 Articles, 7/24
Reply-To: info@astmh.org



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Every donation helps us continue to work towards our mission of reducing the worldwide burden of tropical infectious diseases and improving global health.

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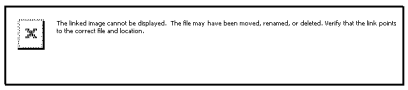

From: Jiang, Wei <jianw@musc.edu>
Sent: Thursday, November 28, 2019 11:14 AM
To: Liu, Shan-Lu; zhengzhiming4@gmail.com; haitguo@iupui.edu; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; wjma@ksu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; shitao.li@okstate.edu; Shan.lu@umassmed.edu; Hu, Haitao; wenzheho@temple.edu; Qfeng4 @central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2 @unl.edu; qiyi.tang@howard.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518 @umd.edu; gaos8@upmc.edu; pewang@uchc.edu; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@ 163.com; xfyu1@zju.edu.cn; bzhao@partners.org; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jun.zhu@nih.gov; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; xiangguo.qiu@canada.ca; Feng Shao; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan; Zhang, Rong; liliwang@upenn.edu; Linheng Li; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; wu@crystal.harvard.edu; Sun.Jie@mayo.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao; Qu, Feng; Hezhao.Ji@umanitoba.ca; Li, Zihai; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; wxiao@temple.edu; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; pzheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong; shuping_tong_md@brown.edu; pinghuif@usc.edu; gaof@im.ac.cn
Subject: Re: Happy Thanksgiving and meeting next year, June 12-13, 2020

Thank you for sharing the information, this was a fantastic meeting, I did enjoy it at Kunming!

Wei Jiang, M.D. & M.S

Associate Professor
Department of Microbiology and Immunology
Division of Infectious Diseases, Department of Medicine
Medical University of South Carolina
173 Ashley Ave. BSB208D
Charleston, SC 29425
Lab phone 843-876-2457
jianw@musc.edu

From: Liu, Shan-Lu <liu.6244@osu.edu>
Sent: Thursday, November 28, 2019 10:57 AM
To: zhengzhiming4@gmail.com <zhengzhiming4@gmail.com>; haitguo@iupui.edu <haitguo@iupui.edu>; tzhou@mail.nih.gov <tzhou@mail.nih.gov>; GCheng@mednet.ucla.edu <GCheng@mednet.ucla.edu>; liangy@umn.edu <liangy@umn.edu>; rli@vcu.edu <rli@vcu.edu>; wjma@ksu.edu <wjma@ksu.edu>; xjmeng@vt.edu <xjmeng@vt.edu>; Zhijian.Chen@UTSouthwestern.edu <Zhijian.Chen@UTSouthwestern.edu>; mluo@gsu.edu <mluo@gsu.edu>; zhangyj@umd.edu <zhangyj@umd.edu>; xzhu1@umd.edu <xzhu1@umd.edu>; jqiu@kumc.edu <jqiu@kumc.edu>; lijun@uic.edu <lijun@uic.edu>; fengwei.bai@usm.edu <fengwei.bai@usm.edu>; andyu@iupui.edu <andyu@iupui.edu>; reachxw@vt.edu <reachxw@vt.edu>; gluo@uab.edu <gluo@uab.edu>; ldu@nybc.org <ldu@nybc.org>; hxu@tulane.edu <hxu@tulane.edu>; liu_fy@berkeley.edu <liu_fy@berkeley.edu>; shitao.li@okstate.edu <shitao.li@okstate.edu>; Shan.lu@umassmed.edu <Shan.lu@umassmed.edu>; haihu@UTMB.edu <haihu@UTMB.edu>; wenzheho@temple.edu <wenzheho@temple.edu>; Qfeng4@central.uh.edu <Qfeng4@central.uh.edu>; tang@bio.fsu.edu <tang@bio.fsu.edu>; feng.li@sdstate.edu <feng.li@sdstate.edu>; ruilu@lsu.edu <ruilu@lsu.edu>; sxiang2@unl.edu <sxiang2@unl.edu>; qiyi.tang@howard.edu <qiyi.tang@howard.edu>; dingsw@ucr.edu <dingsw@ucr.edu>; guohua@missouri.edu <guohua@missouri.edu>; bling@tulane.edu <bling@tulane.edu>; junwang@pharmacy.arizona.edu <junwang@pharmacy.arizona.edu>; lifang@umn.edu <lifang@umn.edu>; wang518@umd.edu <wang518@umd.edu>; gaos8@upmc.edu <gaos8@upmc.edu>; pewang@uchc.edu <pewang@uchc.edu>; xiangy@uthscsa.edu <xiangy@uthscsa.edu>; fzhu@bio.fsu.edu <fzhu@bio.fsu.edu>; chen.liang@mcgill.ca <chen.liang@mcgill.ca>; lyuan@vt.edu <lyuan@vt.edu>; fgao@duke.edu <fgao@duke.edu>; wangjw28@163.com <wangjw28@163.com>; xfyu1@zju.edu.cn <xfyu1@zju.edu.cn>; bzhao@partners.org <bzhao@partners.org>; Jiang, Wei <jianw@musc.edu>; zyang@ksu.edu <zyang@ksu.edu>; yu.cong@nih.gov <yu.cong@nih.gov>; weiming.yuan@usc.edu <weiming.yuan@usc.edu>; Zongdi.feng@nationwidechildrens.org <Zongdi.feng@nationwidechildrens.org>; juh13@psu.edu <juh13@psu.edu>; hengx@missouri.edu <hengx@missouri.edu>; lsu@med.unc.edu <lsu@med.unc.edu>; ywu8@gmu.edu <ywu8@gmu.edu>; jwu@whu.edu.cn <jwu@whu.edu.cn>; tshuo@uic.edu <tshuo@uic.edu>; Shibojiang@fudan.edu.cn <Shibojiang@fudan.edu.cn>; sjiang@nybc.org <sjiang@nybc.org>; pinwang@usc.edu <pinwang@usc.edu>; rzhao@som.umaryland.edu <rzhao@som.umaryland.edu>; shuylong@mail.sysu.edu.cn <shuylong@mail.sysu.edu.cn>; xuefeng.liu@georgetown.edu <xuefeng.liu@georgetown.edu>; yuxingli@som.umaryland.edu <yuxingli@som.umaryland.edu>; shixia.wang@umassmed.edu <shixia.wang@umassmed.edu>; yhe@ipbcams.ac.cn <yhe@ipbcams.ac.cn>; Pinghui.feng@usc.edu <Pinghui.feng@usc.edu>; ju-tao.guo@bblumberg.org <ju-tao.guo@bblumberg.org>; lin.liu@okstate.edu <lin.liu@okstate.edu>; hua.zhu@rutgers.edu <hua.zhu@rutgers.edu>; Jinhong.chang@bblumberg.org <Jinhong.chang@bblumberg.org>; jianzhu1012@gmail.com <jianzhu1012@gmail.com>; ronghai@ucr.edu <ronghai@ucr.edu>; jun.zhu@nih.gov <jun.zhu@nih.gov>; jliu4@uams.edu <jliu4@uams.edu>; xiangpeng.kong@med.nyu.edu <xiangpeng.kong@med.nyu.edu>; haoquanwu@outlook.com <haoquanwu@outlook.com>; Wenjun.liu@defence.gov.au <Wenjun.liu@defence.gov.au>; Liang.shan@wustl.edu <Liang.shan@wustl.edu>; hliao@duke.edu <hliao@duke.edu>; yuan2@upenn.edu <yuan2@upenn.edu>; zxing@umn.edu <zxing@umn.edu>; hongmin.li@health.ny.gov <hongmin.li@health.ny.gov>; pzheng@ihv.umaryland.edu <pzheng@ihv.umaryland.edu>; yaliu@ihv.umaryland.edu <yaliu@ihv.umaryland.edu>; jxw103@case.edu <jxw103@case.edu>; xiangguo.qiu@canada.ca <xiangguo.qiu@canada.ca>; Feng Shao <shaofeng@nibs.ac.cn>; zlshi@wh.iov.cn <zlshi@wh.iov.cn>; klan@whu.edu.cn <klan@whu.edu.cn>; zengmsh@mail.sysu.edu.cn <zengmsh@mail.sysu.edu.cn>; Nan Yan <Nan.Yan@UTSouthwestern.edu>; Zhang, Rong <rongzhang@wustl.edu>; liliwang@upenn.edu <liliwang@upenn.edu>; Linheng Li <LIL@stowers.org>; kli1@uthsc.edu <kli1@uthsc.edu>; tsx@case.edu <tsx@case.edu>; ssun@mdanderson.org <ssun@mdanderson.org>; ysang@tnstate.edu <ysang@tnstate.edu>; Liu, Shan-Lu <liu.6244@osu.edu>; wu@crystal.harvard.edu

<wu@crystal.harvard.edu>; Sun.Jie@mayo.edu <Sun.Jie@mayo.edu>; peijun@strubi.ox.ac.uk <peijun@strubi.ox.ac.uk>; jiayu@coh.org <jiayu@coh.org>; bchen@crystal.harvard.edu <bchen@crystal.harvard.edu>; Wen, Haitao <Haitao.Wen@osumc.edu>; Qu, Feng <qu.28@osu.edu>; Hezhao.Ji@umanitoba.ca <Hezhao.Ji@umanitoba.ca>; Li, Zihai <zihai@musc.edu>; zhengyo@msu.edu <zhengyo@msu.edu>; zhanglinqi@tsinghua.edu.cn <zhanglinqi@tsinghua.edu.cn>; wxiao@temple.edu <wxiao@temple.edu>; Whu@temple.edu <Whu@temple.edu>; RSun@mednet.ucla.edu <RSun@mednet.ucla.edu>; Guangping.Gao@umassmed.edu <Guangping.Gao@umassmed.edu>; PZheng@ihv.umaryland.edu <PZheng@ihv.umaryland.edu>; GMSWANG@nus.edu.sg <GMSWANG@nus.edu.sg>; peshi@UTMB.EDU <peshi@UTMB.EDU>; yaliu@ihv.umaryland.edu <yaliu@ihv.umaryland.edu>; ziying-yan@uiowa.edu <ziying-yan@uiowa.edu>; lqiao@luc.edu <lqiao@luc.edu>; yong.xiong@yale.edu <yong.xiong@yale.edu>; Wang, Qiuhong <wang.655@osu.edu>; shuping_tong_md@brown.edu <shuping_tong_md@brown.edu>; pinghuif@usc.edu <pinghuif@usc.edu>; gaof@im.ac.cn <gaof@im.ac.cn>
Subject: Happy Thanksgiving and meeting next year, June 12-13, 2020

Dear friends and colleagues,

I wish you all a great Thanksgiving holiday!

A few updates:

1. We will have our first scientific meeting on June 12-13, 2020, right before the ASV annual meeting (June 13-17) in Fort Collins, Colorado State University. Organizing and scientific committees will be formed soon.
2. I am excited to share that Dr. Xiang-Jin (XJ) Meng of Virginia Tech, a distinguished virology and a member of the US National Academy of Science, will be the keynote speaker of this meeting. Details will follow.
3. In addition to scientific programs, we will also hold an election; a new leadership team will be elected to serve our community for the next two years.
4. Attached please find a brief report of our Kunming meeting, along with a few photos.

Please let me know if you have comments and suggestions.

All best wishes, and happy holidays!

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

From: Sun, Jie, Ph.D. <Sun.Jie@mayo.edu>
Sent: Thursday, November 28, 2019 11:37 AM
To: Liu, Shan-Lu; zhengzhiming4@gmail.com; haitguo@iupui.edu; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; wjma@ksu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; shitao.li@okstate.edu; Shan.lu@umassmed.edu; Hu, Haitao; wenzheho@temple.edu; Qfeng4 @central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2 @unl.edu; qiyi.tang@howard.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518 @umd.edu; gaos8@upmc.edu; pewang@uchc.edu; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@ 163.com; xfyu1@zju.edu.cn; bzhao@partners.org; jianw@musc.edu; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jun.zhu@nih.gov; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; xiangguo.qiu@canada.ca; Feng Shao; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan; Zhang, Rong; liliwang@upenn.edu; Linheng Li; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; wu@crystal.harvard.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao; Qu, Feng; Hezhao.Ji@umanitoba.ca; Li, Zihai; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; wxiao@temple.edu; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; PZheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong; shuping_tong_md@brown.edu; pinghuif@usc.edu; gaof@im.ac.cn
Subject: Re: [EXTERNAL] Happy Thanksgiving and meeting next year, June 12-13, 2020

Thanks for sharing. Happy Thanksgiving to everyone!

Best wishes,

Jie

Jie Sun, Ph.D.
Associate Professor
Department of Medicine
Department of Immunology
Mayo Clinic
Stabile 8-26
200 1st St SW
Rochester, MN 55905
Tel: 507-284-9503
Email: Sun.Jie@mayo.edu
http://www.mayo.edu/research/faculty/sun-jie-ph-d/bio-20348662

From: "Liu, Shan-Lu" <liu.6244@osu.edu>
Date: Thursday, November 28, 2019 at 10:54 AM
To: "zhengzhiming4@gmail.com" <zhengzhiming4@gmail.com>, "haitguo@iupui.edu" <haitguo@iupui.edu>, "tzhou@mail.nih.gov" <tzhou@mail.nih.gov>, "GCheng@mednet.ucla.edu" <GCheng@mednet.ucla.edu>, "liangy@umn.edu" <liangy@umn.edu>, "rli@vcu.edu" <rli@vcu.edu>, "wjma@ksu.edu" <wjma@ksu.edu>, "xjmeng@vt.edu" <xjmeng@vt.edu>, "Zhijian.Chen@UTSouthwestern.edu" <Zhijian.Chen@UTSouthwestern.edu>, "mluo@gsu.edu" <mluo@gsu.edu>, "zhangyj@umd.edu" <zhangyj@umd.edu>, "xzhu1@umd.edu" <xzhu1@umd.edu>, "jqiu@kumc.edu" <jqiu@kumc.edu>, "lijun@uic.edu" <lijun@uic.edu>, "fengwei.bai@usm.edu" <fengwei.bai@usm.edu>, "andyu@iupui.edu" <andyu@iupui.edu>, "reachxw@vt.edu" <reachxw@vt.edu>, "gluo@uab.edu" <gluo@uab.edu>, "ldu@nybc.org" <ldu@nybc.org>, "hxu@tulane.edu" <hxu@tulane.edu>, "liu_fy@berkeley.edu" <liu_fy@berkeley.edu>, "shitao.li@okstate.edu" <shitao.li@okstate.edu>, "Shan.lu@umassmed.edu" <Shan.lu@umassmed.edu>, "haihu@UTMB.edu" <haihu@UTMB.edu>, "wenzheho@temple.edu" <wenzheho@temple.edu>, "Qfeng4@central.uh.edu" <Qfeng4@central.uh.edu>, "tang@bio.fsu.edu" <tang@bio.fsu.edu>, "feng.li@sdstate.edu" <feng.li@sdstate.edu>, "ruilu@lsu.edu" <ruilu@lsu.edu>, "sxiang2@unl.edu" <sxiang2@unl.edu>, "qiyi.tang@howard.edu" <qiyi.tang@howard.edu>, "dingsw@ucr.edu" <dingsw@ucr.edu>, "guohua@missouri.edu" <guohua@missouri.edu>, "bling@tulane.edu" <bling@tulane.edu>, "junwang@pharmacy.arizona.edu" <junwang@pharmacy.arizona.edu>, "lifang@umn.edu" <lifang@umn.edu>, "wang518@umd.edu" <wang518@umd.edu>, "gaos8@upmc.edu" <gaos8@upmc.edu>, "pewang@uchc.edu" <pewang@uchc.edu>, "xiangy@uthscsa.edu" <xiangy@uthscsa.edu>, "fzhu@bio.fsu.edu" <fzhu@bio.fsu.edu>, "chen.liang@mcgill.ca" <chen.liang@mcgill.ca>, "lyuan@vt.edu" <lyuan@vt.edu>, "fgao@duke.edu" <fgao@duke.edu>, "wangjw28@163.com" <wangjw28@163.com>, "xfyu1@zju.edu.cn" <xfyu1@zju.edu.cn>, "bzhao@partners.org" <bzhao@partners.org>, "jianw@musc.edu" <jianw@musc.edu>, "zyang@ksu.edu" <zyang@ksu.edu>, "yu.cong@nih.gov" <yu.cong@nih.gov>, "weiming.yuan@usc.edu" <weiming.yuan@usc.edu>, "Zongdi.feng@nationwidechildrens.org" <Zongdi.feng@nationwidechildrens.org>, "juh13@psu.edu" <juh13@psu.edu>, "hengx@missouri.edu" <hengx@missouri.edu>, "lsu@med.unc.edu" <lsu@med.unc.edu>, "ywu8@gmu.edu" <ywu8@gmu.edu>, "jwu@whu.edu.cn" <jwu@whu.edu.cn>, "tshuo@uic.edu" <tshuo@uic.edu>, "Shibojiang@fudan.edu.cn" <Shibojiang@fudan.edu.cn>, "sjiang@nybc.org" <sjiang@nybc.org>, "pinwang@usc.edu" <pinwang@usc.edu>, "rzhao@som.umaryland.edu" <rzhao@som.umaryland.edu>, "shuylong@mail.sysu.edu.cn" <shuylong@mail.sysu.edu.cn>, "xuefeng.liu@georgetown.edu" <xuefeng.liu@georgetown.edu>, "yuxingli@som.umaryland.edu" <yuxingli@som.umaryland.edu>, "shixia.wang@umassmed.edu" <shixia.wang@umassmed.edu>, "yhe@ipbcams.ac.cn" <yhe@ipbcams.ac.cn>, "Pinghui.feng@usc.edu"

<Pinghui.feng@usc.edu>, "ju-tao.guo@bblumberg.org" <ju-tao.guo@bblumberg.org>, "lin.liu@okstate.edu" <lin.liu@okstate.edu>, "hua.zhu@rutgers.edu" <hua.zhu@rutgers.edu>, "Jinhong.chang@bblumberg.org" <Jinhong.chang@bblumberg.org>, "jianzhu1012@gmail.com" <jianzhu1012@gmail.com>, "ronghai@ucr.edu" <ronghai@ucr.edu>, "jun.zhu@nih.gov" <jun.zhu@nih.gov>, "jliu4@uams.edu" <jliu4@uams.edu>, "xiangpeng.kong@med.nyu.edu" <xiangpeng.kong@med.nyu.edu>, "haoquanwu@outlook.com" <haoquanwu@outlook.com>, "Wenjun.liu@defence.gov.au" <Wenjun.liu@defence.gov.au>, "Liang.shan@wustl.edu" <Liang.shan@wustl.edu>, "hliao@duke.edu" <hliao@duke.edu>, "yuan2@upenn.edu" <yuan2@upenn.edu>, "zxing@umn.edu" <zxing@umn.edu>, "hongmin.li@health.ny.gov" <hongmin.li@health.ny.gov>, "pzheng@ihv.umaryland.edu" <pzheng@ihv.umaryland.edu>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "jxw103@case.edu" <jxw103@case.edu>, "xiangguo.qiu@canada.ca" <xiangguo.qiu@canada.ca>, Feng Shao <shaofeng@nibs.ac.cn>, "zlshi@wh.iov.cn" <zlshi@wh.iov.cn>, "klan@whu.edu.cn" <klan@whu.edu.cn>, "zengmsh@mail.sysu.edu.cn" <zengmsh@mail.sysu.edu.cn>, Nan Yan <Nan.Yan@UTSouthwestern.edu>, "Zhang, Rong" <rongzhang@wustl.edu>, "liliwang@upenn.edu" <liliwang@upenn.edu>, Linheng Li <LIL@stowers.org>, "kli1@uthsc.edu" <kli1@uthsc.edu>, "tsx@case.edu" <tsx@case.edu>, "ssun@mdanderson.org" <ssun@mdanderson.org>, "ysang@tnstate.edu" <ysang@tnstate.edu>, "Liu, Shan-Lu" <liu.6244@osu.edu>, "wu@crystal.harvard.edu" <wu@crystal.harvard.edu>, "Sun, Jie, Ph.D." <Sun.Jie@mayo.edu>, "peijun@strubi.ox.ac.uk" <peijun@strubi.ox.ac.uk>, "jiayu@coh.org" <jiayu@coh.org>, "bchen@crystal.harvard.edu" <bchen@crystal.harvard.edu>, "Wen, Haitao" <Haitao.Wen@osumc.edu>, "Qu, Feng" <qu.28@osu.edu>, "Hezhao.Ji@umanitoba.ca" <Hezhao.Ji@umanitoba.ca>, "Li, Zihai" <zihai@musc.edu>, "zhengyo@msu.edu" <zhengyo@msu.edu>, "zhanglinqi@tsinghua.edu.cn" <zhanglinqi@tsinghua.edu.cn>, "wxiao@temple.edu" <wxiao@temple.edu>, "Whu@temple.edu" <Whu@temple.edu>, "RSun@mednet.ucla.edu" <RSun@mednet.ucla.edu>, "Guangping.Gao@umassmed.edu" <Guangping.Gao@umassmed.edu>, "PZheng@ihv.umaryland.edu" <PZheng@ihv.umaryland.edu>, "GMSWANG@nus.edu.sg" <GMSWANG@nus.edu.sg>, "peshi@UTMB.EDU" <peshi@UTMB.EDU>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "ziying-yan@uiowa.edu" <ziying-yan@uiowa.edu>, "lqiao@luc.edu" <lqiao@luc.edu>, "yong.xiong@yale.edu" <yong.xiong@yale.edu>, "Wang, Qiuhong" <wang.655@osu.edu>, "shuping_tong_md@brown.edu" <shuping_tong_md@brown.edu>, "pinghuif@usc.edu" <pinghuif@usc.edu>, "gaof@im.ac.cn" <gaof@im.ac.cn>
Subject: [EXTERNAL] Happy Thanksgiving and meeting next year, June 12-13, 2020

Dear friends and colleagues,

I wish you all a great Thanksgiving holiday!

A few updates:

1. We will have our first scientific meeting on June 12-13, 2020, right before the ASV annual meeting (June 13-17) in Fort Collins, Colorado State University. Organizing and scientific committees will be formed soon.
2. I am excited to share that Dr. Xiang-Jin (XJ) Meng of Virginia Tech, a distinguished virology and a member of the US National Academy of Science, will be the keynote speaker of this meeting. Details will follow.
3. In addition to scientific programs, we will also hold an election; a new leadership team will be elected to serve our community for the next two years.
4. Attached please find a brief report of our Kunming meeting, along with a few photos.

Please let me know if you have comments and suggestions.

All best wishes, and happy holidays!

Shan-Lu

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

From: Tang, Qiyi <qiyi.tang@Howard.edu>
Sent: Tuesday, July 7, 2020 10:47 PM
To: Liu, Shan-Lu; zhengzhiming4@gmail.com; haitguo@iupui.edu; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; wjma@ksu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; shitao.li@okstate.edu; Shan.lu@umassmed.edu; Hu, Haitao; wenzheho@temple.edu; Qfeng4 @central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2 @unl.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518@umd.edu; gaos8 @upmc.edu; Wang,Penghua; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@163.com; xfyu1 @zju.edu.cn; bzhao@partners.org; jianw@musc.edu; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jun.zhu@nih.gov; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; xiangguo.qiu@canada.ca; Feng Shao; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan; Zhang, Rong; liliwang@upenn.edu; Linheng Li; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; wu@crystal.harvard.edu; Sun.Jie@mayo.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao; Qu, Feng; Hezhao.Ji@umanitoba.ca; Li, Zihai; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; wxiao@temple.edu; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; pzheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong; shuping_tong_md@brown.edu; pinghuif@usc.edu; gaof@im.ac.cn
Subject: Re: Happy Thanksgiving and meeting next year, June 12-13, 2020

Hi professors,

I apologize if you are bothered by this email. I am helping my friend, Ed Seto to advertise his recruiting post-doc:

Postdoctoral Position

Applications are invited for a postdoctoral fellowship to study the structures, functions, and mechanisms of histone deacetylases. Candidates with experiences in biochemical, molecular, and cell biological approaches are preferred.

Recent selected articles from our lab:
PMID: 32540961
PMID: 32457045
PMID: 31162605
PMID: 30517871
PMID: 30456376
PMID: 29958910

Please send a CV and names of three references to:

Ed Seto, Ph.D.
Email: seto@gwu.edu

From: Liu, Shan-Lu <liu.6244@osu.edu>
Sent: Thursday, November 28, 2019 9:58 AM
To: zhengzhiming4@gmail.com; haitguo@iupui.edu; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; wjma@ksu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; shitao.li@okstate.edu; Shan.lu@umassmed.edu; Hu, Haitao; wenzheho@temple.edu; Qfeng4 @central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2 @unl.edu; qiyi.tang@howard.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518 @umd.edu; gaos8@upmc.edu; pewang@uchc.edu; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@ 163.com; xfyu1@zju.edu.cn; bzhao@partners.org; jianw@musc.edu; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jun.zhu@nih.gov; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; xiangguo.qiu@canada.ca; Feng Shao; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan; Zhang, Rong; liliwang@upenn.edu; Linheng Li; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; Liu, Shan-Lu; wu@crystal.harvard.edu; Sun.Jie@mayo.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao; Qu, Feng; Hezhao.Ji@umanitoba.ca; Li, Zihai; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; wxiao@temple.edu; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; PZheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong; shuping_tong_md@brown.edu; pinghuif@usc.edu; gaof@im.ac.cn
Subject: Happy Thanksgiving and meeting next year, June 12-13, 2020
Attachments: Meeting report_ACVA_SCBA-virology_Kunming.pdf; Junming_1.JPG; Kunming_2.JPG; Kunming_3.JPG; Kunming_4.JPG

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All best wishes, and happy holidays!

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Departments of Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

SCBA-Virology Division Workshop Held in Kunming

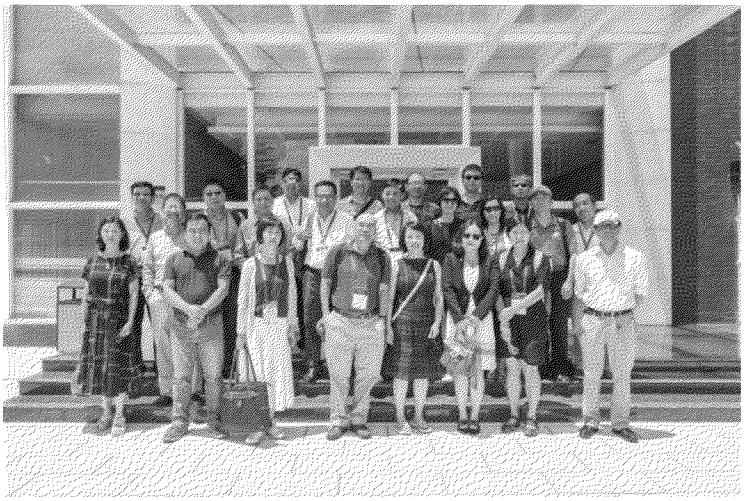
The SCBA-Virology Division held a scientific workshop on July 28, 2019 after the 17th SCBA International Symposium in Kunming, China. The workshop was co-organized by Drs. Genhong Cheng, Haitao Guo, Shan-Lu Liu and Tongqing Zhou of the SCBA-virology Division and by Dr. Qihan Li at the Institute of Medical Biology (IMB), Chinese Academy of Medical Sciences (CAMS).

The meeting was opened by an introductory speech by Prof. Qihan Li, Director of IMB, followed by scientific presentations. The workshop had three sessions, which covered the topics of "Immunity to Viral Infection", "Viral Pathogenesis", and "Vaccine and Primate Models". More than 50 people attended the workshop, many from IMB. Speakers, session chairs, and panelists include: Tian Wang, Shan-Lu Liu, Haitao Hu, Jie Sun, Wenzhe Ho, Lishan Su, Wei Jiang, Xuefeng Liu, Hongyu Deng, Yuntao Wu, Jianming Hu, Genhong Cheng, Lanying Du, Yuan Yan, Kui Li, Shou-Wei Ding, Qi Huang, etc.

Before the scientific sessions, meeting attendees were given a guided tour of the National Medical Primate Research Center located in IMB, CAMS, which hosts the largest P4 primate research facility in China and plays a leading role in breeding, reproduction, disease control, genetic studies of primates in the world. In addition to IMB of CAMS, the workshop was also supported by Drs. Yuelong Shu and Musheng Zeng at Sun Yat-sen University (SYSU), China, Dr. Yuntao Wu at Virongy, LLC and George Mason University, as well as Immune Technology Corp.

This is the first scientific event after the official establishment of the SCBA-Virology Division in 2018. During the 2019 SCBA international symposium and the SCBA-Virology satellite workshop, we also organized opportunities for social networking.


The 17th SCBA
International Symposium
Bioscience for All, All for Bioscience
全球華人生物學家大會
暨第十七屆美洲华人生物科学学会学术研讨会
— 病毒学分会卫星会 —
17th SCBA
病毒学分会卫星会




The 17th SCBA
2019年7月28日
July 28th, 2019
中国 昆明
Kunming, China
International Symposium
Bioscience for All,
All for Bioscience
全球華人生物學家大會
暨第十七届美洲华人生物科学学会学术研讨会
— 病毒学分会卫星会 —
中国医学科学院医学生物学研究所
云南省重大传染病疫苗工程技术中心
云南省重大传染病疫苗研发重点实验室
云南省传染病疫苗研发及产业化国际科技合作基地
病毒学分会卫星会

Suryanarayanan2_TPIA_0000000583


IMBCAMS
IMBCAMS

Suryanarayanan2_TPIA_0000000585

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 5/26/2020 10:29:31 PM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: paper-2020526
Attachments: paper-2020526.docx; GLP2R.pptx

佩勇,

附件是文章的结果。文章很初步，整体结构也需要大的调整。我想这是第一次请教，请你审核数据（文章的主体部分和图表），期待意见和建议，特别是：

1）需要补充的其他实验；

2）文章写作思路和整体布局

另外， 我们正在补充的数据包括：

1）GLP2R蛋白的ECL1结构域和E蛋白DIII直接相互作用证据（合成多肽，SPR分析），

2）缺陷小鼠感染实验（已经构建成功，正在繁殖）。

将在你意见和建议的基础上重新架构文章。

非常感谢！

祝好！

新文

From: 王延轶/Yan-Yi Wang <wangyy@wh.iov.cn>
Sent: Wednesday, October 9, 2019 3:20 AM
To: Shi, Pei yong
Cc: 陈新文; Yuan Zhiming; Bo Zhang
Subject: Re: Wuhan visit from Oct 19 to 21

Dear all,

I would like to invite all of you to a dinner on the 20th. Please let me know if the time is OK.

Best wishes,

Yanyi

> -----原始邮件-----
> 发件人: "Shi, Pei yong" <peshi@UTMB.EDU>
> 发送时间: 2019-10-05 21:10:55 (星期六)
> 收件人: "陈新文" <chenxw@wh.iov.cn>
> 抄送: "'Yanyi Wang'" <wangyy@wh.iov.cn>, "Yuan Zhiming" <yzm@wh.iov.cn>, "Bo Zhang" <zhangbo@wh.iov.cn>
> 主题: Wuhan visit from Oct 19 to 21
>
> Dear Xinwen,
>
> It was great talking to you yesterday. I look forward to discussing the exciting TBEV project. Please feel free to send me the slides to prepare for the discussion.
>
> Ping and I will arrive in Wuhan at 1:35 pm on October 19. The flight number is China Eastern Airline Flight MU2494. We plan to leave Wuhan on October 21. We look forward to seeing you and the colleagues at WIV!
>
> Best wishes from Galveston!
> Pei-Yong
>
>

--
王延轶

Yan-Yi Wang, Ph.D.

Professor

Wuhan Institute of Virology

Chinese Academy of Sciences

TEL: 86-27-87198095

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https://www.washingtonpost.com/opinions/global-opinions/how-did-covid-19-begin-its-initial-origin-story-is-shaky/2020/04/02/1475d488-7521-11ea-87da-77a8136c1a6d_story.html

Please see link to article that appeared today in the Washington Post. I've has inquiries already. Any information you might have to address the work done in the Wuhan CDC would be helpful. BSL2 work there on coronaviruses? True?

Thanks, and I hope you are all well. Things are heating up here but so far everyone is well.

Best wishes, Jim

From: Wei, Guowei <weig@msu.edu>
Sent: Saturday, February 8, 2020 9:40 AM
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Subject: Potentially highly potent drugs for 2019-nCoV
Attachments: 2019-nCoV-Reposition_13.pdf; Anti-2019-nCoV.docx

Dear Researchers,
There is a pressing need to find effective medications for 2019-nCoV. Therefore, I would like to bring your attention to a class of potentially highly potent drugs for 2019-nCoV. Sorry for disturbing your weekend!

We use deep learning to screen 1465 drugs in the DrugBank that have been approved by the U.S. Food and Drug Administration (FDA), based on the inhibition of 2019-nCoV 3CL protease. We found a few market drugs that might be effective for curing 2019-nCoV, ranked by their binding affinities in inhibiting the 2019-nCoV 3CL protease.

Table 1: A summary of potentially highly potent anti2019-nCoV drugs with predicted binding free energies (unit: kcal/mol) and
corresponding trade names.

Drug ID	Type	Trade Name	Predicted Binding Affinity
DB00188	Bortezomib	Velcade, Chemobort, Bortecad	-12.15
DB00690	Flurazepam	Dalmane, Dalmadorm, Fluzepam	-10.38
DB08901	Ponatinib	Iclusig	-10.25
DB00398	Sorafenib	Nexavar	-10.01
DB01254	Dasatinib	Sprycel, Dasanix	-9.87
DB01384	Paramethasone	Cortidene Depot, Dilar, Dilarmine	-9.71
DB00838	Clocortolone	Victrelis	-9.58
DB00301	Flucloxacillin	Flora, Flox, Floxapen	-9.57
DB06144	Sertindole	Serdolect and Serlect	-9.54
DB04920	Clevidipine	Cleviprex	-9.52
DB00673	Aprepitant	Emend	-9.49
DB01076	Atorvastatin	Lipitor, Sortis	-9.49
DB01594	Cinolazepam	Gerodorm	-9.47
DB00845	Clofazimine	Lamprene	-9.43
DB06717	Fosaprepitant	Emend, Ivemend	-9.39

Among FDA approved protease-based antiviral drugs, the most possible one is Boceprevir (binding affinity -9.36 kcal/mol), see Table of the attached manuscript. A brief summary is also given in Chinese.

Best regards,

Guowei Wei
Professor
Mathematics
Electrical and Computer Engineering
Biochemistry and Molecular Biology
Michigan State University
http://users.math.msu.edu/users/wei/

Potentially highly potent drugs for 2019-nCoV

Duc Duy Nguyen[1], Kaifu Gao[1], Jiahui Chen[1], Rui Wang[1], and Guo-Wei Wei[1,2,3] *
[1] Department of Mathematics, Michigan State University, MI 48824, USA
[2] Department of Biochemistry and Molecular Biology
Michigan State University, MI 48824, USA
[3] Department of Electrical and Computer Engineering
Michigan State University, MI 48824, USA

February 5, 2020

Abstract

The World Health Organization (WHO) has declared the 2019 novel coronavirus (2019-nCoV) infection outbreak a global health emergency. Currently, there is no effective anti-2019-nCoV medication. The sequence identity of the 3CL proteases of 2019-nCoV and SARS is 96%, which provides a sound foundation for structural-based drug repositioning (SBDR). Based on a SARS 3CL protease X-ray crystal structure, we construct a 3D homology structure of 2019-nCoV 3CL protease. Based on this structure and existing experimental datasets for SARS 3CL protease inhibitors, we develop an SBDR model based on machine learning and mathematics to screen 1465 drugs in the DrugBank that have been approved by the U.S. Food and Drug Administration (FDA). We found that many FDA approved drugs are potentially highly potent to 2019-nCoV.

Key words: 2019-nCoV, Drug repositioning, DrugBank, deep learning, algebraic topology.

*Address correspondences to Guo-Wei Wei. E-mail:wei@math.msu.edu

1 Introduction

The 2019 novel coronavirus (2019-nCoV) caused the pneumonia outbreak in Wuhan, China, in late December 2019 and has rapidly spread around the world. By Feb 5, 2020, more than 24000 individuals were infected and more than 490 fatalities had been reported. The World Health Organization (WHO) has declared this novel coronavirus outbreak a global health emergency. Currently, there is no specific antiviral drug for this epidemic. Considering the severity of this widespread dissemination and health threats, panic patients misled by media flocked to the pharmacies for Chinese Medicine herbs which were reported to "inhibit" the 2019-nCoV, despite no clinical evidence supporting the claim. Many researchers are engaged in developing anti-2019-nCoV drug s [1, 2]. However, new drug discovery and development is a long, costly and rigorous scientific process. A more effective approach is to search for anti-2019-nCoV therapies from the existing FDA-approved drug database.

Drug repositioning (also known as drug repurposing), which concerns the investigation of existing drugs for new therapeutic target indications, has emerged as a successful strategy for drug discovery due to the reduced costs and expedited approval procedures [3–5]. Several successful examples unveil its great values in practice: Nelfinavir, initially developed to treat the human immunodeficiency virus (HIV), is now being used for cancer treatments. Amantadine was firstly designed to treat influenza caused by type A influenza viral infection and is being used for Parkinson's disease later on [6]. In recent years, the rapid growth of drug-related datasets, as well as open data initiatives, has led to new developments for computational drug repositioning, particularly, structural-based drug repositioning (SBDR). Machine learning, network analysis, and text mining and semantic inference are three major computational approaches commonly applied in drug repositioning [7]. The rapid accumulation of genetic and structural databases [8], the development of low-dimensional mathematical representations of complex biomolecular structures [9, 10], and the availability of advanced deep learning algorithms have made machine learning-based drug reposition a promising approach [7]. Considering the urgent need for anti-2019-nCoV drugs, a computational drug repositioning is one of the most feasible strategies for discovering 2019-nCoV drugs.

In SBDR, one needs to select one or a few effective targets. Study shows that 2019-nCoV genome is very close to that of the severe acute respiratory syndrome (SARS)-CoV [11]. The sequence identities of 2019-nCoV 3CL protease, RNA polymerase, and the spike protein with corresponding SARS-CoV proteins are 96.08%, 96%, and 76%, respectively [12]. We, therefore, hypothesize that a potent SARS 3CL protease inhibitor is also a potent 2019-nCoV 3CL protease inhibitor. Unfortunately, there is no effective SARS therapy at present. Nevertheless, the X-ray crystal structure of SARS 3CL protease has been reported [13] and the binding affinities of 115 potential SARS 3CL protease inhibitors are available in ChEMBL database [14]. Additionally, there are 15,843 protein-ligand complexes in PDBbind 2018 general set with binding affinities and X-ray crystal structures [15]. Moreover, the DrugBank contains about 1600 drugs approved by the U.S. Food and Drug Administration (FDA) [16]. The aforementioned information provides a sound foundation to develop an SBDR machine learning model for 2019-nCoV 3CL protease inhibition.

Recently, we have developed low-dimensional mathematical representations [9, 10] to reduce the structural complexity of macromolecules based on abstract mathematics, such as algebraic topology [17–20], differential geometry, and spectral graph theory [10, 21]. We exploit these representations to extract critical chemical and biological information for protein-ligand pose selection, binding affinity ranking, prediction, ranking, scoring, and screening [9, 10]. Paired with various machine learning, including deep algorithms, these approaches are the top competitor for D3R Grand Challenges, a worldwide competition series in computer-aided drug design in the past few years [22, 23].

In responding to the pressing need for anti-2019-nCoV medications, we develop mathematics-based deep learning models to systematically eventuate FDA approved drugs in the DrugBank for 2019-nCoV 3CL protease inhibition. With the consensus of two deep learning models based on convolutional neural

networks and multitask deep learning, we report the top 15 potentially highly potent anti-2019-nCoV 3CL inhibitors, which provide timely guidance for the further development of anti-2019nCoV drugs.

2 Results

2.1 Sequence identity analysis

The sequence identity is defined as the percentage of characters that match exactly between two different sequences. The sequence identities between 2019-nCoV protease and the protease of SARS-CoV, MERS-CoV, HKU-1, OC43, HCoVNL63, 229E, and HIV are 96.1%, 52.0%, 49.0%, 48.4%, 45.2%, 41.9%, and 23.7%, respectively. It is seen that 2019-nCoV protease is very close to SARS-CoV protease, but is distinguished from other proteases. Clearly, 2019-nCoV has a strong genetic relationship with SARS-CoV, the sequence alignment in Figure 1 further confirms their relationship. Additionally, the available experimental data of SARS-CoV protease inhibitors can be used as the training set to generate new inhibitors of 2019-nCoV protease.

2.2 Structure similarity analysis

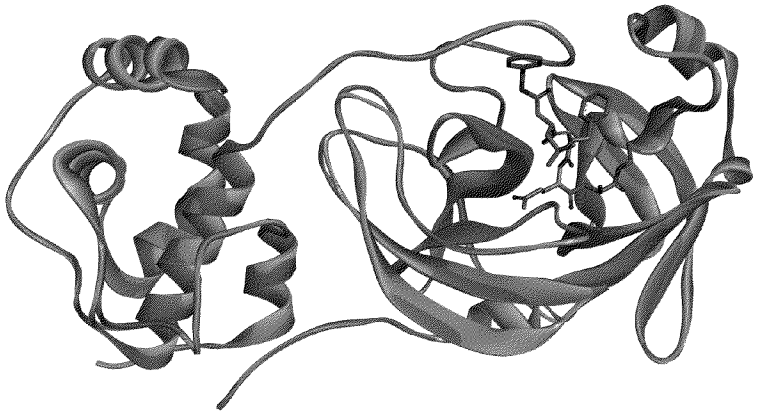

Figure 2: Illustration of the similarity and difference between protease structures of 2019-nCoV 3CL protease (in gold) and SARS-CoV 3CL protease (PDB ID: 2A5I, in green). The anti-SARS inhibitor in dark color indicates the binding site.

Since the sequences are highly identical, the 2019-nCoV protease structure can be built by homology modeling with the SARS-CoV 3CL protease (PDB ID: 2A5I) [13] as a template. It turns out, as shown in Fig. 2, the homology structure of the 2019-nCoV protease is essentially identical to the X-ray structure of SARS-CoV 3CL protease. Particularly, the RMSD of two structures at the binding site is 0.21 Å. The high structural similarity between the two proteases suggests that anti-SARS-CoV chemicals can be equally effective for the treatment of 2019-nCoV.

2.3 Binding analysis

We predict the binding affinities of 1465 3D FDA-approved drugs and 2019-nCoV protease complexes using two models, 3DALL and 3DMT. 3DALL is built with deep convolutional neural networks (CNNs) using the algebraic topology-based representation of protein-ligand complexes, with 84 SARS-CoV protease inhibitors and 15843 complexes from the PDBbind 2018 general set as the training set. 3DMT, a deep

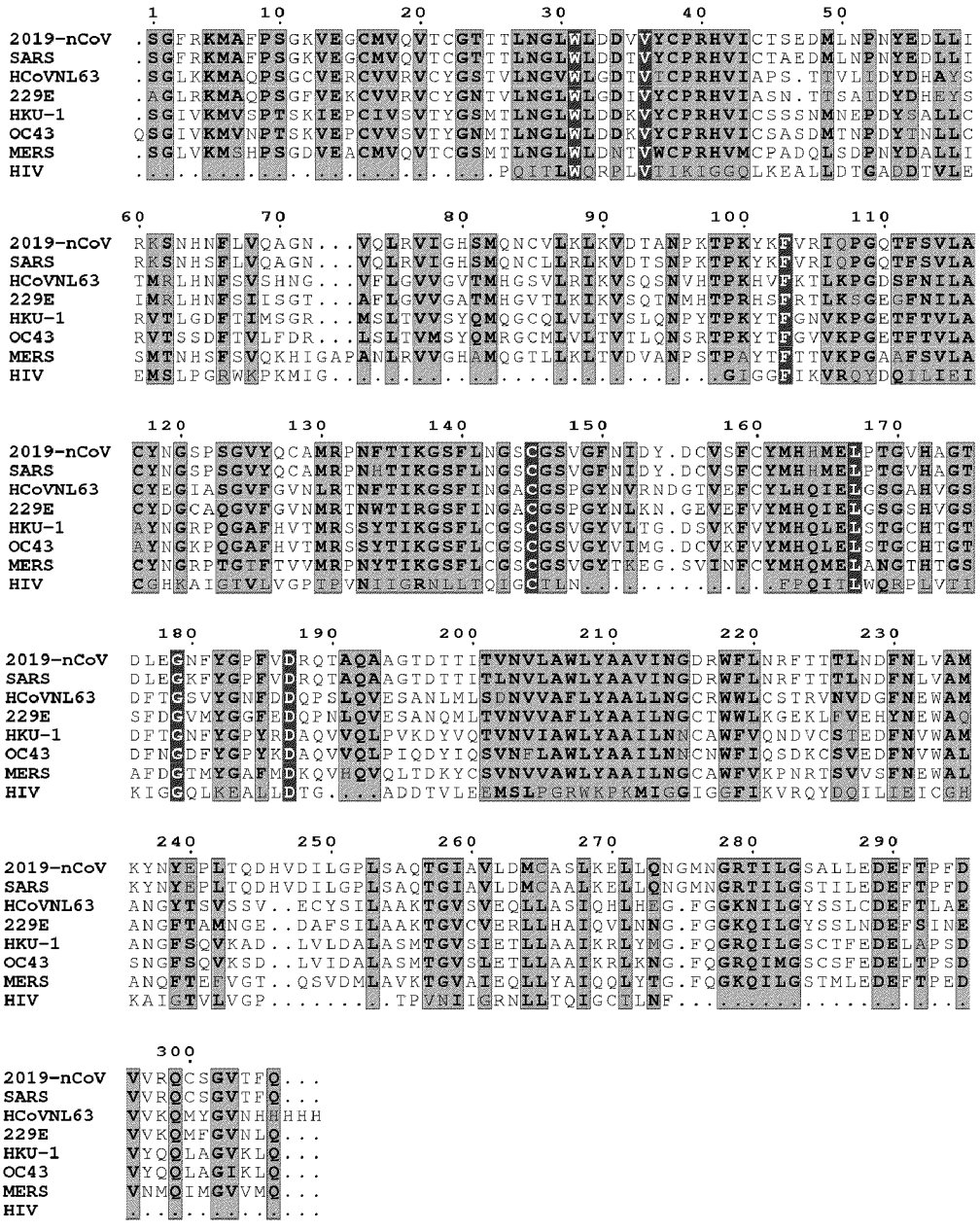

Figure 1: The protease sequence alignment between 2019-nCoV, SARS, MERS, OC43, HCoVNL63, HKU-1, 229E, and HIV.

multitask CNN model based on the algebraic topology representation of protein-ligand complexes is the second model. In the current work, two tasks were developed in the 3DMT. The first task involves 1465 2019-nCoV protease complexes as the test set and 84 SARS-CoV protease inhibitors as the training set. The second task is trained with the PDBbind 2018 general set of 15843 protein-ligand complexes. Our top 15 potential 2019-nCoV inhibitors based on consensus binding affinities of the aforementioned two models are listed in Table 1. A complete list of predicted binding affinities of 1465 FDA-approved drugs is given in the Supplementary Material.

We briefly describe the predicted potentially highly potent anti-2019-nCoV drugs. The most potent one is Bortezomib, an anti-cancer medication, which is known as proteasome inhibitor and can be used to treat multiple myeloma and mantle cell lymphoma. The second drug is Flurazepam, which is a benzodiazepine derivative that possesses anxiolytic, anticonvulsant, hypnotic, sedative, and skeletal muscle

Table 1: A summary of potentially highly potent anti2019-nCoV drugs with predicted binding free energies (unit: kcal/mol) and corresponding trade names.

DrugID	Type	Trade Name	Predicted Binding Affinity
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DB00301	Flucloxacillin	Flora, Flox, Floxapen	-9.57
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DB04920	Clevidipine	Cleviprex	-9.52
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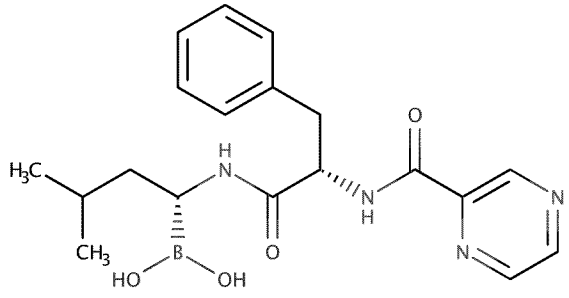
DB00845	Clofazimine	Lamprene	-9.43
DB06717	Fosaprepitant	Emend, Ivemend	-9.39

relaxant properties. The third one, Ponatinib, an oral drug for the treatment of chronic myeloid leukemia and Philadelphia chromosome-positive acute lymphoblastic leukemia, which is a multi-targeted tyrosine kinase inhibitor. It is important to notice that this drug has the risk of life-threatening blood clots and severe narrowing of blood vessels. The next one is Sorafenib, a kinase inhibitor for the treatment of primary kidney cancer and liver cancer. The fifth drug, Dasatinib, is a therapy for treating certain cases of chronic myelogenous leukemia and acute lymphoblastic leukemia. The next one, Paramethasone, is a glucocorticoid with the general properties of corticosteroids. The seventh drug is Clocortolone, a topical steroid that is used in the form of an ester, clocortolone pivalate. It is interesting to note that this drug is always applied as a cream for the treatment of dermatitis. It is considered a medium-strength corticosteroid. Therefore, this drug might be used to clean 2019-nCoV contaminated materials, offering an extra layer of protection. The number eight drug, Flucloxacillin, is a narrow-spectrum beta-lactam antibiotic of the penicillin class. It is used to treat infections caused by susceptible Gram-positive bacteria. The next one, Sertindole, is an antipsychotic medication. The number ten drug, Clevidipine, is a dihydropyridine calcium channel blocker that used for the reduction of blood pressure when oral therapy is not feasible or not desirable. The eleventh drug, Aprepitant, is used to prevent chemotherapy-induced nausea and vomiting, as well as postoperative nausea and vomiting. The number twelve, Atorvastatin, is a statin drug used to prevent cardiovascular disease in those at high risk and treat abnormal lipid levels. The next drug is Cinolazepam, a benzodiazepine derivative. It possesses anxiolytic, anticonvulsant, sedative, and skeletal muscle relaxant properties. The number fourteen drug, Clofazimine, is used together with rifampicin and dapsone to treat leprosy. The fifteenth number drug, Fosaprepitant, is an antiemetic medication used in the prevention of acute and delayed nausea and vomiting associated with chemotherapy treatment.

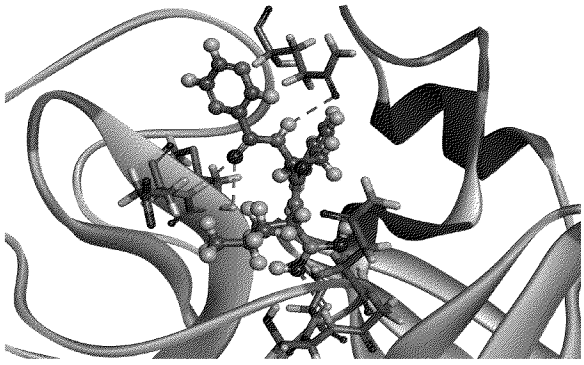
3 Discussion

3.1 The structural analysis of top 3 potent drug candidates

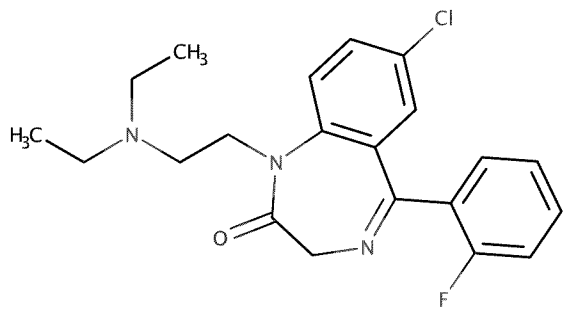
The top-ranking candidate of the existing drugs is Bortezomib (see Figure 3(b)). Its predicted binding affinity to the nCoV-2019 protease is -12.29 kcal/mol. The high binding affinity is due to the strong hydrogen bond network formed between the drug and the nCoV-2019 protease. For example, the strongest hydrogen



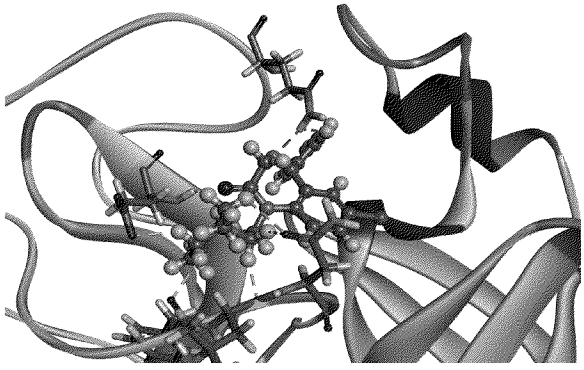
(a) Bortezomib, -12.15 kcal/mol



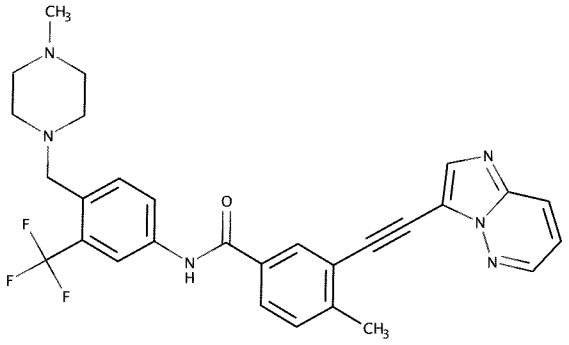
(b) 2019-nCoV protease and Bortezomib complex



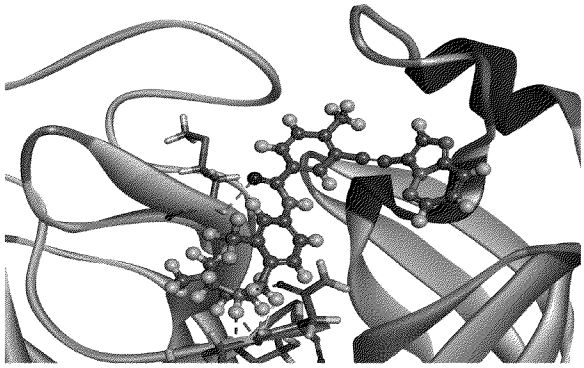
(c) Flurazepam, -10.38 kcal/mol



(d) 2019-nCoV protease and Flurazepam complex



(e) Ponatinib, -10.25 kcal/mol



(f) 2019-nCoV protease and Ponatinib complex

Figure 3: Bortezomib, Flurazepam, Ponatinib and their complexes with 2019-nCoV protease.

bonds are formed by two O atoms in two hydroxyls on the head of Bortezomib and three different aminos in the main chains of residues Gly143, Ser144, and Cys145 of nCoV-2019 protease. Therefore, the head bonds tightly with the side chains of the aforementioned residues. The other two important hydrogen bonds are located at the tail of the drug molecule. The first one is between the O atom in the Hydroxyl on the tail and the two H atoms in the amino acid of the main chain of Glu166 and the methyl of the main chain of Met165. The second one is the H atom in the amino on the tail and the O atom in the side chain of Gln189. As a result, the head, body, and tail of Bortezomib interact firmly with the protease binding site.

The second-best drug is Flurazepam (see Figure 3(d)) with a binding affinity of -10.37 kcal/mol. The strong hydrogen bonds between this molecule and the protease are formed by five different H atoms on the head of the drug with four different O atoms in the main chains of Phe140 , Leu141, as well as the side

chains of Asn142 and Glu166. Another important bond is formed by the H atom in the amino of the side chain of Gln189 with the F atom of the fluorobenzene and one N atom of the 1,4-diazepane in the drug. Additionally, the O atom in the drug adjacent to the 1,4-diazepane is bonded with the amino H atom of the side chain of Glu166. Therefore, the head, tail, and body of the molecule are firmly fixed to the binding site, which promises a strong binding to the 2019-nCoV protease.

The third one, Ponatinib (see Figure 3(f)), has a binding affinity -10.29 kcal/mol. The strong hydrogen bonds between this molecule and the protease are formed by two H atoms of the piperazine with the O atom in the side chain of Ser144 and the main chain of Leu141. Additionally, a bond exists between the O atom in the main chain of the drug and the H atom in the methyl of the main chain of Met165. These hydrogen bonds lead to a high binding affinity with 2019-nCoV protease.

The 3D complexes of 2019-nCoV protease and other 12 potential drugs are given in Supplementary Material.

3.2 Binding affinities of anti-virus protease drugs

It is interesting to analyze the predicted binding affinities of existing antiviral drugs developed as protease inhibitors. Their binding affinities are listed in Table 2. It is interesting to see that except for Boceprevir, which is a protease inhibitor used to treat hepatitis caused by the hepatitis C virus (HCV), the rest of protease inhibitors do not have a strong effect on 2019-nCoV. The predicted values by a recent study [24] are given in the parenthesis. It appears that these values are overestimated.

Table 2: A summary of predicted binding affinities (unit: kcal/mol) of antiviral protease inhibitors. Numbers in parenthesis are results from the literature [24].

DrugID	Predicted Binding Energy	DrugID	Predicted Binding Affinity
Boceprevir	-9.36	Atazanavir	-7.28 (-9.57)
Tipranavir	-8.87	Ritonavir	-7.19 (-8.47)
Fosamprenavir	-7.82	Lopinavir	-7.12
Saquinavir	-7.75	Darunavir	-7.05
Simeprevir	-7.52 (-8.29)	Nelfinavir	-6.74
Telaprevir	-7.50	Amprenavir	-6.73
Indinavir	-7.46		

4 Material and methods

Our deep learning-based drug repositioning models employ mathematical pose (MathPose) and mathematical deep learning (MathDL) to predict 3D poses and protein-ligand binding affinities. The latter is used as a major criterion for searching anti-2019-nCoV therapies from the existing FDA-approved drugs. We first build a 3D 2019-nCoV 3CL protease structure by using homology modeling. A set of SARS-CoV protease inhibitors are docked to the 3D 2019-nCoV 3CL protease structure using our MathPose. The resulting complexes are used as a set of machine learning training. Additionally, a set of protein-ligand complexes from the PDBBind database is collected as another machine learning training set. Our training accuracy in terms of the Pearson correlation coefficient is higher than 0.99 in all deep learning models.

4.1 3D 2019-nCoV protease structure

Homology modeling, a procedure that constructs an atomic-resolution model of a protein from its amino acid sequence and experimental 3D structure of the related homologous protein, i.e., the "template," is used to generate the 3D structure of 2019-nCoV 3CL protease. The SWISS model (https://swissmodel.expasy.org/) is employed with the protease structure of SARS-CoV (PDB ID: 2A5I [13]) as a template. The sequence identity between the 3CL proteases of SARS-CoV and 2019-nCoV is 96.08%.

4.2 SARS-CoV protease inhibitor dataset

ChEMBL [14], an open database that brings chemical, bioactivity, and genomic data together to translate genomic information into effective new drugs, is employed to construct our 2019-nCoV training set. Considering the high sequence identity between viral proteases of 2019-nCoV and SARS-CoV, we take the protease of SARS-CoV as the input target in ChEMBL and a total 115 ChEMBL IDs of the target can be found. The experimental ΔG values of 2019-nCoV 115 SARS-CoV protease inhibition compounds range from -10.0 kcal/mol to 7.5 kcal/mol. We exclude compounds with positive values, resulting in a total of 84 SARS-nCoV protease inhibition compounds for our machine learning training. A collection of these 84 compounds is given in the Supplementary Materials.

4.3 Binding affinity training set

The PDBbind database is a yearly updated collection of experimentally measured binding affinity data (Kd, Ki, and IC50) for the protein-ligand complexes deposited in the Protein Data Bank (PDB). The PDBbind general set, instead of the high-quality refined set, is chosen as our training set because of the FDA approved drugs involve a wide range of protein targets. In the current work, we use a set of 15,843 X-ray crystal structures of protein-ligand complexes and associated binding affinities from the PDBbind v2018 general set [15]. The information of these complexes is provided in the Supplementary Materials.

4.4 FDA approved drugs

DrugBank (www.drugbank.ca) is a richly annotated, freely accessible online database that integrates massive drug, drug target, drug action, and drug interaction information about FDA-approved drugs with the experimental drugs which are going through the FDA approval process [16]. Due to the high quality and sufficient information contained in, the DrugBank has become one of the most popular reference drug resources used all over the world. A total of 1553 FDA-approved drugs are contained in the DrugBank. However, in the present work, a number of FDA-approved drugs encountered difficulties in docking with the target molecule. Therefore, the MathPose successfully created 3D protein-ligand complex structures for 1465 FDA-approved drugs and 2019-nCoV protease.

4.5 MathDL

MathDL, designed for predicting various druggable properties of 3D molecules [23], is capable of efficiently and accurately encoding the high-dimensional biomolecular interactions into low-dimensional representations. Algebraic graph theory-based algorithms [25], differential geometry, and algebraic topology methods [23] are applied to generate three mathematical representations of data in MathDL. These data

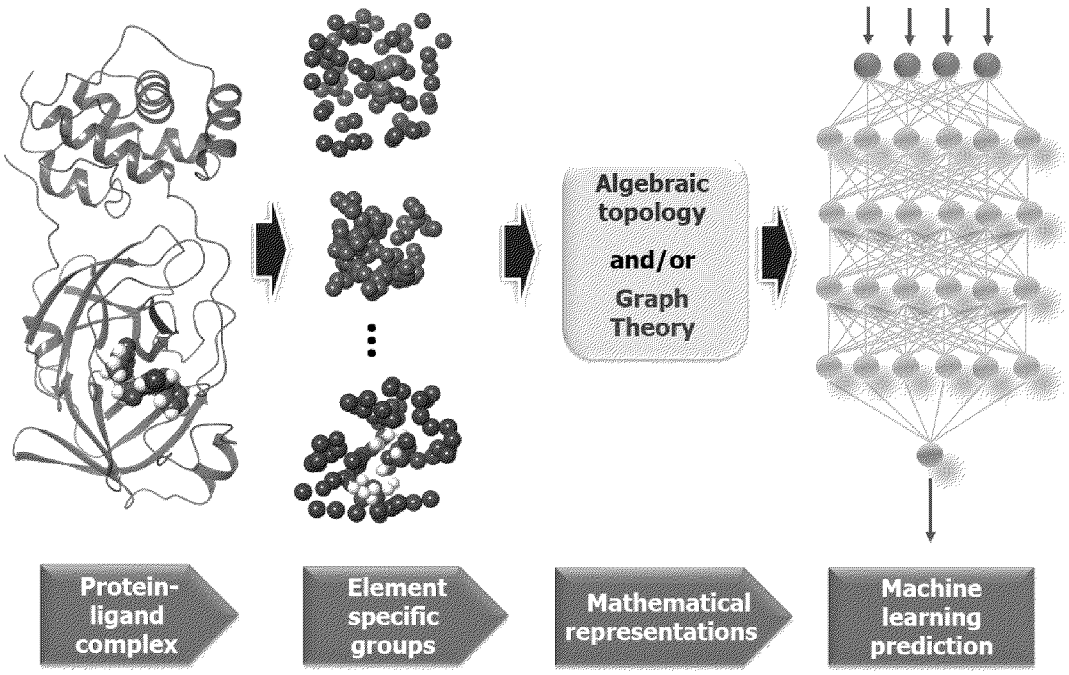


Figure 4: A framework of MathDL energy prediction model which integrates advanced mathematical representations with sophisticated CNN architectures

representations can be integrated with well-designed deep learning models, such as gradient-boosted trees (GBTs) and convolutional neural networks (CNNs), for pose ranking and binding affinity predictions. In D3R Grand Challenges (https://drugdesigndata.org/about/grand-challenge), a worldwide competition series in computer-aided drug design, MathDL had been proved as the top performer in free energy prediction and ranking [22, 23]. Figure 4 illustrates the framework of the MathDL model, which combined the aforementioned mathematical representations with the CNN architecture for druggable properties predictions. The PDBbind 2018 general set [15], along with the SARS 3CL protease related dataset is used in our training process. In this section, we briefly describe the algebraic topology representation used in the present work. Details can be found in the literature [23].

4.5.1 Algebraic topology-based representation

Even with a glimpse of topology, one can realize it dramatically simplifies geometric complexity [9, 17–20]. The study of topology reveals characterizes of different dimensions. As a type of algebraic topology, simplicial homology studies complexes on discrete datasets under various settings, such as the Vietoris-Rips (VR) complex, Čech complex or alpha complex, and identifies the topological invariants of a point-cloud dataset such as atomic coordinates in a protein [26]. Separated components, rings, and cavities can be classified for a given configuration and their numbers are referred to as Betti-0, Betti-1, and Betti-2, respectively. In this topological analysis process, the metrics or coordinates are fully abandoned. Instead, geometric and topological information is captured as data representation. Moreover, as a new development branch of algebraic topology, persistent homology which combines multiscale geometric information and topological invariants to achieve a geometry-enriched topological characteristic, e.g., barcodes. Therefore, the "birth" and "death" of separated components, circles, rings, voids or cavities can be indicated at all spatial scales by topological measurements. Key concepts are briefly shown as following.

In algebraic topology, simplices are the essential building blocks. Let $v_0, v_1, v_2, \cdots, v_k$ be $k+1$ affinely independent points. A (geometric) k-simplex σ^k is the linear combinations of these points in $\mathbb{R}^n$ ($n \geq k$),

whose coefficients are positive and satisfy that their summation equals to 1. For example, a 0, 1, 2, or 3-simplex is considered as a vertex, an edge, a triangle, or a tetrahedron, respectively. A simplicial complex K is a topological space composed of simplices which satisfies that every face of a simplex $\sigma_k \in K$ is also in K and the non-empty intersection of any two simplices is a face for both. To identify the homology group, a k-chain $[\sigma^k]$ is a summation $\sum_i \alpha_i \sigma_i^k$ of k-simplices σ_i^k, and the set of all k-chains of the simplicial complex K equipped with an algebraic field (typically, $\mathbb{Z}_2$) forms an abelian group $C_k(K, \mathbb{Z}_2)$. The homology defined on a series of abelian groups is used to analyze topological invariants which requires boundary operators to connect these chain spaces. The boundary operators $\partial_k : C_k \to C_{k-1}$ for a k-simplex $\sigma^k = \{v_0, v_1, v_2, \cdots, v_k\}$ are homomorphisms defined as $\partial_k \sigma^k = \sum_{i=0}^{k} (-1)^i \{v_0, v_1, \cdots, \hat{v_i}, \cdots, v_k\}$, where $\{v_0, v_1, \cdots, \hat{v_i}, \cdots, v_k\}$ is a $(k-1)$-simplex excluding v_i from the vertex set. Consequently, a important property of boundary operator, $\partial_{k-1}\partial_k = \emptyset$, follows from that boundaries are boundaryless. The algebraic construction to connect a sequence of complexes by boundary maps is called a chain complex

$$\cdots \xrightarrow{\partial_{i+1}} C_i(X) \xrightarrow{\partial_i} C_{i-1}(X) \xrightarrow{\partial_{i-1}} \cdots \xrightarrow{\partial_2} C_1(X) \xrightarrow{\partial_1} C_0(X) \xrightarrow{\partial_0} 0$$

and the kth homology group is the quotient group defined by

$$H_k = Z_k / B_k, \tag{1}$$

where the k-cycle group Z_k and the k-boundary group B_k are the subgroups of C_k defined as, $Z_k = \ker \partial_k = \{c \in C_k \mid \partial_k c = \emptyset\}$, $B_k = \text{im } \partial_{k+1} = \{\partial_{k+1} c \mid c \in C_{k+1}\}$. The aforementioned property implies $B_k \subseteq Z_k \subseteq C_k$. The Betti numbers are defined by the ranks of kth homology group H_k which counts k-dimensional holes, especially, $\beta_0 = \text{rank}(H_0)$ reflects the number of connected components, $\beta_1 = \text{rank}(H_1)$ reflects the number of loops, and $\beta_2 = \text{rank}(H_2)$ reveals the number of voids or cavities. Together, the set of Betti numbers $\{\beta_0, \beta_1, \beta_2, \cdots\}$ indicates the intrinsic topological property of a system.

Persistent homology [18] is devised to track the multiscale topological information over different scales along a filtration. A filtration of a topology space K is a nested sequence of subspaces $\{K^t\}_{t=0,\ldots,m}$ of K such that $\emptyset = K^0 \subseteq K^1 \subseteq K^2 \subseteq \cdots \subseteq K^m = K$. Moreover, on this complex sequence, we obtain a sequence of chain complexes by homomorphisms: $C_*(K^0) \to C_*(K^1) \to \cdots \to C_*(K^m)$ and a homology sequence: $H_*(K^0) \to H_*(K^1) \to \cdots \to H_*(K^m)$, correspondingly. The p-persistent kth homology group of K^t is defined as

$$H_k^{t,p} = Z_k^t / (B_k^{t+p} \bigcap Z_k^t), \tag{2}$$

where $B_k^{t+p} = \text{im}\partial_{k+1}(K^{t+p})$. Intuitively, this homology group records the homology classes of K^t that are persistent at least until K^{t+p}. Under the filtration process, the persistent homology barcodes can be generated. To make use of advanced deep learning algorithms, we vectorize persistent homology barcodes by dividing them into bins and calculating persistence, birth, and death incidents in each bin. Furthermore, the statistics of element-specific persistent homology barcodes are taken into consideration as well in fixed-length features.

4.6 MathPose

MathPose, a 3D pose predictor which converts SMILES strings into 3D poses with references of target molecules, was the top performer in D3R Grand Challenge 4 in predicting the poses of 24 beta-secretase 1 (BACE) binders [23]. For one SMILES string, around 1000 3D structures can be generated by a common docking software tool, i.e., GLIDE [27]. Moreover, a selected set of known complexes is re-docked by the three docking software packages mentioned above to generate at 100 decoy complexes per input ligand as a machine learning training set. The machine learning labels will be the calculated root mean squared deviations (RMSDs) between the decoy and native structures for this training set. Furthermore, MathDL models will be set up and applied to select the top-ranked pose for the given ligand. Additionally, the top poses will be fed into the MathDL for druggable proprieties evaluation.

5 Conclusion

The current pneumonia outbreak caused by a new coronavirus (CoV), called 2019-nCoV in China, has evolved into a global health emergency declared by the World Health Organization. Although there is no effective anti-viral medicine for the 2019-nCoV, the 3CL proteases of 2019-nCoV and SARS-CoV have a sequence identity of 96%, which provides a foundation for us to hypothesize that all potential anti-SARS-CoV chemotherapies are also effective anti-2019-CoV molecules. We build a three-dimensional (3D) 2019-nCoV 3CL protease structure using a SARS-CoV 3CL protease crystal structure as a template and collect a set of 84 SARS-CoV inhibition experimental data. The molecules of this set are docked to the 3D 2019-nCoV 3CL protease structure to form a machine learning training set. Additionally, the PDBbind 2018 general set of 15,843 protein-ligand complexes is also included as an additional machine learning training set. Using these training sets, we develop two deep learning models based on low-dimensional algebraic topology representations of macromolecular complexes. A total of 1465 FDA-approved drugs is evaluated by their binding affinities predicted by the consensus of two models built with 1) a combination of algebraic topology and deep convolutional neural networks (CNNs), and 2) a combination of algebraic topology and deep multitask CNNs. According to the predicted binding affinities, we recommend many FDA-approved drugs as potentially highly potent medications to 2019-nCoV, which serve as a crucial step for the development of anti-2019-nCoV drugs.

Supplementary Materials

Supplementary Materials are available online for 3D structure information and affinities of SARS-CoV inhibitors, FDA-approved drugs, and PDBbind data set.

Acknowledgments

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(A brief summary in Chinese)

潜在的高效抗新冠状病毒药

运用分子生物学, 结构生物学, 药物设计原理, 扑拓学, 大数据, 以及深度学习, 从联邦食品及药物管理局已经批准的1465种药物中筛选出了以下潜在的高效抗新冠病毒药 (按照预测的药物与病毒剪切酶的结合能, i.e, predicted drug-2019-nCoV 3CL protease binding affinity, 由强到弱排列):

1. Bortezomib 万珂, 在台湾的正式商品名为萬科（原用途: 延缓、停止及治疗多发性骨髓瘤和被套细胞淋巴瘤恶化的情况, 属于标靶治疗的新型抗癌药. 潜在抗新冠病毒效果极强. 预测结合能: -12.2 kcal/mol）

2. Flurazepam 盐酸氟西泮（原用途: 抗焦虑药、镇痉剂、镇静剂及肌肉松弛剂. 预测结合能: -10.4 kcal/mol）

3. Ponatinib 普纳替尼（原用途: 白血病治疗药物. 预测结合能: -10.3 kcal/mol）

4. Sorafenib 蕾莎瓦（原用途: 治疗肾细胞癌及肝癌. 预测结合能: -10.0 kcal/mol）

5. Dasatinib 达沙替尼（原用途: 慢性粒细胞性白血病，费城染色体呈阳性的急性髓性白血病该药，前列腺癌等. 预测结合能: -9.9 kcal/mol）

6. Paramethasone 帕拉米松（原用途: 严重的细菌感染和严重的过敏性疾病、各种各种血小板减少性紫癜、粒细胞减少症、严重皮肤病、器官移植的免疫排斥反应、肿瘤的治疗及对糖皮质激素敏感的眼部炎症等. 预测结合能: -9.7 kcal/mol）

7. Clocortolone 氯可托龙（原用途: 各种皮肤病, 例如，湿疹，皮炎，过敏，皮疹. 预测结合能: -9.6 kcal/mol）

8. Flucloxacillin 氟氯西林（原用途: 半合成的耐青霉素酶的青霉素. 预测结合能: -9.6 kcal/mol）

9. Sertindole 舍吲哚（原用途: 非典型抗精神病药物. 预测结合能: -9.5 kcal/mol）

10. Clevidipine 氯维地平（原用途: 治疗高血压. 预测结合能: -9.5 kcal/mol）

11. Aprepitant 阿瑞吡坦胶囊（原用途:止吐. 预测结合能: -9.5 kcal/mol）

12. Atorvastatin 立普妥（原用途: 降低血液胆固醇水平的常见药物. 预测结合能: -9.5 kcal/mol）

13. Cinolazepam 西诺西泮（原用途: 抗焦虑镇静催眠药. 预测结合能: -9.5 kcal/mol）

14. Clofazimine 氯法齐（原用途: 治疗结核病 (TB)、麻风病和其它相关传染病的抗生素. 预测结合能: -9.4 kcal/mol）

15. Fosaprepitant 福沙匹坦（原用途: 一种肿瘤辅助用药. 预测结合能: -9.4 kcal/mol）

另外, 联邦食品及药物管理局已经批准的抗病毒剪切酶的药物中, 分析表明唯有 Boceprevir 博赛泼维（原用途:丙型肝炎蛋白酶抑制剂）可能有一定的效果 (排名18. 预测结合能: -9.3 kcal/mol). 顺便提一下, 以前传的抗艾滋病药, 洛匹那韦/利托那韦片 (Lopinavir/ Ritonavir), 排名很靠后 (预测结合能: -7.1/-7.2 kcal/mol). 达芦那韦 (Darunavir) 排名也很靠后 (预测结合能: -7.1 kcal/mol).

参考文献:

MS ID#: BIORXIV/2020/936013
MS TITLE: Potentially highly potent drugs for 2019-nCoV

From: vinu arumugham <vaccine.safety@aol.com>
Sent: Saturday, June 13, 2020 12:17 AM
To: kanchanmvk@yahoo.com; ushamvk@yahoo.co.in; mike.agogliati@wfsb.com; kienym@who.int; Pasi.Penttinen@ecdc.europa.eu; sbaldwin@idri.org; friedem@who.int; angela.shen@hhs.gov; Bruce.Gellin@sabin.org; cww@austin.utexas.edu; mail@wired.com; submit@wired.com; megan_molteni@wired.com; wjbkwebteam@foxtv.com;; fox2newsdesk@foxtv.com; tyagi@ebi.ac.uk; Nick.Furnham@lshtm.ac.uk; betsy.mckay@wsj.com; spencer.macnaughton@wsj.com; conall.jones@wsj.com; brianna.abbott@wsj.com; Christopher.Weaver@wsj.com; dschui@cuhk.edu.hk; wpchnwr@who.int; wpchnmedia@who.int; wprocom@who.int; mediainquiries@who.int; 13698665 @qq.com; lifang@umn.edu; LDu@nybc.org; kyyuen@hku.hk; mark.woolhouse@ed.ac.uk; Christopher.Whitty@lshtm.ac.uk; Menachery, Vineet; jiwei_yunlong@126.com; Jennifer.Layden@Illinois.gov; rothe@lrz.uni-muenchen.de; zhangyongzhen@shphc.org.cn; sanchak@gmail.com; badrishanthi@hotmail.com; ljli@zju.edu.cn; gmaclaren@iinet.net.au; wiv@wh.iov.cn; suoban@simm.ac.cn; yqi@implad.ac.cn; sunguibo@126.com; kalisvar_marimuthu@ncid.sg; oon_tek_ng@ncid.sg; david.szymkowski@xencor.com; media.relations@roche.com; murthy.aditya@gene.com; joshua.wallach@yale.edu; alexander.egilman@yale.edu; margaret.e.mccarthy@yale.edu; jennifer.miller@nyumc.org; steven.woloshin@dartmouth.edu; lisa.schwartz@dartmouth.edu; joseph.ross@yale.edu; zlshi@wh.iov.cn; Linfa.wang@csiro.au
Subject: Fwd: Re: Confirmation of my predictions on the role of mast cells, histamine in COVID-19

COVID-19 severity is caused by an allergic reaction to the coronavirus involving mast cell degranulation and histamine release (elicitation). The development of this allergy (sensitization) was caused by vaccine components that are similar to coronavirus proteins.

Sharing with permission.

-------- Forwarded Message --------
Subject: Re: Confirmation of my predictions on the role of mast cells, histamine in COVID-19
Date: Sun, 7 Jun 2020 04:07:28 +0000
From: Lawrence Steinman <steiny@stanford.edu>
To:vinu arumugham <vaccine.safety@aol.com>

Dear Vinu,

All very interesting.
Congratulations to you for being correct, on point and prescient!
Thanks for sharing

Larry

Prof. Lawrence Steinman
Zimmermann Professor of Pediatrics, Neurology and Neurological Sciences
Beckman Center for Molecular Medicine
279 Campus Drive
Stanford, CA 94305-5316

From: vinu arumugham <vaccine.safety@aol.com>
Sent: Saturday, June 6, 2020 5:44 PM
To: Lawrence Steinman <steiny@stanford.edu>
Subject: Confirmation of my predictions on the role of mast cells, histamine in COVID-19
ï¿½
Prof. Steinman,

Thought this may be of interest:

I have been predicting for 4 months now that mast cell stabilizers and antihistamines (like H1/H2 blockers) can help in COVID-19.

I described the details, connecting mast cells, histamine, COVID-19 and dengue in my article below (uploaded Apr 11'20):

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

As you may have read, famotidine (an antihistamine, H2 blocker) has been found to help in COVID-19, just like I predicted.

A large group of experts with expertise covering drug discovery, vaccines, pathology etc. recently (May 24'20 report) hypothesized and investigated numerous potential mechanisms involved in famotidine's beneficial effect in COVID-19. The study was funded by the "Department of Defense (DoD), Defense Threat Reduction Agency (DTRA), and the Joint Science and Technology Office (JSTO) of the Chemical and Biological Defense Program (CBDP) for funding under the Discovery of Medical countermeasures Against Novel Entities (DOMANE) initiative."

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
www.researchsquare.com/article/rs-30934/v1

They conclude: "We propose that the principal famotidine mechanism of action for COVID-19 involves on-target histamine receptor H2 activity, and that development of clinical COVID-19 involves dysfunctional mast cell activation and histamine release."

They write: " ... COVID-19 disease progression could share an immunologic basis with Dengue hemorrhagic fever" and

"This model is also supported by the significant overlap in the clinical signs and symptoms of the initial phase of COVID-19 disease and those of mast cell activation syndrome (MCAS) 89-92 as well similarities to Dengue hemorrhagic fever and shock syndrome (including T cell depletion) during the later phase of COVID-19"

"If COVID-19 is partially driven by dysfunctional mast cell degranulation, then a variety of medical interventions employing marketed drugs useful for treating mast cell-related disorders may help to reduce death and disease associated with SARS-CoV-2 infection. Examples include drugs with mast cell stabilizing activity, other histamine antagonists (for example H1 and H4 types), leukotriene antagonists and leukotriene receptor antagonists"

In other words, their findings are in perfect agreement with my prediction and analysis.

Thanks,
Vinu

From: 周缘 [zhouyuan@wh.iov.cn]
Sent: 10/19/2019 10:43:04 PM
To: Shi, Pei yong [peshi@UTMB.EDU]; chenxw [chenxw@wh.iov.cn]
CC: Xie, Xuping [xuxie@UTMB.EDU]; Zhang, Xianwen [zhxianwe@UTMB.EDU]
Subject: about the publishingfee of mBio , ms. mBio02375-19

Dear all ;

I have already paid the membership fee of $90 , and saved the publishing fee for $900！(happy!haha...) I completed the payment of thepublishing.There were some problems logging into the U.S. website those days ,so delayed some time.

By the way,I have changed the invoice information (organization) of publishing fees. But I can't find the invoice about the membership fee. I need to change the organization.

--
周缘
中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2019-10-15 21:59:05 (星期二)
收件人: "周缘" <zhouyuan@wh.iov.cn>
抄送: "Xie, Xuping" <xuxie@UTMB.EDU>, "Zhang, Xianwen" <zhxianwe@UTMB.EDU>
主题: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Thanks, Yuan

Pei-Yong

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Tuesday, October 15, 2019 1:52 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Prof.Pei-yong,

I'll deal with it as soon as possible!

Yuan
--
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中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

> -----原始邮件-----
> **发件人:**"Shi, Pei yong" <peshi@UTMB.EDU>
> **发送时间:**2019-10-14 20:00:19 (星期一)
> **收件人:** "周缘" <zhouyuan@wh.iov.cn>

抄送:

主题: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Yuan,

Please see the forwarded the email. Thanks so much for taking care of it.

Best regards,

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From: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
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Thank you,

ASM Reprint/Billing Account Manager.

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From: Xie, Xuping [xuxie@UTMB.EDU]
Sent: 10/16/2019 12:06:56 PM
To: 周缘 [zhouyuan@wh.iov.cn]; Shi, Pei yong [peshi@UTMB.EDU]; Zhang, Xianwen [zhxianwe@UTMB.EDU]
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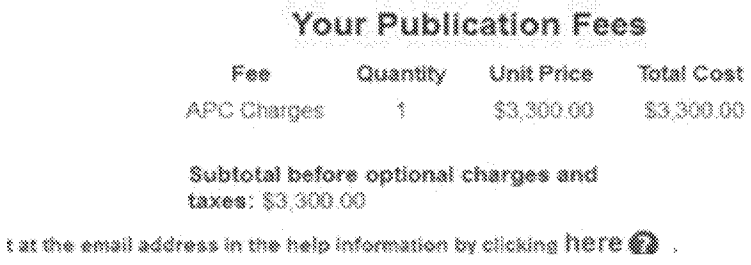

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Subtotal before optional charges and taxes: $3,300.00

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Pei-Yong

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Thank you,

ASM Reprint/Billing Account Manager.

****

From: Xie, Xuping [xuxie@UTMB.EDU]
Sent: 10/18/2019 10:00:51 AM
To: 周缘 [zhouyuan@wh.iov.cn]; Shi, Pei yong [peshi@UTMB.EDU]
CC: Zhang, Xianwen [zhxianwe@UTMB.EDU]; 陈新文 [chenxw@wh.iov.cn]
Subject: RE: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

Please hold on the payment. Pei-Yong is going to renew the member for getting better discounts. Sorry for any inconvenience it may have caused.

Thanks.

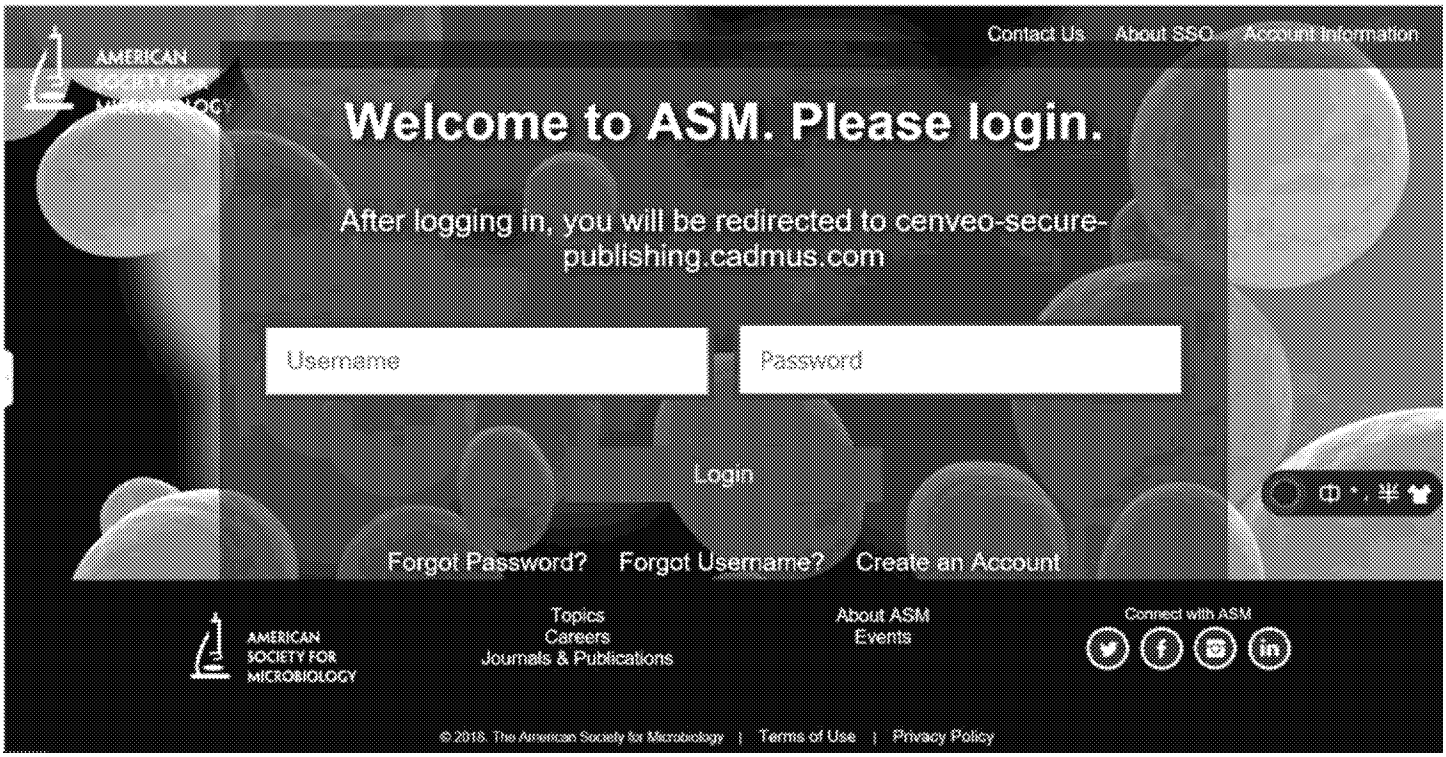
Xuping

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Friday, October 18, 2019 9:14 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Xie, Xuping <xuxie@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>; 陈新文 <chenxw@wh.iov.cn>
Subject: Re: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear all;

ALL the usenames you have told me can't work...Please see the next picture,I need the usename which should be a email.If You all have no the membership,So I'll only pay without discount.

Yours,Yuan



--

周缘
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肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

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44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

-----原始邮件-----

发件人:"Shi, Pei yong" <peshi@UTMB.EDU>

发送时间:2019-10-17 08:16:13 (星期四)

收件人: "Xie, Xuping" <xuxie@UTMB.EDU>, "周缘" <zhouyuan@wh.iov.cn>, "Zhang, Xianwen" <zhxianwe@UTMB.EDU>

抄送: "陈新文" <chenxw@wh.iov.cn>

主题: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

552.136

Please try the following information and see if it works. If my ASV membership has expired, we can renew it easily.

ASM membership and author billing

Username [redacted]

Password: [redacted]

Membership number: [redacted]

We could talk over WeChat if it is easier.

Thanks!

Pei-Yong

From: Xie, Xuping <xuxie@UTMB.EDU>
Sent: Wednesday, October 16, 2019 12:07 PM
To: 周缘 <zhouyuan@wh.iov.cn>; Shi, Pei yong <peshi@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Cc: 陈新文 <chenxw@wh.iov.cn>
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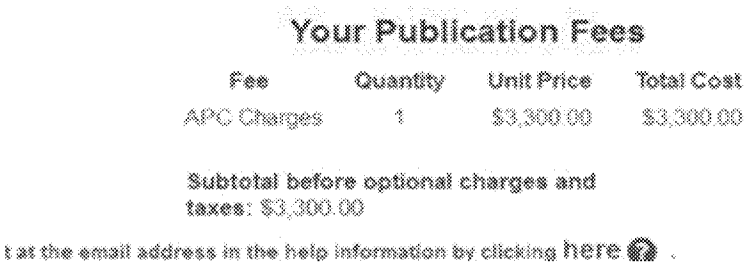

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Yuan

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Email: zhouyuan@wh.iov.cn

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发件人:"Xie, Xuping" <xuxie@UTMB.EDU>

发送时间:2019-10-15 22:04:06 (星期二)

收件人: "周缘" <zhouyuan@wh.iov.cn>

抄送: "Zhang, Xianwen" <zhxianwe@UTMB.EDU>, "Shi, Pei yong" <peshi@UTMB.EDU>

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Subject: Re: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

Please let us know whether it woks. If not, I can help renew it tomorrow.

Best,

Xuping

Sent from my iPhone

On Oct 16, 2019, at 7:16 PM, Shi, Pei yong <peshi@utmb.edu> wrote:

Hi Yuan,

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Subject: Re: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Prof.Pei-yong,

I'll deal with it as soon as possible!

Yuan

--

周缘

中国科学院武汉病毒研究所

肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2019-10-14 20:00:19 (星期一)
收件人: "周缘" <zhouyuan@wh.iov.cn>
抄送:
主题: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Yuan,

Please see the forwarded the email. Thanks so much for taking care of it.

Best regards,

Pei-Yong

From: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Sent: Monday, October 14, 2019 4:00 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: asm.authorservicessupport@cenveo.com
Subject: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Dr. Pei-Yong Shi,

Your article, Zika virus NS2A-mediated virion assembly (Manuscript # mBio02375-19), is scheduled to be published in issue 6 of mBio.

To facilitate prompt publication of your article, please use this link to the Author Services system to do any of the following:

- Pay publication fees
- Pay additional fees (Open Access, supplemental materials, etc.)
- Order reprints or eprints

https://authorservices.cadmus.com/Shibboleth.sso/Login?entityID=https://login.asm.org/idp/shibboleth&target=/DRIPShopperWeb%2Foffer.do%3FarticleID%3D3087836%26emailAddress%3Dpeshi%40utmb.edu

You may pay by credit card, or purchase order. Doing so will create a printable invoice that you can include with your payment, or submit to your funding institution as a pro-forma invoice. The invoice you create will contain information about payment by credit card, bank wire, or check. You must use this system to create an accurate invoice for payment.

ASM Members receive substantial discounts on publication fees and when ordering reprints and eprints. If you are a current ASM member, these discounts are applied automatically when you log in. If you are just now joining or renewing, we must first receive your payment for the membership discounts to be available.

To join or renew your ASM membership, go to: www.asm.org/join.

If you experience problems with your fees or with the Author Services website, please email ASM.AuthorServicesSupport@cenveo.com.

Thank you,

ASM Reprint/Billing Account Manager.

****

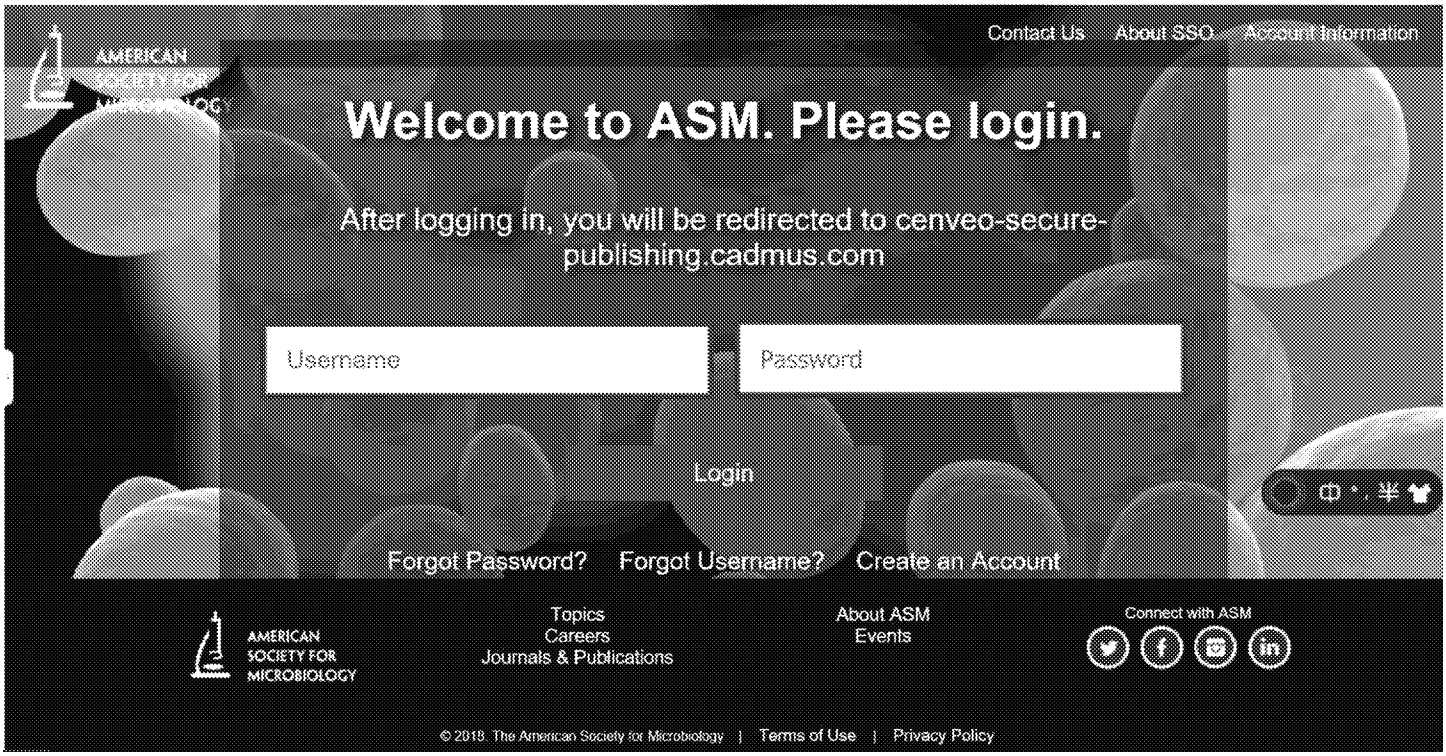
<Pei Yong WeChat QR code.png>

From: 周缘 [zhouyuan@wh.iov.cn]
Sent: 10/18/2019 9:13:44 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
CC: Xie, Xuping [xuxie@UTMB.EDU]; Zhang, Xianwen [zhxianwe@UTMB.EDU]; 陈新文 [chenxw@wh.iov.cn]
Subject: Re: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear all;

ALL the usenames you have told me can't work...Please see the next picture,I need the usename which should be a email.If You all have no the membership,So I'll only pay without discount.

Yours,Yuan



--

周缘
中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China
Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

552.136

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2019-10-17 08:16:13 (星期四)
收件人: "Xie, Xuping" <xuxie@UTMB.EDU>, "周缘" <zhouyuan@wh.iov.cn>, "Zhang, Xianwen" <zhxianwe@UTMB.EDU>
抄送: "陈新文" <chenxw@wh.iov.cn>
主题: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

Please try the following information and see if it works. If my ASV membership has expired, we can renew it easily.

ASM membership and author billing
Username: [redacted]
Password: [redacted]
Membership number: [redacted]

We could talk over WeChat if it is easier.

Thanks!

Pei-Yong

From: Xie, Xuping <xuxie@UTMB.EDU>
Sent: Wednesday, October 16, 2019 12:07 PM
To: 周缘 <zhouyuan@wh.iov.cn>; Shi, Pei yong <peshi@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Cc: 陈新文 <chenxw@wh.iov.cn>
Subject: RE: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Hi Yuan,

We are not the member of the ASM. Based on the linker for the payment, it appears Pei-Yong is also not the member of ASM. I would like to wait for Pei-Yong's confirmation.

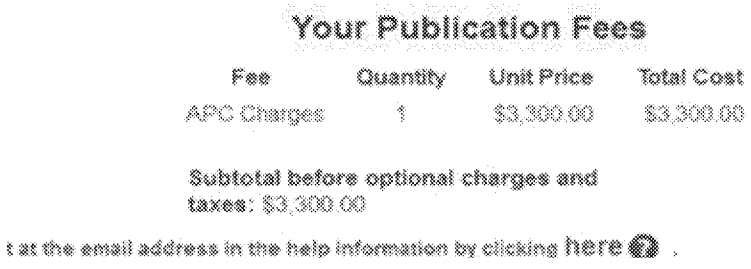
Best,

Xuping

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Tuesday, October 15, 2019 10:01 PM
To: Xie, Xuping <xuxie@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Cc: 陈新文 <chenxw@wh.iov.cn>
Subject: Re: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear all ,How are you?

I need a writer's member name (should be a email) and password on ASM, because members can discount the page fee. I'm not one of the authors,so I can't get a discount even if I pay the membership fee. It's a little expensive(3300 dollars),Please see the picture below.



Your Publication Fees

Fee	Quantity	Unit Price	Total Cost
APC Charges	1	$3,300.00	$3,300.00

Subtotal before optional charges and taxes: $3,300.00

t at the email address in the help information by clicking here .

Yuan

--
周缘
中国科学院武汉病毒研究所

肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
44 Xiao Hong Shan, Wuhan,430071, P.R.China

Email: zhouyuan@wh.iov.cn

Phone: 86-27-87197575

-----原始邮件-----

发件人:"Xie, Xuping" <xuxie@UTMB.EDU>

发送时间:2019-10-15 22:04:06 (星期二)

收件人: "周缘" <zhouyuan@wh.iov.cn>

抄送: "Zhang, Xianwen" <zhxianwe@UTMB.EDU>, "Shi, Pei yong" <peshi@UTMB.EDU>

主题: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Dear Yuan,

Thanks. Please let us know if we can assist.

Best,

Xuping

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, October 15, 2019 8:59 AM
To: 周缘 <zhouyuan@wh.iov.cn>
Cc: Xie, Xuping <xuxie@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>
Subject: RE: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Thanks, Yuan

Pei-Yong

From: 周缘 <zhouyuan@wh.iov.cn>
Sent: Tuesday, October 15, 2019 1:52 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: RE: Payment for your upcoming article in mBio , ms. mBio02375-19

Prof.Pei-yong,

I'll deal with it as soon as possible!

Yuan
--
周缘
中国科学院武汉病毒研究所
肝炎病毒分子生物学学科组，武汉市武昌区小洪山中区44号

Wuhan Institute of Virology, Chinese Academy of Sciences（WIV,CAS）
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Email: zhouyuan@wh.iov.cn
Phone: 86-27-87197575

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Sent: Monday, October 14, 2019 4:00 AM
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- Pay publication fees
- Pay additional fees (Open Access, supplemental materials, etc.)
- Order reprints or eprints

https://authorservices.cadmus.com/Shibboleth.sso/Login?entityID=https://login.asm.org/idp/shibboleth&target=/DRIPShopperWeb%2Foffer.do%3FarticleID%3D3087836%26emailAddress%3Dpeshi%40utmb.edu

You may pay by credit card, or purchase order. Doing so will create a printable invoice that you can include with your payment, or submit to your funding institution as a pro-forma invoice. The invoice you create will contain information about payment by credit card, bank wire, or check. You must use this system to create an accurate invoice for payment.

ASM Members receive substantial discounts on publication fees and when ordering reprints and eprints. If you are a current ASM member, these discounts are applied automatically when you log in. If you are just now joining or renewing, we must first receive your payment for the membership discounts to be available.

To join or renew your ASM membership, go to: www.asm.org/join.

If you experience problems with your fees or with the Author Services website, please email ASM.AuthorServicesSupport@cenveo.com.

Thank you,

ASM Reprint/Billing Account Manager.

****

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; Cervenka, Nicole[NCervenka@nas.edu]; Sharples, Fran[FSharples@nas.edu]; Block, Bruce[BBlock@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Thur 10/15/2020 12:17:33 PM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for participating in the China bio dialogue sessions on Tuesday and Wednesday this week. We have scheduled a short hotwash session so the American participants can discuss the virtual dialogue discussions (from this week and earlier this year) and your get your ideas on future topics and other issues.

The session will take place tomorrow from 5:30-6:30 PM, Zoom link is below. Sorry for the short notice, if you can't make it tomorrow feel free to weigh in by email.

Topic: China Bio Post Dialogue Meeting Discussion
Time: Oct 16, 2020 5:30 PM ET / 4:30 PM CT / 2:30 PM PT
Meeting Link: https://nasem.zoom.us/j/92476126782?pwd= **552.136**
Password: **552.136**

PS I have asked CAS for the ppts from last night, will send those out as soon as I get them.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, October 14, 2020 7:32 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for joining the dialogue session last night. I have attached the slides from the three presentations.

FYI CAS has invited two additional CCDC experts to the session tonight.

Dr. Huaqing Wang, PI, Immunization program, Chinese Center for Disease Control and Prevention
Dr. Zundong Yin, Director of National Immunization Program, Chinese Center for Disease Control and Prevention

Looking forward seeing and hearing from you all in a few hours.
Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, October 12, 2020 12:36 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***
Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**

Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>
Subject: Virtual U.S. China dialogue meeting October 13 and 14
Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another

(4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

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The U.S. National Academy of Sciences
1-202-334-3975

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- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

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We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

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From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 10/12/2020 11:36:05 AM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
October 2020 U.S.-China Bio Dialogue v3.docx

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
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Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
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Subject: Virtual U.S. China dialogue meeting October 13 and 14
Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

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***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**

4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

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As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

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October Bio Dialogue Virtual Sessions

Session 1: Tuesday, October 13, 9-11 PM ET / 6-8 PM PT in U.S.
Wednesday, October 14, 9-11 AM in China

Session 1 Meeting Link: [HYPERLINK "https://nasem.zoom.us/j/92754903815?pwd=
Password: 552.136

552.136

Welcome and Introduction — Diane Griffin and George Gao

Overview of current status of CoVID-19 vaccine development in China — George Gao
Overview of current status of CoVID-19 vaccine development in the U.S. — Nancy Connell

Topic 1: Human vaccine development and delivery
Moderator: Diane Griffin

- Vaccination programs in China: How are vaccine programs for particular subpopulations being implemented?
  - Pediatric populations
  - First responders
  - Elderly population

- Post-vaccination surveillance and monitoring strategies
  - Immunogenicity
  - Monitoring Immunity
  - Vaccine-associated adverse events

- Adapting current vaccine platforms to novel mass vaccination: strategies and issues

- Progress on other vaccines
  - Universal influenza vaccines
  - Enterovirus D68

Topic 2: Animal vaccine development and delivery
Moderator: Linda Saif

- Status of corona virus vaccination for animals
  - Vaccine types
  - Efficacy
  - Complications and other issues?

- African Swine Fever: vaccine progress in China

- New "swine flu" (G4) in China

- H5N1 avian influenza and domestic poultry

Session 2: Wednesday October 14, 9-11 PM ET / 6-8 PM PT in U.S.
Thursday, October 15, 9-11 AM in China

Session 2 Meeting Link: [HYPERLINK "https://nasem.zoom.us/j/98420889232?pwd=552.136
Password: 552.136

Topic 1: Immunity
Moderator: Diane Griffin

- Correlates of immunity – biomarkers predicting susceptibility or progression to severe disease
- Background immunity from circulating "common cold" coronaviruses
- How long will immunity last?

Topic 2: Testing and diagnostics
Moderator: Peggy Hamburg

- Chinese testing strategies for rapid, frequent population-level testing
- Antibody testing
- Importance of T-cell responses
- Long-term sequelae following COVID-19 infection—lung function, neurologic issues, other issues

NASEM Participants

Dr. Ralph Baric, PhD, is a Professor in the Department of Epidemiology at the University of North Carolina's School of Public Health.

Dr. Nancy Connell, PhD, is a Professor at the Johns Hopkins Center for Health Security in Baltimore, MD

Dr. Peter Daszak, PhD, is currently president of EcoHealth Alliance, a nonprofit non-governmental organization that supports various programs on global health.

Dr. Victor Dzau, is the current President of the U.S. National Academy of Medicine in Washington, D.C.

Dr. David R. Franz, DVM, PhD, is currently retired, but served in the U.S. Army Medical Research and Materiel Command for 23 of 27 years on active duty and as Commander of the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID).

Dr. Harvey Fineberg, MD, is currently president of the Gordon and Betty Moore Foundation, immediately prior to which he was President of the Institute of Medicine (now the National Academy of Medicine).

Dr. Diane Griffin, PhD, is University Distinguished Service Professor and Alfred and Jill Sommer Chair of the W. Harry Feinstone Department of Molecular Microbiology and Immunology at Johns Hopkins Bloomberg School of Public Health and the current vice-president of the U.S. National Academy of Sciences.

Dr. Margaret (Peggy) Hamburg, MD, is an American physician and public health administrator. She served as the 21st Commissioner of the U.S. Food and Drug Administration from May 2009 to April 2015 and is currently Foreign Secretary for the U.S. National Academy of Medicine.

Dr. James Le Duc, PhD, is the director of the Galveston National Laboratory, one of the largest active biocontainment facilities on a U.S. academic campus.

Dr. Stanley Perlman, MD, PhD, is Professor of Microbiology and Immunology and of Pediatrics at the University of Iowa Health Care.

Dr. David Relman is a microbiologist and the Thomas C. and Joan M. Merigan Professor in Medicine and in Microbiology & Immunology at the Stanford University School of Medicine.

Dr. Linda J. Saif, PhD,[HYPERLINK "https://en.wikipedia.org/wiki/Linda_Saif" \l "cite_note-:0-3"] is Distinguished University Professor, [HYPERLINK "http://vet.osu.edu/preventive-medicine" \o "Preventive Medicine"], [HYPERLINK "http://www.oardc.ohio-state.edu/fahrp/" \t "_blank"], Ohio Agricultural Research and Development Center of the Ohio State University.

Dr. Pei Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas.

Chinese Participants

George F. Gao, Director-General, Chinese Center for Disease Control and Prevention, Member of Chinese Academy of Sciences

Zhiming Yuan, Professor, Director of Wuhan P4 Lab, Wuhan Institute of Virology, Chinese Academy of Sciences

Zhigao Bu, Director, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences (To be confirmed)

Jianping Weng, Executive Director, Division of Life Sciences and Medicine, University of Science and Technology of China

Xian-En Zhang, Professor, Institute of Biophysics, Chinese Academy of Sciences

Jinhua Liu, Professor, China Agricultural University

Aihua Zheng, Professor, Institute of Zoology, Chinese Academy of Sciences

Xi Zhou, Professor, Wuhan Institute of Virology, Chinese Academy of Sciences

Hongping Wei, Professor, Wuhan Institute of Virology, Chinese Academy of Sciences

Dong Men, Professor, Wuhan Institute of Virology, Chinese Academy of Sciences

Daming Wang, Suzhou Institute of Biomedical Engineering and Technology, Chinese Academy of Sciences

Lianpan Dai, Associate Professor, Institute of Microbiology, Chinese Academy of Sciences

Yong Hu, Associate Professor, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences

To: 'Peter Daszak'[daszak@ecohealthalliance.org]; 'relman@stanford.edu'[relman@stanford.edu]; rbaric_email.unc[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; antoinette_baric.med[antoinette_baric@med.unc.edu]; Alison Andre[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; Cervenka, Nicole[NCervenka@nas.edu]; Sharples, Fran[FSharples@nas.edu]; Block, Bruce[BBlock@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 10/19/2020 10:57:43 PM (UTC-05:00)
Subject: RE: Some bullets following our US-China dialogue discussion on Friday
3-month follow-up-JP Weng.pdf

Greetings,

Thanks again for participating in the China bio dialogue sessions last week. And thank you Peter and others who sent me feedback and thoughts on the future of the dialogue. Additional thoughts and comments are welcome.

Re next steps: The general plan is to try and hold another two night session in 2-3 months, when we have more information to share on vaccines, durability of immunity and the evaluation and uses of different types of tests. More discussion on the origin or "natural history" of the virus focused on preventing future outbreaks (since George Gao seems to be open to it) might be possible as well.

PS I have attached the ppt on learning from Covid patients from the dialogue.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, October 19, 2020 12:21 AM
To: Rusek, Benjamin <BRusek@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; rbaric_email.unc <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; antoinette_baric.med <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: Some bullets following our US-China dialogue discussion on Friday
Importance: High

Thanks for a good discussion on Friday Ben,

I fully support a continued dialog and noted, as did some of those on the call, that George Gao and others were more open in their discussion of investigations into animal reservoirs of SARS-CoV-2 – i.e. discussion about the origin. We discussed ways we could frame a future topic that would allow us to talk about some important issues around the 'natural history' of SARS-CoV-2, that might also be comfortable for our Chinese colleagues. Here are a couple of bullets along the lines you asked me for:

1. Summary of recent findings re. the ability of SARS-CoV-2 to infect other species of animals in the lab, and in the wild, around the world (e.g. mink farm infections Europe and US, experimental infections of ferrets & raccoon dogs, risk assessments of SARS-CoV-2 infecting bats in other countries)

2. From the natural history of the virus, what do we know about the diversity of alpha and beta CoVs in wildlife reservoirs, and in potential intermediate hosts in various countries in Asia.

3. What information can we identify from the receptor binding domain of SARS-related CoVs that might help us predict future potential for emergence of CoVs from other countries

I think a good strategy would be to have the US side give the opening slide deck so that we sort of set the parameters and open up some of the discussion that I'm sure would lead to interesting information. I'd be happy to help on the first 2 points, and I'm sure Ralph could talk to the 3rd point. Linda and Stanley have a great deal of knowledge and could provide supporting comments…

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, October 15, 2020 1:18 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; rbaric_email.unc <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; antoinette_baric.med <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for participating in the China bio dialogue sessions on Tuesday and Wednesday this week. We have scheduled a short hotwash session so the American participants can discuss the virtual dialogue discussions (from this week and earlier this year) and your get your ideas on future topics and other issues.

The session will take place tomorrow from 5:30-6:30 PM, Zoom link is below. Sorry for the short notice, if you can't make it tomorrow feel free to weigh in by email.

Topic: China Bio Post Dialogue Meeting Discussion
Time: Oct 16, 2020 5:30 PM ET / 4:30 PM CT / 2:30 PM PT
Meeting Link: https://nasem.zoom.us/j/92476126782?pwd= **552.136**
Password: **552.136**

PS I have asked CAS for the ppts from last night, will send those out as soon as I get them.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, October 14, 2020 7:32 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for joining the dialogue session last night. I have attached the slides from the three presentations.

FYI CAS has invited two additional CCDC experts to the session tonight.

Dr. Huaqing Wang, PI, Immunization program, Chinese Center for Disease Control and Prevention
Dr. Zundong Yin, Director of National Immunization Program, Chinese Center for Disease Control and Prevention

Looking forward seeing and hearing from you all in a few hours.
Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin

Sent: Monday, October 12, 2020 12:36 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***
Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>
Subject: Virtual U.S. China dialogue meeting October 13 and 14
Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**

5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin

Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

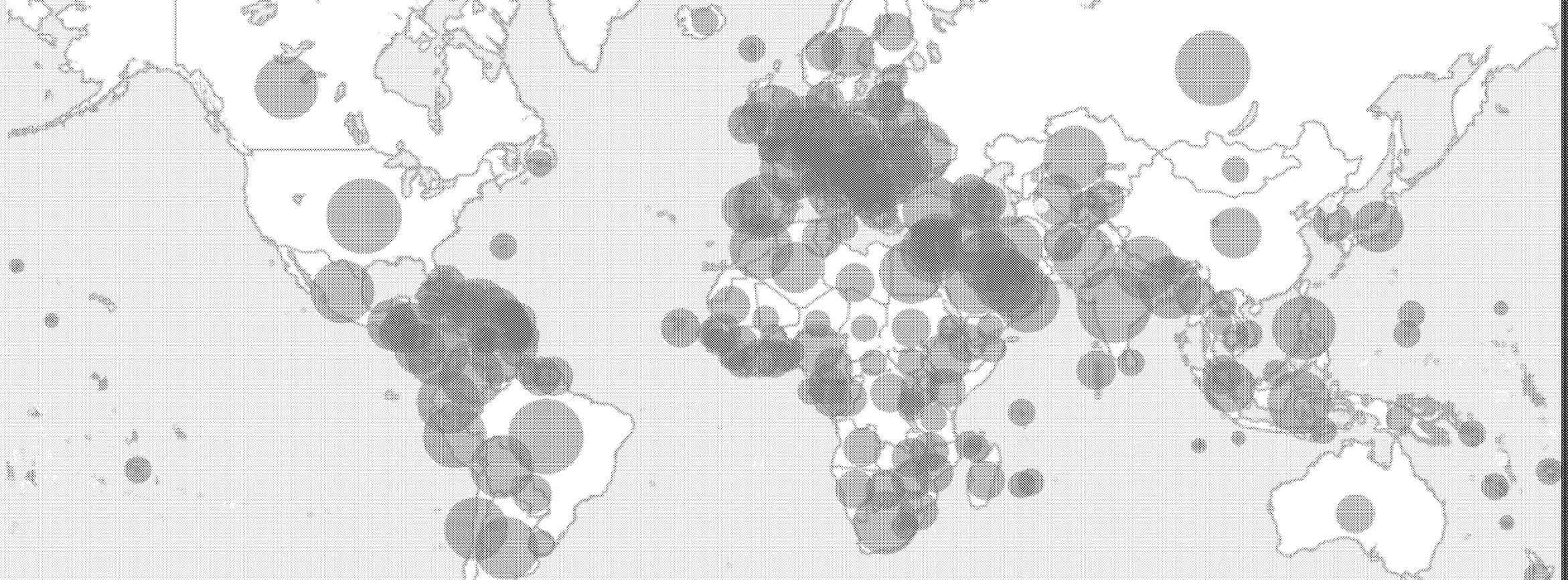
Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

Learning from following up of COVID-19 patients

Jianping Weng October 15, 2020

中国科学技术大学
University of Science and Technology of China



COVID-19 global pandemic: a historical challenge

- Globally, as of 5:06pm CEST, 13 October 2020
- **37,704,153** confirmed cases
- Causing **1,079,029** deaths

1. https://covid19.who.int/ (accessed October 14, 2020)

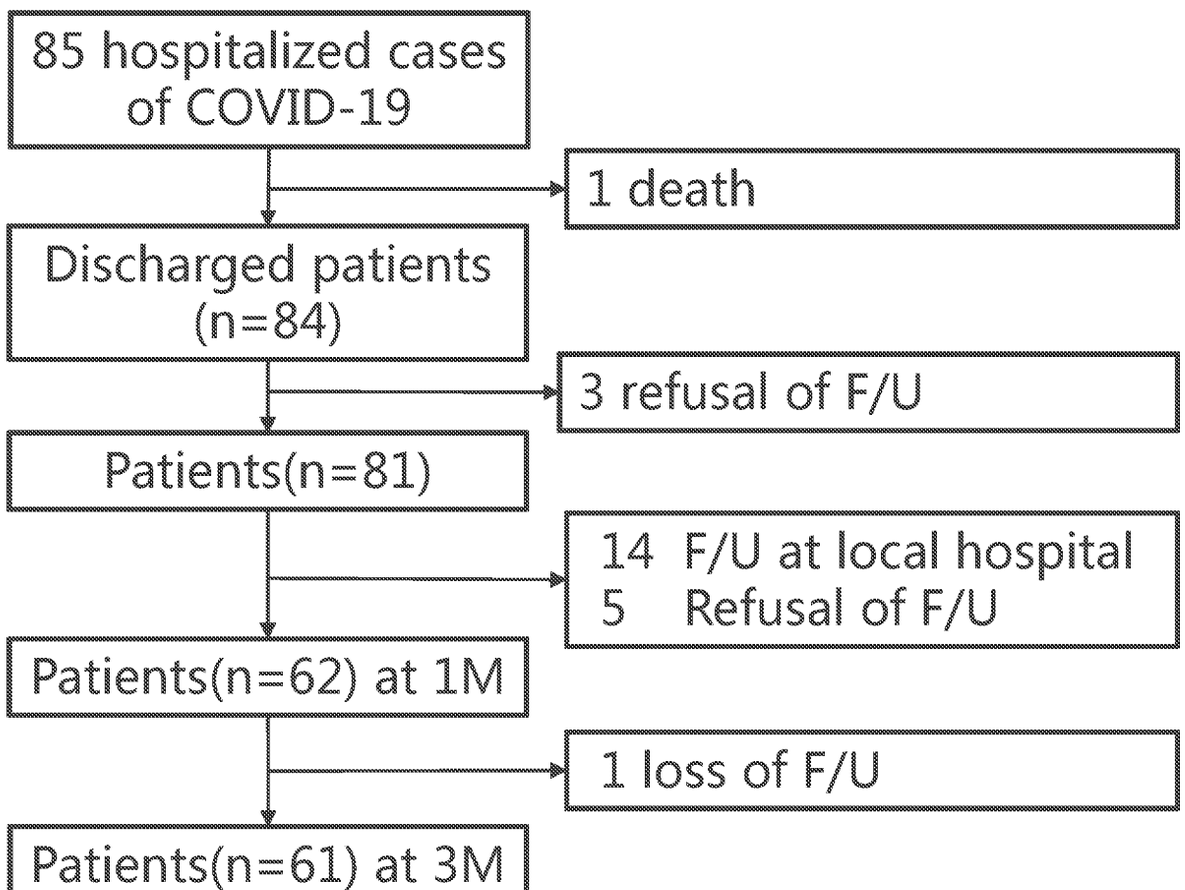
Epidemiology of COVID-19 among Infant and Children in China

- Pediatric cases accounted for approx. 1% of all cases (728/80,000, estimated via China CDC case series)
- Communicability of infection amongst children has been tracked and, as expected, infected children shed virus although, as noted above, they are frequently asymptomatic or only mildly symptomatic.
- Negative breast milk, Amniotic fluid, cord blood, and neonatal throat swab samples by RT-PCR from mothers with COVID-19 reported.
- Cases series of babies breastfed by mothers with overt COVID-19 – not infected

1. Dong Y, et al. Pediatrics. 2020 Jun;145(6):e20200702. 2. Chen H, et al. Lancet. 2020;395(10226):809–815.
3. Liu W, et al. J Hum Lact. In press. 4. Zhu H, et al. Transl Pediatr. 2020;9(1):51–60.
5. Bi Q, et al. Lancet Infect Dis. 2020;20(8):911–919.

Clinical follow-up of COIVD-19 patients after discharge

- A single-center, prospective observational follow-up study to characterize the outcomes in patients with COVID-19 at 1, 3 and 6 months after discharge
- Currently, analysis has finished with the 1- and 3-month data



Manuscript under review

At 3-month COVID-19 patients were not fully recovered

- Baseline characteristics: 58% male; median age 45 years, IQR(34-55) ; 11% had smoking history; 37% had chronic disorders;
- At 3-month (n=61)
  - 1 re-activated virus RT-PCR on D100
  - 38% symptoms persisted: dyspnea(18%), coughing(15%), fatigue(8%)
  - 54% CT scans abnormalities: GGOs (15%), fibrosis (5%)
  - pulmonary ventilating function & physical activity (6MWD) gradually recovering

Potentially more prompt recovery at 3-month compared to SARS

- Compared with SARS, COVID-19 appears to be associated with a prompter resolution on chest CT during the recovery phase.
- Our findings indicate potentially more prompt recovery of COVID-19 patients at 3M in 6MWD compared to those with SARS.
- Preferable to combine FEV1 with DLCO in identifying pulmonary function impairment with higher sensitivity
- No significant difference among the discharged survivors with different severity pneumonia regarding other pulmonary function measures

1. Ng CK, et al.. Thorax. 2004;59(10):889-891.
2. Hui DS, et al. Chest. 2005;128(4):2247-2261.
3. Mo X, et al. Eur Respir J. 2020:2001217.

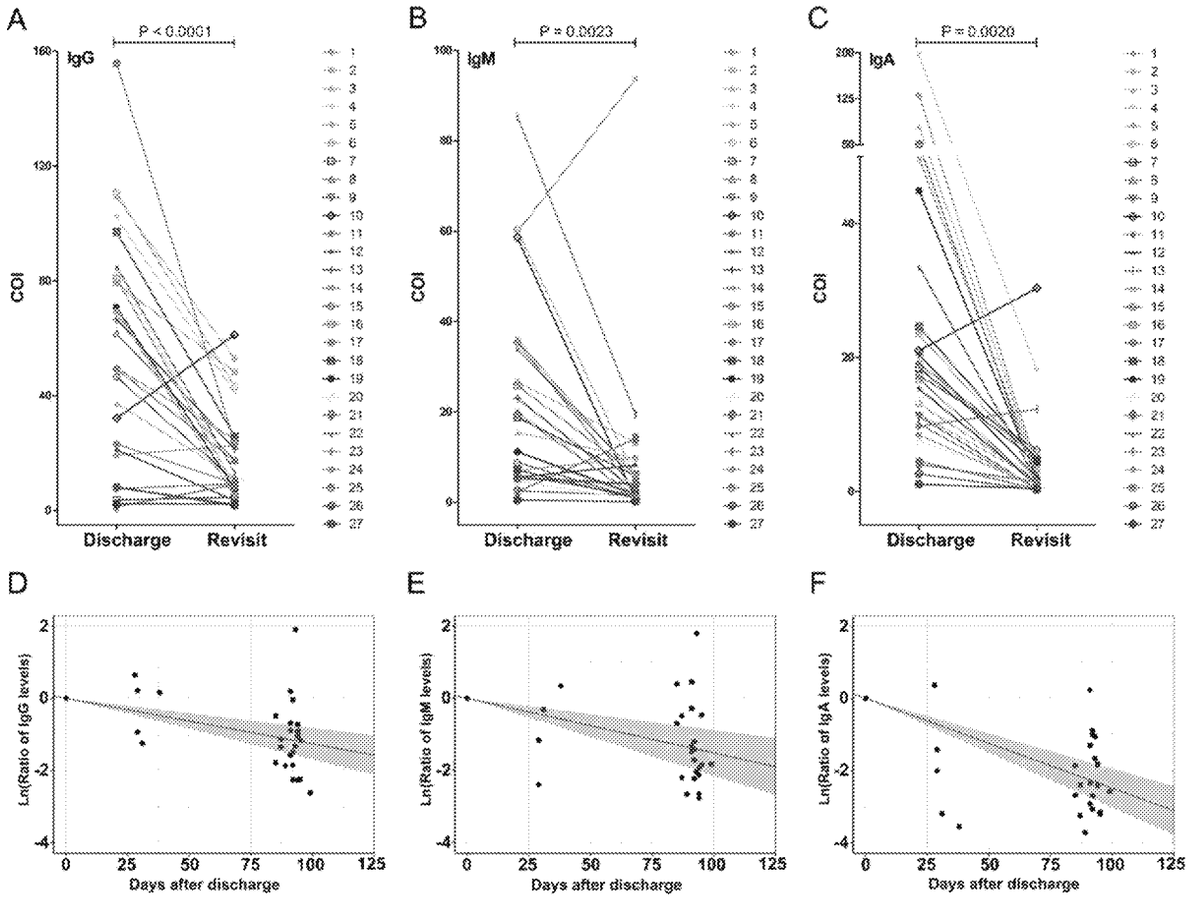
Serological study of COVID-19 patients after recovery

- Previous studies suggest that there is a significant reduction of neutralizing antibodies in the serum of COVID-19 patients in their early convalescent stage.
- Patients recovered from COVID-19 might not have protection against re-infection

1. Robbiani DF, et al. Nature. 2020 Aug;584(7821):437-442. doi: 10.1038/s41586-020-2456-9.
2. Long Q-X, et al. Nat Med. 2020 Aug;26(8):1200-1204. doi: 10.1038/s41591-020-0965-6.

Decline of SARS-CoV-2 specific antibodies in convalescent patients

- Serological study based on 27 patients followed-up after discharge
  - 100% IgG (COI 1.67-61.26) remains positive, 81.5% (COI 0.15-93.73) for IgM and 77.78% (COI 0.25-30.36) for IgA
  - Substantial decline of antibodies level at 3 months



1. Ma et al. Sci China Life Sci, 2020, doi: 10.1007/s11427-020-1805-0

Decline of SARS-CoV-2 specific antibodies in convalescent patients

- IgG antibody would become undetectable after discharge for 273 days
- IgM and IgA would be 150 and 108 days
- Our result suggests humoral immunity diminish in short period, losing the protection for the virus
- Together with previous studies, triggering strong cellular immune response and immune memory is the key for SARS-CoV-2 vaccine development.

1. Ma et al. Sci China Life Sci, 2020, doi: 10.1007/s11427-020-1805-0

Next-generation sequencing revealed influenza and *Chlamydia* infection in recurrent pneumonia in a recovered COVID-19 patient

A 53-year-old man was admitted to hospital with SARS-CoV-2 on January 25, 2020

↓

Discharged on February 9, 2020

↓ 82 days

Recurrence of suspected COVID-19 GGO-like pneumonia On May 1, 2020

↓

NGS showed co-infection with influenza and Chlamydia

↓

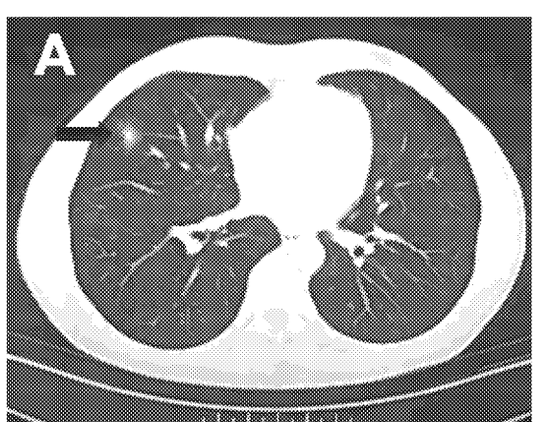
Discharged on May 28, 2020

Table 1 The main pathogens of alveolar lavage fluid sequenced by next generation sequencing.

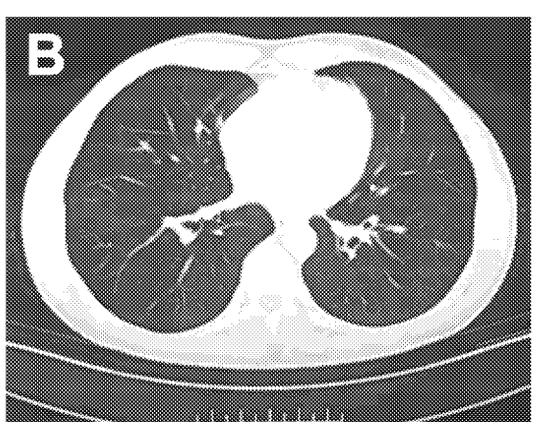
No.	%	Reads	Genus	No.	%	Reads	Genus
1	72.1	28366988	unclassified	15	0.233	91578	Listeria
2	6.948	2733676	Chlamydia	16	0.205	80778	Idiomarina
3	4.764	1874455	cannot be assigned to a genus	17	0.197	77399	Klebsiella
4	2.387	939292	Enterococcus	18	0.195	76888	Salmonella
5	1.956	769431	Lingulodinium	19	0.18	70859	Epulopiscium
6	1.381	543303	Bacillus	20	0.162	63717	Curvibacter
7	1.278	502795	Acinetobacter	21	0.142	55903	Clostridioides
8	1.152	453243	Plasmodium	22	0.111	43483	Sarcocystis
9	0.55	216421	Pseudomonas	23	0.109	42722	Kangiella
10	0.491	193240	Clostridium	24	0.107	41987	Neisseria
11	0.384	151225	Streptococcus	25	0.096	37916	Enterobacter
12	0.362	142335	Escherichia	26	0.095	37467	Burkholderia
13	0.34	133773	Mycobacterium	27	0.095	37280	Viruses
14	0.322	126861	Staphylococcus				

Table 2 The information of influenza viruses sequenced by next generation sequencing.

No.	Reads	Virus	Subtype	Description
1	40	Influenza B virus	Influenza B virus	B/Connecticut/Flu110/2013
2	11	Influenza A virus	H1N1 subtype	A/Brazil/RS-3335/2009
3	4	Influenza A virus		
4	2	Influenza A virus	H3N2 subtype	A/Brazil/RS-3335/2009
5	1	Influenza A virus	H1N2 subtype	
6	1	Influenza A virus	H10N6 subtype	A/American green-winged teal/Alaska/1168/2006



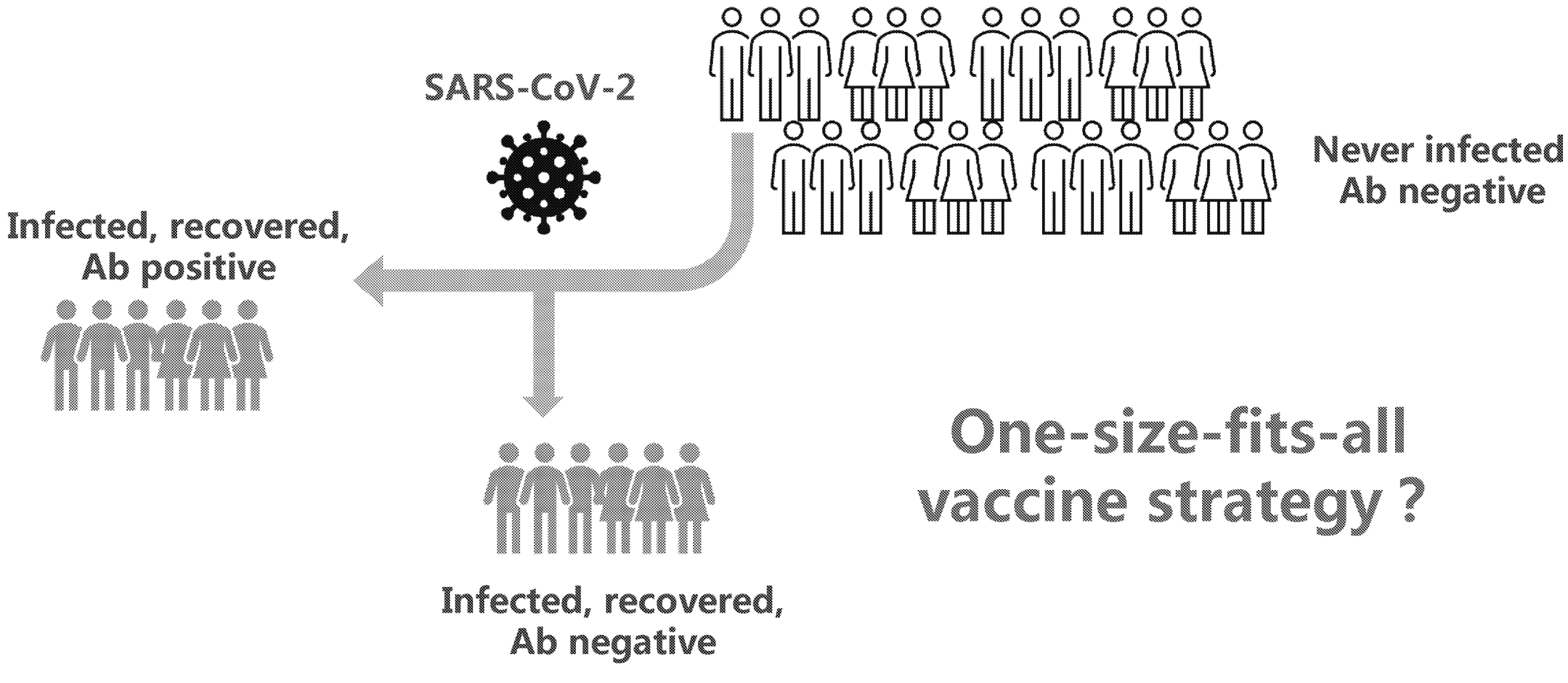
CT on May 1, 2020



CT on May 28, 2020

*Wen W#, Zhang C#, Li C#, Chen Z#, Chen Y, Cai Z, Tao M, Guo M, Xie L, Liu W, Zhang K, Weng J, Zhu S, Xu W, Xu Z. Co-infection of influenza A virus and *Chlamydia* in recurrent pneumonia in a recovered COVID-19 patient. 2020. **Precision Clinical Medicine,** doi:10.1093/pcmedi/pbaa033.

Concerns in developing vaccines…



One-size-fits-all vaccine strategy ?

Thank you for listening!

Jianping Weng

中国科学技术大学
University of Science and Technology of China

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; Cervenka, Nicole[NCervenka@nas.edu]; Sharples, Fran[FSharples@nas.edu]; Block, Bruce[BBlock@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Wed 10/14/2020 6:32:16 PM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
NAS-CAS-Vaccine-20201014.pdf
Emerging CoVs Swine Vaccine China NAS diaglog LJSaif_10-13-20pdf.pdf
20201013Vaccines US update.pdf

Greetings,

Thank you for joining the dialogue session last night. I have attached the slides from the three presentations.

FYI CAS has invited two additional CCDC experts to the session tonight.

Dr. Huaqing Wang, PI, Immunization program, Chinese Center for Disease Control and Prevention
Dr. Zundong Yin, Director of National Immunization Program, Chinese Center for Disease Control and Prevention

Looking forward seeing and hearing from you all in a few hours.
Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, October 12, 2020 12:36 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
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Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
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Subject: Virtual U.S. China dialogue meeting October 13 and 14
Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

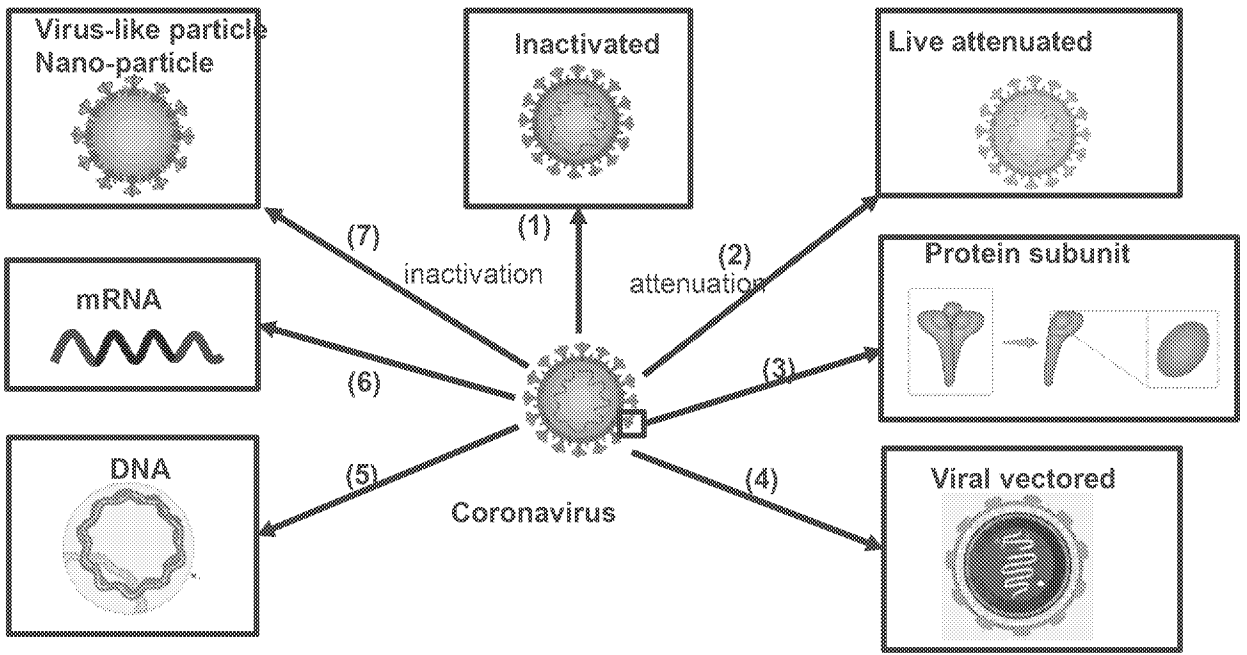
Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

Vaccine development

Future hope

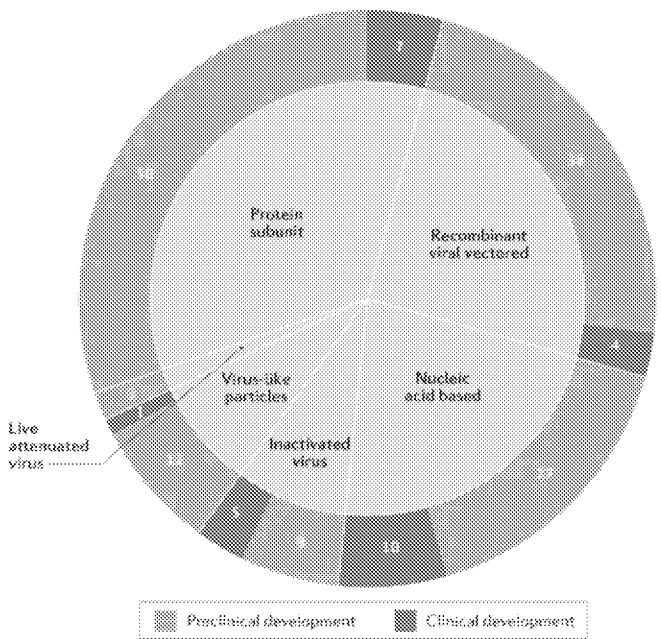
Major forms of coronavirus vaccine



全球新冠疫苗研发现况（截至2020年9月9日，全球有180种候选疫苗）

- 35种进入人体临床试验，9种进入临床Ⅲ期
  - 非复制病毒载体（4）：Ad5 、ChAdOx1、 Ad5+ Ad26、 Ad26
  - RNA（2）：mRNA-1273、mRNA-BNT162b
  - 灭活疫苗（3）：中生北京所、中生武汉所、科兴
  - DNA：INO-4800等
  - 蛋白亚单位：NVX CoV2373等
- 145种在临床前研究阶段，主要技术路线：
  - 蛋白亚单位（51）
  - 非复制病毒载体（19）
  - 复制型病毒载体（19）
  - RNA（17），DNA（12）
  - 病毒样颗粒（12），灭活（9）
  - 减毒（3）

Fig. 1: The global COVID-19 vaccine landscape.



Jeyanathan, M., Afkhami, S., Smaill, F. et al. Immunological considerations for COVID-19 vaccine strategies. Nat Rev Immunol (2020). https://doi.org/10.1038/s41577-020-00434-6
WHO：DRAFT landscape of COVID-19 candidate vaccines – 3 Sep 2020

我国新冠疫苗研发

企业	疫苗类型	临床试验	目标人群	剂次	进展
康希诺公司	Ad5载体疫苗	I期	18-60岁	1	完成
		II期	≥18岁	1	完成
		III期	≥18岁	1	俄罗斯
中生集团（武汉所）	灭活疫苗(Vero)+铝佐剂	I + II期	≥6岁	2	完成
		III期	≥18岁	2	阿联酋、秘鲁、摩洛哥、阿根廷、埃及
中生集团（北京所）	灭活疫苗(Vero))+铝佐剂	I + II期	≥3岁	2	完成
		III期	≥18岁	2	阿联酋、秘鲁、摩洛哥、阿根廷
北京科兴	灭活疫苗(Vero))+铝佐剂	I + II期	18-59岁;≥60岁	2	已完成
		III期	18-59岁, ≥60岁	2	巴西、印尼
医科院昆明所	灭活疫苗(Vero))+铝佐剂	I + II期	18-59岁	2	进行中
智飞龙科马	重组亚单位(CHO))+铝佐剂	I+ II期	18-59岁;≥60岁	2	进行中
华西医院	重组亚单位（Sf9）)+铝佐剂	I期	18-55岁;≥55岁	2	进行中
苏州艾博&沃森生物	mRNA疫苗	I期	18-59岁;≥60岁	2	进行中
复星医药/BioNTech	mRNA疫苗	I期	18-55岁;≥55岁	2	进行中
北京万泰	鼻喷流感病毒载体疫苗	I期	≥18岁	?	9月8日注册
艾棣维欣/Inovio	DNA疫苗	I期	18-59岁	2	9月11日注册

我国新冠疫苗研发进展

企业	类型	Ⅰ期	Ⅱ期	Ⅲ期	备注
艾棣维欣	DNA疫苗	9月11日			
北京万泰	流感病毒载体鼻喷疫苗	9月8日			
上海复星	mRNA疫苗	7月22日			
苏州艾博&云南沃森	mRNA疫苗	6月24日			
四川大学华西医院	重组蛋白疫苗（sf9）	8月28日			
智飞	重组蛋白疫苗（CHO）	6月25日	7月10日		
康希诺	Ad5腺病毒载体	3月18日	4月10日		
昆明所	灭活疫苗（vero）	6月4日			
北京科兴	灭活疫苗（vero）	4月28日			EUA
中生北京所	灭活疫苗（vero）	4月29日			EUA
中生武汉所	灭活疫苗（vero）	4月13日			

Hot Spot：ChAdOx1腺病毒载体疫苗（AZD1222）

➢ 由牛津大学与阿斯利康合作开发

- 腺病毒载体疫苗
- 以复制缺陷型猿猴腺病毒为载体，包含SARS-CoV-2的全长结构表面糖蛋白（S蛋白）的腺病毒载体疫苗
- 该平台尚未用于已批准的疫苗，但已在针对其他病毒（包括埃博拉病毒）的实验性疫苗中进行了测试。

➢ 临床试验分期：Ⅲ期临床试验

- 美国、英国、巴西、南非
- 18-55岁健康成人

※阿斯利康与深圳康泰公司签署了技术转让的合作协议

Folegatti et al., (2020). Safety and immunogenicity of the ChAdOx1 nCoV-19 vaccine against SARS-CoV-2: a preliminary report of a phase 1/2, single-blind, randomised controlled trial. The Lancet, https://doi.org/10.1016/S0140-6736(20)31604-4

AZD1222因疑似不良反应暂停临床试验

- 9月8日，阿斯利康表示一个英国受试者出现一种无法解释的疾病
  - 该公司该疫苗在全球临床试验都暂停，旨在确保受试者安全，
- 9月10日，阿斯利康CEO Pascal Soriot 在电话会议中表示
  - 患上无法解释疾病的受试者是否为**横贯性脊髓炎**仍正在检查
  - 今年7月也曾发现一名疫苗接种者出现了神经系统症状，也一度暂停临床试验，后被诊断患有多发性硬化症，独立审查小组结论为**多发性硬化症**与疫苗接种无关

9月12日，英国恢复了阿斯利康牛津冠状病毒疫苗AZD1222的临床试验

AstraZeneca

阿 斯 利 康

Pascal Soriot 阿斯利康CEO

横贯性脊髓炎

- 脊髓局限性炎性病变过程，导致运动、感觉和自主神经功能障碍
  - 疼痛、肌肉无力、瘫痪、感觉问题或膀胱和肠道功能障碍
- 横贯性脊髓炎的确切病因不清楚
  - 一些影响脊髓的病毒、细菌和真菌感染可能导致横断性脊髓炎

Table 1 Cases of transverse myelitis following vaccination

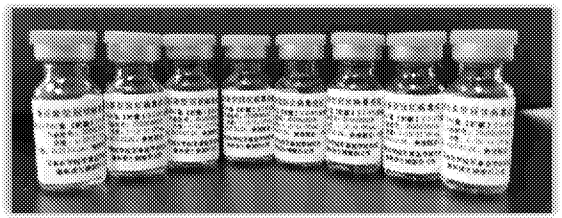
First author	Year of publication	Vaccine	Age (years)	Time from vaccination
Bu[60]	2007	Rabies	25	2 months
Das[7]	2007	Typhoid	19	5 days
Kelly[56]	2006	OPV + DT + Hib	0.5	7 days
Riel-Romero[61]	2006	DTP	0.7	17 days
Lim[62]	2004	Measles or Rubella	9	16 days
Kulkarni[63]	2004	Rabies	45	14 days
Fonseca[53]	2003	HBV	3	10 days
Nakamura[64]	2003	Influenza	70	7 days
Zarei[65]	2002	MMR	1.25	21 days
Matsui[66]	2002	Japanese B encephalitis	4	14 days
Karaali-Savrun[54]	2001	HBV	42	2 months
		HBV	33	4 weeks
		HBV	46	3 weeks
		HBV	42	3 months
Lazrey[67]	2000	Influenza	42	Days9
Bilgen[68]	2000	HBV	15	1 week
Renard[51]	1999	HBV	16	1 week
Tartaglino[69]	1995	HBV	40	2 weeks
Friedrich[70]	1995	OPV	12	6 years
		OPV	8	8 years
		OPV	13	9 years
Joyce[71]	1993	MMR	20	2 weeks
Abdul-Ghaffar[72]	1994	DT	13	3 days
Tzerbani[73]	1993	HBV	31	3 weeks
Read[74]	1992	DTP	50	2weeks
D'Costa[75]	1990	Cholera, typhoid, OPV	24	2 days
Shaw[52]	1988	HBV	41.5	2 weeks
		HBV	*	12 weeks
		HBV	*	20 weeks
		HBV	*	27 weeks
Latef[76]	1982	Rabies	50	2 days†
Clark[77]	1977	Rubella	18	13 days
Whittle[78]	1977	DTP	0.6	6 days
Holt[79]	1976	Rubella	17	2 weeks
	1976	Rubella	13	4 days
Kuleshanpil[80]	1974	Pertussis	6	17 days
Harrington[81]	1971	Rabies	41	14 days

*41.5, average of all four cases presented by Shaw *et al.*[52]

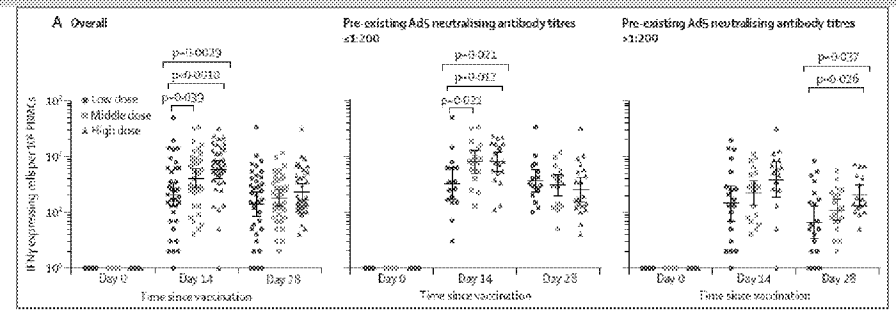
- **Johnson & Johnson: Ad26**

Virus vectored vaccine strategy: Ad5-COVID-19

CanSino Biological Inc. with Beijing Institute of Biotechnology



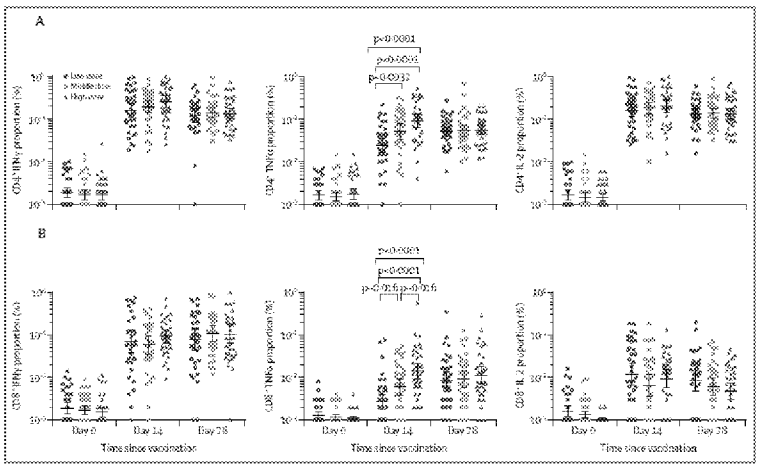
Approved for IND in China on17th, March, 2020



Safety, tolerability, and immunogenicity of a recombinant adenovirus type-5 vectored COVID-19 vaccine: a dose-escalation, open-label, non-randomised, first-in-human trial

Feng-Cai Zhu*, Yu-Hua Li*, Xu-Hua Guan, Li-Hua Hou, Wen-Juan Wang, Jing-Xin Li, Shi-Po Wu, Ben-Sheng Wang, Zheng Wang, Lei Wang, Si-Yu Jia, Hai-Dong Yao, Jing Wang, Peng Jiang, Fu-Xiang Wei, Wei Liu, Qun-Ying Hu, Ying-Mei Liang, Xiao-Bo Luo, Kun-Wei Wang, Wei Wang, Wei-Zhong Chen

In May, Lancet published the data for phase I clinical trials



Safety and immunogenic for both humoral and cellular responses

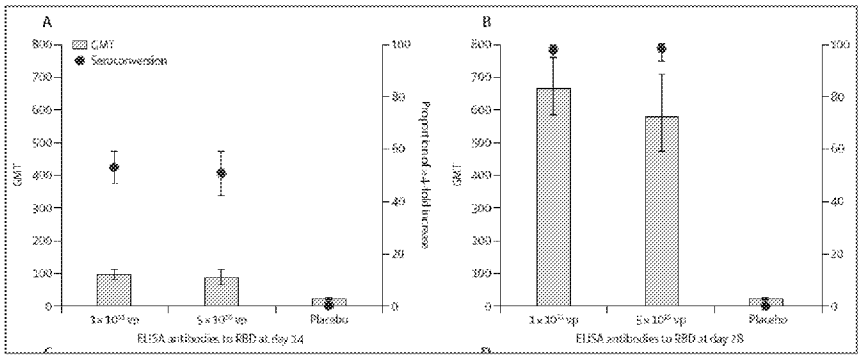
Virus vectored vaccine strategy: Ad5-COVID-19

CanSino Biological Inc. with Beijing Institute of Biotechnology

Immunogenicity and safety of a recombinant adenovirus type-5-vectored COVID-19 vaccine in healthy adults aged 18 years or older: a randomised, double-blind, placebo-controlled, phase 2 trial

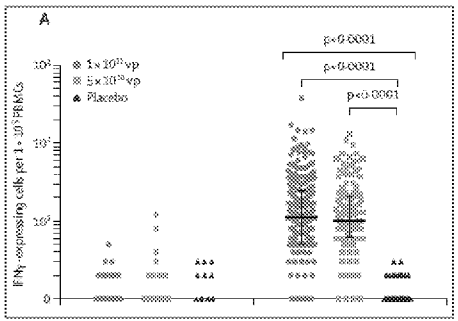
Feng-Cai Zhu*, Xu-Hua Guan*, Yu-Hua Li, Jun-Ying Huang, Bo Jiang, Shi-Hong Tang, Tian Xia, Shi-Tong Zhang, Ru-Yuan Sun, Zhi-Jian Cao, Xiao-Jing Liu, Hong-Yang Wang, Yong Wang, Jing-Xin Gou, Ying-Hao Zhang, Ji-Dong Zang, Wei Zhao, Yong-Xiang Yin, Peng Zhou, Wen-Bo Xu, Wei Chen, Ji-Suo Wang, Wen-Xiao Cheng, Jian-Ping Liu, Hong-Jie Yu, Zhi-Hong Hu, Yu-Tao Wang, Jun-Fa Xia, Yong-Gang Yao, Hua-Chen Zhao, Yong Duan, Qun Wang, Jun Zhang, Xin Li, Xue-Jie Yang, Wen-Hong Zhang, Ai-Hua Wang, Xing-Huan Wang, Wei Chen

In Jul., Lancet published the data for phase II clinical trials



NCT04526990;
NCT04540419

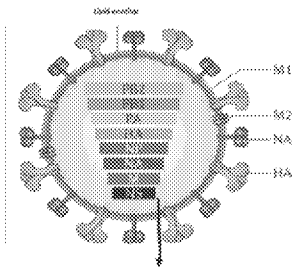
Currently under Phase III overseas multi-center clinical trials



Safety and immunogenic for both humoral and cellular responses

鼻喷流感载体新冠肺炎疫苗

- 由厦门大学、香港大学和北京万泰生物药业股份有限公司共同研发
- 核心技术是CA4-DelNS1，是将California/04/2009(H1N1)流感病毒株的NS1基因敲除后再经低温适应获得的减毒且温度敏感的双重减毒流感载体，缺失NS1可显著增强T细胞免疫应答
- 该疫苗是在CA4-DelNS1内插入新冠病毒RBD基因片段研制而成的活病毒载体疫苗，是目前已获准开展临床试验的新冠肺炎候选疫苗中唯一采用鼻腔喷雾接种方式的疫苗



DelNS1-nCoV-RBD-OPT1

1月27日启动研发　　8月27日获批临床　　9月1日启动一期临床[2]

鼻喷流感载体新冠肺炎疫苗

- 该疫苗在动物模型中呈现出对流感病毒和新冠病毒的双重保护效果：
  - ✓ 小鼠实验显示：对甲型H1N1流感病毒的致死性感染保护率为100%。
  - ✓ hACE2小鼠和仓鼠实验显示：攻毒对照组肺组织出现中至重度病理损伤且体重明显下降，疫苗免疫可明显减轻肺组织病理损伤，体重无明显下降。
- 该疫苗通过模拟呼吸道病毒天然感染途径激活局部和全身性免疫应答，在动物体内可诱导出较强的RBD特异性细胞应答，尤其以肺组织局部T细胞应答为突出特征，同时可检测到RBD特异性抗体应答，包括粘膜局部的IgA。
- 该疫苗于9月1日启动一期临床试验，已完成63名受试者接种，显示出良好安全性：
  - ✓ 正常年龄组 (18-59岁) 不良反应发生率为28.13% (9/32)，其中2级2人，1级7人。

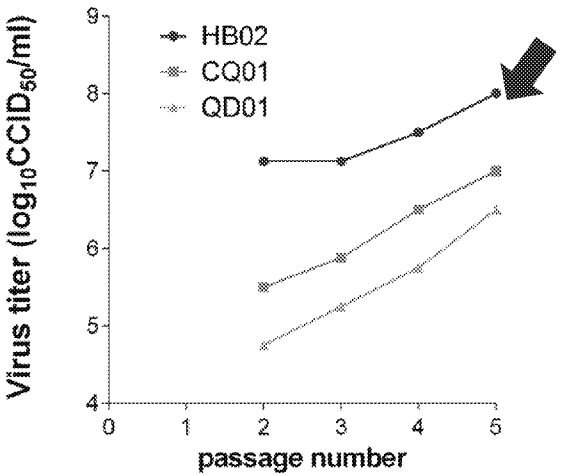
- Inactivated vaccine, BBIBP-CorV
- Protein subunit vaccine

Seed virus selection for COVID-19 vaccine

3 virus strains isolated from broncho-alveolar lavage samples or throat swabs of 3 hospitalized patients

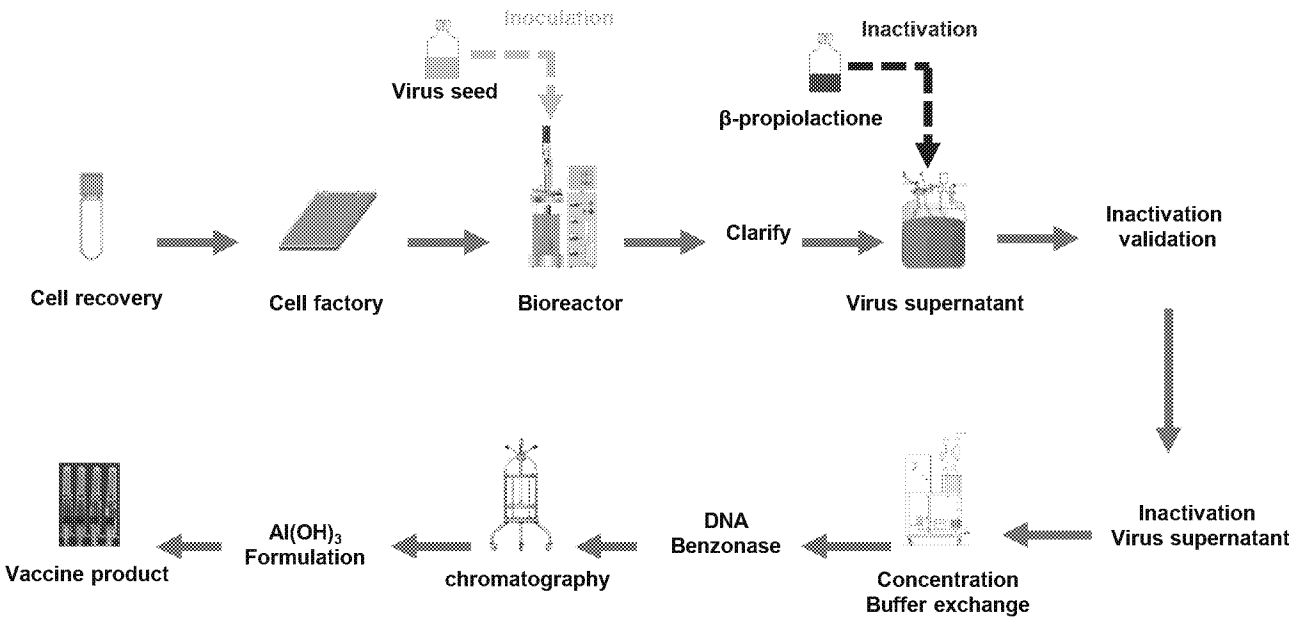
- 19nCoV-CDC-Tan-HB02
- 19nCoV-CDC-Tan-Strain03 (CQ01)
- 19nCoV-CDC-Tan-Strain 04

Lu et al, Lancet, 2020
Zhu et al, NEJM, 2020



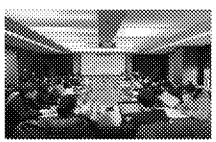
Wang et al., Cell, 2020

Flowchart of preparing the inactivated COVID-19 virus vaccine, BBIBP-CorV



Wang et al., Cell, 2020

Time-course of the BBIBP-CorV vaccine development

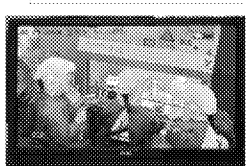


COVID-19 vaccine started

2020.1.25

2020.2

Confirm the workshop design plan



Initiate animal safety evaluation studies

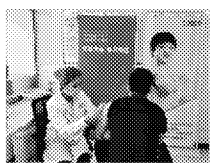
2020.3

The first batch of inactivated stock solution was prepared successfully

Start rolling submission of IND application

2020.4

Many batches of samples obtained the qualified report of the Chinese People's Procuratorate



BBIBP-CorV vacine advanced into Phase II

2020.5

4.27 Obtain clinical trial approval
4.29 First subject inoculation

2020.6

Studies on BBIBP-CorV vacine published in Cell journal

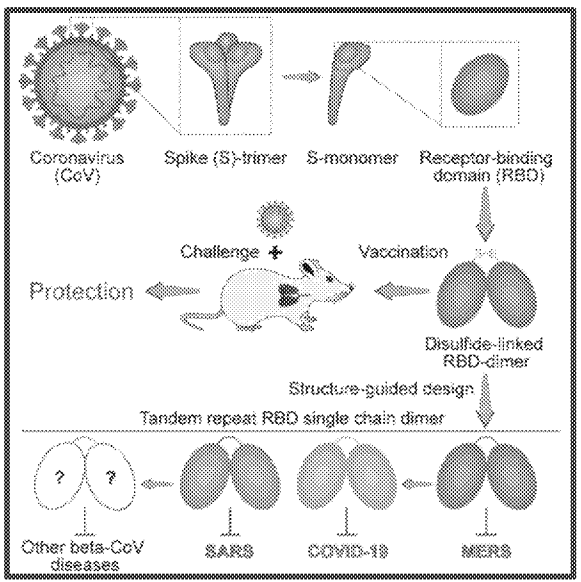
6.28. Phase Ⅰ/Ⅱ clinical trials unblinding. Seroconversion of NAbs are 100% for the all receipients

中国疾病预防控制中心

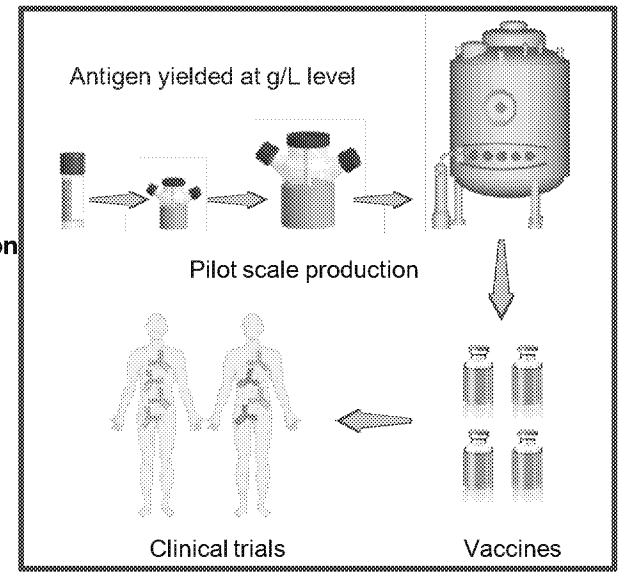
CHINESE CENTER FOR DISEASE CONTROL AND PREVENTION

- Inactivated vaccine, BBIBP-CorV
- Protein subunit vaccine

Overview of the protein subunit COVID-19 vaccine



Translation

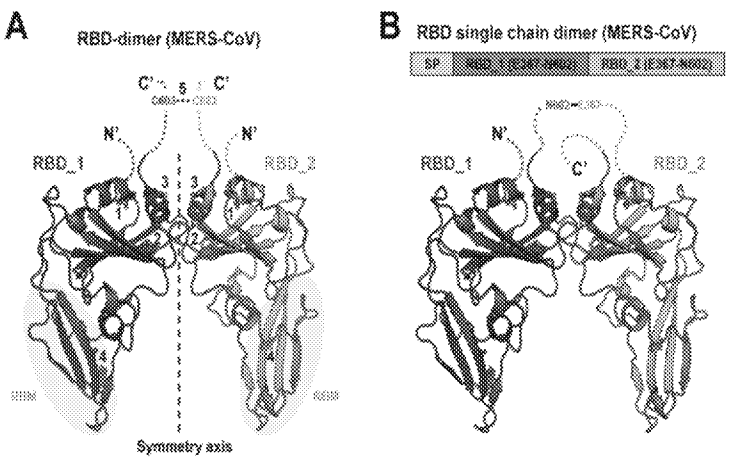


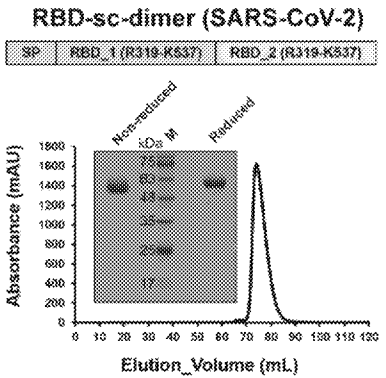
* A universal design of betacoronavirus vaccines

Dai et al., 2020, Cell

* The **first** protein subunit COVID-19 vaccine approved for clinical trials in China and the **second** in the world

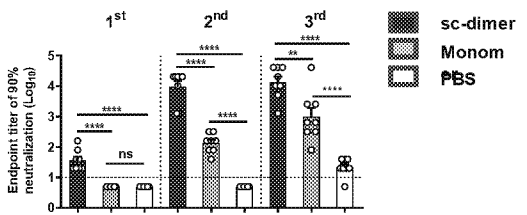
Rational design of tandem repeat RBD single chain dimer





A homogeneous RBD-dimer

- A generalizable strategy to design vaccines against MERS, COVID-19, SARS and other CoV diseases



- RBD-sc-dimer induced significantly higher NAbs compared to conventional monomer

Dai et al., 2020, Cell

Clinical trials of the first protein subunit vaccine in China

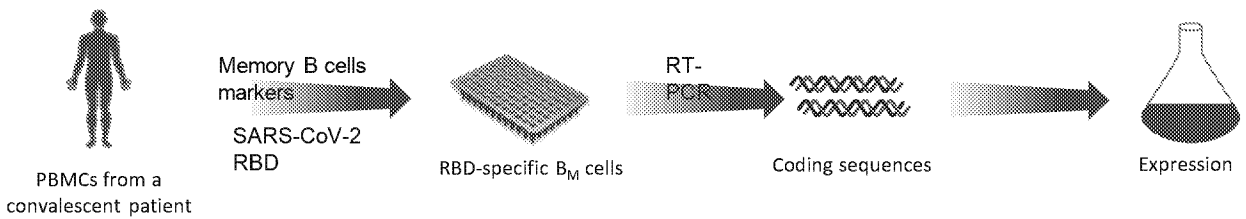
The first human volunteer in trial

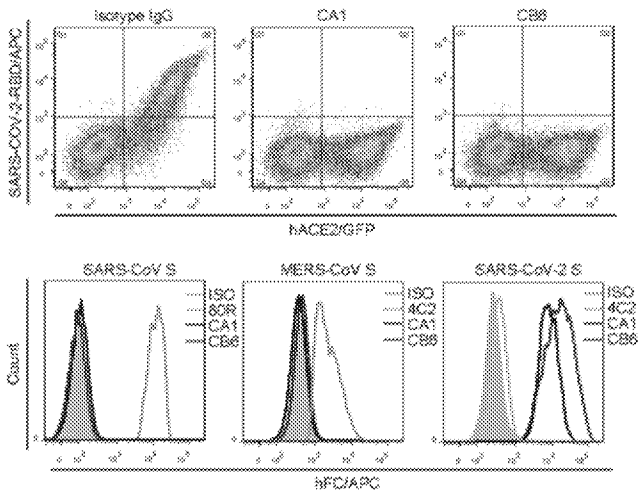
On 19 June 2020, vaccine was approved by the NMPA to enter Phase I clinical trials in China

On 10 July 2020, vaccine enters Phase II clinical trials in China

Platform	Type of candidate vaccine	Developer	Coronavirus target	Current stage of clinical evaluation/regulatory status- Coronavirus candidate	Same platform for non-Coronavirus candidates
Inactivated	Inactivated + alum	Sinovac	SARS-CoV2	Phase 3 NCT04456595 Phase 1/2 NCT04383574 NCT04352608	SARS
Non-Replicating Viral Vector	ChAdOx1-S	University of Oxford/AstraZeneca	SARS-CoV2	Phase 3 ISRCTN89951134 Phase 2b/3 2020-001228-32 Phase 1/2 PACTR202005922165132 2020-001072-15	MERS, Influenza, TB, Chikungunya, Zika, MenB, plague
Non-Replicating Viral Vector	Adenovirus Type 5 Vector	CanSino Biological Inc./Beijing Institute of Biotechnology	SARS-CoV2	Phase 2 ChiCTR2000031781 Phase 1 ChiCTR2000030906	Ebola
Protein Subunit	Adjuvanted recombinant protein (RBD-Dimer)	Anhui Zhifei Longcom Biopharmaceutical/ Institute of Microbiology, Chinese Academy of Sciences	SARS-CoV2	Phase 2 NCT04466085 Phase 1 NCT04445194	MERS

Isolation of RBD-specific memory B cells in a convalescent patient

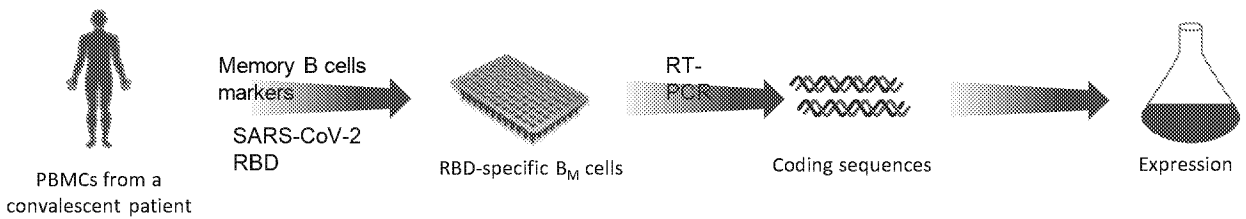


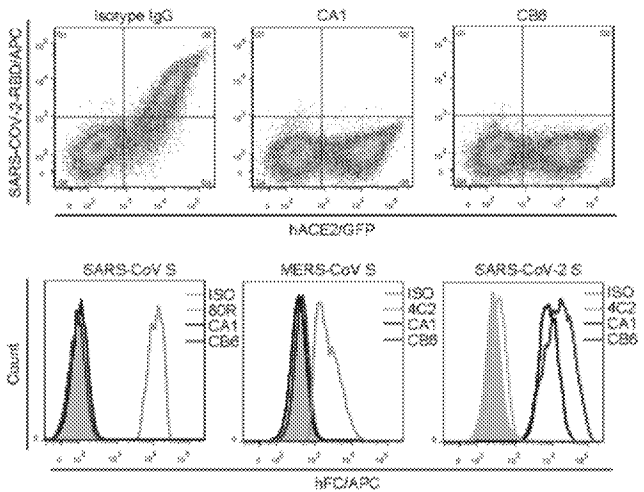


- Two mAbs-containing supernatant blocks the interaction between soluble COVID-19 virus RBD and 293T-hACE2 cells, respectively.
- Both CA1 and CB6 are specific to interact with COVID-19 virus S protein

Shi et al., 2020, Nature

Isolation of RBD-specific memory B cells in a convalescent patient

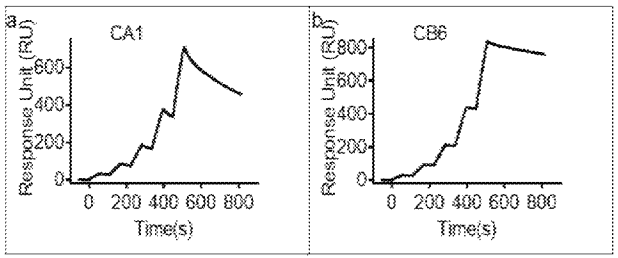




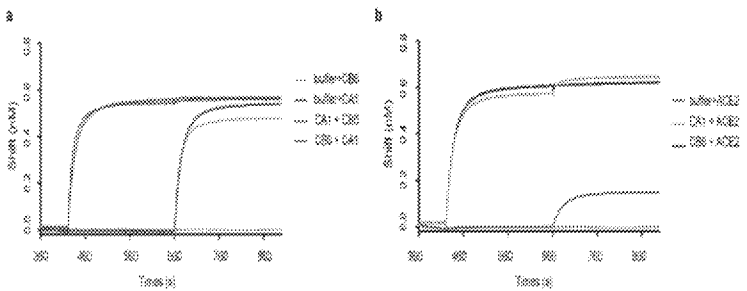
- Two mAbs-containing supernatant blocks the interaction between soluble COVID-19 virus RBD and 293T-hACE2 cells, respectively.
- Both CA1 and CB6 are specific to interact with COVID-19 virus S protein

Shi et al., 2020, Nature

Binding affinity between mAbs and RBD



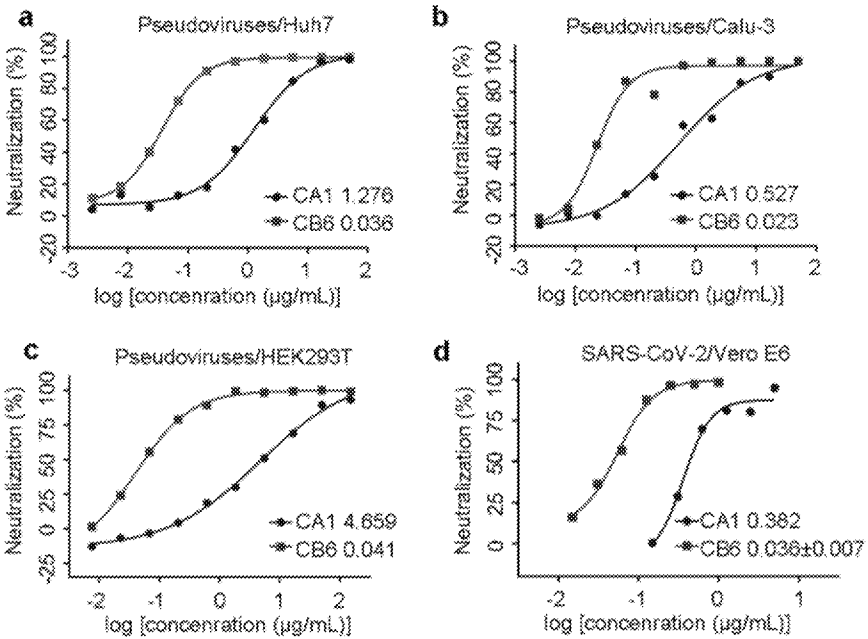
	ka (1/Ms)	kd (1/s)	K_D (M)
CA1/RBD	3.98E+06	1.16E-02	2.92E-09
CB6/RBD	8.95E+05	7.29E-04	0.82E-09
ACE2/RBD	3.82E+04	5.15E-03	133.3E-09



- The binding affinity between mAbs and RBD are stronger than that between the receptor and RBD
- CA1 and CB6 bind to the overlapped epitopes

Shi et al., 2020, Nature

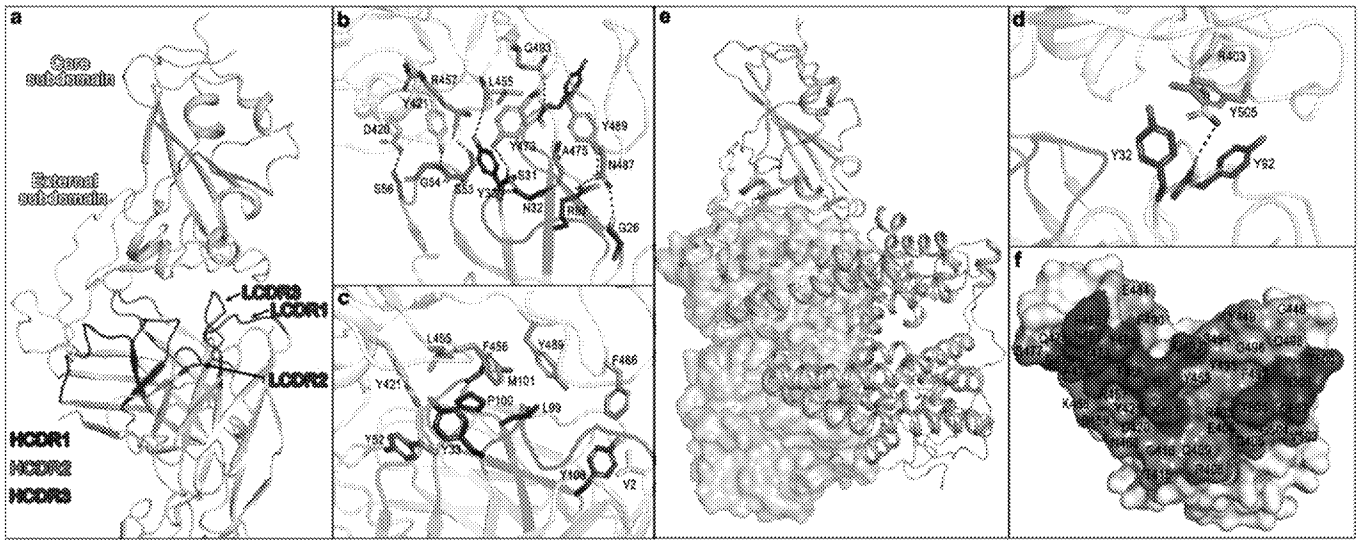
CB6 and CA1 can effectively neutralize COVID-19 virus



- CB6 and CA1 can effectively neutralize COVID-19 virus pseudovirus and live COVID-19 virus *in vitro*.

Shi et al., 2020, Nature

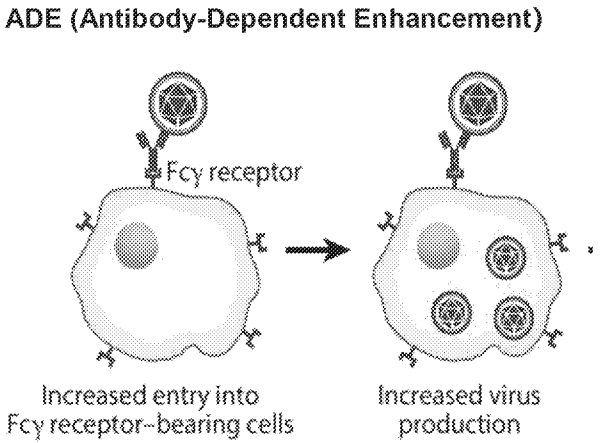
CB6 and CA1 can effectively neutralize COVID-19 virus

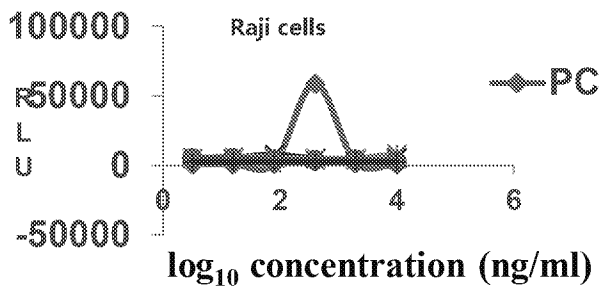


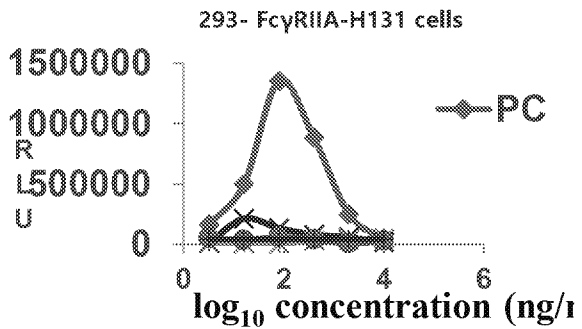
- CB6 competes with the receptor to interact with the same residues of COVID-19 virus RBD
- Both of CB6 heavy chain and light chain sterically hinder the interaction of COVID-19 virus RBD with hACE2

Shi et al., 2020, Nature

CB6-LALA to eliminate the potential ADE effect



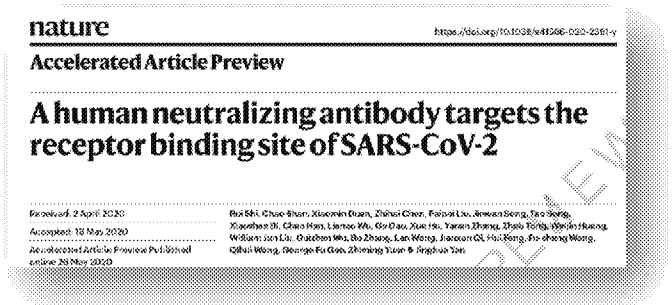


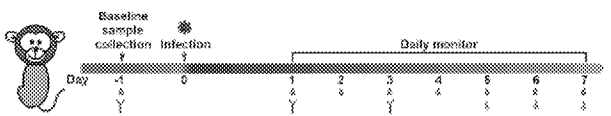


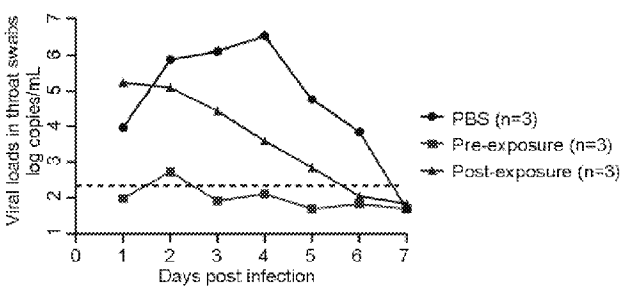
- No detectable ADE effect for CB6-LALA *in vitro*

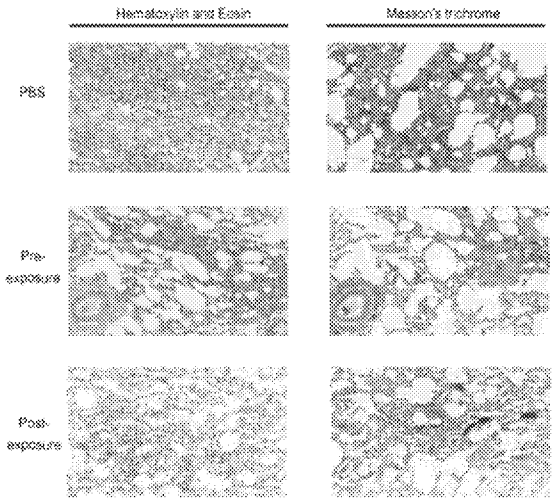
Unpublished data

CB6-LALA protects NHPs from COVID-19 virus infection





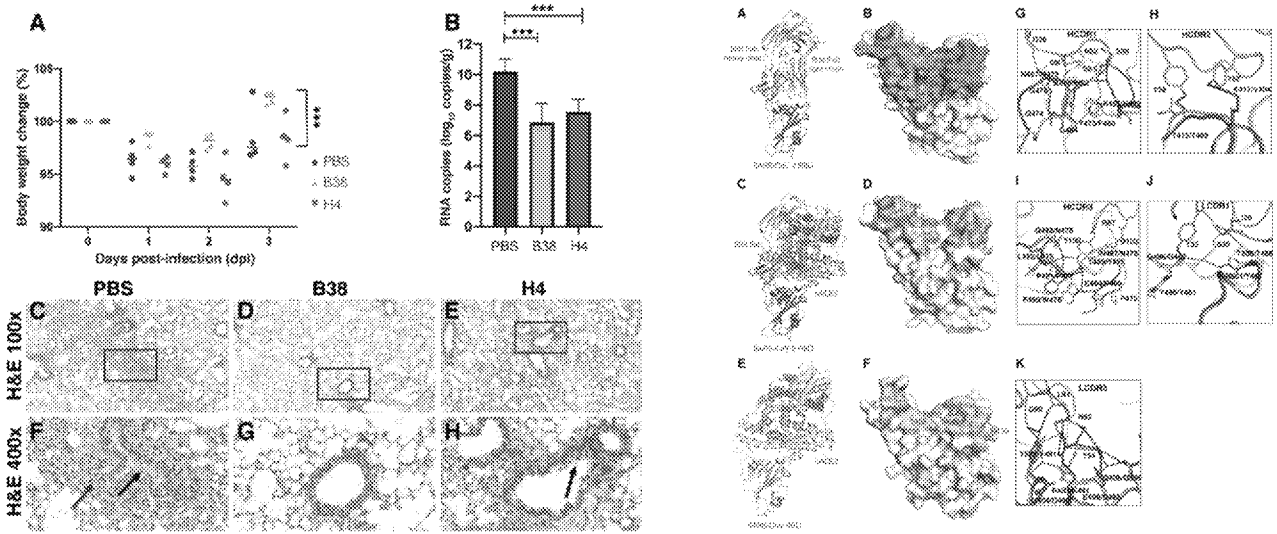




- CB6 decreased the viral loads in the throat swabs in NHPs at both prophylactic and treatment settings
- CB6 reduced the infection-related lung damage of challenged NHPs at both groups

Shi et al., 2020, Nature

Multiple neutralizing MAbs could prevent the escape mutations



- The protection efficiency of MAbs in hACE2 mice model post infection with COVID-19 virus
- Structural analysis of B38 and COVID-19 virus RBD complex and the epitope comparison between B38 and hACE2

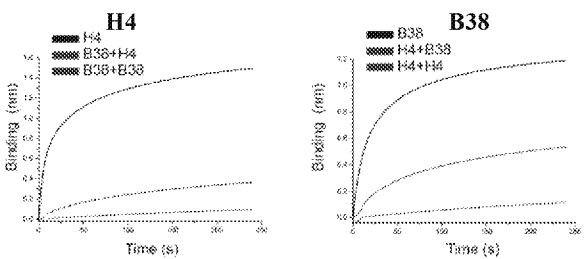
Wu et al., 2020, Science

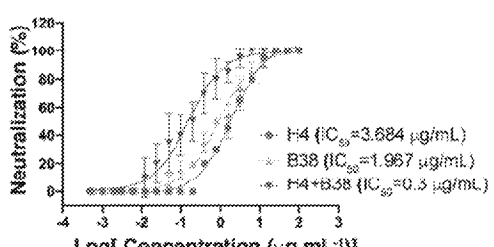
A pair of noncompeting human neutralizing MAbs against COVID-19 virus

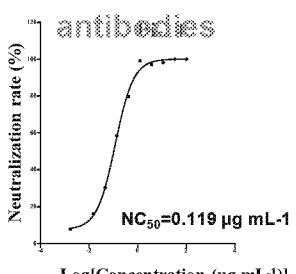

Science

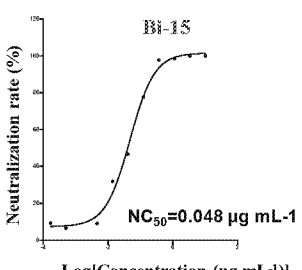
A noncompeting pair of human neutralizing antibodies block COVID-19 virus binding to its receptor ACE2

- H4 and B38, a pair of noncompeting human neutralizing MAbs, synergistically prevent COVID-19 virus infection
- The neutralizing activity of bispecific antibody Bi-15 against COVID-19 pseudovirus is **10 times stronger** than those of parental monoclonal antibodies





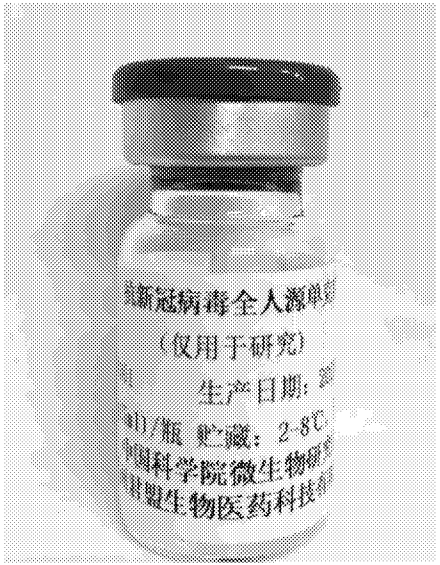




Wu et al., 2020, Science

Unpublished data

CB6 advanced into clinical trials in both China and America

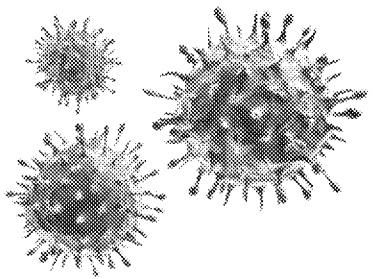


- On 5 June 2020, CB6 was approved by the NMPA to enter Phase I clinical trials in China
- On 8 June 2020, CB6 was approved by the FDA to enter Phase I clinical trials in America

Name ▲	Target ▲	Format ▲	Status ▲	Developer/Reseacher ▲
REGN-COV2 (dual mAb cocktail)	SARS-CoV-2 S protein	mAb	Phase 1	Regeneron
LY-CoV555	SARS-CoV-2 S protein	mAb	Phase 1	AbCellera/Eli Lilly
JS016	SARS-CoV-2 S protein	mAb	Phase 1	Junshi Biosciences/Institute of Microbiology, Chinese Academy of Sciences/Eli Lilly
TY027	SARS-CoV-2 S protein	mAb	Phase 1	Tychan

Outstanding questions

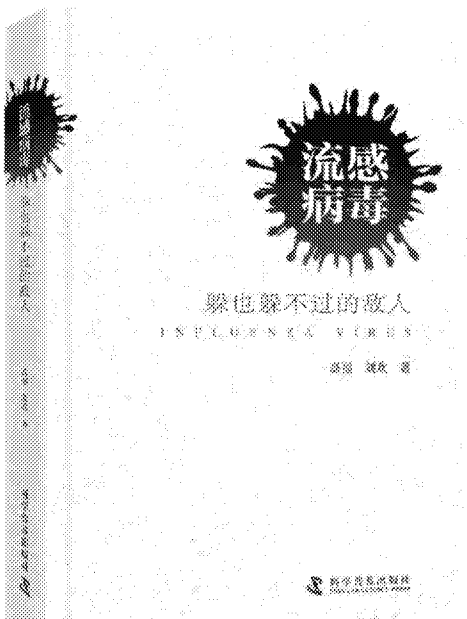
- Correlations of neutralizing MAbs with protection
- Reach of neutralizing MAbs to lung
- Lasting time of neutralizing MAbs in vivo
- Antibody-dependent enhancement (ADE) effect
- Best Immunization programs and the pro and con of all the vaccines
- Stratified/prioritized vaccination program



流感病毒

躲也躲不过的敌人

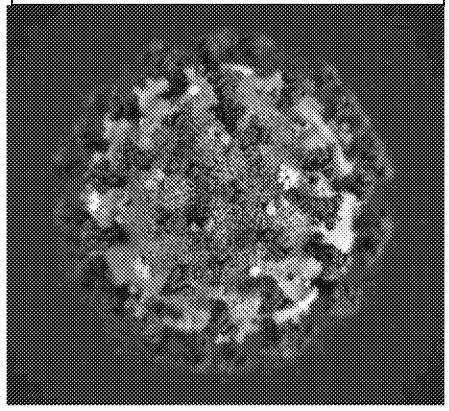
THANK YOU



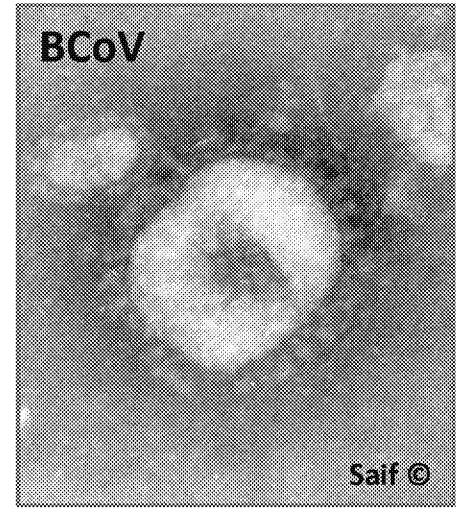
Emerging coronaviruses of humans and animals: Immunity and vaccines

Linda J. Saif

SARS-CoV-2



BCoV



THE OHIO STATE UNIVERSITY
OARDC

Food Animal Health Research Program
Department of Veterinary Preventive Medicine
College of Food, Agricultural, Environmental Sciences
The Ohio State University/OARDC, Wooster, Ohio US

THE OHIO STATE UNIVERSITY
COLLEGE OF FOOD, AGRICULTURAL, AND ENVIRONMENTAL SCIENCES

College of Veterinary Medicine
The Ohio State University

Saif ©

7 Human Coronviruses —Respiratory infections
6 Swine and 1 Bovine CoV —Enteric/respiratory infections

Human CoVs

- **Endemic--Common Cold** (Population has immunity, but lasts only ~1yr)
  - Alpha-CoVs- HC 229E,NL63
  - Beta-CoVs- HC OC43, HC HKU1
- **Epidemic/Pandemic-- Pneumonia** (Naïve population, no immunity)
  - Beta-CoVs- SARS, MERS, SARS-CoV-2

Bovine CoVs

- **Endemic—Respiratory/Diarrhea**
  - Beta-CoV- BCoV

Porcine CoVs

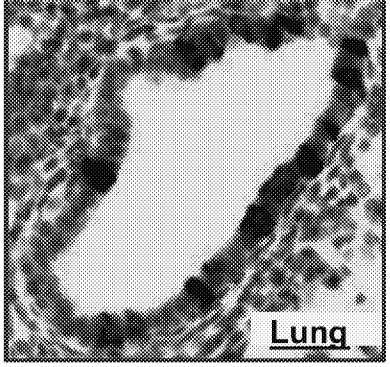
- **Endemic--Gastroenteritis**
  - Alpha-CoVs- TGEV, PEDV
- **Endemic--Respiratory**
  - Alpha-CoV- PRCV
- **Endemic--Encephalomyelitis**
  - Beta-CoV- HEV
- **Epidemic-- Diarrhea** (Naïve population, no immunity)
  - Alpha-CoV- SADS
  - Delta-CoV- PDCoV

Bovine and most human CoVs belong to the *betacoronavirus* genus; most swine CoVs belong to the *alphacoronavirus* genus

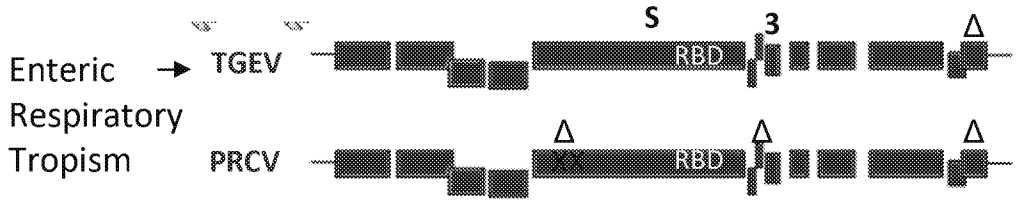
Questions Addressed:
SARS-CoV-2 and Porcine and Bovine CoVs

- How does SARS-CoV-2 cause disease compared with a porcine and bovine respiratory CoV?
- What are the unknowns/gaps for SARS-CoV-2 vaccines and lessons learned based on porcine and bovine CoV vaccines?

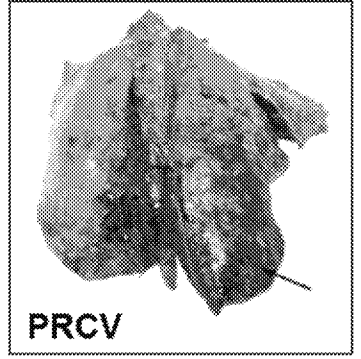
  -- What are the correlates of protection?
  -- What are the lessons for immunity from similar next Gen platform swine experimental CoV vaccines?
  -- What are the correlates of immunity based on immunity to bovine respiratory CoV infections?



Porcine respiratory CoV (PRCV) mutant of TGEV



XX S 681nt Δ
-Loss SA binding
ORF 3 Δ
-Nonfunctional



- TGEV causes fatal diarrhea in baby pigs
- PRCV--S gene deletion mutant of TGEV (621 – 682 bp, N-terminus) emerged in 1980s
- TGEV and PRCV share APN receptor; tissue tropisms differ due to loss of SA binding (gut mucins) by PRCV Spike *(Schultze et al 1996)*
- Lost of enteric tropism and virulence

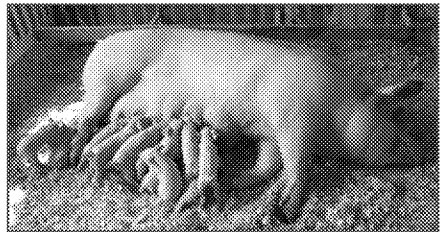
Similarities to SARS CoV-2 respiratory infections

- PRCV infects epithelial cells of upper/lower respiratory tract and type I and 2 pneumoctyes *(Jung/Saif et al 2007 JVI)*
- Most infections mild or subclinical— walking pneumonia like > 50% asymptomatic COVID-19 cases *(Long, QX et al 2020 Nat Med)*
- Atypical pneumonia in most pigs resembles SARS-CoV-2 lesions *(Saif, Jung, 2020 JCM)*: ***PRCV as a BSL2 respiratory CoV model for COVID-19***

Lessons from Swine Coronavirus Veterinary Vaccines

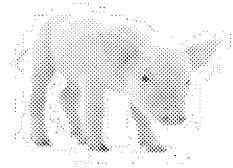
Swine Enteric/Respiratory Coronaviruses: TGEV/PRCV

- Only 2-3X attenuated oral enteric CoV vaccine induced gut/milk IgA Abs: Correlate of immune protection *(Chatta, Roth, Saif 2015 ARAB; Langel/Saif et al 2020 Pathogens)*
  - *GALT-Mammary gland SIgA axis*



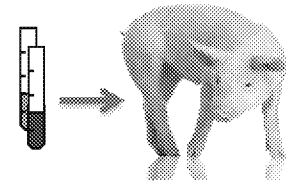
Mother

Gut IgA Ab- Immunity against CoV



Suckling piglet

Milk IgA Abs-Passive immunity



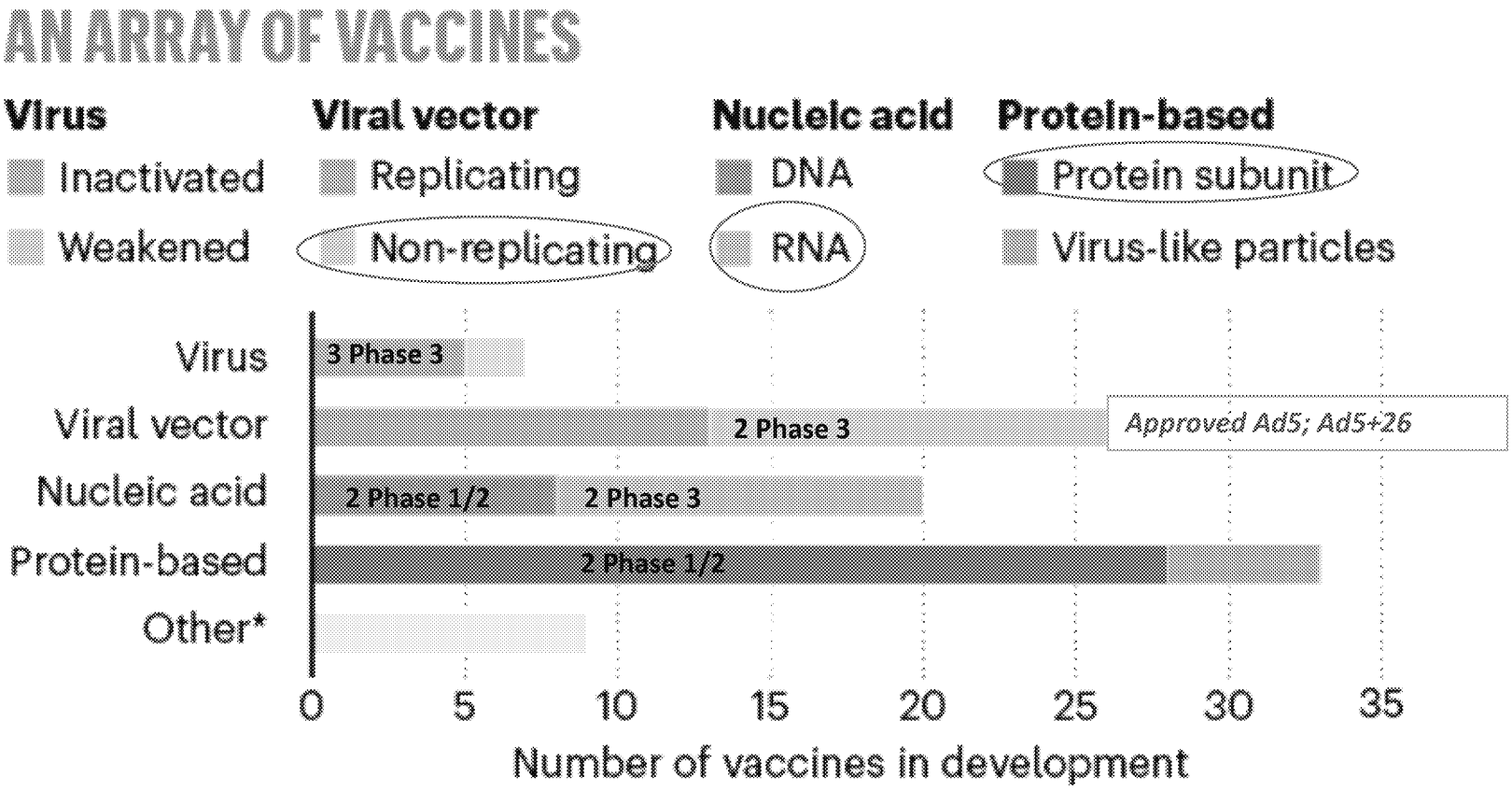
Weaned piglet

Gut IgA Ab-Active immunity: Prevent disease and infection

- Repeated PRCV infections induce IgA Abs and immunity to TGEV *(Sestak/Saif et al 1996 AJVR)*
  - *BALT-Mammary gland SIgA axis*

PRCV as naturally occurring TGEV vaccine

COVID-19 Vaccines



* Other efforts include testing whether existing vaccines against poliovirus or tuberculosis could help to fight SARS-CoV-2 by eliciting a general immune response (rather than specific adaptive immunity), or whether certain immune cells could be genetically modified to target the virus.

(Modified E Callaway Nature 30 April 2020)

©nature

Saif ©

Lessons from Molecular Vaccines for Swine CoVs

➢ Molecular next Gen vaccines have advantages (if safe & effective)

-- Provide a platform for rapid production of vaccines for new emerging diseases

-- Backbone constructs to insert key antigens for new viruses with established manufacturing

Will these unproven vaccines be effective to prevent disease and shedding (transmission)?

Recombinant vector vaccines:

PRCV respiratory vaccine

— Recominant experimental human adenovirus (Ad)+PRCV S1

Enteric CoV vaccines — PEDV

— PEDV -Recominant experimental human Ad5+PEDV S1

— PEDV- iPEDV+ (PED RNA)vaccine—Viral Replicon Particle (VRP)= VEEV based replicon vaccine encoding PEDV S replicon RNA

- Non-replicating single cycle RNA in DCs

Recombinant Vector Vaccines: rAd vaccines for porcine CoVs

Antigen/ Vector	Route (dose)	Challenge Inoculum	VN Ab Serum	Protection against Morbidity	Protection against Infection
PRCV respir.			*(Callebaut et al, J Gen Virol 1996;4-wk-old pigs)*		
H Ad5 /S_{A+D} (1220aa) (A+)	**Oronasal 1x**	**PRCV**	**Yes (low)**	**NT**	**Partial (shorter)**
H Ad5 Control	**Oronasal 1x**	**PRCV**	**No**	**NT**	**None**
PEDV enteric			*(Crawford et al, Virus Res 2016; 8 and 20-wk-old pigs)*		
H Ad5/S1 PEDV	**IN 1X**	**PEDV**	**(PreC) No (Post) Yes (3x)**	**Partial**	**No**
Control	**--**	**PEDV**	**No Yes**	**No**	**No**

The human Adeno-S vaccine 1x elicited only partial respiratory immunity to PRCV and marginal enteric immunity to PEDV: multiple doses needed?

Lessons from Molecular Vaccines for Swine CoVs

Recombinant vector/virus and subunit vaccines:

Enteric CoV vaccines — TGEV and PEDV

- TGEV -S recombinant vaccine—ineffective in naïve pigs, but effective as booster vaccine after 1x oral attenuated vaccine *(Shoup/Saif et al, 1997; Park/Saif et al,1998)*

- PEDV -PED RNA (iPEDV+) vaccine—Viral Replicon Particle (VRP) VEEV+ PEDV S replicon RNA
  - 1-3X IM doses in pregnant sows showed low efficacy (only 14-22% less mortality vs controls) in piglet protection in manufacturer's studies *(Crawford et al 2016)* and only 3% less in an independent study *(Greiner et al 2015)*
  - Low milk VN Ab titers (50%+,<80) vs milk (100%,>320) of wt PEDV orally inoculated sows *(Sherba et al 2016)*

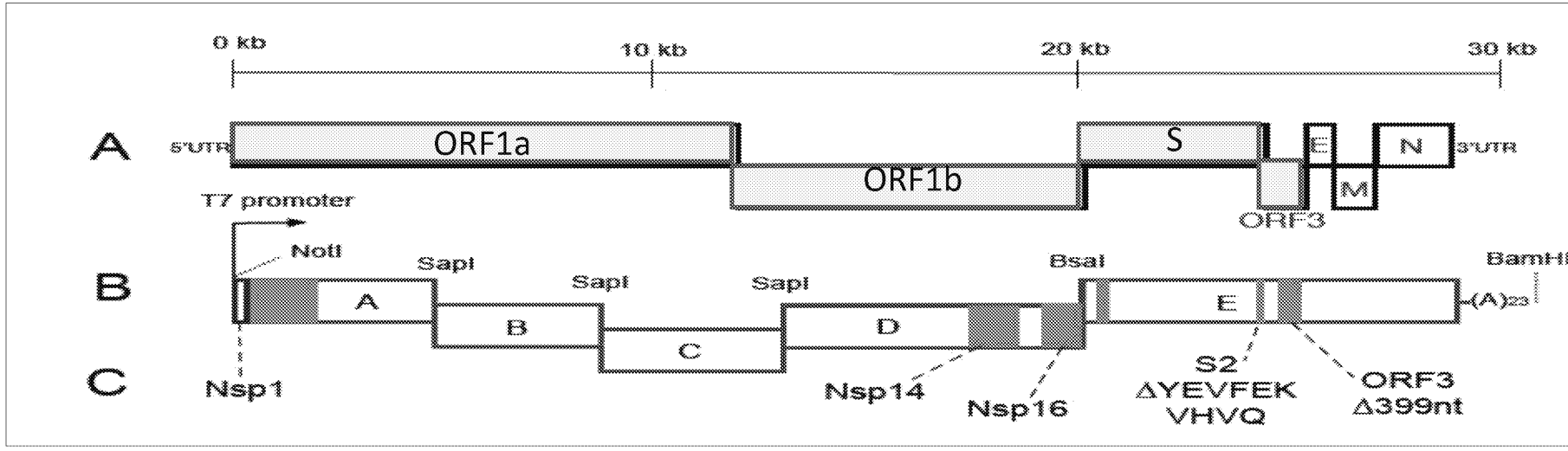
- PEDV -Recominant live attenuated virus vaccine developed by introduction of attenuating mutations into infectious clone (Lead PI: Dr Q. Wang, OSU)

Strategy to generate safe attenuated CoV vaccines using iclones

PEDV

- Target genes that encode innate immune response modulators (nsp1,nsp16) and virus replication (nsp14), non-essential sequences of S protein and the accessory gene ORF3

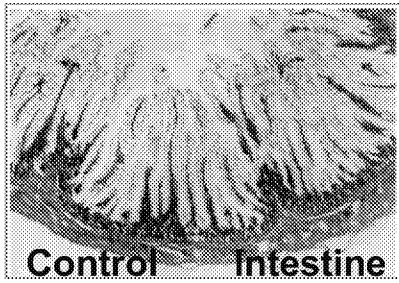
- Introduce at least 2 distinct mutations into separate genes that attenuate the virus to increase genetic stability



(Hou Y, Ke H, Kim J, Yoo D, Su Y, Boley P, Saif LJ, Wang Q. 2019. J Virol)

Saif ©

Three Clinical Syndromes Occur for Bovine Beta-CoV A Infections



Enteric Infections

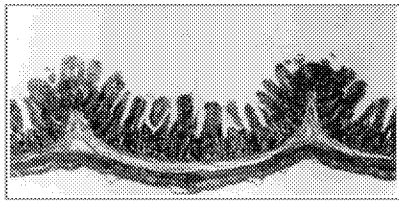
Calf diarrhea

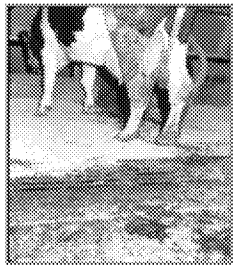
- Diarrhea, dehydration
- Intestinal villous atrophy

Age Groups/Vaccines

Birth to 4 wks of age

IM inact or atten virus vaccine in pregnant cow



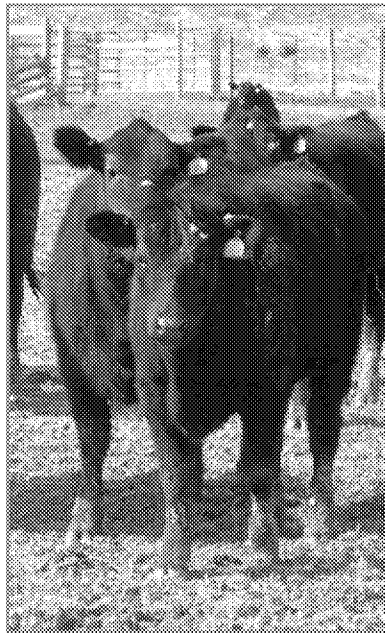


Winter dysentery

- Bloody diarrhea ± upper respiratory infection
- Intestinal villous atrophy

Adults, but not calves

No Vaccine



Respiratory Infections

Calf respiratory disease

Bovine respiratory disease complex (Shipping Fever)

•Cough, nasal discharge, pneumonia

2 wks to 6 months

6-9-mo-old feedlot cattle

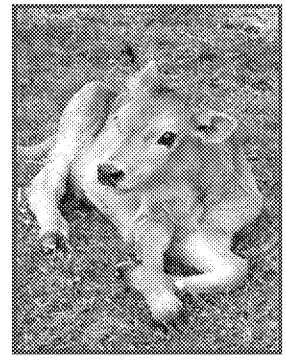
No Vaccine

Saif ©

BCoVs are endemic, pneumoenteric, age effects for clinical syndromes *(Saif, Jung 2020 JCM)*

Some SARS-CoV-2 patients have diarrhea, shed virus in stools

Lessons from BCoV respiratory infection: Correlates of protective immunity in calves



- Strong correlation between serum antibody titers to BCoV and respiratory disease and IgA antibody titers in nasal secretions and nasal shedding in field studies

Calves (Heckert/Saif et al, 1990, 1991)

- *Calves (birth to 20 weeks) shed BCoV repeatedly in nasal secretions, often subclinically (short lived mucosal immunity?)*
- *Calves with IgA antibodies (titer >100) in nasal secretions did not show recurrent BCoV nasal shedding*
- *Correlation between serum antibody titers to BCoV at 24hrs of age and subsequent number of respiratory sick days*

Develop COVID-19 vaccines that elicit both systemic and mucosal immunity?

Lessons from BCoV respiratory infections: Correlates of protective immunity in feedlot cattle

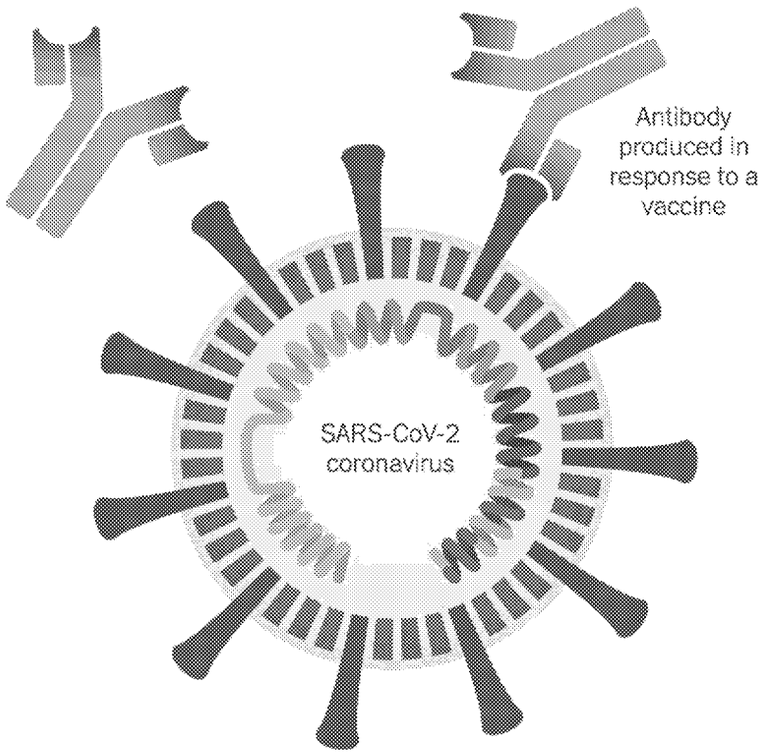
- In Feedlot cattle BCoV serum antibody titers may be a marker for respiratory protection
  - *Antibody isotype (IgG, IgA) and neutralizng titer in serum of cattle at arrival in feedlots were correlated with protection against respiratory disease, pneumonia or BCoV shedding* *(Cho/Saif et al, 2001; Lin et al, 2001; Hasoksuz/Saif et al 2002; Thomas/Saif et al, 2005)*

Strategy: Use vaccines to boost memory antibody responses to BCoV to rapidly increase antibody titers

- *Calves vaccinated IN with an attenuated BCoV vaccine at entry to feedlots had reduced risk for treatment for shipping fever pneumonia* *(Plummer et al, 2004)*

Challenges for COVID-19 Vaccines

- Rapidly deployed nucleic acid or viral vector vaccines may be a 1st generation vaccine to reduce mortality in high risk groups
  - May not prevent nasal shedding (NHP: ChAdOx1, BioRxiv; Inact vaccine, Sci)
  - May require annual booster doses to maintain immunity (common cold CoVs)
- 2nd generation (more potent, efficacious) vaccines (attenuated) may be needed to prevent severe disease and reduce shedding
- Many vaccines have reduced efficacy in elderly (or those with chronic diseases)
  - Require higher dose like flu vaccines, better adjuvants or multiple doses
  - Animal models may not reflect vaccine responses in these high risk groups
- Vaccines will be used in two populations: naïve vs recovered individuals with variable levels of pre-existing immunity
  - Efficacy/adverse effects (ADE?) may vary



COVID-19 vaccines in the US an update

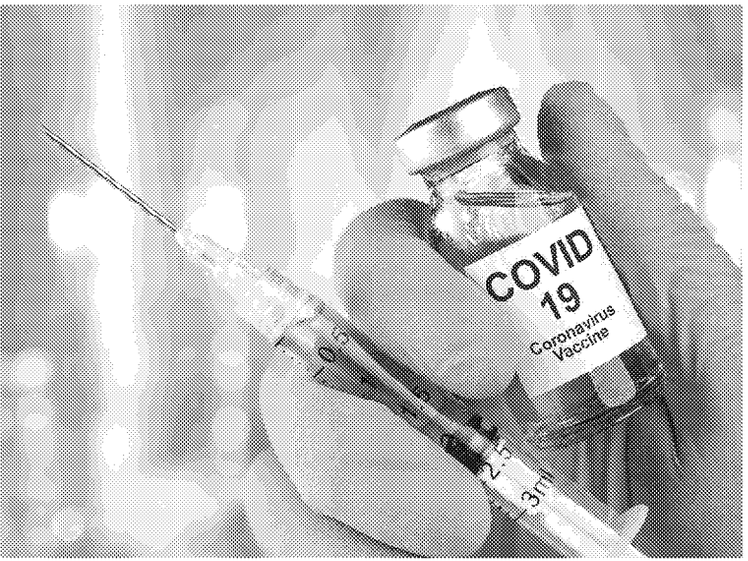
13 OCT 2020

Nancy Connell

Professor and Senior Scholar

Johns Hopkins Center for Health Security

JOHNS HOPKINS BLOOMBERG SCHOOL of PUBLIC HEALTH | Center for Health Security



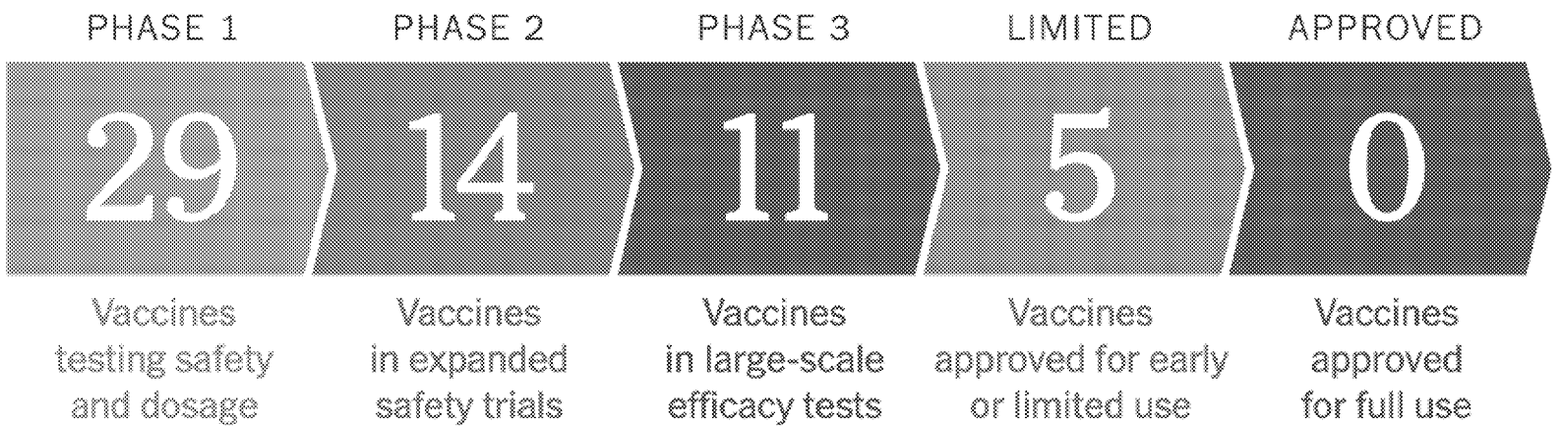
World Health Organization

Health Topics | Countries | Newsroom

Home / Publications / Overview / Draft landscape of COVID-19 candidate vaccines

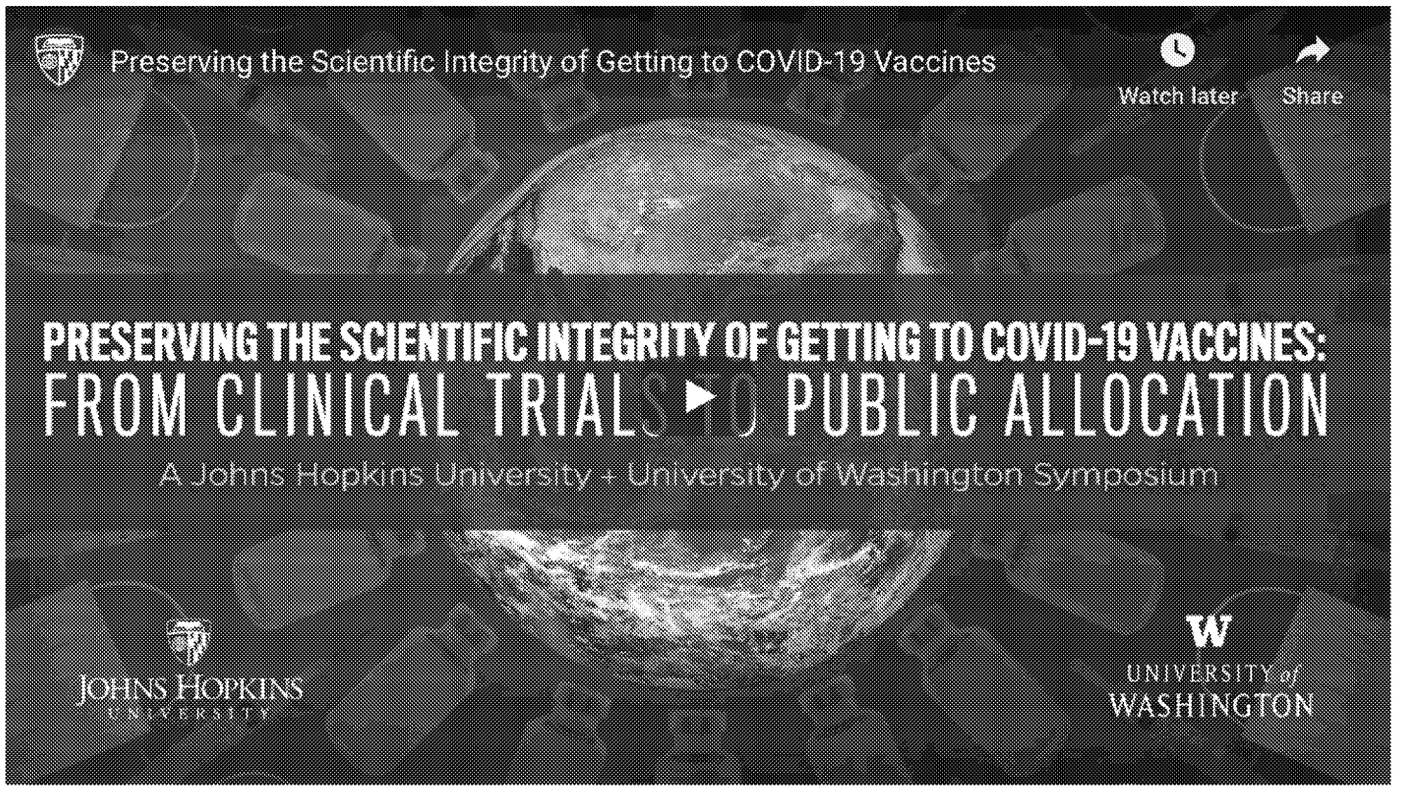
Draft landscape of COVID-19 candidate vaccines

2 October 2020 | Publication



NY Times Oct 12, 2020

Preserving the Scientific Integrity of Getting to COVID-19 Vaccines: From Clinical Trials to Public Allocation



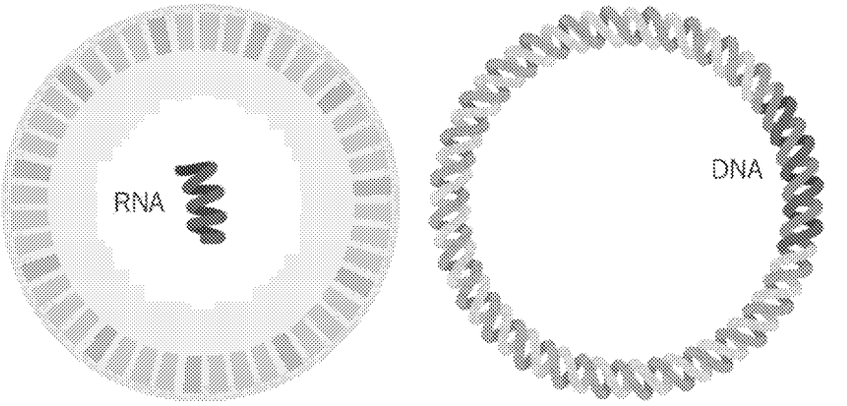
Moncef Slaoui
Chief Advisor

Four platforms, 2 vaccines in each

- Parameters for choice
  - Speed of development
  - Likelihood of efficacy
  - Expected safety profile
  - Scaleup of manufacturing
  - Capacity of owners to execute

- 1. mRNA vaccine
- 2. non-replicating live vectored
- 3. adjuvanted recombinant protein
- 4. live replicating vectored vaccine
  - Oral? Single does?

mRNA vaccines



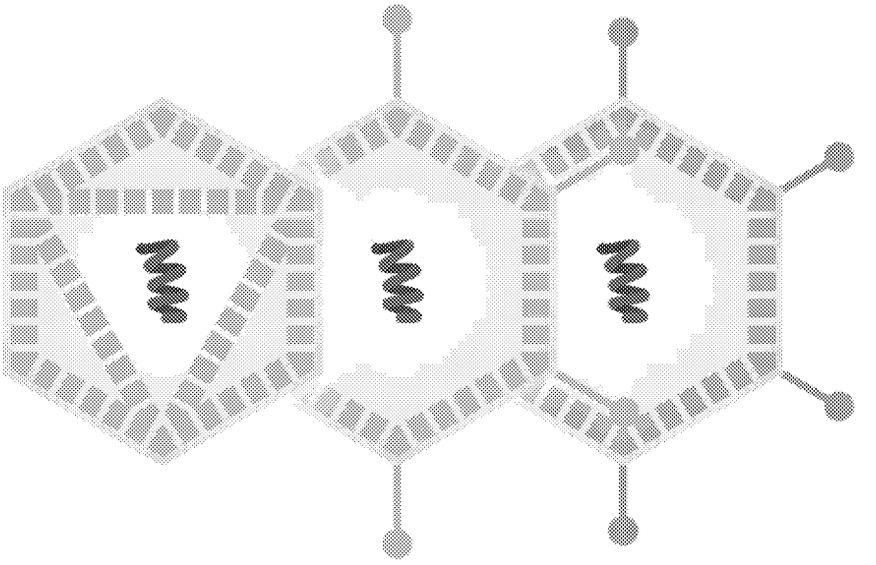
- Who?
  - Moderna
  - BioNtech/Pfizer/Fosun Pharma

Previous uses?
- none

MF and dose availability:
- single digit millions Nov
- 10s millions – Dec
- 100s million - Jan

- Stuctures
  - mRNA encoding Spike protein
  - Encapsulated in lipid nanoparticles – to survive attack by blood cells
  - Pass through cell membranes
  - Chemicals – ease of manufacture
  - Ultracold chain required

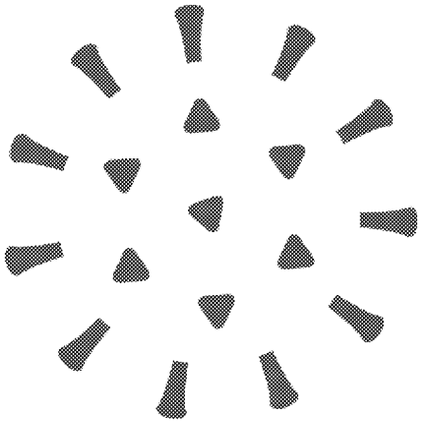
Non-replicative live vector



- Who?
  - Johnson & Johnson
  - Oxford/Astrazeneca
- Previous use?
  - Ebola
- MF and dose availability
  - Oxford 10s millions Jan
  - J&J 6-8 weeks behind

- Mechanism:
  - Virus infects one cell –induced viral immune response
  - Carries S protein gene
  - Immunity to vector?
    - J&J: Adenovirus Ad26 (obscure)
    - Oxford/AZ: (ChAdOx1) (chimp)

Adjuvanted recombinant protein



- Who?

  Novovax

  Sanofi/GSK

- Previous use?
  - multiple
- MF and dose availability:
  - Doses available 1st Q 2021
  - Novovax: NC and TX
  - Sanofi: MA and NJ
- Mechanism
  - Each protein and expression system is different
  - Novovax: nanoparticle with adjuvant
  - Sanofi: based on flu vaccine technology (“FluBlock”)

Four waves of roll-out

- RNA vaccines — November/December
- Non-replicating live vectors — January/February
- Adjuvanted proteins — March-April
- Replicating live vectors — mid-late 2021

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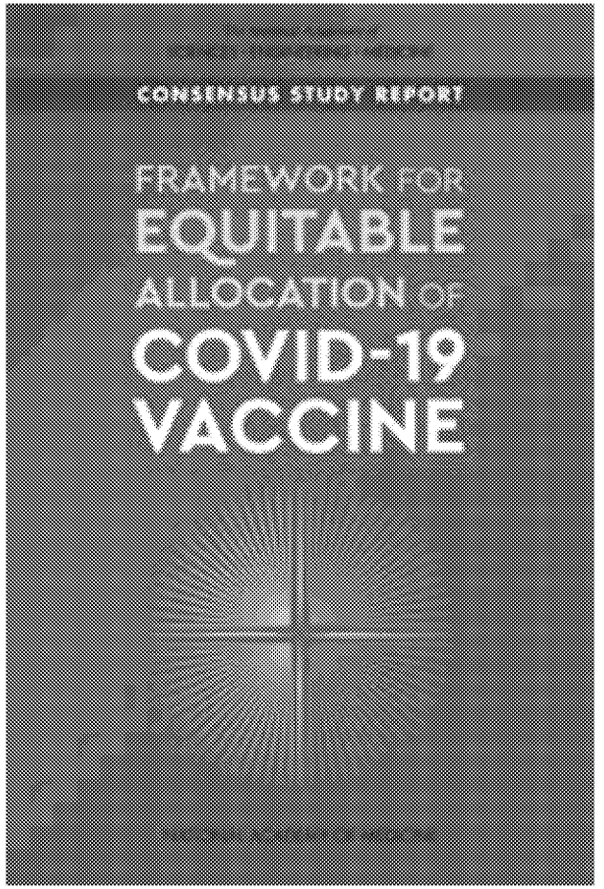
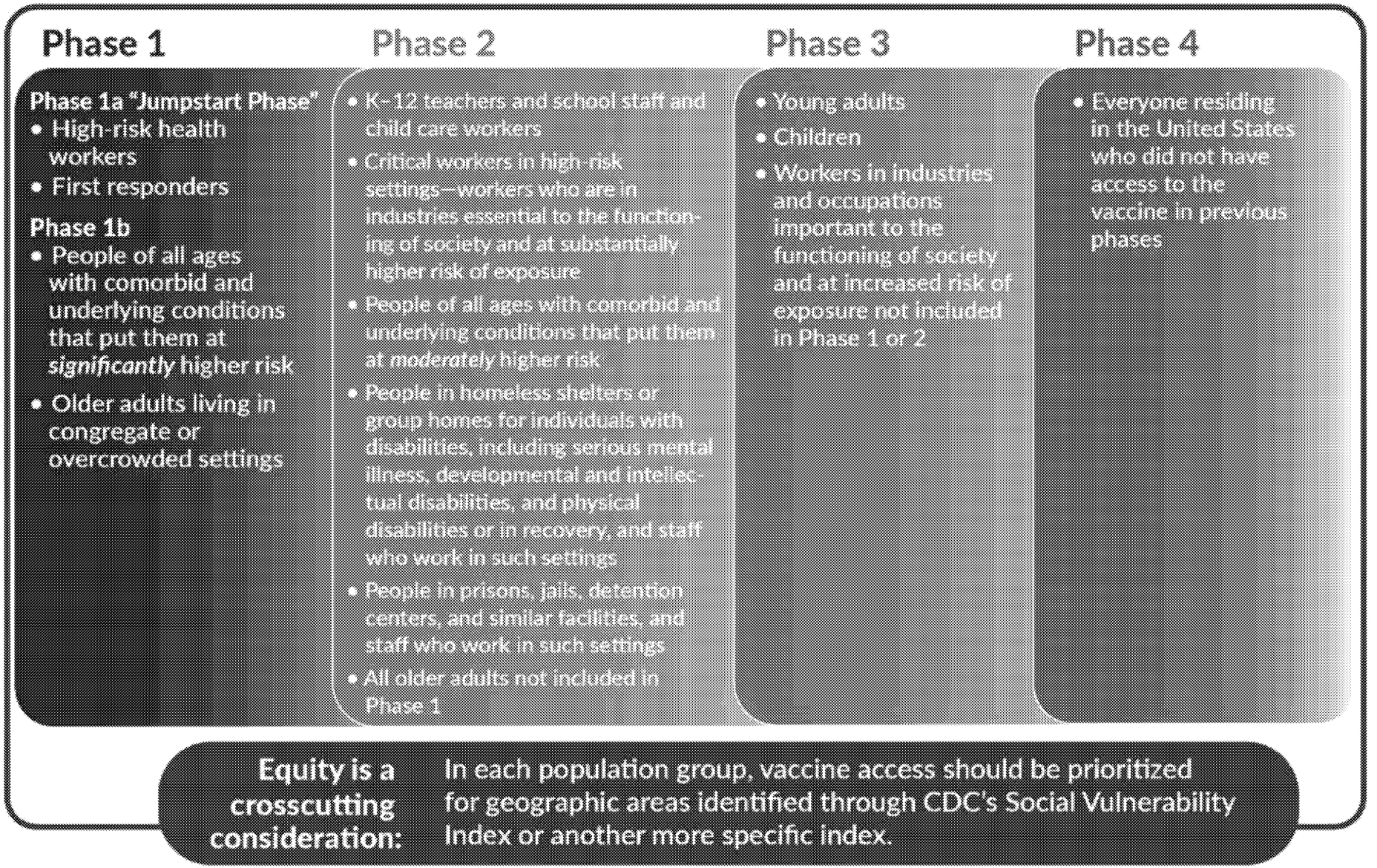


Equitable allocation of COVID-19 vaccine

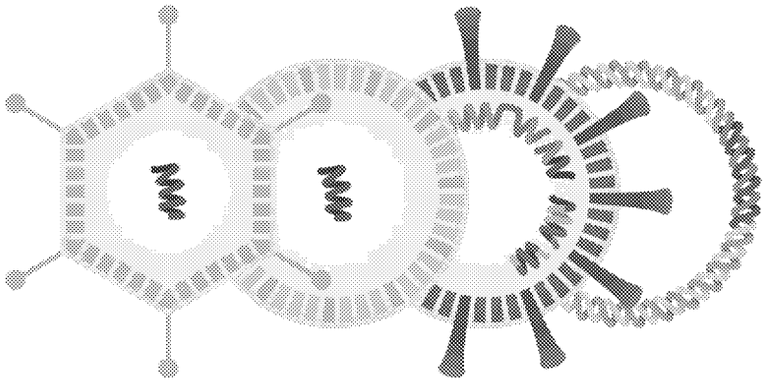
- Four-phased equitable framework, for state, tribal, local and territorial authorities (demand exceeds supply)
- Use existing programs;
- Promotion campaign with risk communication and engagement;
- Support of equitable global allocation



NATIONAL ACADEMY of MEDICINE

FIGURE: A Phased Approach to Vaccine Allocation for COVID-19

The National Academies of SCIENCES ENGINEERING MEDICINE



- *Fauci:* I could say… as a public health person, as a scientist, it will end. We will get through this for absolutely certain. We've already suffered through a lot of pain—a lot of economic and personal pain and inconvenience. But it will end. It will end because the public health efforts will succeed ultimately. And science will get us through this. We will get a vaccine. We will get therapies for early disease and for late disease. So the only message that I think we can jointly tell the American public and the global public is that we will get through this. Hang in there. It will end, we promise you.

Anthony Fauci, August 2020

To: Rusek, Benjamin[BRusek@nas.edu]; 'relman@stanford.edu'[relman@stanford.edu]; rbaric_email.unc[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; antoinette_baric.med[antoinette_baric@med.unc.edu]; Alison Andre[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; Cervenka, Nicole[NCervenka@nas.edu]; Sharples, Fran[FSharples@nas.edu]; Block, Bruce[BBlock@nas.edu]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Sun 10/18/2020 11:21:02 PM (UTC-05:00)
Subject: Some bullets following our US-China dialogue discussion on Friday

Thanks for a good discussion on Friday Ben,

I fully support a continued dialog and noted, as did some of those on the call, that George Gao and others were more open in their discussion of investigations into animal reservoirs of SARS-CoV-2 – i.e. discussion about the origin. We discussed ways we could frame a future topic that would allow us to talk about some important issues around the 'natural history' of SARS-CoV-2, that might also be comfortable for our Chinese colleagues. Here are a couple of bullets along the lines you asked me for:

1. Summary of recent findings re. the ability of SARS-CoV-2 to infect other species of animals in the lab, and in the wild, around the world (e.g. mink farm infections Europe and US, experimental infections of ferrets & raccoon dogs, risk assessments of SARS-CoV-2 infecting bats in other countries)

2. From the natural history of the virus, what do we know about the diversity of alpha and beta CoVs in wildlife reservoirs, and in potential intermediate hosts in various countries in Asia.

3. What information can we identify from the receptor binding domain of SARS-related CoVs that might help us predict future potential for emergence of CoVs from other countries

I think a good strategy would be to have the US side give the opening slide deck so that we sort of set the parameters and open up some of the discussion that I'm sure would lead to interesting information. I'd be happy to help on the first 2 points, and I'm sure Ralph could talk to the 3rd point. Linda and Stanley have a great deal of knowledge and could provide supporting comments…

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Thursday, October 15, 2020 1:18 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; rbaric_email.unc <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; antoinette_baric.med <antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for participating in the China bio dialogue sessions on Tuesday and Wednesday this week. We have scheduled a short hotwash session so the American participants can discuss the virtual dialogue discussions (from this week and earlier this year) and your get your ideas on future topics and other issues.

The session will take place tomorrow from 5:30-6:30 PM, Zoom link is below. Sorry for the short notice, if you can't make it tomorrow feel free to weigh in by email.

Topic: China Bio Post Dialogue Meeting Discussion
Time: Oct 16, 2020 5:30 PM ET / 4:30 PM CT / 2:30 PM PT
Meeting Link: https://nasem.zoom.us/j/92476126782?pwd= **552.136**
Password: **552.136**

PS I have asked CAS for the ppts from last night, will send those out as soon as I get them.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, October 14, 2020 7:32 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Greetings,

Thank you for joining the dialogue session last night. I have attached the slides from the three presentations.

FYI CAS has invited two additional CCDC experts to the session tonight.

Dr. Huaqing Wang, PI, Immunization program, Chinese Center for Disease Control and Prevention
Dr. Zundong Yin, Director of National Immunization Program, Chinese Center for Disease Control and Prevention

Looking forward seeing and hearing from you all in a few hours.
Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, October 12, 2020 12:36 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>
Subject: Virtual U.S. China dialogue meeting October 13 and 14
Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT)** to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics

set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Karen Makar[Karen.Makar@gatesfoundation.org]

Attendees: Harry Kleanthous; Holger Kanzler; Max Silverman; David Vaughn; Anastazia Older Aguilar; Colleen Woods; Kriti Arora; Susan Barnett; Ajoke Sobanjo-ter Meulen; Anna DU; Emilio Emini; Judy Hubbard; David Robinson; Nina Russell; Anushri Singhvi; Chris Karp; Peter Dull; Scott Dowell; Vivian Hsu; Kristen Earle; Julia Kuhn; Steve Hadley; Janet White; Heather Ann Brauer; Jacqueline Kirchner; Max Silverman; Kavita Malling (Camber Collective); Natalie Revelle; Chris Chen; Vidya Vasu-Devan; Ros Hollingsworth; Laura Powell; Email Recovery Approval; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; Monalisa Chatterji; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; Kai Dallmeier; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; Dillen, Carly; edohm@uab.edu; Ruben.Donis@hhs.gov; William Dowling; mariette.ducatez@envt.fr; pduprex@pitt.edu; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence; joanne@pitt.edu; thomasf@primate.wisc.edu; Frieman, Matthew; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Garcia-Sastre, Adolfo; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; henaorestrepoa@who.int; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; kazif@who.int; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline Kirchner; knezevici; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; philip.krause@fda.hhs.gov; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; Roger Le Grand; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; moorthyv; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; Johan Neyts; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; lauriex@who.int; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; salamik@who.int; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; Erica Ollmann Saphire; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; schwartzl@who.int; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; Shi, Pei yong; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; yoos@who.int; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; swaminathans@who.int; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov;

JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Tseng, Chien-Te K.; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David Vaughn; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; woodd@who.int; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; zhout@who.int; Jin.Zhu@health.gov.au; alex.sigal@ahri.org; rawcraig@yahoo.com; Gerald.Kovacs@hhs.gov; Ashley.Smith1@hhs.gov; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; valentina.bernasconi@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; Arun Kumar; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; MNELSON@dstl.gov.uk; Georgia Tomaras, Ph.D.; david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Ragini.Shivji@ema.europa.eu; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; cheryl@gisaid.org; christian.brechot@pasteur.fr; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; Sharon Schendel; alex@lji.org; sujan@lji.org; daniela@lji.org; liz.miller@lshtm.ac.uk; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; janet.lathey@nih.gov; larry.wolfraim@nih.gov; johnsonreed@niaid.nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Christine.bruce@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; Goldblatt, David; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; gustavo.f.palacios.civ@mail.mil; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; costaa@who.int; omorgan@who.int; perkinsm@who.int; subissil@who.int; dj56wood@gmail.com; STRÖHER, Ute; sandsa@who.int; irahetar@who.int; zlshi@wh.iov.cn; Youngmee Jee; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; Jiae Kim; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; Pillai, Satish; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; fernando.p.polack@vanderbilt.edu; Celeste.Marsh@health.gov.au; kim.Mulholland@lshtm.ac.uk; achidi.eric@gmail.com; macalvo@uach.cl; rodewaldl@chinacdc.cn; AFO@ssi.dk; hutiny@Who.int; sylvain.baize@pasteur.fr; mariangela.cavarelli@cea.fr; alariqil@who.int; may@bnitm.de; Jakob Cramer; Harish Iyer; Gagandeep Kang; Kayla Laserson; alemseged.abdissa@ahri.gov.et; azimt@who.int; cawthornea@who.int; adane.mihret@ahri.gov.et; ephcicm@nus.edu.sg; Vernon_LEE@moh.gov.sg; cherylc@nicd.ac.za; madhis@rmpru.co.za; mdohmd@snu.ac.kr; joser.arribas@salud.madrid.org; marta.diaz@salud.madrid.org; Katrin.Leitmeyer@ecdc.europa.eu; bergerii@who.int; feikind@who.int; grantr@who.int; Stephan.Harbarth@hcuge.ch; vankerkhovem@who.int; kum.ungchusak@gmail.com; albert.jan.van.hoek@rivm.nl; chantal.reusken@rivm.nl; mawiddowson@itg.be; Gayatri.Amirthalingam@phe.gov.uk; Nick Andrews; Andrew.Gorringe@phe.gov.uk; Bassam.Hallis@phe.gov.uk; Liz.Miller@phe.gov.uk; ccassetti@niaid.nih.gov; glynnsa@nhlbi.nih.gov; Graham, Barney (NIH/VRC) [E]; kdk6@cdc.gov; Barbara Mahon; MCELROYA@pitt.edu; ztq9@cdc.gov; Padmini Srikantiah; Jordan Tappero; jqt8@cdc.gov; rgonzalez@uaem.mx; hopr@uaem.mx; m.addo@uke.de; Mark_Ic_Chen@ncid.sg; Romain.Martischang@hcuge.ch; shimian.zou@nih.gov; Christina.Bareja@health.gov.au; John.Forde@phe.gov.uk; JinalB@nicd.ac.za; vekemansj@who.int; paola.stefanelli@iss.it; liya.wassie@ahri.gov.et; vongs@who.int; starkullaj@who.int; mahamuda@who.int; reveizl@paho.org; rodrigueza@paho.org; leitejul@paho.org; vicarian@paho.org; pebodyr@who.int; rawleigh.howe@ahri.gov.et; THOMAS.JAENISCH@CUANSCHUTZ.EDU; ayola-akim.adegnika@medizin.uni-tuebingen.de; t.brehm@uke.de; adamou.rafiou@gmail.com; bernadettemrg5@gmail.com; bernadette.murgue@inserm.fr; gmackenzie@mrc.gm; Anthony.Scott@lshtm.ac.uk; SUyoga@kemri-wellcome.org; atanuri1@gmail.com; ggj2@cdc.gov; wbrooks3@jhu.edu; kkotloff@som.umaryland.edu;

ADriscoll@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; SHakre@eidresearch.org; derrick.crook@ndcls.ox.ac.uk; csv@ssi.dk; schwartz@pasteur.fr; marc.eloit@pasteur.fr; srinivas.murthy; matthew.cheng@mcgill.ca; nymadawa@gyals.mn; wuzy@263.net; gaofu@chinacdc.cn; Mpasetti@som.umaryland.edu; aleksandra.wesolowska@wum.edu.pl; cuchip@who.int; per.ashorn@tuni.fi; kwatrag@rmpru.co.za; jmarien@itg.be; KArien@itg.be; adebola.olayinka@ncdc.gov.ng; bcowling@hku.hk; Suellen.Nicholson@vidrl.org.au; paul.licciardi@mcri.edu.au; lienanhha.do@mcri.edu.au; marc-alexandre.lafrance.1@ulaval.ca; paul.fine@lshtm.ac.uk; krystian.jazdzewski@warsawgenomics.pl; jzejda@sum.edu.pl; freidlg@who.int; taufiqur@icddrb.org; fqadri@icddrb.org; r.heyderman@ucl.ac.uk; mff7@cdc.gov; Heather.Whitaker@phe.gov.uk; tonoletej@who.int; annev@nicd.ac.za; shinj@who.int; johnvparry@ntlworld.com; leli@who.int; krishnanv@who.int; revans@who.int; belll@who.int; juneja@tifr.res.in; violetafonsecaocampos@gmail.com; twosned@googlemail.com; alain.townsend@imm.ox.ac.uk; sanchezg@une.net.co; muldersm@who.int; pereyaslovd@who.in; mueller@wehi.edu.au; leanne.robinson@burnet.edu.au; claudioc@gsespa.cl; drmlaman@yahoo.com; ffntoumi@hotmail.com; rajatonirinas@who.int; Kirsty Le Doare; Joe.Fitchett@mologic.co.uk; hstaines@sgul.ac.uk; thall@sgul.ac.uk; okeibunorj@who.int; barnorj@who.int; heather.gidding@sydney.edu.au; mayara_bastos@yahoo.com.br; faiz.ahmadkhan@mcgill.ca; louis.patrick.haraoui@usherbrooke.ca; yuemei.fan@tuni.fi; almonther@hotmail.com; philippa.matthews@ndm.ox.ac.uk; Abbie.Bown@phe.gov.uk; hsaeb@phcc.gov.qa; intl@ibto.ir; dorits@imbm.org; dthea@bu.edu; yoshiyama1962@yahoo.co.jp; ullas@tifr.res.in; jsshastri@gmail.com; Audrey Hutter; cooldrdax@gmail.com; inbanathanf@who.int; muhammadqasim.qasim@otago.ac.nz; ofrinr@who.int; payden@who.int; vokatya@who.int; tranminhn@who.int; cgomez@javeriana.edu.co; jccastellanos@husi.org.co; katom@who.int; snsmarlowe@doctors.org.uk; arashirot@who.int; lOwusu@noguchi.ug.edu.gh; eric.osoro@wsu.edu; HarbiNa2@NGHA.MED.SA; amhashem@kau.edu.sa; bwilliams@who.int; radegbola@hotmail.com; jean-luc.gala@uclouvain.be; rosemaryaudu@yahoo.com; sandeepdogra@gmail.com; allergypk@gmail.com; maghsoodlu@yahoo.com; peshghi64@gmail.com; a.a.khazaeli@gmail.com; Bethany_Gauthier@hms.harvard.edu; vittoria.offeddu@ird.global; MAHIPALAP@who.int; ian.marr@menzies.edu.au; Abena.Amoah@lshtm.ac.uk; Mia.Crampin@lshtm.ac.uk; Antonia.Ho@glasgow.ac.uk; javadi11@hzdr.de; asmronger@gmail.com; Kaitlyn.Vette@health.nsw.gov.au; magdalena.spolnicka@policja.gov.pl; aleksander.masny@policja.gov.pl; marc.veldhoen@medicina.ulisboa.pt; MRabeh@dha.gov.ae; susie.dunachie@ndm.ox.ac.uk; necla.tulek@atilim.edu.tr; sophiev@hku.hk; koningsf@who.int; Lloyd.Mulenga@moh.gov.zm; lbmulenga@yahoo.com; mastershakil@hotmail.com; rahul.arora@balliol.ox.ac.uk; christian.cao@ucalgary.ca; liu.michael222@gmail.com; niklas.bobrovitz@mail.utoronto.ca; tingting.yan@mail.utoronto.ca; a.pan@asst-cremona.it; s.testa@asst-cremona.it; alessia.zoncada@tin.it; nicolew@nicd.ac.za; GWarimwe@kemri-wellcome.org; HKaranja@kemri-wellcome.org; dancohen@tauex.tau.ac.i; sabinoec@usp.br; patricia.garcia@upch.pe; zobstfeld@wesleyan.edu; amyjanel@gmail.com; liliana.brown@nih.gov; lori.newman@nih.gov; descherm@bni-hamburg.de; emmerich@bnitm.de; charlotte.thalin@sll.se; voneijek@who.int; avillarreal@indicasat.org.pa; agoodridge@indicasat.org.pa; r.a.mckendry@ucl.ac.uk; jint@ustc.edu.cn; Email; monika.lindemann@uk-essen.de; ygrad@hsph.harvard.edu; KHerbst@ahri.org; daniel.larremore@colorado.edu; william.windsor@cuanschutz.edu; Molly.Lamb@cuanschutz.edu; rolf.fendel@uni-tuebingen.de; jguthmiller@uchicago.edu; mzrein@infynity-biomarkers.com; mike.fisher@oncimmune.com; kjambo@mlw.mw; petra.budde@oncimmune.com; oon_tek_ng@ncid.sg; kalisvar_marimuthu@ttsh.com.sg; Farah_MOHAMED_HANIFF@ncid.sg; a.t.decruz.20@ucl.ac.uk; ben.miller.13@ucl.ac.uk; mafarodriguez@unisalle.edu.co; Anna.JefferySmith@phe.gov.uk; keti.glonti@gmail.com; imaginapolo@gmail.com; Maria.Zambon@phe.gov.uk; Jennifer.Yates@health.ny.gov; gingras@lunenfeld.ca; jen.gommerman@utoronto.ca; lewish@who.int; daclark@sgul.ac.uk; omar.nyabi@uclouvain.be; giorgio.fedele@iss.it; Rachel.Halkerston@phe.gov.uk; pamela.proud@phe.gov.uk; kpancer@pzh.gov.pl; wegene.borena@i-med.ac.at; wrastawicki@pzh.gov.pl; sungskim63@gmail.com; vfa3@cdc.gov; teodora.aktas@folkhalsomyndigheten.se; Email: jplested@novavax.com; bkhatri@lunenfeld.ca; tesfaye.gelanew@ahri.gov.et; juan.moliva@nih.gov; anne.werner@nih.gov; gabriela.alvarado@nih.gov; Breeze Cavell; wangling@niaid.nih.gov; eunsung.yang@nih.gov; yi.zhang3@nih.gov; nicole.doriarose@nih.go; lorna.mcinroy@phe.gov.uk; mazhari@wehi.edu.au; zhuna@ivdc.chinacdc.cn; maony@ivdc.chinacdc.cn; zhuzhen@ivdc.chinacdc.cn; zhangyan@ivdc.chinacdc.cn; wangpw@ivdc.chinacdc.cn; sanghwan.seo@ivi.int; vfumado@hsjdbcn.org; xhatzi@med.uth.gr; tatjana.vilibic-cavlek@hzjz.hr; annap@auth.gr; andargachew.mulu@ahri.gov.et; viki.indenbaum@sheba.health.gov.il; colwill@lunenfeld.ca; ytakahas@niid.go.jp; sayamrym@niid.go.jp; tksuzuki@niid.go.jp; raquel.guiomar@insa.min-saude.pt; merit.melin@thl.fi; katarina.prosenc@nlzoh.si; jwilbur@meso-scale.com; Celine.Parsy-Kowalska@oncimmune.com; Imran Nisar; Fyezah Jehan; lcorey@fredhutch.org; m.noursadeghi@ucl.ac.uk; fabienne.brilot@sydney.edu.au; lja2002@qatar-med.cornell.edu; mdjjh@nmc.or.kr; AAgweyu@kemri-wellcome.org; katherine.gallagher@lshtm.ac.uk; AEtyang@kemri-wellcome.org; ekagucia@kemri-wellcome.org; Christian.Bottomley@LSHTM.ac.uk; SPortillo@som.umaryland.edu; nicole.gilberger@bnitm.de; sudhirbabji@cmcvellore.ac.in; Mallory.Shriver@som.umaryland.edu; freedmanne@mail.nih.gov; galter@mgh.harvard.edu; kristian@andersen-lab.com; trvrb; pbieniasz@rockefeller.edu; Bjorkman, Pamela J.; jbloom@fredhutch.org; burton@scripps.edu; mmdavis@stanford.edu; deoliveira@ukzn.ac.za; gd312@cam.ac.uk; embrya@niaid.nih.gov; katie.ewer@ndm.ox.ac.uk; agartlan@fredhutch.org; r.fouchier@erasmusmc.nl; ggaiha@mgh.harvard.edu; dh2994@cumc.columbia.edu; Nick Jackson; yoshihiro.kawaoka@wisc.edu;

akiko.iwasaki@yale.edu; paul.kellam@kymab.com; neil@ipd.uw.edu; btk@lanl.gov; karin.lore@ki.se; J. Christopher Love; darrenpatrickmartin@gmail.com; monte@duke.edu; felipe.naveca@fiocruz.br; nussen@mail.rockefeller.edu; Erica Ollmann Saphire; sjp97@medschl.cam.ac.uk; mpepper@uw.edu; bpulend@stanford.edu; rino.r.rappuoli@gsk.com; sabinoec@gmail.com; senjutisaha@gmail.com; schief@scripps.edu; gideon.schreiber@weizmann.ac.il; gavin.screaton@medsci.ox.ac.uk; djs200@cam.ac.uk; varadar; dveesler@uw.edu; bwalker@mgh.harvard.edu; andrew@scripps.edu; wilson@scripps.edu; wyatt@scripps.edu

Sent: Mon 3/29/2021 9:56:00 PM (UTC-05:00)

Subject: Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

Dear All

The goal of the workshop is to discuss how to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. This requires connecting local pathogen genomic sequencing and epidemiology with high quality virology and immunology. There will also be a discussion of how immunological knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making.

Agenda and registration link forthcoming.

Thank you.
Karen

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-

perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; Port, Julia (NIH/NIAID) [F]; Kortekaas, Jeroen; S. Herfst; Thomas Friedrich; Stylianos Bournazos; Griffiths, Anthony; Reed, Douglas S; Malkevich, Nina (OS/ASPR/BARDA) (CTR); Sinha, Tanima (OS/ASPR/BARDA); Revelli, David; Andrew Jones

Sent: Sun 5/30/2021 10:21:59 AM (UTC-05:00)

Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jmkperrine@gmail.com; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-

perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; julia.port@nih.gov; benjamin.murrell@ki.se; d.vanriel@erasmusmc.nl; Cherry, Sara; Robert JEFF Hogan; Jeffrey V. Ravetch; Stylianos Bournazos; Kortekaas, Jeroen; Griffiths, Anthony; Thomas Friedrich; Andrew Jones; Diane Bolton; Revelli, David; Flynn, Joanne L

Sent: Sun 6/6/2021 10:23:38 AM (UTC-05:00)

Subject: Canceled: WHO COVID-19 Animal Models Group Call

Due to a conflicting WHO meeting, we are cancelling the call this week.

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jmkperrine@gmail.com; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-

perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; julia.port@nih.gov; benjamin.murrell@ki.se; d.vanriel@erasmusmc.nl; Cherry, Sara; Griffiths, Anthony; Kortekaas, Jeroen; S. Herfst; Jeffrey V. Ravetch; Thomas Friedrich; Stylianos Bournazos; Reed, Douglas S; Diane Bolton; Sinha, Tanima (OS/ASPR/BARDA); Danielle Anderson; Danielle Anderson

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Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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Meeting ID: 361 256 8290

From: Lisa CHAKRABARTI[lisa.chakrabarti@pasteur.fr]

Attendees: Tony.Schountz@colostate.edu; Techakitiroj Chatkul (tverakit@gmail.com); Segales, Joaquim; kupke (kupke@staff.uni-marburg.de); qinchuan (qinchuan@pumc.edu.cn); Karl.Erlandson (Karl.Erlandson@hhs.gov); erica (erica@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; mary.lane@nih.gov; Andrew.Phipps; Eitzen, Melissa M.; Florence, Clint (NIH/NIAID) [E]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Riccardo Russo; anja.kipar@uzh.ch; feldmannh@niaid.nih.gov; Levis, Robin; Hodgson, Paul; SBradfute@salud.unm.edu; wim.vanderpoel@wur.nl; Cartner, Samuel Corbin; lok-yinroy-wong; thomasf@primate.wisc.edu; danielle.anderson (danielle.anderson@duke-nus.edu.sg); sodas; BRANGEL, Polina; MNELSON@mail.dstl.gov.uk; William Dowling (william.dowling@cepi.net); Brasel, Trevor; RIVEROS BALTA, Ximena; sekim (sekim@krict.re.kr); estefania.rodriguez (estefania.rodriguez@bnitm.de); lgralins@email.unc.edu; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); De wit, Emmie (NIH/NIAID) [E]; Cherry, Sara; jeroen.kortekaas (jeroen.kortekaas@wur.nl); JOHN JAMES BACZENAS; Hwan K Kim (hwan.kim@stonybrook.edu); Neil Berry (Neil.Berry@nibsc.org); marlene.espinozamoraga; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Manki Song (mksong@ivi.int); Jason.Mott; DAVID H O'CONNOR (dhoconno@wisc.edu); hlchen (hlchen@hku.hk); Vandenberghe, Luk; MSLEVER (MSLEVER@dstl.gov.uk); Donis, Ruben (OS/ASPR/BARDA); Miles.Carroll (Miles.Carroll@phe.gov.uk); Perlman, Stanley; Bukreyev, Alexander; SHELBY L O'CONNOR; Kayvon Modjarrad (kmodjarrad@eidresearch.org); Romain Volmer (romain.volmer@envt.fr); langermans (langermans@bprc.nl); Dohm, Erik Daniel; bosioc@niaid.nih.gov; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); patrick.reid@unmc.edu; Seungtaek Kim (seungtaek.kim@ip-korea.org); john.c.trefry.civ (john.c.trefry.civ@mail.mil); dbolton@hivresearch.org; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); res2025; wenchun0617; Amelia Karlsson (amelia.karlsson@duke.edu); fkoide (fkoide@southernresearch.org); Hevey, Michael (CTR); Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); WaickmaA@upstate.edu; croy (croy@tulane.edu); Juan García Arriaza (jfgarcia@cnb.csic.es); sheahan; Tony.Wang (Tony.Wang@fda.hhs.gov); dean.smith (dean.smith@canada.ca); t.sulpice; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); horer@ku.edu.tr; Elliot Lilley - NC3Rs; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); HENAO RESTREPO, Ana Maria; dmissiak (dmissiak@bsd.uchicago.edu); bobomok@hku.hk; Falzarano, Darryl; kevinharrod (kevinharrod@uabmc.edu); Luis.Lugo.mil@afrims.org; Tadaki (tksuzuki@nih.go.jp); dgdiel@cornell.edu; kandeil_a@hotmail.com; Sivko, Gloria S; Krammer, Florian; Little, James (OS/ASPR/BARDA); Sally Sharpe (Sally.Sharpe@phe.gov.uk); Graham, Barney (NIH/VRC) [E]; anna (anna@thsti.res.in); Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); tenoever@gmail.com; JTorrelles@txbiomed.org; sean.li (sean.li@canada.ca); Frieman, Matthew; d.vanriel; KNEZEVIC, Ivana; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); lisambrosseau@gmail.com; verstrepen@bprc.nl; Albrecht, Randy; tcs38@psu.edu; sharon.daye2.mil@mail.mil; peter.palese@mssm.edu; PREZIOSI, Marie-pierre; tyamamoto@ciea.or.jp; Benjamin Murrell; Oreshkova, Nadia; Yper.Hall (Yper.Hall@phe.gov.uk); y.jacob.hou@unc.edu; WOOD, David John; Lee-Parritz, David; paul-mccray (paul-mccray@uiowa.edu); snumouse (snumouse@snu.ac.kr); kanta.subbarao (kanta.subbarao@influenzacentre.org); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); kyle.rosenke; Kobie, James J; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); seos@cnu.ac.kr; kai.dallmeier

(kai.dallmeier@kuleuven.be); salgampa (salgampa@njms.rutgers.edu); Stemmy, Erik (NIH/NIAID) [E]; Matthew.Reed.mil@afrims.org; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); l.enjuanes@cnb.csic.es; Volker.gerdts (Volker.gerdts@usask.ca); mariette.ducatez@envt.fr; Victoria.Wahl; que.dang@nih.gov; caroline.melo@rivm.nl; ygoez; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); David Vaughn (David.Vaughn@gatesfoundation.org); B.H.G. Rockx (b.rockx@erasmusmc.nl); SATHIYAMOORTHY, Vaseeharan; REIRELAND (REIRELAND@mail.dstl.gov.uk); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); CDillen@som.umaryland.edu; Munir, Muhammad; SPERGEL@email.chop.edu; YOO, Si Hyung; Stewart, James; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); Kristine Macartney (kristine.macartney@health.nsw.gov.au); daniel.martinez-arguelles; Pickett, Thames (NIH/NIAID) [E]; sutter (sutter@micro.vetmed.uni-muenchen.de); gustavo.palacios (gustavo.palacios@gmail.com); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); S. Herfst; Holbrook, Michael (NIH/NIAID) [C]; lisette.cornelissen; LESELLIER Sandrine (sandrine.lesellier@anses.fr); MacGill, Tracy; Schotsaert, Michael; Paul.Dabisch; Krause, Philip; angierasmussen@gmail.com; Barbara.Schnierle (Barbara.Schnierle@pei.de); grace.m.lidl.mil@mail.mil; antoine.nougairede; alankhoo.imr; JLPRIOR (JLPRIOR@dstl.gov.uk); LMartinez@txbiomed.org; caroline.foo; Vergara, Julia; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); Garcia-Sastre, Adolfo; Paul.Lambert (Paul.Lambert@unige.ch); Crozier, Ian (NIH) [C]; julia.port; Olinger, Gene; neeltje.vandoremalen@nih.gov; scordo (scordo@qb.fcen.uba.ar); Philip Minor (Philip.Minor2@gmail.com); Pauline Maisonnasse (pauline.maisonnasse@cea.fr); verschoor (verschoor@bprc.nl); ZHU, Jin; tomeri (tomeri@iibr.gov.il); ivan.marazzi; stittelaar (stittelaar@viroclinics.com); christian.c.hofer.mil@mail.mil; f.briand; Jayashankar, Lakshmi (OS/ASPR/BARDA); Damron, Fredrick; franck.TOURET@univ-amu.fr; ZHOU, Tiequn; mopargal (mopargal@rams.colostate.edu); Yusibov, Vidadi (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Roger Le Grand (roger.le-grand@cea.fr); Honko, Anna; Christiane GERKE; mdiamond (mdiamond@wustl.edu); rhakami@gmu.edu; dbarouch (dbarouch@bidmc.harvard.edu); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Shi, Pei yong; Simon Funnell (simon.funnell@phe.gov.uk); Nicola Rose (Nicola.Rose@nibsc.org); jfwchan (jfwchan@hku.hk); lawton.stubbert@canada.ca; jmkperrine; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); SWAMINATHAN, Soumya; troyrandall (troyrandall@uabmc.edu); marzia; SALAMI, Kolawole; ravetch; Vasan, Vasan (H&B, Geelong ACDP); gabriella.worwa; mito@ciea.or.jp; Chris Miller (cjmiller@ucdavis.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); rbaric (rbaric@email.unc.edu); dsreed@cvr.pitt.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); darwyn.kobasa@canada.ca; ramadany; GREY Finn (fgrey@exseed.ed.ac.uk); Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Tseng, Chien-Te K.; Gerhards, Nora; Treanor, John (OS/ASPR/BARDA) (CTR); Nadia KHELEF; Hensley, Lisa (NIH/NIAID) [E]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Griffiths, Anthony; Alyson Kelvin; rcarrion (rcarrion@TxBiomed.org); nnagata@niid.go.jp; Golding, Hana; sanath.rao; Javier Salguero (Javier.Salguero@phe.gov.uk); jhogan@uga.edu; nirp (nirp@iibr.gov.il); Karen Gooch; mto@umn.edu; Ann Rawkins (Ann.Rawkins@phe.gov.uk); sinabavari@comcast.net; Julia Tree (Julia.Tree@phe.gov.uk); Carolyn Clark (carolyn.clark@cepi.net); BAMFORD, Pearl; Duprex, Paul; White, Alexander G; IVMARTINEZ; anice.lowen; Munster,

	Vincent (NIH/NIAID) [E]; Idenisy (Idenisy@yahoo.com); Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); Karen Makar (Karen.Makar@gatesfoundation.org); Flynn, Joanne L; Chi Van Dang (cdang@lcr.org); Russell.Ray@bcm.edu; Hild, Sheri (NIH/OD) [E]; Juergen Richt (jricht@vet.k-state.edu); Kathryn Ryan; shanchao (shanchao@wh.iov.cn); sid.byrareddy; johan.neyts (johan.neyts@kuleuven.be); mesteban (mesteban@cnb.csic.es); KAZI, Fatema; sbournazos@mail.rockefeller.edu; B.L. Haagmans (b.haagmans@erasmusmc.nl); Martin.Beer (Martin.Beer@fli.de); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); yu.cong@nih.gov; Mark Prescott - NC3Rs; mitchell.palmer@usda.gov; Asisa.Volz (Asisa.Volz@tiho-hannover.de); esulkowska@rics.bwh.harvard.edu; rkiatchula (rkiatchula@gmail.com); Mark Page (Mark.Page@nibsc.org); ajones; bradley.pickering (bradley.pickering@canada.ca); dustin.johnson (dustin.johnson@canada.ca); David Revelli (drevelli@lovelacebiomedical.org); mlewis (mlewis@bioqual.com); Flynn, Joanne L; Jeffrey V. Ravetch; Revelli, David; Griffiths, Anthony; THOMAS C FRIEDRICH (tfriedri@wisc.edu); Sinha, Tanima (OS/ASPR/BARDA); Stylianos Bournazos; Robert JEFF Hogan; Andrew Jones; Diane Bolton; Kortekaas, Jeroen
Sent:	Wed 6/9/2021 3:19:40 PM (UTC-05:00)
Subject:	Canceled: WHO COVID-19 Animal Models Group Call

Due to a conflicting WHO meeting, we are cancelling the call this week.

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Luis.Lugo.mil@afrims.org; Matthew.Reed.mil@afrims.org; franck.TOURET@univ-amu.fr; LESELLIER Sandrine (sandrine.lesellier@anses.fr); Romain Volmer (romain.volmer@envt.fr); BAMFORD, Pearl; ZHU, Jin; Donis, Ruben (OS/ASPR/BARDA); Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Little, James (OS/ASPR/BARDA); Andrew.Phipps; Sabourin, Carol (OS/ASPR/BARDA); Treanor, John (OS/ASPR/BARDA) (CTR); Yusibov, Vidadi (OS/ASPR/BARDA); Sivko, Gloria S; Russell.Ray@bcm.edu; verschoor (verschoor@bprc.nl); verstrepen@bprc.nl; langermans (langermans@bprc.nl); mlewis (mlewis@bioqual.com); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); estefania.rodriguez (estefania.rodriguez@bnitm.de); Griffiths, Anthony; Honko, Anna; dustin.johnson (dustin.johnson@canada.ca); sean.li (sean.li@canada.ca); dean.smith (dean.smith@canada.ca); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); Roger Le Grand (roger.le-grand@cea.fr); Pauline Maisonnasse (pauline.maisonnasse@cea.fr); sekim (sekim@krict.re.kr); kandeil_a (kandeil_a@hotmail.com); Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); shanchao (shanchao@wh.iov.cn); rkiatchula (rkiatchula@gmail.com); seos@cnu.ac.kr; lisambrosseau@gmail.com; mto@umn.edu; mito@ciea.or.jp; tyamamoto@ciea.or.jp; mesteban (mesteban@cnb.csic.es); Juan García Arriaza (jfgarcia@cnb.csic.es); l.enjuanes@cnb.csic.es; mopargal (mopargal@rams.colostate.edu); Tony.Schountz@colostate.edu; angierasmussen@gmail.com; scordo (scordo@qb.fcen.uba.ar); sinabavari@comcast.net; dgdiel@cornell.edu; res2025; Vasan, Vasan (H&B, Geelong ACDP); Duprex, Paul; Flynn, Joanne L; White, Alexander G; Alyson Kelvin; john.c.trefry.civ (john.c.trefry.civ@mail.mil); jennifer.m.kishimori.mil@mail.mil; kanta.subbarao (kanta.subbarao@influenzacentre.org); REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON@mail.dstl.gov.uk; JLPRIOR (JLPRIOR@dstl.gov.uk); Amelia Karlsson (amelia.karlsson@duke.edu); danielle.anderson (danielle.anderson@duke-nus.edu.sg); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); anice.lowen; mariette.ducatez@envt.fr; S. Herfst; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); Golding, Hana; MacGill, Tracy; Tony.Wang (Tony.Wang@fda.hhs.gov); Krause, Philip; Levis, Robin; Martin.Beer (Martin.Beer@fli.de); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); ldenisy (ldenisy@yahoo.com); rhakami@gmu.edu; Asisa.Volz (Asisa.Volz@tiho-hannover.de); dbarouch (dbarouch@bidmc.harvard.edu); esulkowska@rics.bwh.harvard.edu; Vandenberghe, Luk; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; daniel.martinez-arguelles; lawton.stubbert@canada.ca; jfwchan (jfwchan@hku.hk); hlchen (hlchen@hku.hk); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); Krammer, Florian; lisa.chakrabarti@pasteur.fr; Christiane Gerke (christiane.gerke@pasteur.fr); Nadia KHELEF (nadia.khelef@pasteur.fr); Seungtaek Kim (seungtaek.kim@ip-korea.org); Manki Song (mksong@ivi.int); Segales, Joaquim; Vergara, Julia; tomeri (tomeri@iibr.gov.il); nirp (nirp@iibr.gov.il); nnagata@niid.go.jp; Tadaki (tksuzuki@nih.go.jp); terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Juergen Richt (jricht@vet.k-state.edu); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); horer@ku.edu.tr; snumouse (snumouse@snu.ac.kr); kai.dallmeier (kai.dallmeier@kuleuven.be); johan.neyts (johan.neyts@kuleuven.be); caroline.foo; erica (erica@lji.org); Munir, Muhammad; David Revelli (drevelli@lovelacebiomedical.org); Chi Van Dang (cdang@lcr.org); sutter (sutter@micro.vetmed.uni-muenchen.de); kupke (kupke@staff.uni-marburg.de); Albrecht, Randy; Garcia-Sastre, Adolfo; peter.palese@mssm.edu; Schotsaert, Michael; tenoever@gmail.com; Olinger, Gene; marlene.espinozamoraga; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Mark Page (Mark.Page@nibsc.org); Florence, Clint (NIH/NIAID) [E]; mary.lane@nih.gov; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; feldmannh@niaid.nih.gov; Munster, Vincent (NIH/NIAID) [E]; Graham, Barney (NIH/VRC) [E]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Elliot Lilley - NC3Rs; Mark Prescott - NC3Rs; Kristine Macartney (kristine.macartney@health.nsw.gov.au); patrick.reid@unmc.edu; yu.cong@nih.gov; marzia; bosioc@niaid.nih.gov; gabriella.worwa; Neil Berry (Neil.Berry@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Nicola Rose (Nicola.Rose@nibsc.org); que.dang@nih.gov; Hild, Sheri (NIH/OD) [E]; neeltje.vandoremalen@nih.gov; kyle.rosenke; Cassels, Fred; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); Barbara.Schnierle (Barbara.Schnierle@pei.de); qinchuan (qinchuan@pumc.edu.cn); SPERGEL@email.chop.edu; darwyn.kobasa@canada.ca; bradley.pickering (bradley.pickering@canada.ca); t.sulpice; f.briand; tcs38@psu.edu; Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Yper.Hall (Yper.Hall@phe.gov.uk); Ann Rawkins (Ann.Rawkins@phe.gov.uk); Javier Salguero (Javier.Salguero@phe.gov.uk); Sally Sharpe (Sally.Sharpe@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); caroline.melo@rivm.nl; ajones; ravetch; Riccardo Russo; salgampa (salgampa@njms.rutgers.edu); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); ramadany; fkoide (fkoide@southernresearch.org); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); Hwan K Kim (hwan.kim@stonybrook.edu); WaickmaA@upstate.edu; alankhoo.imr; rcarrion (rcarrion@TxBiomed.org); LMartinez@txbiomed.org; JTorrelles@txbiomed.org;

Techakitiroj Chatkul (tverakit@gmail.com); bobomok@hku.hk; anna (anna@thsti.res.in); Lee-Parritz, David; croy (croy@tulane.edu); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); Chris Miller (cjmiller@ucdavis.edu); sodas; rbaric (rbaric@email.unc.edu); lgralins@email.unc.edu; sheahan; gustavo.palacios (gustavo.palacios@gmail.com); dmissiak (dmissiak@bsd.uchicago.edu); GREY Finn (fgrey@exseed.ed.ac.uk); dsreed@cvr.pitt.edu; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); Paul.Lambert (Paul.Lambert@unige.ch); y.jacob.hou@unc.edu; Cartner, Samuel Corbin; Dohm, Erik Daniel; kevinharrod (kevinharrod@uabmc.edu); Kobie, James J; troyrandall (troyrandall@uabmc.edu); jhogan@uga.edu; paul-mccray (paul-mccray@uiowa.edu); Perlman, Stanley; Stewart, James; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); CDillen@som.umaryland.edu; Frieman, Matthew; SBradfute@salud.unm.edu; JOHN JAMES BACZENAS; SHELBY L O'CONNOR; thomasf@primate.wisc.edu; DAVID H O'CONNOR (dhoconno@wisc.edu); anja.kipar@uzh.ch; christian.c.hofer.mil@mail.mil; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); grace.m.lidl.mil@mail.mil; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mitchell.palmer@usda.gov; Brasel, Trevor; Bukreyev, Alexander; Eitzen, Melissa M.; Shi, Pei yong; Tseng, Chien-Te K.; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; stittelaar (stittelaar@viroclinics.com); wim.vanderpoel@wur.nl; Gerhards, Nora; jeroen.kortekaas (jeroen.kortekaas@wur.nl); Oreshkova, Nadia; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Kayvon Modjarrad (kmodjarrad@eidresearch.org); mdiamond (mdiamond@wustl.edu); BRANGEL, Polina; HENAO RESTREPO, Ana Maria; KAZI, Fatema; KNEZEVIC, Ivana; SATHIYAMOORTHY, Vaseeharan; PREZIOSI, Marie-pierre; RIVEROS BALTA, Ximena; SALAMI, Kolawole; YOO, Si Hyung; SWAMINATHAN, Soumya; WOOD, David John; ZHOU, Tiequn; dbolton@hivresearch.org; sharon.daye2.mil@mail.mil; Damron, Fredrick; IVMARTINEZ; lisette.cornelissen; ivan.marazzi; wenchun0617; Victoria.Wahl; Hevey, Michael (CTR); Paul.Dabisch; Stylianos Bournazos

Sent: Sun 4/25/2021 11:56:43 AM (UTC-05:00)

Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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+1 651 372 8299 US (Minnesota)
+1 786 635 1003 US (Miami)
+1 267 831 0333 US (Philadelphia)
+1 301 715 8592 US (Washington D.C)

+1 312 626 6799 US (Chicago)
Meeting ID: 361 256 8290
Find your local number: https://who.zoom.us/u/acLh9DwRd3

Join by SIP
3612568290@zoomcrc.com

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
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From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; sweaver@utmb.edu; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA;

Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif; Warner, Blake (NIH/NIDCR) [E]; Joseph, Paule (NIH/NIAAA) [E]; Kim, Sonnie (NIH/NIAID) [E]; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E]

Sent: Fri 4/23/2021 12:05:50 PM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal
Start Time: Tue 5/4/2021 1:00:00 PM (UTC)
End Time: Tue 5/4/2021 2:00:00 PM (UTC)
Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Mark Denison; Routh, Andrew L.

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Thanks,
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Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal
Start Time: Tue 8/17/2021 1:00:00 PM (UTC)
End Time: Tue 8/17/2021 2:00:00 PM (UTC)
Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Mark Denison; Routh, Andrew L.

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 6/22/2021 1:00:00 PM (UTC)
End Time:	Tue 6/22/2021 2:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Mark Denison; Routh, Andrew L.

Importance: Normal
Start Time: Tue 6/15/2021 1:00:00 PM (UTC)
End Time: Tue 6/15/2021 2:00:00 PM (UTC)
Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Mark Denison; Routh, Andrew L.

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Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 4/27/2021 1:00:00 PM (UTC)
End Time:	Tue 4/27/2021 2:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Mark Denison; Routh, Andrew L.

To: Stevens, Rick L.[stevens@anl.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]

Cc: Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

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Subject: SARS-CoV-2 Weekly Investigators Meeting - May 4, 2021

Good morning!

Hope everyone had a wonderful weekend!

On Tuesday, April 27th, Jennifer Gribble-Bowser gave a presentation on "**Defining the determinants and products of coronavirus recombination**". Thank you to the presenter and to everyone who was able to join.

Tomorrow, Tuesday, May the 4th be with you, presentation will be:
Oral Cavity Infection with SARS-CoV-2: Pathology, Transmission Potential, and Symptoms

- Part 1 – Oral Cavity Infection- Blake Warner, PhD
- Part 2 – Symptoms- Paule Joseph, PhD

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Stevens, Rick L.[stevens@anl.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]

Cc: Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Thur 5/6/2021 9:51:57 AM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - May 11th

Happy Thursday!

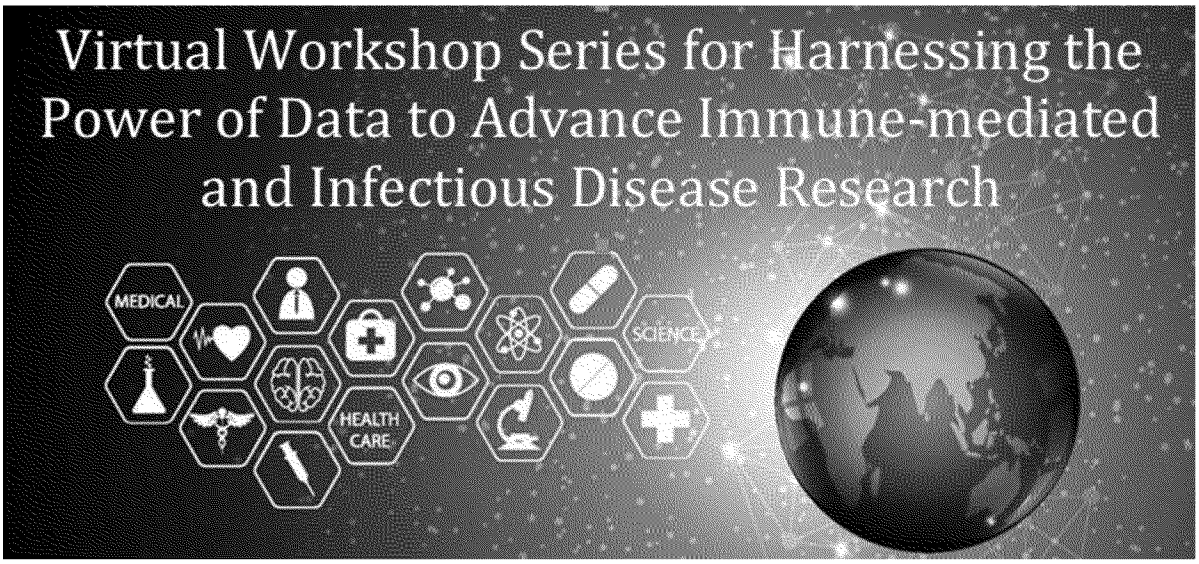
I hope you all enjoyed the presentation on Tuesday, May 4th.
Oral Cavity Infection with SARS-CoV-2: Pathology, Transmission Potential, and Symptoms

- Part 1 – Oral Cavity Infection- Blake Warner, PhD
- Part 2 – Symptoms- Paule Joseph, PhD

Thank you to our presenters and those that joined.

On Tuesday, May 11th, Dr. Pardis Sabeti will be giving a presentation on the "**Outbreak Preemption and Response in the Genomic and Information Age".**

Also….



The National Institute of Allergy and Infectious Diseases (NIAID) is excited to advance discovery and innovation in infectious diseases and immune-mediated disorders research by leveraging data and data science approaches. Towards this end, NIAID will conduct a series of ideas and innovation webinars that bring together experts and stakeholders in data science, infectious diseases, immunology, and immune-mediated disorders.

Through the webinar series, participants will have the opportunity to provide insights into the current landscape of data science research and development, as well as offer ideas that promise to shape the future of data-driven immune-mediated and infectious disease research. The webinar series will serve as a platform for collaboration, idea generation, and networking among participants and generate foundational materials that is expected to inform the prospective role of data science in advancing NIAID's mission.

THIRD EVENT : **Breaking the Silos: Opportunities and Challenges of Harnessing the Power of Data to Advance Immune-Mediated and Infectious Disease Research**

WHEN: May 14th, 2021 2-3:30 pm ET

WHERE: Virtually hosted on Zoom - register to receive meeting link

REGISTRATION : https://zoom.us/webinar/register/WN_jjHo246UQieRTKWtDdSHug
AGENDA : https://apply.hub.ki/datascience4niaid/

WHAT: Our expert panel will engage in a moderated discussion following short talks where they will define the traditional silos that may impede broad data sharing and highlight examples of where breaking those silos facilitated advancement that otherwise could not have been achieved.

WHO: Invited Speakers include Dr. Raphael Gottardo (Fred Hutchinson Cancer Research Center), Dr. Alexa McCray (Harvard Medical School), Dr. Ewan Harrison (University of Cambridge). Moderated by Dr. Stephany Duda (Vanderbilt University) and Dr. Purvesh Khatri (Stanford University).

CONTACTS: Event Organizing Committee (NIAIDODSET@niaid.nih.gov)

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Stevens, Rick L.[stevens@anl.gov]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jesse Erasmus[jerasmus@uw.edu]; Katzelnick, Leah (NIH/NIAID) [E][leah.katzelnick@nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID)

[E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Eva HARRIS[eharris@berkeley.edu]; Fausto Bustos[bustos.fausto@gmail.com]; Ricotta, Emily (NIH/NIAID) [E][emily.ricotta@nih.gov]

Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Fri 5/21/2021 2:48:48 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - May 25th

Hi Everyone,

On Tuesday, May 18th, Dr. Neal Freedman went over "**The COVID-19 SeroHub: a seroprevalence studies resource**". Thank you to our presenter and those that were able to join.

We will have two presentations on Tuesday, May 25th:

1. **SARS-CoV-2 in the Nicaraguan Household Cohort: Spectrum of illness and protection from reinfection**,

   Aubree Gordon, PhD
2. **Four epidemics of chikungunya, Zika, and COVID-19 in Nicaragua reveal bias in case-based mapping**,

   Fausto Bustos Carrillo, PhD

Hope everyone is able to join!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Freedman, Neal (NIH/NCI) [E][freedmanne@mail.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves,

Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]

Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Mon 5/17/2021 11:58:17 AM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - May 18th

Happy Monday!
On Tuesday, May 11th, Dr. Pardis Sabeti gave a wonderful presentation on the "**Outbreak Preemption and Response in the Genomic and Information Age".** Thank you to our presenter and to those that were able to join.
Tomorrow, May 18th, Dr. Neal Freedman will be going over "**The COVID-19 SeroHub: a seroprevalence studies resource**". If you or someone you know is interested in listening in, please join. ☺
Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 6/1/2021 8:00:00 AM (UTC-05:00)

End Time: Tue 6/1/2021 9:00:00 AM (UTC-05:00)

Required Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal;

Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Zendt, Mackenzie (NIH/NIAID) [E]

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Stevens, Rick L.[stevens@anl.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Weaver, Scott[sweaver@UTMB.EDU]; Sabra Klein[sklein2@JHU.EDU]; Matthew Frieman[mfrieman@som.umaryland.edu]; Ghazi Kayali[ghazi@human-link.org]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; Jennifer Hyde[jlhyde4@uw.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino,

Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]

Cc: Graham, Rachel[rlgraham@ad.unc.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Tue 6/1/2021 8:13:51 AM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi All,

As a reminder, today's meeting is CANCELLED due to the holiday weekend. We will resume next week.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Stevens, Rick L.[stevens@anl.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Weaver, Scott[sweaver@UTMB.EDU]; Sabra Klein[sklein2@JHU.EDU]; Matthew Frieman[mfrieman@som.umaryland.edu]; Ghazi Kayali[ghazi@human-link.org]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; Jennifer Hyde[jlhyde4@uw.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; 'Marta Gaglia'[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; 'Turpin, Jim (NIH/NIAID) [E]'[JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino,

Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]

Cc: Graham, Rachel[rlgraham@ad.unc.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Mon 6/7/2021 12:30:56 PM (UTC-05:00)

Subject: RE: SARS-CoV-2 Weekly Investigators Meeting - June 8th

Hi All,

This meeting has been canceled for tomorrow and will be rescheduled. A meeting calendar cancelation has been sent.

Thanks,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C]
Sent: Wednesday, June 2, 2021 11:10 AM
To: Stevens, Rick L. <stevens@anl.gov>; Patterson, Jean (NIH/NIAID) [E] <jean.patterson@nih.gov>; Nelson, Martha (NIH/NIAID) [C] <nelsonma@mail.nih.gov>; 'Coughlan, Lynda' <LCoughlan@som.umaryland.edu>; 'Miller, Benjamin' <Benjamin_Miller@URMC.Rochester.edu>; Priya Luthra <pluthra@trudeauinstitute.org>; 'sweaver@utmb.edu' <sweaver@utmb.edu>; Sabra Klein <sklein2@jhu.edu>; Matthew Frieman <mfrieman@som.umaryland.edu>; Ghazi Kayali <ghazi@human-link.org>; Pickett, Thames (NIH/NIAID) [E] <pickettte@niaid.nih.gov>; Karla Satchell <k-satchell@northwestern.edu>; 'WVanVoorhis@medicine.washington.edu' <WVanVoorhis@medicine.washington.edu>; Cammarata, Sue (OS/ASPR/IO) (CTR) <Sue.Cammarata@hhs.gov>; 'paul-mccray@uiowa.edu' <paul-mccray@uiowa.edu>; marlene.espinozamoraga@mssm.edu; 'rebecca.dutch@uky.edu' <rebecca.dutch@uky.edu>; 'Thomas Friedrich' <tfriedri@wisc.edu>; Brooke, Christopher Byron <cbrooke@illinois.edu>; 'Jennifer Hyde' <jlhyde4@uw.edu>; 'cmichelo@rzhrg-mail.org' <cmichelo@rzhrg-mail.org>; 'ckabengele@rzhrg-mail.org' <ckabengele@rzhrg-mail.org>; McKenzie, Pamela <Pamela.McKenzie@STJUDE.ORG>; cpage001@umaryland.edu; Hoffman, James <James.Hoffman@STJUDE.ORG>; Leo Poon <llmpoon@hku.hk>; 'Hou, Yixuan Jacob' <y.jacob.hou@unc.edu>; Richard Webby <richard.webby@stjude.org>; malik <malik@hku.hk>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; yguan@hku.hk; 'cthio@jhmi.edu' <cthio@jhmi.edu>; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. <apekosz@jhsph.edu>; 'Simons, Mark' <mark.simons@usuhs.edu>; Stacey Schultz-Cherry <stacey.schultz-cherry@stjude.org>; 'david_topham@urmc.rochester.edu'; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>; Baric, Ralph <rbaric@email.unc.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; daszak@ecohealthalliance.org; zhu huachen <zhuhch@hku.hk>; Aubree Gordon <gordonal@umich.edu>; 'Robert E. Schwartz' <res2025@med.cornell.edu>; Munster, Vincent (NIH/NIAID) [E] <Vincent.Munster@nih.gov>; PETERPALESE <peter.palese@mssm.edu>; Florian Krammer <florian.krammer@mssm.edu>; Esona, Mathew D. (CDC/DDID/NCIRD/DVD) <mdi4@CDC.GOV>; Ben Cowling <bcowling@hku.hk>; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD) <ydk5@cdc.gov>; jwramme@emory.edu; Aneesh Mehta <aneesh.mehta@emory.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>; MASATO HATTA <masato.hatta@wisc.edu>; Hendricks, Tanya J <thendr19@uthsc.edu>; pduprex@cvr.pitt.edu; McElroy, Anita Katherine <MCELROYA@pitt.edu>; Prabhudas,

Mercy (NIH/NIAID) [E] <mprabhudas@niaid.nih.gov>; Marta Gaglia <Marta.Gaglia@tufts.edu>; Williams, Mark (NIH/NIAID) [E] <mark.williams4@nih.gov>; Woodson, Sara (NIH/NIAID) [E] <sara.woodson@nih.gov>; Florence, Clint (NIH/NIAID) [E] <clint.florence@nih.gov>; Wolfraim, Larry (NIH/NIAID) [E] <larry.wolfraim@nih.gov>; Hsu, Christopher (CDC/DDID/NCIRD/DVD) <ydh2@cdc.gov>; Kirking, Hannah L. (CDC/DDPHSIS/CGH/DGHT) <hrj7@cdc.gov>; Plumb, Ian (CDC/DDID/NCIRD/DVD) <ydk9@cdc.gov>; Zendt, Mackenzie (NIH/NIAID) [E] <mackenzie.zendt@nih.gov>; Logue, James <James.Logue@som.umaryland.edu>; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E] <jennifer.gordon2@nih.gov>; Hauguel, Teresa (NIH/NIAID) [E] <teresa.hauguel@nih.gov>; Gabi Neumann <gabriele.neumann@wisc.edu>; Kanta Subbarao <kanta.subbarao@influenzacentre.org>; Mathur, Punam (NIH/NIAID) [E] <mathurpu@niaid.nih.gov>; jmclellan@austin.utexas.edu; Mark Denison <mark.denison@vumc.org>; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E] <johnsonreed@niaid.nih.gov>; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E] <kstemple@niaid.nih.gov>; Sutton, Troy Clavell <tcs38@psu.edu>; Simon, Viviana <viviana.simon@mssm.edu>; Van bakel, Harm <harm.vanbakel@mssm.edu>; Deckhut, Alison (NIH/NIAID) [E] <augustine@niaid.nih.gov>; Donald K. Milton <dmilton@umd.edu>; Hensley, Scott <hensley@pennmedicine.upenn.edu>; Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Fry, Alicia (CDC/DDID/NCIRD/ID) <agf1@CDC.GOV>; Pallansch, Mark A. (CDC/DDID/NCIRD/OD) <map1@CDC.GOV>; Hall, Aron (CDC/DDID/NCIRD/DVD) <esg3@CDC.GOV>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Andy Pekosz <apekosz1@jhu.edu>; Topham, David <David_Topham@URMC.Rochester.edu>; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED) <bhx1@cdc.gov>; zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E] <brooke.bozick@nih.gov>; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Wentworth, David E. (CDC/DDID/NCIRD/ID) <gll9@cdc.gov>; Charles Russell <charles.russell@stjude.org>; Cooper, Michael (NIH/NIAID) [E] <michael.cooper3@nih.gov>; Weiss, Susan <weisssr@pennmedicine.upenn.edu>; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina <weina.sun@mssm.edu>; Roberts, Chris (NIH/NIAID) [E] <paul.roberts@nih.gov>; S. Mark Tompkins <smt@uga.edu>; Uccellini, Melissa <melissa.uccellini@mssm.edu>; Paul Thomas <paul.thomas@stjude.org>; B.H.G. Rockx <b.rockx@erasmusmc.nl>; Michael Chan <mchan@hku.hk>; S. Herfst <s.herfst@erasmusmc.nl>; Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>; Park, Eun-Chung (NIH/NIAID) [E] <EPark@niaid.nih.gov>; Crozier, Ian (NIH) [C] <ian.crozier@nih.gov>; Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; Andrea Sant <andrea_sant@urmc.rochester.edu>; Ali Ellebedy <ellebedy@wustl.edu>; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E] <readsa@niaid.nih.gov>; Finzi, Diana (NIH/NIAID) [E] <DFINZI@niaid.nih.gov>; Turpin, Jim (NIH/NIAID) [E] <JTurpin@niaid.nih.gov>; jae jung (jaeujung@med.usc.edu) <jaeujung@med.usc.edu>; SAMANTHA LOEBER <sloeber@wisc.edu>; Cherry, Sara <cherrys@pennmedicine.upenn.edu>; akuki@trudeauinstitute.org; Hui-Ling Yen <hyen@hku.hk>; Andrew Mesecar <amesecar@purdue.edu>; Jonsson, Colleen Beth <cjonsson@uthsc.edu>; Strome, Scott Eric <sstrome@uthsc.edu>; Fitzpatrick, Elizabeth A <efitzpat@uthsc.edu>; Ryan A. Langlois <langlois@umn.edu>; Seema Lakdawala <seemal@pitt.edu>; amesecar@gmail.com; Runstadler, Jonathan A. <Jonathan.Runstadler@tufts.edu>; Pruijssers, Ardina <ardina.pruijssers@vumc.org>; David.Renner@pennmedicine.upenn.edu; Fremont, Daved <fremont@wustl.edu>; 'Isabelle.Phan@seattlechildrens.org' <Isabelle.Phan@seattlechildrens.org>; Piantadosi, Anne L. <anne.piantadosi@emory.edu>; Richt, Juergen <jricht@vet.k-state.edu>; Khurana, Surender (FDA/CBER) <Surender.Khurana@fda.hhs.gov>; 'Neu, Donna' <Donna_Neu@URMC.Rochester.edu>; Golding, Hana (FDA/CBER) <Hana.Golding@fda.hhs.gov>; Gaur, Aditya <Aditya.Gaur@STJUDE.ORG>; 'hlarman1@jhmi.edu' <hlarman1@jhmi.edu>; Mary Rode <mrode4@jhmi.edu>; 'lsauer2@jhmi.edu' <lsauer2@jhmi.edu>; Kathryn Shaw-Saliba <kshaw15@jhu.edu>; 'Andino, Raul' <Raul.Andino@ucsf.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; Shiho Chiba <shiho.chiba@wisc.edu>; Brown, Liliana (NIH/NIAID) [E] <liliana.brown@nih.gov>; 'lhughes@scripps.edu' <lhughes@scripps.edu>; 'asu@scripps.edu' <asu@scripps.edu>; 'andersen@scripps.edu' <andersen@scripps.edu>; 'mmcgraw@scripps.edu' <mmcgraw@scripps.edu>; Shabman, Reed (NIH/NIAID) [E] <reed.shabman@nih.gov>; Chandramouliswaran, Ishwar (NIH/NIAID) [E] <ishwar.chandramouliswaran@nih.gov>; Evans, Jared D. <Jared.Evans@jhuapl.edu>; Chaves, Francisco <Francisco_Chaves@URMC.Rochester.edu>; Lambert, Kris <Kris_Lambert@URMC.Rochester.edu>; Reilly, Emma C (CVBI) <Emma_Reilly@URMC.Rochester.edu>; Fitzgerald, Theresa <Theresa_Fitzgerald@URMC.Rochester.edu>; Nguyen, Phuong <Phuong_Nguyen@URMC.Rochester.edu>; Jesse Erasmus <jerasmus@uw.edu>; 'fullerdh@uw.edu' <fullerdh@uw.edu>; Anthony, Simon J. <sja2127@cumc.columbia.edu>; Katherine Fenstermacher <kfenste1@jhu.edu>; Zhou, Bin (CDC/DDID/NCIRD/ID) <nmb7@cdc.gov>; 'alr2105@cumc.columbia.edu' <alr2105@cumc.columbia.edu>; Dillen, Carly <CDillen@som.umaryland.edu>; 'Koelle, Katharina V.' <katia.koelle@emory.edu>; Holbrook, Michael (NIH/NIAID) [C] <michael.holbrook@nih.gov>; Blocker, Wendy (NIH/NIAID) [E] <wendy.blocker@nih.gov>; 'Suthar, Mehul' <mehul.s.suthar@emory.edu>; 'Andrea Cox' <acox@jhmi.edu>; Cong, Yu (NIH/NIAID) [C] <yu.cong@nih.gov>; Jain, Sanjay <sjain5@jhmi.edu>; Alvaro Ordonez <aordone2@jhmi.edu>; Joseph Mankowski <jmankows@jhmi.edu>; Hildebrand, Kristen <Kristen.Hildebrand@STJUDE.ORG>; Breen, Joseph (NIH/NIAID) [E] <JBREEN@niaid.nih.gov>; Newman, Lori (NIH/NIAID) [E] <lori.newman@nih.gov>; Williams, Carolyn (NIH/NIAID) [E] <CWilliams@niaid.nih.gov>; 'Jim Heath' <jim.heath@isbscience.org>; Marshall Strome <stromemhnsg@gmail.com>; RDBViral <NIAIDRDBViral@mail.nih.gov>; Marazzi, Ivan <ivan.marazzi@mssm.edu>; Trovao, Nidia (NIH/FIC) [F] <nidia.trovao@nih.gov>; Ray, Russell Scott <Russell.Ray@bcm.edu>; 'tenOever, Benjamin' <benjamin.tenoever@mssm.edu>; 'andrzejj@anl.gov' <andrzejj@anl.gov>; 'Michael J Gale' <mgale@uw.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Sheldon Shih-han Tai <stai1@umd.edu>; Jennifer

Rebecca German <jgerman@umd.edu>; Paul Jacob Bueno de Mesquita <jbueno@umd.edu>; Oluwasanmi Oladapo Adenaiye <adenaiye@umd.edu>; Lafont, Bernard (NIH/NIAID) [E] <BLAFONT@niaid.nih.gov>; 'Martinez, David Rafael' <davidmar@email.unc.edu>; Rutvisuttinunt, Wiriya (NIH/NIAID) [E] <wiriya.rutvisuttinunt@nih.gov>; Saydah, Sharon (CDC/DDID/NCIRD/DVD) <zle0@CDC.GOV>; 'Olson, Daniel' <Daniel.Olson@childrenscolorado.org>; Sarah Cobey <cobey@uchicago.edu>; Qifang Bi <qbi@uchicago.edu>; 'Emma Hodcroft' <emmahodcroft@gmail.com>; Becker, Patrice (NIH/NIAID) [E] <patrice.becker@nih.gov>; 'Denis Nash' <Denis.Nash@sph.cuny.edu>; 'Dutta, Jayeeta' <jayeeta.dutta@mssm.edu>; 'Ramilo, Octavio' <Octavio.Ramilo@nationwidechildrens.org>; 'Keri Althoff' <kalthoff@jhu.edu>; Jennifer Kishimori <Jennifer.M.Kishimori.mil@mail.mil>; Biggins, Julia E CTR (USA) <julia.e.biggins.ctr@mail.mil>; Katarina Braun <kmbraun2@wisc.edu>; Gage Moreno <gkmoreno@wisc.edu>; DAVID H O'CONNOR <dhoconno@wisc.edu>; SHELBY L O'CONNOR <slfeinberg@wisc.edu>; Bruno, Robert (OS/ASPR/BARDA) (CTR) <Robert.Bruno@hhs.gov>; Eisnor, Derek (OS/ASPR/BARDA) <Derek.Eisnor@hhs.gov>; Walker, Robert (OS/ASPR/BARDA) <Robert.Walker@hhs.gov>; 'ns2@medicine.wisc.edu' <ns2@medicine.wisc.edu>; 'jon.temte@fammed.wisc.edu' <jon.temte@fammed.wisc.edu>; Katie Mulka <kmulka1@jhmi.edu>; Richard G Wunderink <r-wunderink@northwestern.edu>; Alexander Misharin <a-misharin@northwestern.edu>; Rogan Grant <rogangrant2022@u.northwestern.edu>; 'james.mancuso@usuhs.edu' <james.mancuso@usuhs.edu>; Ghedin, Elodie (NIH/NIAID) [E] <elodie.ghedin@nih.gov>; Roder, Allison (NIH/NIAID) [E] <allison.roder@nih.gov>; 'amushegian@gmail.com' <amushegian@gmail.com>; Mcgugan, Glen (NIH/NIAID) [E] <gmcgugan@niaid.nih.gov>; 'abdullah.syed@gladstone.ucsf.edu' <abdullah.syed@gladstone.ucsf.edu>; 'ksplante@UTMB.EDU' <ksplante@UTMB.EDU>; McDonald, David (NIH/NIAID) [E] <david.mcdonald@nih.gov>; 'marcjohnson@missouri.edu' <marcjohnson@missouri.edu>; 'mshukla@anl.gov' <mshukla@anl.gov>; 'rscheuermann@jcvi.org' <rscheuermann@jcvi.org>; Stevens, Laura J <laura.j.stevens@vumc.org>; 'samantha.l.grimes@vanderbilt.edu' <samantha.l.grimes@vanderbilt.edu>; 'jordan.m.anderson-daniels.1@vumc.org' <jordan.m.anderson-daniels.1@vumc.org>; 'jennifer.gribble@vanderbilt.edu' <jennifer.gribble@vanderbilt.edu>; 'sdhakal3@jhmi.edu' <sdhakal3@jhmi.edu>; Mclendon, Molly (OS/ASPR/BARDA) <Molly.Mclendon@hhs.gov>; 'Kevin.Messacar@childrenscolorado.org' <Kevin.Messacar@childrenscolorado.org>; 'pcreish1@jhmi.edu' <pcreish1@jhmi.edu>; 'mmoonga@rzhrg-mail.org' <mmoonga@rzhrg-mail.org>; 'cchanda@rzhrg-mail.org' <cchanda@rzhrg-mail.org>; 'smwangelwa@rzhrg-mail.org' <smwangelwa@rzhrg-mail.org>; 'chimukumbwa@rzhrg-mail.org' <chimukumbwa@rzhrg-mail.org>; 'kmumba@rzhrg-mail.org' <kmumba@rzhrg-mail.org>; Lee, John (OS/ASPR/BARDA) <John.Lee@hhs.gov>; Feldstein, Leora (CDC/DDID/NCIRD/DVD) <nqw5@cdc.gov>; Malloy, Allison <allison.malloy@usuhs.edu>; Otieno, James (NIH/FIC) [G] <james.otieno@nih.gov>; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US) <kimberly.a.bishop-lilly.civ@mail.mil>; 'alrouth@utmb.edu' <alrouth@utmb.edu>; Jones, Jefferson (CDC/DDID/NCIRD/DVD) <ioe8@cdc.gov>; Bratt, Debbie (NIH/NIAID) [C] <debbie.bratt@nih.gov>; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT) <VKA5@cdc.gov>; Nanishi, Etsuro <Etsuro.Nanishi@childrens.harvard.edu>; Borriello, Francesco <Francesco.Borriello@childrens.harvard.edu>; Dowling, David <David.Dowling@childrens.harvard.edu>; 'Huyen.cao@hhs.gov' <Huyen.cao@hhs.gov>

Cc: Graham, Rachel <rlgraham@ad.unc.edu>; cobeywork@gmail.com; Asturias, Edwin <Edwin.Asturias@childrenscolorado.org>; Martin Blaser <martin.blaser@cabm.rutgers.edu>; Krafft, Amy (NIH/NIAID) [E] <kraffta@niaid.nih.gov>; Duprex, Paul <pduprex@pitt.edu>; Ferguson, Stacy (NIH/NIAID) [E] <fergusonst@niaid.nih.gov>; Davis, Mindy (NIH/NIAID) [E] <mindy.davis@nih.gov>; Goldstein, Jason (CDC/DDID/NCEZID/DSR) <fex0@CDC.GOV>; Lockmuller, Jane (NIH/NIAID) [E] <lockj@niaid.nih.gov>; Timothy Burgess <timothy.burgess@usuhs.edu>; Gergen, Peter (NIH/NIAID) [E] <PGergen@niaid.nih.gov>; ZHANG, JIAJIA <JZHANG@mailbox.sc.edu>; Thompson, Mark (CDC/DDID/NCIRD/ID) <isq8@cdc.gov>; Staat, Mary Allen <Mary.Staat@cchmc.org>; Robien, Mark (NIH/NIAID) [E] <mark.robien@nih.gov>; Monica McNeal <monica.mcneal@cchmc.org>; Siriruk Changrob <siriruk@uchicago.edu>; Fulkerson, Patricia (NIH/NIAID) [E] <patricia.fulkerson@nih.gov>; Halasa, Natasha <natasha.halasa@vumc.org>; Nayak, Seema (NIH/NIAID) [E] <seema.nayak@nih.gov>; Baqar, Shahida (NIH/NIAID [E] <shahida.baqar@nih.gov>; 'Rogier van Doorn' <rvandoorn@oucru.org>; Lee, Marina (NIH/NIAID) [E] <marina.lee@nih.gov>; Whelan, Sean <spjwhelan@wustl.edu>; Haslam, David <David.Haslam@cchmc.org>; Gordon, Robin (Robin Gordon) <Robin.Gordon@cchmc.org>; Lerner, Andrea (NIH/NIAID) [E] <andrea.lerner@nih.gov>; Alaa Abdel Latif <aabdellatif@scripps.edu>; kga1978@gmail.com; Warner, Blake (NIH/NIDCR) [E] <blake.warner@nih.gov>; Joseph, Paule (NIH/NIAAA) [E] <paule.joseph@nih.gov>; Kim, Sonnie (NIH/NIAID) [E] <Sonnie.Kim@nih.gov>; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E] <dyallj@niaid.nih.gov>

Subject: SARS-CoV-2 Weekly Investigators Meeting - June 8th

Hi All!

I hope your week is going well.

On Tuesday, June 8th, Dr. Sara Cherry will be presenting on "**SARS-CoV-2 and antiviral therapeutics**".

Looking forward to seeing all your names on Zoom next week!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= 552.136

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 6/8/2021 8:00:00 AM (UTC-05:00)

End Time: Tue 6/8/2021 9:00:00 AM (UTC-05:00)

Required Attendees: Stevens, Rick L.; Patterson, Jean (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Coughlan, Lynda; Miller, Benjamin; Priya Luthra; Weaver, Scott; Sabra Klein; Matthew Frieman; Ghazi Kayali; Pickett, Thames (NIH/NIAID) [E]; Karla Satchell; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; cmichelo@rzhrg-mail.org; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; Simon, Viviana; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; rscheuermann@jcvi.org; Stevens, Laura J;

samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Bratt, Debbie (NIH/NIAID) [C]; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov

****CANCELING** due to time conflicts with the nidovirus meeting**

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Stevens, Rick L.[stevens@anl.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Weaver, Scott[sweaver@UTMB.EDU]; Sabra Klein[sklein2@JHU.EDU]; Matthew Frieman[mfrieman@som.umaryland.edu]; Ghazi Kayali[ghazi@human-link.org]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; Jennifer Hyde[jlhyde4@uw.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino,

Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]

Cc: Graham, Rachel[rlgraham@ad.unc.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Wed 6/2/2021 10:09:30 AM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - June 8th

Hi All!

I hope your week is going well.

On Tuesday, June 8th, Dr. Sara Cherry will be presenting on "**SARS-CoV-2 and antiviral therapeutics**".

Looking forward to seeing all your names on Zoom next week!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Sabra Klein[sklein2@JHU.EDU]; Logue, James[James.Logue@som.umaryland.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Hoffman, James[James.Hoffman@STJUDE.ORG]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Ghazi Kayali[ghazi@human-link.org]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Matthew Frieman[mfrieman@som.umaryland.edu]; amushegian@gmail.com[amushegian@gmail.com]; Simon, Viviana[viviana.simon@MSSM.EDU]; fullerdh@uw.edu[fullerdh@uw.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana

(NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Priya Luthra[pluthra@trudeauinstitute.org]; Malloy, Allison[allison.malloy@usuhs.edu]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; Stevens, Rick L.[stevens@anl.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; Stevens, Laura J[laura.j.stevens@vumc.org]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]

Cc: Jacques Banchereau[Jacques.Banchereau@jax.org]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Alaa Abdel Latif[aabdellatif@scripps.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Duprex, Paul[pduprex@pitt.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Thur 6/10/2021 2:35:46 PM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - June 15th

Hi Everyone!

Dr. Florian Krammer will help get us back to our regularly scheduled presentation series by presenting on "**Antibody responses to SARS-CoV-2 vaccination**". Looking forward to virtually seeing everyone on Tuesday, June 15th!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 6/1/2021 8:00:00 AM (UTC-05:00)

End Time: Tue 6/1/2021 9:00:00 AM (UTC-05:00)

Required Attendees: Aubree Gordon; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu;

Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David

CANCELING to give you all time to catch up from the long weekend

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: Jennifer Rebecca German; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Patterson, Jean (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Coughlan, Lynda; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Bratt, Debbie (NIH/NIAID) [C]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Warner, Blake

(NIH/NIDCR) [E]; Joseph, Paule (NIH/NIAAA) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif; kga1978@gmail.com; Kim, Sonnie (NIH/NIAID) [E]; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E]

Sent: Tue 5/25/2021 2:21:02 PM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

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Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: McDonald, David (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Sabra Klein; Logue, James; Isabelle.Phan@seattlechildrens.org; Van bakel, Harm; Eisnor, Derek (OS/ASPR/BARDA); Jennifer Hyde; Thomas Friedrich; Pickett, Thames (NIH/NIAID) [E]; Breen, Joseph (NIH/NIAID) [E]; McKenzie, Pamela; Hsu, Christopher (CDC/DDID/NCIRD/DVD); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; Holbrook, Michael (NIH/NIAID) [C]; Cammarata, Sue (OS/ASPR/IO) (CTR); Hoffman, James; WVanVoorhis@medicine.washington.edu; Ghazi Kayali; tenOever, Benjamin; rebecca.dutch@uky.edu; Matthew Frieman; amushegian@gmail.com; Simon, Viviana; fullerdh@uw.edu; cpage001@umaryland.edu; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; mshukla@anl.gov; rscheuermann@jcvi.org; samantha.l.grimes@vanderbilt.edu; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Bratt, Debbie (NIH/NIAID) [C]; Patterson, Jean (NIH/NIAID) [E]; marcjohnson@missouri.edu; Stevens, Rick L.; Stevens, Laura J; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Jacques Banchereau; Goldstein, Jason (CDC/DDID/NCEZID/DSR); Alaa Abdel Latif;

cobeywork@gmail.com; Duprex, Paul; Gergen, Peter (NIH/NIAID) [E]; Martin Blaser; Lerner, Andrea (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); kga1978@gmail.com; Warner, Blake (NIH/NIDCR) [E]; Joseph, Paule (NIH/NIAAA) [E]; Kim, Sonnie (NIH/NIAID) [E]; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E]

Sent: Tue 5/25/2021 2:21:04 PM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Location: https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09
Importance: Normal
Subject: SARS-CoV-2 Variant Testing pipeline
Start Time: Fri 3/12/2021 7:30:00 AM (UTC-06:00)
End Time: Fri 3/12/2021 8:30:00 AM (UTC-06:00)
Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; Routh, Andrew L.; dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]
Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott

Research Update Template.xlsx

From: marciela.degrace@nih.gov
When: 7:30 AM - 8:30 AM March 12, 2021
Subject: SARS-CoV-2 Variant Testing pipeline
Location: https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

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From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Thursday, February 25, 2021 10:05:10 PM (UTC) Coordinated Universal Time
To: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]
Cc: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott
Subject: SARS-CoV-2 Variant Testing pipeline

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		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Monthly Call
Start Time:	Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen

Importance:	Normal
Start Time:	Fri 4/24/2020 2:30:00 PM (UTC)
End Time:	Fri 4/24/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

From: Young, Jennifer (AE)[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=939434B3DC894CAAB01C10E93943D292-YOUNG, JENN]

Attendees: "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.

Location: https://zoom.us/j/9095677699?pwd=552.136

Importance: Normal

Subject: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2

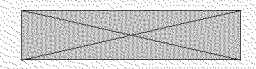
Start Time: Tue 9/1/2020 1:00:00 PM (UTC-05:00)

End Time: Tue 9/1/2020 2:00:00 PM (UTC-05:00)

Required Attendees: Young, Jennifer (AE); Toni Baric; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.

Please see the below teleconference information for tomorrow s meeting at 1pm 2pm (CDT)/ 2pm 3pm (EDT).

Required Attendees: Young, Jennifer (AE); Toni Baric; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.



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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Monthly Call
Start Time:	Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Monthly Call
Start Time:	Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen

Importance: Normal

Start Time: Fri 6/19/2020 2:30:00 PM (UTC)

End Time: Fri 6/19/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen; Bouvier, Nicole

Dear A38 Task Order Team,

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

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End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
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Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
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Best,
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

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Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

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Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

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Optional Attendees:	Richard Bowen; Bouvier, Nicole

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Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
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Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 3/26/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 3/26/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/26/2021 Agenda:

- General Updates (Chelsea)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (*3/26: UNC*; 4/9: UTMB; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/23/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 4/23/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/23/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~*3/26: UNC; 4/9: UTMB*~~; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: 425732

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 4/9/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 4/9/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Viner, Rebekah L.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 5, 2021 1:17 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Cc: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Subject: A38 Task Order Bi-weekly Call
When: Friday, April 9, 2021 10:30 AM-12:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToMeeting

WARNING: This email originated from outside of UTMB's email system. Do not click links or open attachments unless you recognize the sender and know the content is safe.

4/9/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (~~3/26: UNC~~; ~~*4/9: UTMB*~~; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

Join ZoomGov Meeting

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Meeting ID: 161 887 1310
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Viner, Rebekah L.; Beasley, David; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Taylor, Ebony (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 6/18/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 6/18/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Viner, Rebekah L.; Beasley, David; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Taylor, Ebony (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/18/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~5/21: UNC~~; ~~6/4: UTMB~~; 6/18: USU; 7/30: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 1/29/2021 9:30:00 AM (UTC-06:00)

End Time: Fri 1/29/2021 11:00:00 AM (UTC-06:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

***Note*:** for this Friday, January 29th, please include within your site's presentations whether your site is able to perform aerosol delivery of Tx compounds (and if so, what methods you use). A slide or two max should be sufficient.

1/29/2021 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (*1/29: UNC*; 2/12: UTMB; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 6/4/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 6/4/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/4/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~5/21: UNC~~; 6/4: UTMB; 6/18: USU; 7/2: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 2/12/2021 9:30:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 11:00:00 AM (UTC-06:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

***Note*:** for this Friday, February 12th, please be prepared for a discussion on testing of dexamethasone (that your site has already conducted, or that is in your queue). Please refer to the email that I sent on Thursday, 2/4/2020.

2/12/2021 Agenda:

- General Updates (Erik)
- First 15minutes – discussion regarding testing of dexamethasone
- *Brief* 10-15 minute updates for all A38 contractor sites
- Rotating check-in with individual sites (~~1/29: UNC~~; *2/12: UTMB*; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

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Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 2/26/2021 9:30:00 AM (UTC-06:00)

End Time: Fri 2/26/2021 11:00:00 AM (UTC-06:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

2/26/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites
- Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~; *2/26: USU*; 3/12: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 3/12/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 3/12/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/12/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites. *Note*: please include about a 5 minute high level summary on your thoughts/experiences on positive controls (for Tx studies) for the model(s) that you are developing. If you have any data you can summarize, that would be great. It is okay if you don't have extensive experience with this.**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~;~~2/26: USU~~; *3/12: CSU*)**

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/9/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 4/9/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/9/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~3/26: UNC~~; *4/9: UTMB*; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

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Erik & Chelsea

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Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 5/7/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 5/7/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/7/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~*3/26: UNC; 4/9: UTMB*~~; ~~*4/23: USU*~~; 5/7: CSU)

Dear A38 Task Order Team,

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Erik & Chelsea

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Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 5/21/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 5/21/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/21/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (5/21: UNC; 6/4: UTMB; 6/18: USU; 7/2: CSU)

Dear A38 Task Order Team,

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Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Macoubray, Aaron[amacoubray@rti.org]

Attendees: Macoubray, Aaron; kga1978@gmail.com; rfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; rwcross@UTMB.EDU; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Dyall, Julie (NIH/NIAID) [E]; Florese, Ruth (NIH/NIAID) [E]

Location: https://rtiorg.zoom.us/j/98355183025?pwd= **552.136**

Importance: Normal

Subject: CREID EBOV Discussion

Start Time: Fri 4/23/2021 2:00:00 PM (UTC-05:00)

End Time: Fri 4/23/2021 3:00:00 PM (UTC-05:00)

Required Attendees: Macoubray, Aaronrfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Megan Averill; Vasilakis, Nikolaos

Optional Attendees: kga1978@gmail.com; Dyall, Julie (NIH/NIAID) [E]; Florese, Ruth (NIH/NIAID) [E]

Greetings,

This Friday, April 23rd 3-4 pm EDT, we will hold a focused meeting to discuss the EBOV outbreaks in the DRC and Guinea to support Dr. Robert Garry's (and others) outbreak research response to these outbreaks.

Below are two topics that Dr. Garry would like discussed with this group, although we expect other topics to arise during a discussion.

Agenda:

1. Relevance of and most pressing research questions of purported 5 yr recrudescence of EBOV
2. Options/recommendations for enhancing infrastructure including biorepository and inventory system – specifically cold chain power supply. Also, recommendations for inventory software and SOPs

If you are interested in joining this conversation, please reach out to Claire Quiner or Aaron Macoubray and we will forward the invite.

Best,

Claire

Required Attendees: Macoubray, Aaronrfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Megan Averill; Vasilakis, Nikolaos

Hi there,

Aaron Macoubray is inviting you to a scheduled Zoom meeting.

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213.244.140.110 (Germany)

103.122.166.55 (Australia Sydney)
103.122.167.55 (Australia Melbourne)
209.9.211.110 (Hong Kong SAR)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada Toronto)
65.39.152.160 (Canada Vancouver)
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Passcode: **552.136**

Skype for Business (Lync)

https://rtiorg.zoom.us/skype/98355183025

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance:	Normal
Start Time:	Fri 9/25/2020 2:30:00 PM (UTC)
End Time:	Fri 9/25/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**

Importance:	Normal
Start Time:	Fri 10/9/2020 2:30:00 PM (UTC)
End Time:	Fri 10/9/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Start Time:	Fri 10/23/2020 2:30:00 PM (UTC)
End Time:	Fri 10/23/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

Join ZoomGov Meeting
https://www.zoomgov.com/j/1618871310?pwd= **552.136**

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Password: **552.136**
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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 11/6/2020 3:30:00 PM (UTC)
End Time:	Fri 11/6/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 11/20/2020 3:30:00 PM (UTC)
End Time:	Fri 11/20/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Hi all,
Just to let you all know in advance, we are expecting NIAID leadership to be joining this call on Friday. Please be prepared to present all the work you have completed thus far for model development and any MCM studies (if applicable). Please also be prepared to mention your capacity for MCM studies starting in January 2021.

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Macoubray, Aaron[amacoubray@rti.org]

Attendees: Macoubray, Aaron; kga1978@gmail.com; rfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; rwcross@UTMB.EDU; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Dyall, Julie (NIH/NIAID) [E]; Florese, Ruth (NIH/NIAID) [E]

Location: https://rtiorg.zoom.us/j/98355183025?pwd= **552.136**

Importance: Normal

Subject: CREID EBOV Discussion

Start Time: Fri 4/23/2021 2:00:00 PM (UTC-05:00)

End Time: Fri 4/23/2021 3:00:00 PM (UTC-05:00)

Required Attendees: Macoubray, Aaronrfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Megan Averill; Vasilakis, Nikolaos

Optional Attendees: kga1978@gmail.com; Dyall, Julie (NIH/NIAID) [E]; Florese, Ruth (NIH/NIAID) [E]

Hi all,

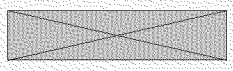
I've added others from your Research Centers to this invite. Please feel free to forward this invitation to the most appropriate representative on the topic from your RC, and to other CREID Network members as you see fit.

Thank you very much,

Aaron

Required Attendees: Macoubray, Aaronrfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov; Weldon, Caroline; li@ecohealthalliance.org; firth@ecohealthalliance.org; linfa.wang@duke-nus.edu.sg; eric.laing@usuhs.edu; rbaric@email.unc.edu; christopher.broder@usuhs.edu; chmura@ecohealthalliance.org; hagan@ecohealthalliance.org; peshi@UTMB.EDU; sumclell@UTMB.EDU; SLPAESSL@utmb.edu; Megan Averill; Vasilakis, Nikolaos

Optional Attendees: kga1978@gmail.com; Dyall, Julie (NIH/NIAID) [E]; Florese, Ruth (NIH/NIAID) [E]



Hi there,

Aaron Macoubray is inviting you to a scheduled Zoom meeting.

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213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia Sydney)
103.122.167.55 (Australia Melbourne)
209.9.211.110 (Hong Kong SAR)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada Toronto)
65.39.152.160 (Canada Vancouver)
207.226.132.110 (Japan Tokyo)
149.137.24.110 (Japan Osaka)

Meeting ID: 983 5518 3025

Passcode:

SIP: 98355183025@zoomcrc.com

Passcode: **552.136**

Skype for Business (Lync)

https://rtiorg.zoom.us/skype/98355183025

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal
Subject: FW: A38 Task Order Monthly Call
Start Time: Fri 5/22/2020 2:30:00 PM (UTC)
End Time: Fri 5/22/2020 4:00:00 PM (UTC)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Massey, Christopher; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees: Richard Bowen

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Cc: Richard Bowen
Subject: A38 Task Order Monthly Call
When: Friday, May 22, 2020 10:30 AM-12:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToMeeting

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Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 7/17/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 7/17/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 8/14/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 8/14/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

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Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 9/25/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 9/25/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310

Password: 552.136

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Importance: Normal

Subject: Canceled: A38 Task Order Bi-weekly Call

Start Time: Fri 1/1/2021 10:30:00 AM (UTC-05:00)

End Time: Fri 1/1/2021 12:00:00 PM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Canceling our meeting on 1/1/2021 due to the holiday

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 10/9/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 10/9/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310

Password: 552.136

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees: Massey, Christopher
Location: GoToMeeting
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Massey, Christopher

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal
Subject: FW: A38 Task Order Monthly Call
Start Time: Fri 5/22/2020 2:30:00 PM (UTC)
End Time: Fri 5/22/2020 4:00:00 PM (UTC)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Massey, Christopher; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees: Richard Bowen

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Cc: Richard Bowen
Subject: A38 Task Order Monthly Call
When: Friday, May 22, 2020 10:30 AM-12:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToMeeting

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 7/17/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 7/17/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 8/14/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 8/14/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Dear A38 Task Order Team,

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Best,
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal
Subject: FW: A38 Task Order Monthly Call
Start Time: Fri 5/22/2020 2:30:00 PM (UTC)
End Time: Fri 5/22/2020 4:00:00 PM (UTC)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Massey, Christopher; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees: Richard Bowen

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Cc: Richard Bowen
Subject: A38 Task Order Monthly Call
When: Friday, May 22, 2020 10:30 AM-12:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToMeeting

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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161.199.136.10 (US East)
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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 7/17/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 7/17/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
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Start Time: Fri 8/14/2020 9:30:00 AM (UTC-05:00)
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Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 9/25/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 9/25/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310

Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: GoToMeeting Invitation - A38 Task Order Kickoff Meeting
Start Time: Fri 3/27/2020 12:00:00 PM (UTC-05:00)
End Time: Fri 3/27/2020 2:00:00 PM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C

Hello gents,

Please see below for details of the A38 kickoff teleconference on Friday afternoon. Please plan on joining for as much of the meeting as you are able to. I think we will all be connecting from remote locations so I will not reserve a conference room.

David B.

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Wednesday, March 25, 2020 2:18 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C
Subject: GoToMeeting Invitation - A38 Task Order Kickoff Meeting
When: Friday, March 27, 2020 1:00 PM-3:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToMeeting

WARNING: This email originated from outside of UTMB's email system. Do not click links or open attachments unless you recognize the sender and know the content is safe.

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the A38 kickoff meeting. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be adding an agenda soon, so please stay tuned. Looking forward to virtually meeting everyone soon!

Best,
Erik & Chelsea
Fri, Mar 27, 2020 1:00 PM - 3:00 PM (EDT)

Please join my meeting from your computer, tablet or smartphone.
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Access Code: 464-670-373

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
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Importance:	Normal
Start Time:	Fri 4/24/2020 2:30:00 PM (UTC)
End Time:	Fri 4/24/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

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Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
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Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
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Chelsea
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Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**

Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance:	Normal
Start Time:	Fri 5/22/2020 2:30:00 PM (UTC)
End Time:	Fri 5/22/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance: Normal

Start Time: Fri 9/25/2020 2:30:00 PM (UTC)

End Time: Fri 9/25/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 10/9/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 10/9/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 10/23/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 10/23/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 11/6/2020 9:30:00 AM (UTC-06:00)
End Time:	Fri 11/6/2020 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 11/20/2020 9:30:00 AM (UTC-06:00)
End Time:	Fri 11/20/2020 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 1/29/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 1/29/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 1/29/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 1/29/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 2/12/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 2/12/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 2/26/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 2/26/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 3/12/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 3/12/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 4/9/2021 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/9/2021 11:00:00 AM (UTC-05:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 4/23/2021 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/23/2021 11:00:00 AM (UTC-05:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

To: Beasley, David W.[dwbeasle@UTMB.EDU]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]
Cc: Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Fri 4/24/2020 10:30:43 AM (UTC-05:00)
Subject: A38 Task Order Monthly Call
A38 Task Order Update_Template.docx

Hi All,

Thanks again for joining the A38 call this morning. As mentioned during the call, please email your site's update to Erik Stemmy (erik.stemmy@nih.gov), me (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov) by **COB, Tuesday 4/28**. Please use the attached template, and as mentioned, for those of you further along in the model development process, please include a one pager/descriptor of the model as discussed.

Lastly, for those that are having issues with obtaining PPE, please reach out to Charles Jackson (Charles.Jackson@nih.gov) and Miranda Adams (miranda.adams@nih.gov).

Hope you all have a lovely weekend,
Chelsea

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
5601 Fishers Lane, Room ***8A19***
Bethesda, MD 20892-9826
[FedEx, UPS, DHL Address is Rockville, MD 20852]
Phone: (240) 627-3741
Cell: (240) 478-8653

Click to link to A Universal Influenza Vaccine: The Strategic Plan for the National Institute of Allergy and Infectious Diseases

A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status (including any new data)
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Study capacity
- Any resources needed? Any hurdles/challenges?

Also, as model development nears completion – please send us a one pager/description of the model including animal background (e.g. mouse background & any information on promoters, etc., route of inoculum & dose, days post inoculation for determining viral loads & histopathology, etc...)

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

To: Beasley, David W.[dwbeasle@UTMB.EDU]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
Cc: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Wed 5/6/2020 8:43:50 AM (UTC-05:00)
Subject: A38 Task Order Bi-weekly Update
A38 Task Order Update_Template.docx

Hi All,

Hope you are all doing well! As mentioned during our last call, please email your site's bi-weekly update to Erik Stemmy (erik.stemmy@nih.gov), me (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov) by **COB, Friday 5/8**. Please use the attached template, and as mentioned, for those of you further along in the model development process, please include a one pager/descriptor of the model as discussed. If you have any updates to your one pager/descriptor, please feel free to send us an update.

Lastly, if any of you are still having issues with obtaining PPE, please reach out to Charles Jackson (Charles.Jackson@nih.gov) and Miranda Adams (miranda.adams@nih.gov).

Hope you all have a lovely week,
Chelsea

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
5601 Fishers Lane, Room ***8A19***
Bethesda, MD 20892-9826
[FedEx, UPS, DHL Address is Rockville, MD 20852]
Phone: (240) 627-3741
Cell: (240) 478-8653

A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status (including any new data)
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Study capacity (how many MCM studies would you be able to conduct at a given time)
- Any resources needed? Any hurdles/challenges?

Also, as model development nears completion – please send us a one pager/description of the model including animal background (e.g. mouse background & any information on promoters, etc., route of inoculum & dose, days post inoculation for determining viral loads & histopathology, etc...)

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

To: Beasley, David W.[dwbeasle@UTMB.EDU]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
Cc: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Thur 6/4/2020 1:18:01 PM (UTC-05:00)
Subject: RE: DUE Friday, 6/5: A38 biweekly email update
A38 Task Order Update_Template.docx

Hi All,

Just a friendly reminder that this biweekly email update is due by **tomorrow COB**.

For CSU and UNC: please also indicate the following: How many MCM candidates can you test at one time (and how many animals can you run per study)? How often can you initiate a study (e.g. every two weeks?).

Thanks all!
Chelsea

From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, June 1, 2020 4:34 PM
To: Beasley, David <Dwbeasle@utmb.edu>; Liz.grinstead@colostate.edu; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Julie Harvey <Julie.harvey@colostate.edu>; Bowen, Richard <richard.bowen@colostate.edu>; Chandra Caldwell <ccaldwel@email.unc.edu>; Victoria Moore <victoria_moore@unc.edu>; Baric, Ralph <rbaric@email.unc.edu>; Christy Taylor Bray <cjtaylor@utmb.edu>; Rebekah Viner <rlviner@UTMB.EDU>; Devin Hansen <devin.hansen@usu.edu>; Jennipher Hulse <jennipher.hulse@usu.edu>; Bart Tarbet <bart.tarbet@usu.edu>; Katie Dana <katie.dana@usu.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>; Graham, Rachel <rlgraham@ad.unc.edu>; Menachery, Vineet <vimenach@UTMB.EDU>; Brett Hurst <brett.hurst@usu.edu>; LeGros, Erika <erlegros@UTMB.EDU>; Schilling, Beth A. <baschill@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>; Bouvier, Nicole <Nicole.Bouvier@mountsinai.org>; Zhongde Wang <zonda.wang@usu.edu>; Morrey, John <john.morrey@usu.edu>; Richard Bowen <rbowen@rams.colostate.edu>
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Subject: DUE Friday, 6/5: A38 biweekly email update

Hi All,
Hope you are all doing well! I wanted to send you a reminder re: our next biweekly email update for the A38 task order, which is this **Friday, June 5th**. As a reminder, please use the attached template outlining the updates on your site's SARS2 animal model(s) that are in development. Please email your site's update to Erik Stemmy (erik.stemmy@nih.gov), Chelsea Lane (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov).
Thanks, and have a great week!

Chelsea & Erik

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases

NIAID/NIH/DHHS
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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Mon 6/29/2020 5:22:20 PM (UTC-05:00)
Subject: DUE Monday, 7/6: A38 biweekly email update
A38 Task Order Update_Template.docx

Dear Colleagues,
Hope this message finds you well! I wanted to send you a reminder re: our next biweekly email update for the A38 task order. Given the holiday this upcoming weekend (and that we have all been working extremely hard), I figured we could extend the email update deadline to **COB, Monday, July 6th**. As a reminder, please use the attached template outlining the updates on your site's SARS2 animal model(s) that are in development. Please email your site's update to Erik Stemmy (erik.stemmy@nih.gov), Chelsea Lane (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov).
Thanks, and have a great week!

Chelsea & Erik & Thames

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A38 Task Order Update

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To: Beasley, David W.[dwbeasle@UTMB.EDU]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Mon 7/6/2020 9:29:37 AM (UTC-05:00)
Subject: FW: DUE Monday, 7/6: A38 biweekly email update
A38 Task Order Update_Template.docx

Hi all – I hope that you had a lovely 4th! Thanks to those of you who have already sent in your site's updates. For those that haven't responded yet, this is just a friendly reminder that A38 updates are due by COB, today. *

From: Lane, Chelsea (NIH/NIAID) [E]
Sent: Monday, June 29, 2020 6:22 PM
To: Beasley, David <Dwbeasle@utmb.edu>; Liz.grinstead@colostate.edu; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Julie Harvey <Julie.harvey@colostate.edu>; Bowen, Richard <richard.bowen@colostate.edu>; Chandra Caldwell <ccaldwel@email.unc.edu>; Victoria Moore <victoria_moore@unc.edu>; Baric, Ralph <rbaric@email.unc.edu>; Christy Taylor Bray <cjtaylor@utmb.edu>; Rebekah Viner <rlviner@UTMB.EDU>; Devin Hansen <devin.hansen@usu.edu>; Jennipher Hulse <jennipher.hulse@usu.edu>; Bart Tarbet <bart.tarbet@usu.edu>; Katie Dana <katie.dana@usu.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>; Graham, Rachel <rlgraham@ad.unc.edu>; Menachery, Vineet <vimenach@UTMB.EDU>; Brett Hurst <brett.hurst@usu.edu>; LeGros, Erika <erlegros@UTMB.EDU>; Schilling, Beth A. <baschill@UTMB.EDU>; McNees, Andrew G. <amcnees@UTMB.EDU>; Bouvier, Nicole <Nicole.Bouvier@mountsinai.org>; Zhongde Wang <zonda.wang@usu.edu>; Morrey, John <john.morrey@usu.edu>; Richard Bowen <rbowen@rams.colostate.edu>
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Subject: DUE Monday, 7/6: A38 biweekly email update

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Thanks, and have a great week!

Chelsea & Erik & Thames

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current animal model development study status
- Timelines for availability of MCM studies. Should **emphasize** earliest possible date for study start and numbers of animals able to test per vaccine or therapeutic study (i.e. study capacity).
- Any resources needed? Any hurdles/challenges?

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To: Beasley, David W.[dwbeasle@UTMB.EDU]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
Cc: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Mon 7/13/2020 12:32:54 PM (UTC-05:00)
Subject: A38 Task Order Monthly Call_Friday July 17th

Dear Colleagues,

I wanted to send you a reminder for our upcoming A38 task order monthly call, to be held virtually this **Friday, July 17th from 10:30am-12pm EST**. As a reminder, please be prepared to share a brief slide presentation outlining the updates on your site's SARS-CoV-2 animal model(s) that are in development.

Thanks so much – looking forward to seeing your updates on Friday!
Chelsea & Erik

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Mon 7/27/2020 7:20:37 PM (UTC-05:00)
Subject: DUE Friday, 7/31: A38 biweekly email update
A38 Task Order Update_Template.docx

Hi All,
Hope you are all doing well! I wanted to send you a reminder re: our next biweekly email update for the A38 task order, which is this **Friday, July 31st**. As a reminder, please use the attached template outlining the updates on your site's SARS2 animal model(s) that are in development. Please email your site's update to Erik Stemmy (erik.stemmy@nih.gov), Chelsea Lane (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov).
Thanks, and have a great week!

Chelsea & Erik

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Cc: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Tue 8/25/2020 2:12:37 PM (UTC-05:00)
Subject: DUE Friday, 8/28: A38 biweekly email update
A38 Task Order Update_Template.docx

Dear Colleagues,
Hope this message finds you well! I wanted to send you a reminder re: our next biweekly email update for the A38 task order. As a reminder, please use the attached template outlining the updates on your site's SARS2 animal model(s) that are in development. Please email your site's update to Erik Stemmy (erik.stemmy@nih.gov), Chelsea Lane (mary.lane@nih.gov), and Thames Pickett (pickettte@niaid.nih.gov).
Thanks, and have a great week!

Chelsea & Erik & Thames

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
5601 Fishers Lane, Room ***8A19***
Bethesda, MD 20892-9826
[FedEx, UPS, DHL Address is Rockville, MD 20852]
Phone: (240) 627-3741
Cell: (240) 478-8653

Click to link to A Universal Influenza Vaccine: The Strategic Plan for the National Institute of Allergy and Infectious Diseases

A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current animal model development study status
- Timelines for availability of MCM studies. Should **emphasize** earliest possible date for study start and numbers of animals able to test per vaccine or therapeutic study (i.e. study capacity).
- Any resources needed? Any hurdles/challenges?

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To: Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Beasley, David W.[dwbeasle@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; bart.tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; antoinette_baric[antoinette_baric@med.unc.edu]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]; Zhongde Wang[zonda.wang@usu.edu]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Massey, Christopher[chmassey@UTMB.EDU]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Taylor, Kimberly (NIH/NIAID) [E][kimberly.taylor3@nih.gov]
Cc: Richard Bowen[rbowen@rams.colostate.edu]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hewitt, Judith (NIH/NIAID) [E][jhewitt@niaid.nih.gov]; Challberg, Mark (NIH/NIAID) [E][mchallberg@niaid.nih.gov]; Young, Jennifer (AE)[jenyoung@UTMB.EDU]; Vily, Aytaj (NIH/NIAID) [E][aytaj.vily@nih.gov]; Palin, Amy (NIH/NIAID) [E][amy.palin@nih.gov]; Sciotti, Rick (NIH/NIAID) [E][rick.sciotti@nih.gov]; Venkatraman Siddharthan[venkat.siddharthan@usu.edu]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Tue 6/8/2021 2:00:46 PM (UTC-05:00)
Subject: A38 Task Order Bi-weekly Call

Dear A38 Sites,

You should all have received an updated meeting invitation for Friday, July 16th. Please note the shift in time by 30 minutes – and that the meeting will start at 11am EST.

We have been asked by NIAID SARS-CoV-2 leadership to take another big picture view of where we are with all of our SARS2 small animal models. Hence, the update to our standard agenda for the 7/16 meeting (as shown at the bottom of this email). Many of our NIAID SARS-CoV-2 team members (from the Vaccine, mAb, and Therapeutics team) will be attending, so I'd like to keep these slides as a high level overview – similar to the 1 pager or information sheets that we asked you to develop. The goal will be that we (NIAID) can then utilize these slides as well and send them to External Requestors interested in testing their medical countermeasure of interest. I'd like to make sure that we are clear with the caveats/limitations of each model – i.e. if you think that the given model at your site is not best for testing of anti-inflammatory agents, please be sure to note that.

At the end of your presentation, please be sure to include 2-3 slides capturing final data on the pilot dexamethasone study conducted at your site. I know that many of you are still awaiting histopathology analyses, but I'm hoping that we can have all these final data (and cytokine data if applicable) in by July 16th.

Should you have any questions, please let me or Erik know ☺
Chelsea

7/16/2021 Agenda:

- General Updates (Erik)
- Brief slide deck (~6-10 slides) on models developed at each A38 site. Please include:
  - Model kinetics & pathology phenotypes (as noted in your 1-pager/info sheets);
  - Whether your model is suitable for testing of vaccines, antivirals, anti-inflammatory agents, mAbs, etc., and what controls can be utilized in your model (and the optimal timing and routes for dosing, etc.);
  - What assays/reagents are available for testing of immune responses in your model (and please include any relevant cytokine data if available);
- Another 2-3 slides with your Site's final data for testing of dexamethasone. Please ensure that histopathology analyses (and any additional analyses, e.g. cytokine if appropriate) can be completed by this date.

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch

Division of Microbiology and Infectious Diseases
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Tue 4/7/2020 1:40:40 PM (UTC-05:00)
Subject: PPE shortages & scheduling for monthly update teleconferences

Dear A38 Task Order Team (Colleagues),

It has come to the attention of Erik Stemmy and me that certain labs are having issues with ordering PPE and/or critical reagents from Fisher and VWR for conducting essential research under the A38 task order. In an effort to determine how widespread this issue is (and to help find potential solutions), we are assembling a list of PPE/reagents that are in short supply per contractor site. If possible, please let me and Erik know by noon tomorrow, whether your site has had any issues in obtaining necessary PPE or reagents for your task order studies.

Also, as per the instructions from the kickoff meeting, big thanks to the contractor sites that have already emailed Erik and me updates on your site's model development efforts. Again, we do not need a detailed update at this point in time – just a high level update on the availability of the animals that you are testing (e.g. if you are breeding animals, how that is coming along) and any updates on SARS-CoV-2 testing if that work has commenced. For those that have not provided updates, please send Erik and me (with a Cc to Thames and Miranda) your updates by noon tomorrow as well.

Last but not least, I wanted to begin polling for days/times during the week for our monthly update teleconferences. Based on Erik's and my calendars – the best day/time windows during the week are: Mondays (after 1pm EST); Friday mornings (between 10am-12pm EST); and Friday afternoons (after 1pm). For each contractor site, please let me know whether any of these day/time windows does not work for your team (by Friday COB if possible). If you could first consult with your specific site and reply to me in a single email, that would be most helpful.

Thanks all, and I hope that you are all staying healthy and safe. Should you have any additional questions, please let me or Erik know.

Sincerely,
Chelsea

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Bouvier, Nicole; Richard Bowen
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Monthly Call
Start Time:	Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Richard Bowen

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.]**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

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Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

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Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

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- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
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Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 6/4/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 6/4/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/4/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~5/21: UNC~~; 6/4: UTMB; 6/18: USU; 7/2: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 6/18/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 6/18/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/18/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~5/21: UNC~~; ~~6/4: UTMB~~; 6/18: USU; 7/30: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 5/21/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 5/21/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/21/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (5/21: UNC; 6/4: UTMB; 6/18: USU; 7/2: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 5/22/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 5/22/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen; Bouvier, Nicole

Location: Zoom meeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 6/19/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 6/19/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen; Bouvier, Nicole

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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To: Beasley, David W.[dwbeasle@UTMB.EDU]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
Cc: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Tue 8/11/2020 12:15:29 PM (UTC-05:00)
Subject: RE: A38 Task Order Monthly Call_Friday August 14th

Dear Colleagues,

I wanted to send you a reminder for our upcoming A38 task order monthly call, to be held virtually this **Friday, August 14th from 10:30am-12pm EST**. As a reminder, please be prepared to share a brief slide presentation outlining the updates on your site's SARS-CoV-2 animal model(s) that are in development.

Thanks so much!
Chelsea & Erik

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
5601 Fishers Lane, Room ***8A19***
Bethesda, MD 20892-9826
[FedEx, UPS, DHL Address is Rockville, MD 20852]
Phone: (240) 627-3741
Cell: (240) 478-8653

Click to link to A Universal Influenza Vaccine: The Strategic Plan for the National Institute of Allergy and Infectious Diseases

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 8/14/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 8/14/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Dear A38 Task Order Team,

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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To: Beasley, David W.[dwbeasle@UTMB.EDU]; Liz.grinstead@colostate.edu[Liz.grinstead@colostate.edu]; Julie Harvey[Julie.harvey@colostate.edu]; Bowen, Richard[richard.bowen@colostate.edu]; Chandra Caldwell[ccaldwel@email.unc.edu]; Victoria Moore[victoria_moore@unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Taylor Bray, Christy J.[cjtaylor@utmb.edu]; Viner, Rebekah L.[rlviner@UTMB.EDU]; Devin Hansen[devin.hansen@usu.edu]; Jennipher Hulse[jennipher.hulse@usu.edu]; Bart Tarbet[bart.tarbet@usu.edu]; Katie Dana[katie.dana@usu.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Brett Hurst[brett.hurst@usu.edu]; LeGros, Erika[erlegros@UTMB.EDU]; Schilling, Beth A.[baschill@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; McNees, Andrew G.[amcnees@UTMB.EDU]; Bouvier, Nicole[Nicole.Bouvier@mountsinai.org]; Zhongde Wang[zonda.wang@usu.edu]; Morrey, John[john.morrey@usu.edu]; Richard Bowen[rbowen@rams.colostate.edu]
Cc: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Adams, Miranda (NIH/NIAID) [E][miranda.adams@nih.gov]; Bryan, Jonathan (NIH/NIAID) [E][jonathan.bryan@nih.gov]; Jackson, Charles (NIH/NIAID) [E][charles.jackson@nih.gov]
From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Sent: Wed 9/9/2020 1:20:57 PM (UTC-05:00)
Subject: A38 Task Order Monthly Call_Friday September 11th

Dear Colleagues,

I wanted to send you a reminder for our upcoming A38 task order monthly call, to be held virtually this **Friday, September 11th from 10:30am-12pm EST**. As a reminder, please be prepared to share a brief slide presentation outlining the updates on your site's SARS-CoV-2 animal model(s) that are in development.

Also, we have received a number of questions from external requestors regarding the capacity for performing immune assays. It would be great if you could present a couple general slides on your site's assay capabilities this Friday as well.

Thanks so much – looking forward to seeing your updates on Friday!
Chelsea & Erik

M. Chelsea Lane, Ph.D.
Influenza Immunity Program Officer
Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases
NIAID/NIH/DHHS
5601 Fishers Lane, Room ***8A19***
Bethesda, MD 20892-9826
[FedEx, UPS, DHL Address is Rockville, MD 20852]
Phone: (240) 627-3741
Cell: (240) 478-8653

Click to link to A Universal Influenza Vaccine: The Strategic Plan for the National Institute of Allergy and Infectious Diseases

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 9/25/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 9/25/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 11/20/2020 9:30:00 AM (UTC-06:00)

End Time: Fri 11/20/2020 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 12/4/2020 9:30:00 AM (UTC-06:00)

End Time: Fri 12/4/2020 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

On December 4th, we will go more in depth into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: Canceled: A38 Task Order Bi-weekly Call
Start Time: Fri 1/1/2021 10:30:00 AM (UTC-05:00)
End Time: Fri 1/1/2021 12:00:00 PM (UTC-05:00)
Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Canceling our meeting on 1/1/2021 due to the holiday

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 12/4/2020 9:30:00 AM (UTC-06:00)

End Time: Fri 12/4/2020 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

Thanks again to UNC and UTMB for their presentations today. On December 4th, we will go into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

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Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 12/18/2020 9:30:00 AM (UTC-06:00)

End Time: Fri 12/18/2020 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

12/18/2020 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (~~11/20: UNC~~;~~12/4: UTMB~~; 12/18: USU; 1/15: CSU)

Note: this will be our last bi-weekly meeting of 2020.

Dear A38 Task Order Team,

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Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: Canceled: A38 Task Order Bi-weekly Call
Start Time: Fri 1/15/2021 9:30:00 AM (UTC-06:00)
End Time: Fri 1/15/2021 11:00:00 AM (UTC-06:00)
Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

****Canceling our A38 bi-weekly call next week on Jan. 15th due to a meeting conflict for both me and Erik. We will resume our bi-weekly meetings on Friday, January 29th****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Location: GoToMeeting

Importance: Normal

Subject: Canceled: A38 Task Order Bi-weekly Call

Start Time: Fri 1/15/2021 9:30:00 AM (UTC-06:00)

End Time: Fri 1/15/2021 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 1/29/2021 9:30:00 AM (UTC-06:00)

End Time: Fri 1/29/2021 11:00:00 AM (UTC-06:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

1/29/2021 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (1/29: UNC; 2/12: UTMB; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 3/26/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 3/26/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/26/2021 Agenda:

- General Updates (Chelsea)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (*3/26: UNC*; 4/9: UTMB; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: 425732

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 5/7/2021 9:30:00 AM (UTC-05:00)

End Time: Fri 5/7/2021 11:00:00 AM (UTC-05:00)

Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/7/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~*3/26: UNC; 4/9: UTMB*~~; ~~*4/23: USU*~~; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: 425732

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Password: **552.136**

Importance:	Normal
Start Time:	Fri 4/24/2020 2:30:00 PM (UTC)
End Time:	Fri 4/24/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password **552.136**

Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance:	Normal
Start Time:	Fri 9/25/2020 2:30:00 PM (UTC)
End Time:	Fri 9/25/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/9/2020 2:30:00 PM (UTC)
End Time:	Fri 10/9/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/23/2020 2:30:00 PM (UTC)
End Time:	Fri 10/23/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/6/2020 3:30:00 PM (UTC)
End Time:	Fri 11/6/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/20/2020 3:30:00 PM (UTC)
End Time:	Fri 11/20/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Hi all,
Just to let you all know in advance, we are expecting NIAID leadership to be joining this call on Friday. Please be prepared to present all the work you have completed thus far for model development and any MCM studies (if applicable). Please also be prepared to mention your capacity for MCM studies starting in January 2021.

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/4/2020 3:30:00 PM (UTC)
End Time:	Fri 12/4/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

On December 4th, we will go more in depth into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/18/2020 3:30:00 PM (UTC)
End Time:	Fri 12/18/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

12/18/2020 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (~~11/20: UNC~~;~~12/4: UTMB~~; 12/18: USU; 1/15: CSU)

Note: this will be our last bi-weekly meeting of 2020.

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Subject:	Canceled: A38 Task Order Bi-weekly Call
Start Time:	Fri 1/15/2021 3:30:00 PM (UTC)
End Time:	Fri 1/15/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 1/29/2021 3:30:00 PM (UTC)
End Time:	Fri 1/29/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

1/29/2021 Agenda:

- **General Updates (Erik)**
- **Brief updates for all A38 contractor sites**
- **Rotating check-in with individual sites** (1/29: UNC; 2/12: UTMB; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 1/29/2021 9:30:00 AM (UTC-06:00)
End Time: Fri 1/29/2021 11:00:00 AM (UTC-06:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

1/29/2021 Agenda:

- **General Updates (Erik)**
- **Brief updates for all A38 contractor sites**
- **Rotating check-in with individual sites** (1/29: UNC; 2/12: UTMB; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Koop, Douglas; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Subject: A38 Task Order Monthly Call
When: Occurs every 4 week(s) on Friday effective 4/24/2020 until 10/9/2020 from 10:30 AM to 12:00 PM Eastern Standard Time.
Where: GoToMeeting

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David W.; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David W.; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: 552.136

Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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161.199.136.10 (US East)
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Password: **552.136**

Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

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Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Password: **552.136**

Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance:	Normal
Start Time:	Fri 9/25/2020 2:30:00 PM (UTC)
End Time:	Fri 9/25/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 10/9/2020 2:30:00 PM (UTC)
End Time:	Fri 10/9/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/23/2020 2:30:00 PM (UTC)
End Time:	Fri 10/23/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/6/2020 3:30:00 PM (UTC)
End Time:	Fri 11/6/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Start Time:	Fri 11/20/2020 3:30:00 PM (UTC)
End Time:	Fri 11/20/2020 5:00:00 PM (UTC)
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Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Hi all,
Just to let you all know in advance, we are expecting NIAID leadership to be joining this call on Friday. Please be prepared to present all the work you have completed thus far for model development and any MCM studies (if applicable). Please also be prepared to mention your capacity for MCM studies starting in January 2021.

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/4/2020 3:30:00 PM (UTC)
End Time:	Fri 12/4/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

On December 4th, we will go more in depth into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/18/2020 3:30:00 PM (UTC)
End Time:	Fri 12/18/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

12/18/2020 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (~~11/20: UNC~~;~~12/4: UTMB~~; 12/18: USU; 1/15: CSU)

Note: this will be our last bi-weekly meeting of 2020.

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 1/29/2021 3:30:00 PM (UTC)
End Time:	Fri 1/29/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Note: for this Friday, January 29th, please include within your site's presentations whether your site is able to perform aerosol delivery of Tx compounds (and if so, what methods you use). A slide or two max should be sufficient.

1/29/2021 Agenda:

- **General Updates (Erik)**
- **Brief updates for all A38 contractor sites**
- **Rotating check-in with individual sites (*1/29: UNC*; 2/12: UTMB; 2/26: USU; 3/12: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 2/12/2021 3:30:00 PM (UTC)
End Time:	Fri 2/12/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

***Note*:** for this Friday, February 12th, please be prepared for a discussion on testing of dexamethasone (that your site has already conducted, or that is in your queue). Please refer to the email that I sent on Thursday, 2/4/2020.

2/12/2021 Agenda:

- **General Updates (Erik)**
- **First 15minutes – discussion regarding testing of dexamethasone**
- ***Brief* 10-15 minute updates for all A38 contractor sites**
- **Rotating check-in with individual sites (~~1/29: UNC~~; *2/12: UTMB*; 2/26: USU; 3/12: CSU)**

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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End Time:	Fri 2/26/2021 5:00:00 PM (UTC)
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Optional Attendees:	Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

2/26/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~; *2/26: USU*; 3/12: CSU)**

Dear A38 Task Order Team,

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Importance:	Normal
Start Time:	Fri 3/12/2021 3:30:00 PM (UTC)
End Time:	Fri 3/12/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/12/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites. *Note*: please include about a 5 minute high level summary on your thoughts/experiences on positive controls (for Tx studies) for the model(s) that you are developing. If you have any data you can summarize, that would be great. It is okay if you don't have extensive experience with this.**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~;~~2/26: USU~~; *3/12: CSU*)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.136.10 (US East)

Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 3/26/2021 2:30:00 PM (UTC)
End Time:	Fri 3/26/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/26/2021 Agenda:

- **General Updates (Chelsea)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC*; 4/9: UTMB; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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+1 646 828 7666 US (New York)
833 568 8864 US Toll-free
Meeting ID: 161 887 1310
Password: **552.136**
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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 4/9/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 4/9/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/9/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (~~3/26: UNC~~; *4/9: UTMB*; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Password: **552.136**
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Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 4/23/2021 2:30:00 PM (UTC)
End Time:	Fri 4/23/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/23/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC; 4/9: UTMB*; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
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Importance:	Normal
Start Time:	Fri 5/7/2021 2:30:00 PM (UTC)
End Time:	Fri 5/7/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/7/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC; 4/9: UTMB*; *4/23: USU*; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

Join ZoomGov Meeting
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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal

Start Time: Fri 5/21/2021 2:30:00 PM (UTC)

End Time: Fri 5/21/2021 4:00:00 PM (UTC)

Required Attendees: Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Menachery, Vineet; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Massey, ChristopherLane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David W.; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Vily, Aytaj (NIH/NIAID) [E]Young, Jennifer (AE)Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/21/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (5/21: UNC; 6/4: UTMB; 6/18: USU; 7/2: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310

Password: **552.136**

To: Baric, Ralph S[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
Cc: mtferris[mtferris@email.unc.edu]
From: Plante, Jessica A.[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=23798af99bc14d6e80c3fc0adb52d51f-Plante, Jes]
Sent: Tue 1/21/2020 10:06:35 AM (UTC-06:00)
Subject: Re:

Hi Ralph,

Sounds good, do you guys have any availability on Thursday or Friday? Other than the Marty genetics I should be able to have all of your comments incorporated by then.

Thanks again,
Jessica

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, January 17, 2020 8:57 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Plante, Jessica A. <japlante@UTMB.EDU>; mtferris <mtferris@email.unc.edu>
Subject:

Hi Vineet and Jess, Hope you are having a nice new year. Nice job on the paper. I have appended my comments on the paper. I think marty needs to discuss genotyping in the methods section. Be glad to chat. Ralph

To: "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,
From: Microsoft Outlook[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MICROSOFTEXCHANGE329E71EC88AE4615BBC36AB6CE41109E1F8FAAA8]
Sent: Mon 8/31/2020 9:09:32 AM (UTC-05:00)
Subject: Undeliverable: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2
A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2

Delivery has failed to these recipients or groups:

"Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,

The format of the email address isn't correct. A correct address looks like this: someone@example.com. Please check the recipient's email address and try to resend the message.

Diagnostic information for administrators:

Generating server: SN4PR0201MB3407.namprd02.prod.outlook.com

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Remote Server returned '550 5.1.3 STOREDRV.Submit; invalid recipient address'

Original message headers:

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Received: from SN4PR0201MB3407.namprd02.prod.outlook.com
 ([fe80::2c34:294a:70d3:e7d8]) by SN4PR0201MB3407.namprd02.prod.outlook.com
 ([fe80::2c34:294a:70d3:e7d8%7]) with mapi id 15.20.3326.025; Mon, 31 Aug 2020
 14:09:32 +0000
Content-Type: application/ms-tnef; name="winmail.dat"
Content-Transfer-Encoding: binary
From: "Young, Jennifer (AE)" <jenyoung@UTMB.EDU>
To: "\"Baric, Toni C\" <antoinette_baric@med.unc.edu>, \"Baric, Ralph S\"
 <rbaric@email.unc.edu>, \"McGlaughon, Ben\" <benmcg@email.unc.edu>, \"Graham,
 Rachel\" <rlgraham@ad.unc.edu> : \"Baric, Toni C\"
 <antoinette_baric@med.unc.edu>, \"Baric, Ralph S\" <rbaric@email.unc.edu>,
 \"McGlaughon, Ben\" <benmcg@email.unc.edu>, \"Graham, Rachel\"
 <rlgraham@ad.unc.edu>,"
         <"Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>,
"McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C"
<antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben"
<benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,>,
         "Beasley, David W." <dwbeasle@UTMB.EDU>, "Tseng, Chien-Te K."
         <sktseng@UTMB.EDU>, "Menachery, Vineet" <vimenach@UTMB.EDU>, "Massey,
 Christopher" <chmassey@UTMB.EDU>, "Viner, Rebekah L." <rlviner@UTMB.EDU>
Subject: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2
Thread-Topic: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2
Thread-Index: AdZ/oBbC3tl+V8WhQDOMLSGWbaEFaAAAED9A
X-MS-Exchange-Calendar-Originator-Id: 89e9f51b-b637-4ff7-bf03-c59c6c11ee6d;/o=ExchangeLabs/ou=Exchange
 Administrative Group
 (FYDIBOHF23SPDLT)/cn=Recipients/cn=939434b3dc894caab01c10e93943d292-Young,
 Jenn
X-MS-Exchange-Calendar-Series-Instance-Id:
BAAAAIIA4AB0xbcQGoLgCAAAAAAwXOUvdX/WAQAAAAAAAAAAEAAAAEQ0Svk7t89BgWHhuy+8se0=
Date: Mon, 31 Aug 2020 14:09:31 +0000
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Message-ID: <SN4PR0201MB3407DFC6099BA53ABB1139F2A5510@SN4PR0201MB3407.namprd02.prod.outlook.com>
Accept-Language: en-US
Content-Language: en-US
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
<SN4PR0201MB3407DFC6099BA53ABB1139F2A5510@SN4PR0201MB3407.namprd02.prod.outlook.com>
x-ms-publictraffictype: Email
MIME-Version: 1.0
X-Originating-IP: [98.196.240.18]

From: Young, Jennifer (AE)[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=939434B3DC894CAAB01C10E93943D292-YOUNG, JENN]

Location: https://zoom.us/j/9095677699?pwd= **552.136**

Importance: Normal

Subject: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2

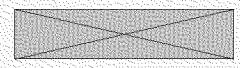
Start Time: Tue 9/1/2020 1:00:00 PM (UTC-05:00)

End Time: Tue 9/1/2020 2:00:00 PM (UTC-05:00)

Required Attendees: "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.

Please see the below teleconference information for tomorrow's meeting at 1pm – 2pm (CDT)/ 2pm – 3pm (EDT).

Required Attendees: "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.



Hi there,

Jennifer Young is inviting you to a scheduled Zoom meeting.

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Meeting ID: 909 567 7699

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Passcode: **552.136**

International numbers

Skype for Business (Lync)

https://zoom.us/skype/9095677699

Importance: Normal
Start Time: Fri 5/22/2020 2:30:00 PM (UTC)
End Time: Fri 5/22/2020 4:00:00 PM (UTC)

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Cc: Richard Bowen
Subject: A38 Task Order Monthly Call
When: Occurs every 4 week(s) on Friday effective 4/24/2020 until 10/9/2020 from 10:30 AM to 12:00 PM Eastern Standard Time.
Where: GoToMeeting

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Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal
Start Time: Fri 4/24/2020 2:30:00 PM (UTC)
End Time: Fri 4/24/2020 4:00:00 PM (UTC)

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
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Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 7/17/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 7/17/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 8/14/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 8/14/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 9/25/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 9/25/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Meeting ID: 161 887 1310

Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 10/9/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 10/9/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Password: **552.136**

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 10/23/2020 9:30:00 AM (UTC-05:00)
End Time:	Fri 10/23/2020 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

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Password: **552.136**

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 11/6/2020 9:30:00 AM (UTC-06:00)
End Time:	Fri 11/6/2020 11:00:00 AM (UTC-06:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

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Best,
Erik & Chelsea

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161.199.136.10 (US East)
Meeting ID: 161 887 1310

Password: 552.136

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 11/20/2020 9:30:00 AM (UTC-06:00)

End Time: Fri 11/20/2020 11:00:00 AM (UTC-06:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Hi all,
Just to let you all know in advance, we are expecting NIAID leadership to be joining this call on Friday. Please be prepared to present all the work you have completed thus far for model development and any MCM studies (if applicable). Please also be prepared to mention your capacity for MCM studies starting in January 2021.

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 12/4/2020 9:30:00 AM (UTC-06:00)
End Time: Fri 12/4/2020 11:00:00 AM (UTC-06:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

On December 4th, we will go more in depth into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

Dear A38 Task Order Team,

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Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 12/18/2020 9:30:00 AM (UTC-06:00)
End Time: Fri 12/18/2020 11:00:00 AM (UTC-06:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

12/18/2020 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (~~11/20: UNC~~;~~12/4: UTMB~~; 12/18: USU; 1/15: CSU)

Note: this will be our last bi-weekly meeting of 2020.

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 1/29/2021 9:30:00 AM (UTC-06:00)
End Time: Fri 1/29/2021 11:00:00 AM (UTC-06:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Note: for this Friday, January 29th, please include within your site's presentations whether your site is able to perform aerosol delivery of Tx compounds (and if so, what methods you use). A slide or two max should be sufficient.

1/29/2021 Agenda:

- **General Updates (Erik)**
- **Brief updates for all A38 contractor sites**
- **Rotating check-in with individual sites (*1/29: UNC*; 2/12: UTMB; 2/26: USU; 3/12: CSU)**

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 2/12/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 2/12/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Note: for this Friday, February 12th, please be prepared for a discussion on testing of dexamethasone (that your site has already conducted, or that is in your queue). Please refer to the email that I sent on Thursday, 2/4/2020.

2/12/2021 Agenda:

- General Updates (Erik)
- First 15minutes – discussion regarding testing of dexamethasone
- *Brief* 10-15 minute updates for all A38 contractor sites
- Rotating check-in with individual sites (~~1/29: UNC~~; *2/12: UTMB*; 2/26: USU; 3/12: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 2/26/2021 9:30:00 AM (UTC-06:00)
End Time:	Fri 2/26/2021 11:00:00 AM (UTC-06:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

2/26/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~; *2/26: USU*; 3/12: CSU)**

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 3/12/2021 9:30:00 AM (UTC-06:00)
End Time: Fri 3/12/2021 11:00:00 AM (UTC-06:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/12/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites. *Note*: please include about a 5 minute high level summary on your thoughts/experiences on positive controls (for Tx studies) for the model(s) that you are developing. If you have any data you can summarize, that would be great. It is okay if you don't have extensive experience with this.
- Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~;~~2/26: USU~~; *3/12: CSU*)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 3/26/2021 9:30:00 AM (UTC-05:00)
End Time:	Fri 3/26/2021 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/26/2021 Agenda:

- General Updates (Chelsea)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (*3/26: UNC*; 4/9: UTMB; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 4/9/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 4/9/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/9/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (~~3/26: UNC~~; *4/9: UTMB*; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal
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Start Time: Fri 4/23/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 4/23/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees: Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/23/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~*3/26: UNC; 4/9: UTMB*~~; 4/23: USU; 5/7: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 5/7/2021 9:30:00 AM (UTC-05:00)
End Time:	Fri 5/7/2021 11:00:00 AM (UTC-05:00)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/7/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC; 4/9: UTMB*; *4/23: USU*; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Importance: Normal
Subject: A38 Task Order Bi-weekly Call
Start Time: Fri 5/21/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 5/21/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Menachery, Vineet; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Massey, ChristopherLane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, ChristopherDevin Hansen
Optional Attendees: Vily, Aytaj (NIH/NIAID) [E]Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/21/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (5/21: UNC; 6/4: UTMB; 6/18: USU; 7/2: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: A38 Task Order Monthly Call
Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)
End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)
Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Young, Jennifer (AE); Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees: Richard Bowen

-----Original Appointment-----
From: Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>
Sent: Monday, April 13, 2020 3:27 PM
To: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Cc: Richard Bowen
Subject: A38 Task Order Monthly Call
When: Occurs every 4 week(s) on Friday effective 4/24/2020 until 10/9/2020 from 10:30 AM to 12:00 PM Eastern Standard Time.
Where: GoToMeeting

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
Cc: Lokugamage, Kumari G.[kglokuga@UTMB.EDU]; Carlin, Aaron F[acarlin@health.ucsd.edu]
From: Ramirez, Sydney[sir011@health.ucsd.edu]
Sent: Thur 4/9/2020 10:54:13 PM (UTC-05:00)
Subject: Introductions and collaborations

Vineet,

I am sorry that we are not able to meet in person given the current circumstances.

I am an MD, PhD, and I did my PhD in Shinji Makino's lab at UTMB when Kumari was still in the lab. Since then, I have moved to UCSD to do my Internal Medicine and Infectious Disease clinical training, and I recently joined Shane Crotty's lab at La Jolla Institute (LJI).

Congratulations on the recent manuscript regarding type I interferon pre-treatment and SARS-CoV-2 vs SARS-CoV. It was posted to our lab's Slack #coronavirus thread.

As you can imagine, there are a number of excellent scientists with diverse backgrounds eager to study SARS-CoV-2. However, there are not many coronavirologists around. Given your lab's expertise in the area, including your own expertise from your time in the Baric lab and your time as an independent investigator, it would be great to be able to put you in touch with a number of PIs here in San Diego.

Shane and multiple other PIs at LJI are focused on understanding the immune response (mainly T and B cell responses) to SARS-CoV-2. We are also collaborating with a number of PIs at UCSD.

Aaron Carlin is one of our collaborators at UCSD. He is an MD, PhD Infectious Diseases physician scientist who did his postdoc in Chris Glass' lab and has gone on to start his own lab, studying innate immunity and pathogen-host interactions with flaviviruses (among other things). He is hoping to study pathogen-host interactions with SARS-CoV-2, and ultimately hopes to do so in a lung organoid model. However, he does not have experience culturing CoV.

Would you be willing/able to share your SOPs for making SARS-CoV-2 stock virus? I think that it would be useful for him to have an SOP for plaque assays in Vero E6 as well.

I have copied Aaron and Kumari on this email to try to help facilitate this. Aaron can correct me or add details as needed.

Thank you.

Best,

Sydney

To: Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 2/18/2021 2:02:02 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - February 23rd

Hi Everyone!

Apologies for the last minute cancelation last week.

Dr. Laura Hughes saved me from disappointing you all two weeks in a row. She will be giving a presentation titled "**Real-time surveillance of SARS-CoV-2 mutations and variants**".

As a reminder, if you are interested in presenting, please reach out to me so I can get you on the schedule.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 2/16/2021 8:00:00 AM (UTC-06:00)

End Time: Tue 2/16/2021 11:00:00 AM (UTC-06:00)

Required Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane

(NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]

Hi Everyone!

Due to a last minute cancellation, we will NOT be having tomorrow's weekly Investigators meeting. We will resume on Tuesday, February 23rd.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; 'Marta Gaglia'[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Rick L.[stevens@anl.gov]; mshukla@anl.gov[mshukla@anl.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 2/19/2021 4:13:15 PM (UTC-06:00)
Subject: UPDATE: SARS-CoV-2 Weekly Investigators Meeting - February 23rd

Hi Everyone!

SURPRISE! We will now have TWO presenters on Tuesday, February 23rd to make up for the last minute cancellation last week.

Presenter 1:

Dr. Laura Hughes
"**Real-time surveillance of SARS-CoV-2 mutations and variants**"

Presenter 2:

Dr. Richard Scheuermann
"Toward an Early warning system for SARS-CoV-2 Variants of Concern"

As a reminder, if you are interested in presenting, please reach out to me so I can get you on the schedule.

Have a great weekend,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 2/15/2021 7:06:34 PM (UTC-06:00)
Subject: CANCELLED: SARS-CoV-2 Weekly Investigators Meeting - February 16th

Hi Everyone,

Apologies for the late notice but tomorrow's meeting will be CANCELLED due to a last minute cancellation. We will resume next week on Tuesday, February 23rd.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager

Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 2/26/2021 3:04:33 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - March 2nd

Hi Everyone,

On Tuesday, February 23rd, we had two wonderful presentations given by the presenters below:
Presenter 1:

Dr. Laura Hughes
"**Real-time surveillance of SARS-CoV-2 mutations and variants**"

Presenter 2:

Dr. Richard Scheuermann
"Toward an Early warning system for SARS-CoV-2 Variants of Concern"

Next week, Dr. Robert "Rob" Schwartz will be giving a presentation titled "**The landscape of host responses and disease pathology in SARS-CoV-2 infection**" on Tuesday, March 2nd.

As a reminder, if you are interested in presenting, please reach out to me so I can get you on the schedule.

Have a great weekend,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Koelle, Katharina V.[katia.koelle@emory.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Priya Luthra[pluthra@trudeauinstitute.org]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu];

Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 3/4/2021 10:42:23 AM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - March 9th

Hi Everyone,

On Tuesday, **March 2nd,** Dr. Robert "Rob" Schwartz gave a wonderful presentation titled "**The landscape of host responses and disease pathology in SARS-CoV-2 infection**". Thank you to our presenter and those that were able to join.

Next up, we have Dr. Rory de Vries who will be giving a presentation on how "**Intranasal fusion inhibitory lipopeptide prevents**

direct-contact SARS-CoV-2 transmission in ferrets" on Tuesday, March 9th.

Presenter needed: March 23rd! Please let me know if you'd like to claim that spot. ☺

Have a great rest of the week,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 3/25/2021 2:10:44 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - March 30th

Hi Everyone,

On March 23rd, Dr. Ben tenOever presented data on "**Aging and the immune response to SARS-CoV-2 in the golden hamster**".

Thank you to our presenter for his time and to those that were able to join.
Our last March presenter will be Dr. Christopher Brooke who will be presenting on the "**Substantial person-to-person heterogeneity in viral dynamics during acute SARS-CoV-2 infection".**

Hope you all have a wonderful rest of the week!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]

Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Mon 4/19/2021 12:49:53 PM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - April 20th

Hi Everyone!

I hope you all had a great weekend!

Dr. Liz Thompson gave us all an overview on the "**Metabolic programs define dysfunctional immune responses in severe COVID-19 patients".** Thank you to our presenter and to everyone who was able to join.

Tomorrow, Dr. Santosh Dhakal will be presenting on the "**Sex differences in lung imaging and SARS-CoV-2 antibody responses in a COVID-19 golden Syrian hamster model**". Hope you all are able to join!

If you are interested in presenting in the future or would like to add someone to this call, please feel free to reach out.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Stevens, Rick L.[stevens@anl.gov]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID)

[E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]

Cc: Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 4/23/2021 9:22:05 AM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - April 27th

Happy Friday, Everyone!

Thank you all who attended the presentation given by Dr. Santosh Dhakal on the "**Sex differences in lung imaging and SARS-CoV-2 antibody responses in a COVID-19 golden Syrian hamster model**" and thank you to the presenter.

On Tuesday, April 27th, Dr. Jennifer Gribble-Bowser will be giving a presentation on "**Defining the determinants and products of coronavirus recombination**".

Hope you all have a great weekend! Look forward to seeing your names on Tuesday!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: DAVID H O'CONNOR[dhoconno@wisc.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Aubree Gordon[gordonal@umich.edu]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Charles Russell[charles.russell@stjude.org]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu];

Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Feldstein, Leora (CDC/DDID/NCIRD/ID)[nqw5@cdc.gov]

Cc: Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Tue 4/6/2021 8:12:34 AM (UTC-05:00)
Subject: 4/6 CANCELLED: SARS-CoV-2 Weekly Investigators Meeting

Hi Everyone,

We had a last minute cancelation and will NOT be having the SARS-CoV-2 Investigators meeting this morning.

However, we will resume next week with Dr. Liz Thompson who will be presenting on the "**Metabolic programs define dysfunctional immune responses in severe COVID-19 patients**".

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Graham, Jessica B[jgraham@fredhutch.org]; Swarts, Jessica L[jswarts@fredhutch.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Gralinski, Lisa E[lgralins@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; clayton.r.morrison@gmail.com[clayton.r.morrison@gmail.com]; Kathleen Voss[katvoss@uw.edu]; Gabrielle Choonoo[gchoonoo@gmail.com]; Sophia Jeng[jengs@ohsu.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Shannon McWeeney[mcweeney@ohsu.edu]; mtferris[mtferris@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Michael J Gale[mgale@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; richardgreen.98109@gmail.com[richardgreen.98109@gmail.com]
From: Lund, Jennifer[jlund@fredhutch.org]
Sent: Tue 9/3/2019 11:27:02 AM (UTC-05:00)
Subject: Co-authored manuscript - conflict of interest forms required
coi_disclosure.pdf

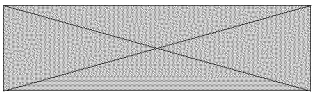
Dear Co-authors,

Our manuscript, "Immune predictors of mortality following RNA virus infection", has been reviewed at a couple of places – Cell Reports wanted additional experiments that we aren't willing to do (requiring a lot more mice), so we submitted to the Journal of Infectious Diseases, where it was quite favorably reviewed. We're preparing our revision, and in the meantime, they require each author to complete the attached conflict of interest form.

Could you each fill this out and return to me ASAP?

Thanks!
Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org



Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

To: Lund, Jennifer[jlund@fredhutch.org]; Graham, Jessica B[jgraham@fredhutch.org]; Swarts, Jessica L[jswarts@fredhutch.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Gralinski, Lisa E[lgralins@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; clayton.r.morrison@gmail.com[clayton.r.morrison@gmail.com]; Kathleen Voss[katvoss@uw.edu]; Gabrielle Choonoo[gchoonoo@gmail.com]; Sophia Jeng[jengs@ohsu.edu]; Michael Mooney[mooneymi@ohsu.edu]; Shannon McWeeney[mcweeney@ohsu.edu]; mtferris[mtferris@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Michael J Gale[mgale@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; richardgreen.98109@gmail.com[richardgreen.98109@gmail.com]
From: Miller, Darla[darla_miller@med.unc.edu]
Sent: Thur 9/19/2019 12:48:38 PM (UTC-05:00)
Subject: Re: Co-authored manuscript

Congratulations Jenny and all!

Darla Miller
UNC Systems Genetics Core Facility
UNC at Chapel Hill
5047 Genetic Medicine Building, CB 7264
120 Mason Farm Road
Chapel Hill, NC 27599-7264
919 843-6471

COO, International Mammalian Genome Society
865 250-9173

From: Lund, Jennifer <jlund@fredhutch.org>
Sent: Thursday, September 19, 2019 1:37 PM
To: Graham, Jessica B <jgraham@fredhutch.org>; Swarts, Jessica L <jswarts@fredhutch.org>; Menachery, Vineet <vimenach@UTMB.EDU>; Gralinski, Lisa E <lgralins@email.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; ksplante@utmb.edu <ksplante@utmb.edu>; clayton.r.morrison@gmail.com <clayton.r.morrison@gmail.com>; Kathleen Voss <katvoss@uw.edu>; Gabrielle Choonoo <gchoonoo@gmail.com>; Sophia Jeng <jengs@ohsu.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Shannon McWeeney <mcweeney@ohsu.edu>; mtferris <mtferris@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Michael J Gale <mgale@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; richardgreen.98109@gmail.com <richardgreen.98109@gmail.com>
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Hi everyone,

I just wanted to pass on the good news that our manuscript was accepted for publication in The Journal of Infectious Diseases. Thanks to everyone for their contributions to this paper, and I hope there are many more to come!

Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
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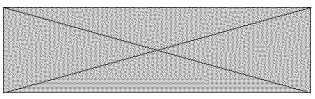

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Lund, Jennifer" <jlund@fredhutch.org>
Date: Tuesday, September 3, 2019 at 9:27 AM
To: "Graham, Jessica B" <jgraham@fredhutch.org>, "Swarts, Jessica L" <jswarts@fredhutch.org>, "Menachery, Vineet" <vimenach@UTMB.EDU>, Lisa Gralinski <lgralins@email.unc.edu>, "Schaefer, Alexandra" <aschaefe@email.unc.edu>, "ksplante@utmb.edu" <ksplante@utmb.edu>, "clayton.r.morrison@gmail.com" <clayton.r.morrison@gmail.com>, Kathleen Voss <katvoss@uw.edu>, Gabrielle Choonoo <gchoonoo@gmail.com>, Sophia Jeng <jengs@ohsu.edu>, "Miller, Darla" <darla_miller@med.unc.edu>, Michael Mooney <mooneymi@ohsu.edu>, Shannon McWeeney <mcweeney@ohsu.edu>, mtferris <mtferris@email.unc.edu>, "Pardo Manuel de Villena, Fernando" <fernando_pardo-manuel@med.unc.edu>, Michael J Gale <mgale@uw.edu>, "Heise, Mark T" <mark_heisem@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "richardgreen.98109@gmail.com" <richardgreen.98109@gmail.com>
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Could you each fill this out and return to me ASAP?

Thanks!
Jenny

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Associate Member
Vaccine and Infectious Disease Division
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F 206.667.7767
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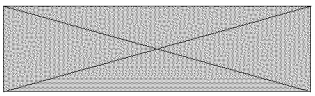

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fredhutch.org

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From: Lund, Jennifer[jlund@fredhutch.org]
Sent: Thur 9/19/2019 12:37:15 PM (UTC-05:00)
Subject: Re: Co-authored manuscript

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Associate Member
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O 206.667.2217
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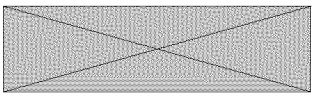

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Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
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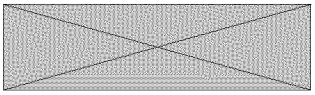

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

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From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 9/19/2019 12:48:39 PM (UTC-05:00)
Subject: RE: Co-authored manuscript

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To: Graham, Jessica B <jgraham@fredhutch.org>; Swarts, Jessica L <jswarts@fredhutch.org>; Menachery, Vineet <vimenach@UTMB.EDU>; Gralinski, Lisa E <lgralins@email.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; ksplante@utmb.edu; clayton.r.morrison@gmail.com; Kathleen Voss <katvoss@uw.edu>; Gabrielle Choonoo <gchoonoo@gmail.com>; Sophia Jeng <jengs@ohsu.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Shannon McWeeney <mcweeney@ohsu.edu>; mtferris <mtferris@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Michael J Gale <mgale@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; richardgreen.98109@gmail.com
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University of North Carolina
CB 7292
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From: Heise, Mark T[mark_heisem@med.unc.edu]
Sent: Thur 9/19/2019 1:35:25 PM (UTC-05:00)
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From: Michael J Gale[mgale@uw.edu]
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Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

To: Heise, Mark T[mark_heisem@med.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; McWeeney, Shannon[mcweeney@ohsu.edu]; Morrison, Thomas[THOMAS.MORRISON@CUANSCHUTZ.EDU]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Menachery, Vineet[vimenach@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]
Cc: Noll, Kelsey[kenoll@email.unc.edu]; mtferris[mtferris@email.unc.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Mon 3/16/2020 3:06:11 PM (UTC-05:00)
Subject: RE: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Awesome, Congrats Kelsey! Congrats Everyone!

From: Heise, Mark T <mark_heisem@med.unc.edu>
Sent: Monday, March 16, 2020 3:41 PM
To: Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Morrison, Thomas <THOMAS.MORRISON@CUANSCHUTZ.EDU>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
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    - Original/source data for [figures/datatype] in the paper is available [i.e. Mendeley Data DOI]
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Gail Teitzel, Ph.D.
Deputy Editor, Cell Reports

Reviewer comments:

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Reviewer #2: Author's were responsive to previous reviewer concerns. No further comments.

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Super, congratulations.
Klaus

Von: Heise, Mark T <mark_heisem@med.unc.edu>
Gesendet: Montag, 16. März 2020 20:41
An: Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Morrison, Thomas <THOMAS.MORRISON@CUANSCHUTZ.EDU>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
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    - All unique/stable reagents generated in this study are available from the Lead Contact with a completed Materials Transfer Agreement.
- Under the Data and Code Availability subheading in the Resource Availability section, we require a Data and Code Availability Statement.
- Examples of "Data and Code Availability Statements" are below. Statements with multiple types of datasets may use a combination of statements.
    - The [datasets/code] generated during this study are available at [NAME OF REPOSITORY] [ACCESSION CODE/WEB LINK]
    - The published article includes all [datasets/code] generated or analyzed during this study.
    - The [datasets/code] supporting the current study have not been deposited in a public repository because [REASON WHY DATA ARE NOT PUBLIC], but are available from the corresponding author on request.
    - There are restrictions to the availability of [dataset/code] due to [REASON WHY RESTRICTIONS EXIST]
    - Original/source data for [figures/datatype] in the paper is available [i.e. Mendeley Data DOI]
    - Original/source data for [figures/datatype] in the paper is available in supplemental figure X
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- If the paper does not generate any new data or code, it is appropriate to state the following:
    - This study did not generate any unique datasets or code.
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Please upload your final files to our https://www.editorialmanager.com/cell-reports/ as a revision of CELL-REPORTS-D-19-04583R1. When you submit your revised files, our team will check them and will contact you if there are any remaining formatting issues that need to be resolved. We will also share any editorial comments on the revised files at this point.

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Sincerely,
Gail

Gail Teitzel, Ph.D.
Deputy Editor, Cell Reports

Reviewer comments:

Reviewer #1: (Comments for the author)
The authors have addressed my concerns and the concerns of the other reviewer and have significantly strengthened what was already a strong manuscript.

Reviewer #2: Author's were responsive to previous reviewer concerns. No further comments.

To: Morrison, Thomas[THOMAS.MORRISON@CUANSCHUTZ.EDU]; Baric, Ralph S[rbaric@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; McWeeney, Shannon[mcweeney@ohsu.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Menachery, Vineet[vimenach@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]
Cc: Noll, Kelsey[kenoll@email.unc.edu]; mtferris[mtferris@email.unc.edu]
From: Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]
Sent: Mon 3/16/2020 3:15:43 PM (UTC-05:00)
Subject: Re: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Agree, Congrats!!

f

From: Morrison, Thomas <THOMAS.MORRISON@CUANSCHUTZ.EDU>
Sent: Monday, March 16, 2020 4:14 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Cc: Noll, Kelsey <kenoll@email.unc.edu>; mtferris <mtferris@email.unc.edu>
Subject: Re: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Congratulations! Nice to receive some good news!!

From: "Baric, Ralph S"
Date: Monday, March 16, 2020 at 2:06 PM
To: "Heise, Mark T", "Pardo Manuel de Villena, Fernando", "McWeeney, Shannon", "Morrison, Thomas", "Schughart, Klaus", "Menachery, Vineet", "Plante, Kenneth S."
Cc: "Noll, Kelsey", mtferris
Subject: RE: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Awesome, Congrats Kelsey! Congrats Everyone!

From: Heise, Mark T <mark_heisem@med.unc.edu>
Sent: Monday, March 16, 2020 3:41 PM
To: Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Morrison, Thomas <THOMAS.MORRISON@CUANSCHUTZ.EDU>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Cc: Noll, Kelsey <kenoll@email.unc.edu>; mtferris <mtferris@email.unc.edu>
Subject: FW: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Hi Everyone,
Good news. Kelsey's manuscript was accepted. Thank you for all of the help on this and please pass on to the other authors in your research groups.
Best
Mark

From:em.cell-reports.0.69fa61.aaee7413@editorialmanager.com <em.cell-reports.0.69fa61.aaee7413@editorialmanager.com>
On Behalf Of Cell Reports
Sent: Monday, March 16, 2020 1:47 PM
To: Heise, Mark T <mark_heisem@med.unc.edu>
Subject: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Dr. Mark Heise
The University of North Carolina

Genetics
9039 Burnett Womack Building
Campus Box 7292
Chapel Hill, NC 27599
UNITED STATES

Complex genetic architecture underlies regulation of influenza A virus-specific antibody responses in the Collaborative Cross
CELL-REPORTS-D-19-04583R1

Mar 16, 2020

Dear Dr. Heise,

I am pleased to let you know that, based on your revisions and the reviewer comments below, your manuscript has now been "accepted in principle" as a Research Article at Cell Reports.

Before we can formally accept your manuscript, we require that the final files are uploaded according to our production guidelines as outlined in our Final Files Checklist. We would like to have your final materials within 10 days, but please let us know if you think that you may need more time. Once we receive your final files, we can move forward with accepting your manuscript and scheduling it for publication.

Please note that our article length guidelines have been recently adjusted to reflect that references are no longer counted towards the overall character count of the manuscript. The revised manuscript should conform to the general length restriction for a Research Article, which is **45,000 characters** (including spaces and figure legends) and no more than **7 figures and/or tables**. This count does not include STAR Methods or any supplemental legends, or the reference list. There is some flexibility here, so please contact us to discuss this further.

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- To avoid errata, you should **double check all files carefully and ensure that all figure panels are accurate.**
- **Author names cannot be corrected later, thus you should ask all co-authors to carefully check the spelling of their names.**
- I have a few suggestions for the eTOC blurb to trim this to within our guidelines as the eTOC blurb can be up to 50 words. I will email these to you separately I will email these to you separately. Please feel free to modify my suggestions while keeping within these length limits.
- Please submit the main-text figures in individual high resolution files (TIF or high resolution PDF) and ensure that gel and microscopy images are at least 300 pixels per inch at final print size. For clear and accurate presentation of your data, we strongly recommend a vector graphics program (such as Adobe Illustrator or Inkscape) to assemble the figures and verify that at final print size, each displayed image is at least 300 pixels per inch. Note that programs such as Word or Powerpoint often reduce the resolution of primary data images and this should be checked carefully before resubmission.
- Figure legends should include information on biological and technical replicates.
- We routinely implement post-accept figure checks for papers at Cell Press. Thus, we may need to see the original data (uncropped, unlabeled images) for your figures. If so, I'll be in touch with specific instructions. Please ensure you have all raw data underlying the figures quickly accessible in case this is necessary.
- When you split up your single PDF for final file submission, please ensure that the Supplemental information (figures, tables, and legends) is uploaded as a single PDF file.
- The supplemental section should be organized so that the relevant figure legend is placed beneath each Supplementary figure. The text should be Times New Roman (10 point) with single (left) justification of all text in the Supplemental document.
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STAR Methods

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- RESOURCE AVAILABILITY: We have just changed our guidelines for this section to require three subsections: Lead Contact, Materials Availability, and Data and Code Availability.
- In the Lead Contact subsection, we require identification and contact information for a Lead Contact, who is the main point of contact for responding to material and resource requests. Please provide the full name and email address for the author taking responsibility for the Lead Contact role. Sample text to include: Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Jane Doe (janedoe@qwerty.com).
- Under the Materials Availability subheading in the Resource Availability section, we require a "Materials Availability Statement" even if no reagents were generated in the study.
- Examples of the types of appropriate "Materials Availability Statements" are below and the Information for Authors provides further details on the Cell Press Materials Sharing policy. A combination of these Statements may be appropriate:
    - Plasmids generated in this study have been deposited to [Addgene, name and catalog number or unique identifier].
    - Mouse lines generated in this study have been deposited to [the Knockout Mouse Project (KOMP), name and catalog number or unique identifier].
    - This study did not generate new unique reagents.
    - There are restrictions to the availability of [reagent] due to the lack of an external centralized repository for its distribution and our need to maintain the stock. We are glad to share [reagent] with reasonable compensation by requestor for its processing and shipping.
    - [Reagent] generated in this study will be made available on request, but we may require a payment and/or a completed Materials Transfer Agreement if there is potential for commercial application.
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    - The published article includes all [datasets/code] generated or analyzed during this study.
    - The [datasets/code] supporting the current study have not been deposited in a public repository because [REASON WHY DATA ARE NOT PUBLIC], but are available from the corresponding author on request.
    - There are restrictions to the availability of [dataset/code] due to [REASON WHY RESTRICTIONS EXIST]
    - Original/source data for [figures/datatype] in the paper is available [i.e. Mendeley Data DOI]
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Sincerely,
Gail

Gail Teitzel, Ph.D.
Deputy Editor, Cell Reports

Reviewer comments:

Reviewer #1: (Comments for the author)
The authors have addressed my concerns and the concerns of the other reviewer and have significantly strengthened what was already a strong manuscript.

Reviewer #2: Author's were responsive to previous reviewer concerns. No further comments.

To: Heise, Mark T[mark_heisem@med.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Morrison, Thomas[THOMAS.MORRISON@CUANSCHUTZ.EDU]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Menachery, Vineet[vimenach@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]
Cc: Noll, Kelsey[kenoll@email.unc.edu]; mtferris[mtferris@email.unc.edu]
From: Shannon McWeeney[mcweeney@ohsu.edu]
Sent: Mon 3/16/2020 3:07:16 PM (UTC-05:00)
Subject: Re: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Great news!! Whoo hoo Kelsey ! Great job all
S

Shannon McWeeney PhD
Professor and Division Head, Bioinformatics and Computational Biology
Associate Director, Computational Biomedicine
OHSU Knight Cancer Institute

Administrative Assistant: Nicole Durchanek
Email: durchane@ohsu.edu
Phone: 503-418-9667

From: Mark T Heise <mark_heisem@med.unc.edu>
Date: Monday, March 16, 2020 at 12:46 PM
To: "fernando_pardo-manuel@med.unc.edu" <fernando_pardo-manuel@med.unc.edu>, Ralph Baric <rbaric@email.unc.edu>, Shannon McWeeney <mcweeney@ohsu.edu>, "Morrison, Thomas" <THOMAS.MORRISON@CUANSCHUTZ.EDU>, "Schughart, Klaus" <Klaus.Schughart@helmholtz-hzi.de>, "Menachery, Vineet" <vimenach@UTMB.EDU>, "Plante, Kenneth S." <ksplante@UTMB.EDU>
Cc: "Noll, Kelsey" <kenoll@email.unc.edu>, Marty Ferris <mtferris@email.unc.edu>
Subject: FW: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Hi Everyone,
Good news. Kelsey's manuscript was accepted. Thank you for all of the help on this and please pass on to the other authors in your research groups.
Best
Mark

From: em.cell-reports.0.69fa61.aaee7413@editorialmanager.com <em.cell-reports.0.69fa61.aaee7413@editorialmanager.com>
On Behalf Of Cell Reports
Sent: Monday, March 16, 2020 1:47 PM
To: Heise, Mark T <mark_heisem@med.unc.edu>
Subject: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Dr. Mark Heise
The University of North Carolina
Genetics
9039 Burnett Womack Building
Campus Box 7292
Chapel Hill, NC 27599
UNITED STATES

Complex genetic architecture underlies regulation of influenza A virus-specific antibody responses in the Collaborative

Cross
CELL-REPORTS-D-19-04583R1

Mar 16, 2020

Dear Dr. Heise,

I am pleased to let you know that, based on your revisions and the reviewer comments below, your manuscript has now been "accepted in principle" as a Research Article at Cell Reports.

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    - The published article includes all [datasets/code] generated or analyzed during this study.
    - The [datasets/code] supporting the current study have not been deposited in a public repository because [REASON WHY DATA ARE NOT PUBLIC], but are available from the corresponding author on request.
    - There are restrictions to the availability of [dataset/code] due to [REASON WHY RESTRICTIONS EXIST]
    - Original/source data for [figures/datatype] in the paper is available [i.e. Mendeley Data DOI]
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Gail

Gail Teitzel, Ph.D.
Deputy Editor, Cell Reports

Reviewer comments:

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Cc: Noll, Kelsey[kenoll@email.unc.edu]; mtferris[mtferris@email.unc.edu]
From: Morrison, Thomas[THOMAS.MORRISON@CUANSCHUTZ.EDU]
Sent: Mon 3/16/2020 3:14:53 PM (UTC-05:00)
Subject: Re: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Congratulations! Nice to receive some good news!!

From: "Baric, Ralph S"
Date: Monday, March 16, 2020 at 2:06 PM
To: "Heise, Mark T", "Pardo Manuel de Villena, Fernando", "McWeeney, Shannon", "Morrison, Thomas", "Schughart, Klaus", "Menachery, Vineet", "Plante, Kenneth S."
Cc: "Noll, Kelsey", mtferris
Subject: RE: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Awesome, Congrats Kelsey! Congrats Everyone!

From: Heise, Mark T <mark_heisem@med.unc.edu>
Sent: Monday, March 16, 2020 3:41 PM
To: Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Morrison, Thomas <THOMAS.MORRISON@CUANSCHUTZ.EDU>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Cc: Noll, Kelsey <kenoll@email.unc.edu>; mtferris <mtferris@email.unc.edu>
Subject: FW: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Hi Everyone,
Good news. Kelsey's manuscript was accepted. Thank you for all of the help on this and please pass on to the other authors in your research groups.
Best
Mark

From:em.cell-reports.0.69fa61.aaee7413@editorialmanager.com <em.cell-reports.0.69fa61.aaee7413@editorialmanager.com>
On Behalf Of Cell Reports
Sent: Monday, March 16, 2020 1:47 PM
To: Heise, Mark T <mark_heisem@med.unc.edu>
Subject: Editorial Decision on Cell Reports manuscript CELL-REPORTS-D-19-04583R1

Dr. Mark Heise
The University of North Carolina
Genetics
9039 Burnett Womack Building
Campus Box 7292
Chapel Hill, NC 27599
UNITED STATES

Complex genetic architecture underlies regulation of influenza A virus-specific antibody responses in the Collaborative Cross
CELL-REPORTS-D-19-04583R1

Mar 16, 2020

Dear Dr. Heise,

I am pleased to let you know that, based on your revisions and the reviewer comments below, your manuscript has now been "accepted in principle" as a Research Article at Cell Reports.

Before we can formally accept your manuscript, we require that the final files are uploaded according to our production guidelines as outlined in our Final Files Checklist. We would like to have your final materials within 10 days, but please let us know if you think that you may need more time. Once we receive your final files, we can move forward with accepting your manuscript and scheduling it for publication.

Please note that our article length guidelines have been recently adjusted to reflect that references are no longer counted towards the overall character count of the manuscript. The revised manuscript should conform to the general length restriction for a Research Article, which is **45,000 characters** (including spaces and figure legends) and no more than **7 figures and/or tables**. This count does not include STAR Methods or any supplemental legends, or the reference list. There is some flexibility here, so please contact us to discuss this further.

Please pay attention to the following points when preparing your revised paper:

- To avoid errata, you should **double check all files carefully and ensure that all figure panels are accurate.**
- **Author names cannot be corrected later, thus you should ask all co-authors to carefully check the spelling of their names.**
- I have a few suggestions for the eTOC blurb to trim this to within our guidelines as the eTOC blurb can be up to 50 words. I will email these to you separately I will email these to you separately. Please feel free to modify my suggestions while keeping within these length limits.
- Please submit the main-text figures in individual high resolution files (TIF or high resolution PDF) and ensure that gel and microscopy images are at least 300 pixels per inch at final print size. For clear and accurate presentation of your data, we strongly recommend a vector graphics program (such as Adobe Illustrator or Inkscape) to assemble the figures and verify that at final print size, each displayed image is at least 300 pixels per inch. Note that programs such as Word or Powerpoint often reduce the resolution of primary data images and this should be checked carefully before resubmission.
- Figure legends should include information on biological and technical replicates.
- We routinely implement post-accept figure checks for papers at Cell Press. Thus, we may need to see the original data (uncropped, unlabeled images) for your figures. If so, I'll be in touch with specific instructions. Please ensure you have all raw data underlying the figures quickly accessible in case this is necessary.
- When you split up your single PDF for final file submission, please ensure that the Supplemental information (figures, tables, and legends) is uploaded as a single PDF file.
- The supplemental section should be organized so that the relevant figure legend is placed beneath each Supplementary figure. The text should be Times New Roman (10 point) with single (left) justification of all text in the Supplemental document.
- Each Supplemental figure or table should be linked to at least one main-text figure or table, and/or to STAR Methods. This is indicated in the legend for the Supplemental figure; for example, "Figure S1. Flies lacking YFG do not exhibit changes in grooming behavior. Related to Figures 1 and 3." Every Supplemental figure must be cited at least once in the main text.

STAR Methods

Thank you for including the STAR Methods and Key Resources Table with your revised manuscript. I am including a few further suggestions, particularly as our guidelines are currently changing.

- GENERAL:STAR Methods follows a standardized structure. Please include these specific headings in the following order: RESOURCE AVAILABILITY; EXPERIMENTAL MODEL AND SUBJECT DETAILS; METHOD DETAILS; QUANTIFICATION AND STATISTICAL ANALYSIS; ADDITIONAL RESOURCES. The list below details the information that should be reported in each section. Please see the STAR Methods guide

for more information or contact me for help.

- RESOURCE AVAILABILITY: We have just changed our guidelines for this section to require three subsections: Lead Contact, Materials Availability, and Data and Code Availability.
- In the Lead Contact subsection, we require identification and contact information for a Lead Contact, who is the main point of contact for responding to material and resource requests. Please provide the full name and email address for the author taking responsibility for the Lead Contact role. Sample text to include: Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Jane Doe (janedoe@qwerty.com).
- Under the Materials Availability subheading in the Resource Availability section, we require a "Materials Availability Statement" even if no reagents were generated in the study.
- Examples of the types of appropriate "Materials Availability Statements" are below and the Information for Authors provides further details on the Cell Press Materials Sharing policy. A combination of these Statements may be appropriate:
    - Plasmids generated in this study have been deposited to [Addgene, name and catalog number or unique identifier].
    - Mouse lines generated in this study have been deposited to [the Knockout Mouse Project (KOMP), name and catalog number or unique identifier].
    - This study did not generate new unique reagents.
    - There are restrictions to the availability of [reagent] due to the lack of an external centralized repository for its distribution and our need to maintain the stock. We are glad to share [reagent] with reasonable compensation by requestor for its processing and shipping.
    - [Reagent] generated in this study will be made available on request, but we may require a payment and/or a completed Materials Transfer Agreement if there is potential for commercial application.
    - All unique/stable reagents generated in this study are available from the Lead Contact without restriction.
    - All unique/stable reagents generated in this study are available from the Lead Contact with a completed Materials Transfer Agreement.
- Under the Data and Code Availability subheading in the Resource Availability section, we require a Data and Code Availability Statement.
- Examples of "Data and Code Availability Statements" are below. Statements with multiple types of datasets may use a combination of statements.
    - The [datasets/code] generated during this study are available at [NAME OF REPOSITORY] [ACCESSION CODE/WEB LINK]
    - The published article includes all [datasets/code] generated or analyzed during this study.
    - The [datasets/code] supporting the current study have not been deposited in a public repository because [REASON WHY DATA ARE NOT PUBLIC], but are available from the corresponding author on request.
    - There are restrictions to the availability of [dataset/code] due to [REASON WHY RESTRICTIONS EXIST]
    - Original/source data for [figures/datatype] in the paper is available [i.e. Mendeley Data DOI]
    - Original/source data for [figures/datatype] in the paper is available in supplemental figure X
    - The [datasets/code] supporting the current study have not been deposited in a public repository because [REASON WHY DATA ARE NOT PUBLIC] but are available from the corresponding author on request.
- If the paper does not generate any new data or code, it is appropriate to state the following:
    - This study did not generate any unique datasets or code.
- KEY RESOURCES TABLE (KRT): Some citations also include journal name and this can be removed so that the citations use author name and year as in the main text. Please add the DOIs for the Mendeley Data datasets

Please be sure that the STAR Methods section is in the main Word document and appears after the figure legends. Note that there should be no Supplemental Experimental Procedures or supplemental references section. You can consult the STAR Methods website for further details and for the Key Resources Table template. You may also create the Key Resources Table using this interactive webform. The following are specific issues that need to be addressed in your STAR Methods. **Please email me with any questions (**gteitzel@cell.com**).**

The Final Files Checklist is provided to make sure your paper complies with our guidelines and everything is in order. We suggest having multiple authors review the checklist and revised materials to ensure that all items are complete. If you have any questions about any of the points in the final file checklist, please email us at reports@cell.com.

Please upload your final files to our https://www.editorialmanager.com/cell-reports/ as a revision of CELL-REPORTS-D-19-04583R1. When you submit your revised files, our team will check them and will contact you if there are any remaining formatting issues that need to be resolved. We will also share any editorial comments on the revised files at this point.

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Consider submitting one of your protocols to STAR Protocols, the new protocols journal from Cell Press. STAR Protocols aims to make the daily work of the scientific researcher easier by providing complete, authoritative, and consistent instructions on how to conduct experiments. STAR Protocols gives scientists the space they need to explain what worked and, perhaps more importantly, what didn't. The primary criteria for publication in STAR Protocols is usability and reproducibility. You can check out their most recent protocols here. If would like to submit your Protocol, please visit their submissions site. If you have any questions, please email starprotocols@cell.com.

Please note that your paper is not formally accepted at this stage and cannot be until we receive the materials listed above. Please let me know if you have any questions, and I look forward to hearing from you.

Sincerely,
Gail

Gail Teitzel, Ph.D.
Deputy Editor, Cell Reports

Reviewer comments:

Reviewer #1: (Comments for the author)
The authors have addressed my concerns and the concerns of the other reviewer and have significantly strengthened what was already a strong manuscript.

Reviewer #2: Author's were responsive to previous reviewer concerns. No further comments.

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: McDonald, David (NIH/NIAID) [E]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif; Jacques Banchereau

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif

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Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi Everyone,

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Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. 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Subject: SARS-CoV-2 Weekly Investigators Meeting

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Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal
Start Time: Tue 2/9/2021 2:00:00 PM (UTC)
End Time: Tue 2/9/2021 3:00:00 PM (UTC)
Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Weaver, Scott; Plante, Kenneth S.

Hi Everyone,

We will be incorporating COVID-19 Cohort presentations to our arsenal of talks. As a reminder, the goal for the weekly SARS-CoV-2 Investigators meeting is to provide a platform that is informative and encourages collaboration.

If you would like to present your research, please let me know. *

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Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 2/16/2021 2:00:00 PM (UTC)

End Time: Tue 2/16/2021 5:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. 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Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID)

[E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]

Hi Everyone!

Due to a last minute cancellation, we will NOT be having tomorrow's weekly Investigators meeting. We will resume on Tuesday, February 23rd.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 2/23/2021 2:00:00 PM (UTC)

End Time: Tue 2/23/2021 3:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Wentworth, David E. (CDC/DDID/NCIRD/ID); cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. 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Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 6/15/2021 1:00:00 PM (UTC)

End Time: Tue 6/15/2021 2:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. 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Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. 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samantha.l.grimes@vanderbilt.edu; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Bratt, Debbie (NIH/NIAID) [C]; Patterson, Jean (NIH/NIAID) [E]; Priya Luthra; Malloy, Allison; ckabengele@rzhrg-mail.org

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 5/25/2021 1:00:00 PM (UTC)
End Time:	Tue 5/25/2021 2:00:00 PM (UTC)
Required Attendees:	Stevens, Rick L.; Jesse ErasmusLampley, Rebecca (NIH/NIAID) [C]; Lockmuller, Jane (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Katzelnick, Leah (NIH/NIAID) [E]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID)

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Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 6/1/2021 1:00:00 PM (UTC)

End Time: Tue 6/1/2021 2:00:00 PM (UTC)

Required Attendees: Stacey Schultz-Cherry; vimenach@UTMB.EDU; Michael J Gale; sweaver@utmb.edu; alrouth@utmb.edu; Lampley, Rebecca (NIH/NIAID) [C]; Aubree Gordon; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. 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cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); Routh, Andrew L.; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David

CANCELING to give you all time to catch up from the long weekend

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 6/22/2021 1:00:00 PM (UTC)
End Time:	Tue 6/22/2021 2:00:00 PM (UTC)
Required Attendees:	Jennifer Rebecca German; Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy

(NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Bratt, Debbie (NIH/NIAID) [C]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Patterson, Jean (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Coughlan, Lynda; Midgley, Claire (CDC/DDID/NCIRD/DVD); Miller, Benjamin; Priya Luthra; sweaver@utmb.edu; Lowen, Anice; Pickett, Thames (NIH/NIAID) [E]; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela; Rogan Grant

Importance: Normal

Start Time: Tue 6/8/2021 1:00:00 PM (UTC)

End Time: Tue 6/8/2021 2:00:00 PM (UTC)

Required Attendees: Stevens, Rick L.; Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Huyen.cao@hhs.gov; Patterson, Jean (NIH/NIAID) [E]; Coughlan, Lynda; Miller, Benjamin; Priya Luthra; sweaver@utmb.edu; Sabra Klein; Ghazi Kayali; Pickett, Thames (NIH/NIAID) [E]; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; cmichelo@rzhrg-mail.org; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan

A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Bratt, Debbie (NIH/NIAID) [C]; Nanishi, Etsuro; Borriello, Francesco; Dowling, David

Importance: Normal

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End Time: Tue 8/17/2021 2:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Charles Russell; S. Mark Tompkins; Paul Thomas; Andrea Sant; Ali Ellebedy; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Roberts, Chris (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Priya Luthra; Sabra Klein; Ghazi Kayali; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; Malloy, Allison; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Uccellini, Melissa; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.;

Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; sweaver@utmb.edu; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Coughlan, Lynda; Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov

Importance:	Normal
Start Time:	Tue 6/29/2021 1:00:00 PM (UTC)
End Time:	Tue 6/29/2021 2:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Huyen.cao@hhs.gov; Seema Lakdawala; sweaver@utmb.edu; Ghazi Kayali; WVanVoorhis@medicine.washington.edu; Pickett, Thames (NIH/NIAID) [E]; Cammarata, Sue (OS/ASPR/IO) (CTR); rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; andrzejj@anl.gov; fullerdh@uw.edu; cmichelo@rzhrg-mail.org; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-

mccray@uiowa.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Nanishi, Etsuro; Borriello, Francesco; Dowling, David

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott

Location: https://www.zoomgov.com/j/1602664950?pwd= **552.136** **552.136**

Importance: Normal

Subject: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 2/12/2021 7:30:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 8:30:00 AM (UTC-06:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil;

irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]

Importance: Normal

Start Time: Fri 3/12/2021 1:30:00 PM (UTC)

End Time: Fri 3/12/2021 2:30:00 PM (UTC)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Meeting ID: 160 266 4950
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+16692545252,,1602664950#,,,, **552.136** US (San Jose)
+16468287666,,1602664950#,,,, US (New York)

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
833 568 8864 US Toll-free

Meeting ID: 160 266 4950
Passcode: 552.136
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP
1602664950@sip.zoomgov.com

Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
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From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar,

Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif; Warner, Blake (NIH/NIDCR) [E]; Joseph, Paule (NIH/NIAAA) [E]; Kim, Sonnie (NIH/NIAID) [E]; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E]

Sent: Tue 2/9/2021 8:13:02 AM (UTC-06:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 2/9/2021 8:00:00 AM (UTC-06:00)

End Time: Tue 2/9/2021 9:00:00 AM (UTC-06:00)

Required Attendees: Weaver, Scott; Plante, Kenneth S.; Weaver, Scott; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-

mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.govLampley, Rebecca (NIH/NIAID) [C]; Weaver, Scott

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Hi Everyone,

We will be incorporating COVID-19 Cohort presentations to our arsenal of talks. As a reminder, the goal for the weekly SARS-CoV-2 Investigators meeting is to provide a platform that is informative and encourages collaboration.

If you would like to present your research, please let me know. *

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 2/23/2021 2:00:00 PM (UTC)

End Time: Tue 2/23/2021 3:00:00 PM (UTC)

Required Attendees: Stacey Schultz-Cherry; vimenach@UTMB.EDU; Michael J Gale; ksplante@UTMB.EDU; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.govLampley, Rebecca (NIH/NIAID) [C]; Wentworth, David E. 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Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu;

jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 6/15/2021 1:00:00 PM (UTC)

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Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. 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Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. 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pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Bratt, Debbie (NIH/NIAID) [C]; Patterson, Jean (NIH/NIAID) [E]; Priya Luthra; Malloy, Allison; ckabengele@rzhrg-mail.org

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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

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(CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. 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Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno,

James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Eva Harris; Fausto Bustos; Ricotta, Emily (NIH/NIAID) [E]; Coughlan, Lynda

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Rebecca

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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

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Required Attendees: Jennifer Rebecca German; Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. 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marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela; Rogan Grant

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Stay safe,
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Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

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Required Attendees: Stevens, Rick L.; Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. 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Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. 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Rebecca

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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 8/17/2021 1:00:00 PM (UTC)

End Time: Tue 8/17/2021 2:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. 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rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; Malloy, Allison; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela

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Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

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Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. 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Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD);

Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Nanishi, Etsuro; Borriello, Francesco; Dowling, David

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso (Anthony.Macaluso@tonixpharma.com); boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman (coleman@codagenix.com); rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; Thien Do (dothuanthien@vabiotech.com.vn); dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo (fguirakhoo@geovax.com); farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); greanggrai.h@bionet-asia.com; guido.grandi@unitn.it; 秀樹 長谷川 (hasegawa@nih.go.jp); hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen (hlchen@hku.hk); Holger.Martinius@neovii.com; hotez (hotez@bcm.edu); huyl@sinovac.com; james.hayward (james.hayward@adnas.com); James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; Ilse Roodink (iroodink@immunoprecise.com); JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice (jprice@greffex.com); jwolf (jwolf@heatbio.com); kandeil_a (kandeil_a@hotmail.com); Kapil Maithal (Kapil.Maithal@zyduscadila.com); khirullin@mail.ru; Kayvon Modjarrad (kmodjarrad@eidresearch.org); kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban (mesteban@cnb.csic.es); mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; Munir, Muhammad; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; Hodgson, Paul; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd (prasadsd@bharatbiotech.com); qinjian_zhao (qinjian_zhao@xmu.edu.cn); Liang Qu (Jenny) (quliang@sinopharm.com); Ricardo.Gazzinelli@umassmed.edu; Webby, Richard; roland.tschismarov@themisbio.com; Christiane Gerke (christiane.gerke@pasteur.fr); Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker (stucker@vaxart.com); sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg (vgarg@altimmune.com); wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar

(Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; GILBERT Nick; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; GILBERT Nick; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

Sent: Sun 1/3/2021 10:32:39 PM (UTC-06:00)
Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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149.137.40.110 (Singapore)
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69.174.57.160 (Canada)
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From: Stephanie Moore[smoore@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; Amelia George; Anish Avadukoot; Ardina Pruijssers; Ashish Pathak; Babu Tekwani; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; Chelsea Tompkins; Clare O'Regan; Corinne Augelli-Szafran; 'Daniel Streblow'; 'Erica Bitten'; Fahim Ahmad; George Painter; Greg Bluemling; 'Jay Nelson'; Jessica Smith; Jim Chappell; Kathy Keith; Lynn Rasmussen; 'Maria Agostini'; Mark Denison ; Mark Heise; 'Mark Suto'; Mason Wu; 'Michael Diamond'; 'Miranda Nebane'; Narayan Chaurasiya; Nichole Tower; Nicole Haese; Omar Moukha-Chafiq; Shi, Pei yong; Rachel Graham; 'Ralph Baric'; Richard Whitley, M.D.; Ron Swanstrom; Sarah M. Dowdy; Shalisa Sanders; Shilpa Dutta; Shuntai Zhou; Sixue Zhang; Tameca Winston; Thomas Morrison; Tia Hughes; Tim Sheahan; 'Toni Baric'; Victor DeFilippis

Location: https://uab.zoom.us/j/96769424930?pwd=[redacted] S05hZzdsZz09

Importance: Normal

Subject: FW: AD3C Monthly Meeting

Start Time: Thur 1/28/2021 3:30:00 PM (UTC-06:00)

End Time: Thur 1/28/2021 5:00:00 PM (UTC-06:00)

Required Attendees: Stephanie Moore; 'Alana Centilli'; 'Alec Hirsch'; Amelia George; Anish Avadukoot; Ardina Pruijssers; Ashish Pathak; Babu Tekwani; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; Chelsea Tompkins; Clare O'Regan; Corinne Augelli-Szafran; 'Daniel Streblow'; 'Erica Bitten'; Fahim Ahmad; George Painter; Greg Bluemling; 'Jay Nelson'; Jessica Smith; Jim Chappell; Kathy Keith; Lynn Rasmussen; 'Maria Agostini'; Mark Denison ; Mark Heise; 'Mark Suto'; Mason Wu; 'Michael Diamond'; 'Miranda Nebane'; Narayan Chaurasiya; Nichole Tower; Nicole Haese; Omar Moukha-Chafiq; Shi, Pei yong; Rachel Graham; 'Ralph Baric'; Richard Whitley, M.D.; Ron Swanstrom; Sarah M. Dowdy; Shalisa Sanders; Shilpa Dutta; Shuntai Zhou; Sixue Zhang; Tameca Winston; Thomas Morrison; Tia Hughes; Tim Sheahan; 'Toni Baric'; Victor DeFilippis

-----Original Appointment-----
From: Stephanie Moore
Sent: Wednesday, January 6, 2021 12:21 PM
To: Stephanie Moore; Antiviral Drug Discovery and Development Center-AD3C; Sara Davis
Subject: AD3C Monthly Meeting
When: Occurs the fourth Thursday of every 1 month(s) effective 1/28/2021 until 10/28/2021 from 3:30 PM to 5:00 PM (UTC-06:00) Central Time (US & Canada).
Where:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fuab.zoom.us%2Fj%2F96769424930%3Fpwd%3DMm9Wd3EwOC8rZXFKaHR6S05hZzdsZz09&data=04%7C01%7Cpeshi%40utmb.edu%7C4724f355f369472934ec08d8b27273b5%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637455551923655613%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=wMYNPG5w2QwN0i1XdTCbZF7BcQvvo0HxFXp2xD2UtXk%3D&reserved=0

When: Thursday, January 28, 2021 3:30 PM-5:00 PM. (UTC-06:00) Central Time (US & Canada)

Where:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fuab.zoom.us%2Fj%2F96769424930%3Fpwd%3DMm9Wd3EwOC8rZXFKaHR6S05hZzdsZz09&data=04%7C01%7Cpeshi%40utmb.edu%7C4724f355f369472934ec08d8b27273b5%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637455551923655613%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=wMYNPG5w2QwN0i1XdTCbZF7BcQvvo0HxFXp2xD2UtXk%3D&reserved=0

+~+~+~+~+~+~+~+~+~+
Hello all,

Here is the invite for our monthly AD3C meeting, scheduled for the fourth Thursday of each month from 3:30 to 5:00 pm Central Time.

Thank you!

AD3C administrative team

Join Zoom Meeting
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Meeting ID: 967 6942 4930
Passcode: **552.136**

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov

Sent: Sun 1/10/2021 4:22:20 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela

Sent: Sun 1/24/2021 4:00:53 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Please note this meeting will be 1.5hrs instead of the usual one hour to allow for an additional presentation and discussion on the new variant.

Agenda to follow.

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From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

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Importance: Normal

Subject: SARS-CoV2 Variant Testing Discussion

Start Time: Thur 1/28/2021 7:00:00 AM (UTC-06:00)

End Time: Thur 1/28/2021 8:00:00 AM (UTC-06:00)

Required Attendees: Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina; gweiss@uci.edu; ZHOU, Tiequn; YOO, Si Hyung; Sutter Roland

Sent: Mon 11/9/2020 2:45:41 AM (UTC-06:00)

Subject: [COVID-19] 37th WHO TC - Assays

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela

Sent: Sun 1/31/2021 11:16:11 AM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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103.122.166.55 (Australia)
149.137.40.110 (Singapore)

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69.174.57.160 (Canada)
207.226.132.110 (Japan)
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From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Importance:	Normal
Subject:	Canceled: Monthly AD3C Project/Core Teleconference Call
Start Time:	Thur 1/23/2020 4:30:00 PM (UTC-05:00)
End Time:	Thur 1/23/2020 6:00:00 PM (UTC-05:00)
Required Attendees:	'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Tameca Winston; 'Nicole Haese'; Jessica Eagar
Optional Attendees:	'Suto, Mark J.'; 'Rasmussen, Lynn'; 'Swanstrom, Ronald I'; 'Morrison, Thomas'; 'Sides, Kate'

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute; alain.townsend (alain.townsend@imm.ox.ac.uk)

Sent: Sun 2/7/2021 1:27:29 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and call-in information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday February 10 2:30PM CET (Geneva Time)

1. Alain Townsend (University of Oxford)- *A haemagglutination test for rapid detection of antibodies to SARS-CoV-2*
2. David Montefiori (Duke) - *SARS-CoV-2 variant B.1.1.7 is susceptible to neutralizing antibodies elicited by ancestral Spike vaccines*

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute

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Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org);

david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute; alain.townsend (alain.townsend@imm.ox.ac.uk)

Sent: Sun 2/7/2021 1:27:14 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]

Importance: Normal

Subject: Canceled: Monthly AD3C Project/Core Teleconference Call

Start Time: Thur 1/23/2020 4:30:00 PM (UTC-05:00)

End Time: Thur 1/23/2020 6:00:00 PM (UTC-05:00)

Required Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Tameca Winston; 'Nicole Haese'

Optional Attendees: 'Suto, Mark J.'; 'Rasmussen, Lynn'; 'Swanstrom, Ronald I'; 'Morrison, Thomas'; 'Sides, Kate'

Hello To Everyone:

Just to be safe, I am sending a second message to confirm the cancellation of the monthly AD3C Project/Core Zoom Meeting call at this time. I may have cancelled the Zoom meeting, but not removed this entry from your calendars. This message should accomplish the latter, and remove it from your Outlook calendar. At this time, because many of our institutions are not operating at full capacity, there isn't a lot of monthly progress to report at this time. When we are back to normal operations, we will send a new meeting notice.

However, if anyone would like to discuss anything during this time, please reach out to our Admin Core group and we can arrange a call as needed.

Thank you!

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
Cell Phone: 205.725.0543 | sadavis@peds.uab.edu

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak (daszak@ecohealthalliance.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim

Sent: Sun 3/7/2021 10:51:20 AM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

Join Zoom Meeting
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213.244.140.110 (Germany)
103.122.166.55 (Australia)

149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak (daszak@ecohealthalliance.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; Kemp, Troy (NIH/NCI) [C]; Pinto, Ligia (NIH/NCI) [C]

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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; 'HENAO RESTREPO, Ana Maria'; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya; zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; viviana.simon@mssm.edu;

pintol@mail.nih.gov; kemptj@mail.nih.gov; Jacqueline.Fryer@nibsc.org; Kevin Bewley (Kevin.bewley@phe.gov.uk); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; euiho.kim@ip-korea.org; David Vaughn; Eddins, Ryan (OS/ASPR/BARDA); Maria Keramarou; Sinha, Tanima (OS/ASPR/BARDA); Chaitram, Jasmine (CDC/DDPHSS/CSELS/DLS); Camille Escadafal; Knight, Brittany; Lohman, Kent

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); viviana.simon; pintol; kemptj; Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Camille Escadafal; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA)

Sent: Sun 4/11/2021 9:47:41 AM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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69.174.57.160 (Canada)
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From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; Sara Davis

Location: Zoom format, please see instructions contained in the message

Importance: Normal

Subject: AD3C Monthly Meeting for Project/Core Discussions

Start Time: Thur 6/25/2020 3:30:00 PM (UTC-05:00)

End Time: Thur 6/25/2020 5:00:00 PM (UTC-05:00)

Required Attendees: Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'

Optional Attendees: Sara Davis

AD3C Zoom Meeting invitation

Steph Moore is inviting you to a scheduled Zoom meeting.
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13.19.144.110 (EMEA)
03.122.166.55 (Australia)
09.9.211.110 (Hong Kong SAR)
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assword: **552.136**

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); viviana.simon; pintol; kemptj; Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Camille Escadafal; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA)

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Agenda to follow.

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Attendees:	'Fred Hayden'; 'Kara Carter'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'
Location:	Connection Details and Meeting Platform will be communicated closer to the meeting date
Importance:	Normal
Subject:	AD3C Annual Meeting (VIRTUAL)
Start Time:	Thur 11/12/2020 1:00:00 AM (UTC-05:00)
End Time:	Fri 11/13/2020 1:00:00 AM (UTC-05:00)
Required Attendees:	Antiviral Drug Discovery and Development Center-AD3C; 'Fred Hayden'; 'Kara Carter'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'

From:	Macoubray, Aaron[amacoubray@rti.org]
Attendees:	Bronwyn MacInnis; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan
Location:	https://rtiorg.zoom.us/j/98355183025?pwd= **552.136** **552.136**
Importance:	Normal
Subject:	CREID EBOV Discussion
Start Time:	Fri 4/23/2021 2:00:00 PM (UTC-05:00)
End Time:	Fri 4/23/2021 3:00:00 PM (UTC-05:00)
Required Attendees:	Bronwyn MacInnis; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Vasan, Vasan (H&B, Geelong ACDP); a.luttick; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); tlying (tlying@fudan.edu.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); baihe (baihe@nmpa.gov.cn); zlshi (zlshi@wh.iov.cn); Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); rawcraig@yahoo.com; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); christian.drosten (christian.drosten@charite.de); Barbara.Schnierle (Barbara.Schnierle@pei.de); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; epstein@ecohealthalliance.org; Peter Daszak; christian.brechot (christian.brechot@pasteur.fr); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); Boyle, David; de los Santos, Tala; Leader, Troy; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; malik (malik@hku.hk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); Daniel Cohen (dancohen@tauex.tau.ac.il); Youngmee Jee (jeey62@gmail.com); alankhoo.imr; Celine Gurry (Celine.gurry@cepi.net); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); ramadany; linfa.wang (linfa.wang@duke-nus.edu.sg); engeong.ooi; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); qiang.pan-hammarstrom@ki.se; Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); pilailuk.o (pilailuk.o@dmsc.mail.go.th); pawinee.k@redcross.or.th; B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Javier Castillo-Olivares Pallardo; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); r.tedder@imperial.ac.uk; katie.doores (katie.doores@kcl.ac.uk); Liz Miller (Liz.Miller@lshtm.ac.uk); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; jma; GILBERT Nick; Goldblatt, David; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Griffiths, Anthony; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Chu, May; eric.vangieson@darpa.mil; john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); Sarah Mudrak, Ph.D.; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; McElrath MD PhD, Julie; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Vidadi Yusibov (vyusibov@indianabiosciences.org); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; daniela@lji.org; Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Lee, William T (HEALTH); tcs38@psu.edu; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Marc L Salit (msalit@stanford.edu); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu);

wilsonp@uchicago.edu; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); rbaric (rbaric@email.unc.edu); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); Theodora Hatziioannou; jakim; Donis, Ruben (OS/ASPR/BARDA); renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; viviana.simon; pintol; kemptj; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA); Iturriza-Gomara, Miren; david.montefiori@duke.edu; sujan@lji.org; Camille Escadafal

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162.255.36.11 (US East)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; Sara Davis

Location: Zoom format, please see instructions contained in the message

Importance: Normal

Subject: AD3C Monthly Meeting for Project/Core Discussions

Start Time: Thur 6/25/2020 3:30:00 PM (UTC-05:00)

End Time: Thur 6/25/2020 5:00:00 PM (UTC-05:00)

Required Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'

Optional Attendees: Sara Davis

AD3C Zoom Meeting invitation

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Password: **552.136**
Or iPhone one-tap :
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Dial(for higher quality, dial a number based on your current location):
US: +1 646 558 8656 or +1 301 715 8592 or +1 312 626 6799 or +1 669 900 6833 or +1 253 215 8782 or +1 346 248 7799
Meeting ID: 946 2553 1176
International numbers available: https://uasystem.zoom.us/u/aiNDytfdU
Or an H.323/SIP room system:
H.323:
62.255.37.11 (US West)
62.255.36.11 (US East)
15.114.131.7 (India Mumbai)
15.114.115.7 (India Hyderabad)
13.19.144.110 (EMEA)
03.122.166.55 (Australia)
09.9.211.110 (Hong Kong SAR)
4.211.144.160 (Brazil)
9.174.57.160 (Canada)
07.226.132.110 (Japan)
Meeting ID: 946 2553 1176
assword: **552.136**

IP: 94625531176@zoomcrc.com
assword: **552.136**

From: Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]

Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Ho, David D.

Location: https://nih.zoomgov.com/j/1619922848?pwd=bzUxRXErSFJ6STNSZklpYXU4cWNIdz09

Importance: Normal

Subject: Leah Vincent (NIAID)'s Zoom Meeting

Start Time: Fri 4/30/2021 7:30:00 AM (UTC-05:00)

End Time: Fri 4/30/2021 8:30:00 AM (UTC-05:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk;

jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov

From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Attendees:	'Fred Hayden'; 'Kara Carter'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'
Location:	Connection Details and Meeting Platform will be communicated closer to the meeting date
Importance:	Normal
Subject:	AD3C Annual Meeting (VIRTUAL)
Start Time:	Thur 11/12/2020 1:00:00 AM (UTC-05:00)
End Time:	Fri 11/13/2020 1:00:00 AM (UTC-05:00)
Required Attendees:	'Fred Hayden'; 'Kara Carter'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'

From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; Sara Davis; Kathy Keith; 'Diamond, Michael'; 'Graham, Rachel'; 'Bostwick, Bob'; 'Suto, Mark J.'; 'Evans, Carrie W.'; 'Swanstrom, Ronald I'

Location: Zoom format, please see instructions contained in the message

Importance: Normal

Subject: AD3C Monthly Meeting for Project/Core Discussions

Start Time: Thur 7/30/2020 3:30:00 PM (UTC-05:00)

End Time: Thur 7/30/2020 5:00:00 PM (UTC-05:00)

Required Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'

Optional Attendees: Sara Davis; Kathy Keith; 'Diamond, Michael'; 'Graham, Rachel'; 'Bostwick, Bob'; 'Suto, Mark J.'; 'Evans, Carrie W.'; 'Swanstrom, Ronald I'

AD3C Zoom Meeting invitation

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Password: **552.136**
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Meeting ID: 946 2553 1176
International numbers available: https://uasystem.zoom.us/u/aiNDytfdU
Or an H.323/SIP room system:
H.323:
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62.255.36.11 (US East)
15.114.131.7 (India Mumbai)
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13.19.144.110 (EMEA)
03.122.166.55 (Australia)
09.9.211.110 (Hong Kong SAR)
4.211.144.160 (Brazil)
9.174.57.160 (Canada)
07.226.132.110 (Japan)
Meeting ID: 946 2553 1176
assword: **552.136**

IP: 94625531176@zoomcrc.com
assword: **552.136**

To: Kara Carter[Kara.Carter@evotec.com]; Shi, Pei yong[peshi@UTMB.EDU]; Ralph Baric[rbaric@email.unc.edu]; Denison, Mark[mark.denison@vumc.org]; Daniel Streblow[streblow@ohsu.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Mike Bray[mikebray10@gmail.com]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Mon 2/10/2020 8:26:20 PM (UTC-06:00)
Subject: NIAID Location tomorrow
Fishers Lane map[1].pptx

Hello all,
Just figured I'd send these details below out again for quick reference. Attached is the map for the meeting location too.

See you in the morning!
-Steph

Meeting Location:
NIAID
5601 Fishers Lane
Rockville MD 20852

Building Access: It is very important that you arrive at the building by **8:30 am Eastern Time** to allow sufficient time to get through security. Domestic travelers will need a government issued ID (i.e. driver's license) to enter the building. We plan to meet as a group in the lobby, but if you are early/late, please call Maureen Beanan at 301-339-4753 when you arrive at the lobby security station and she or one of her colleagues will come down to escort you.

Parking: Parking is available in the garage at 5635 Fishers Lane, Rockville, MD 20852 – the road to the garage is the first left after turning on to Fisher's Lane. The garage will be at the end of a road. Walk back out to Fisher's Lane, turn left and walk one block, cross the street to reach our building, about a 3 minute walk.

Meeting schedule: 9:00 to 11:00 am Part I: (~2.0 hours, including time for questions)
(Audience: This part of the meeting is open to all NIAID staff, including CETR Program Staff and all other interested NIAID staff)

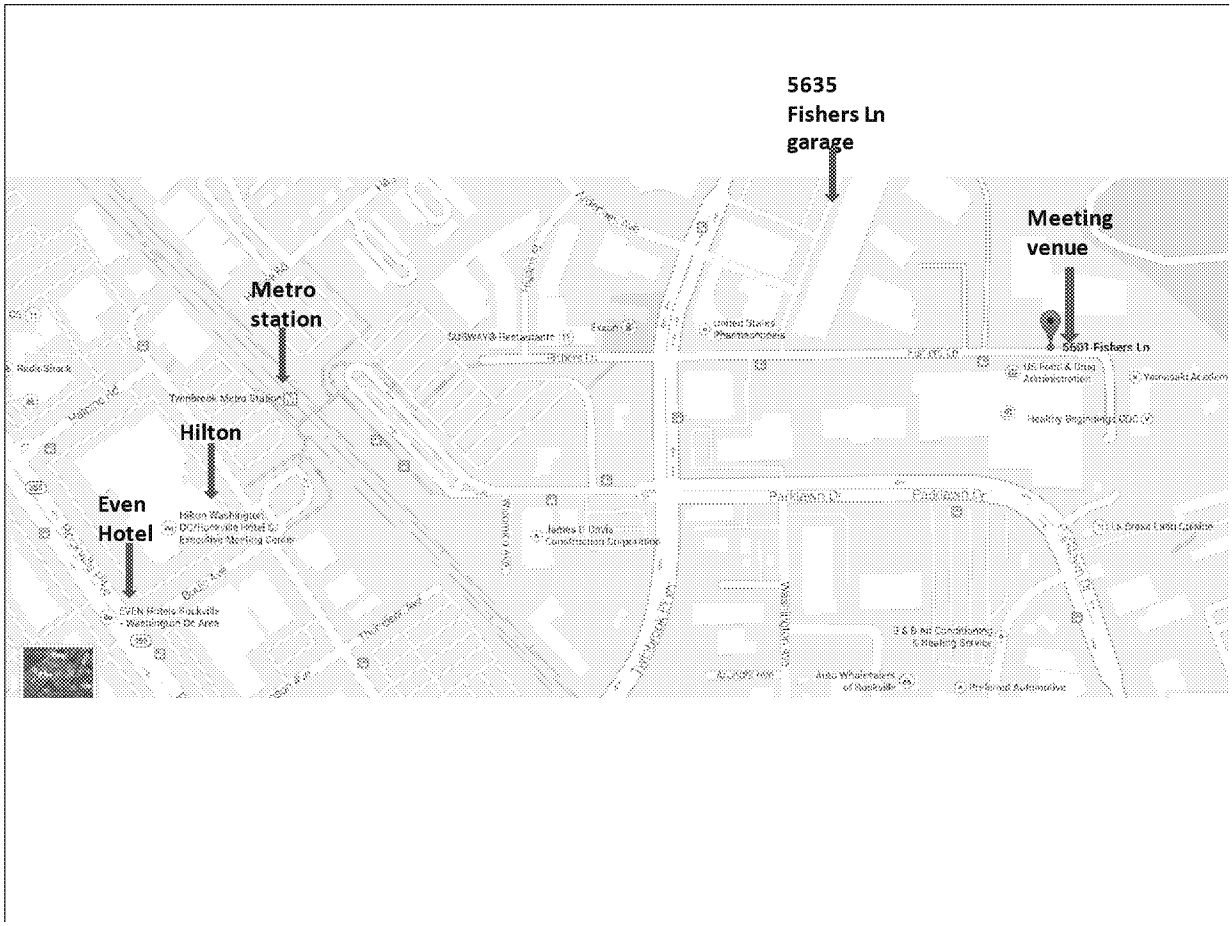
9:00 am NIAID CETR staff welcome participants and Introductions (5 minutes)

9:05 am CETR presentations:

- Brief overview of the Center including the goals, administrative structure, projects, and cores – please include a slide summarizing the progress of depositing the genome sequences into NCBI in this part of the presentation;
- Report on Year 1 activities for each project (~15-20 minutes per project)
- Summarize the status of the project at the end of Year 1 (1 slide)
- Describe the progress on each project during year 1 and plans for remaining 4 years

11:00 am to 12:00 pm Part II: Discussion with CETR Program staff (~0.5 - 1 hour)
Possible topics:

- Senior NIAID staff questions
- Issues that have arisen during year and proposed options
- CETR Program updates
- Annual Progress Report questions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garage
Meeting
venue
Metro
station
Hilton
Even
Hotel
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Parklawn Dr
Parklawn Dr

From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Location:	Zoom format, please see instructions contained in the message
Importance:	Normal
Subject:	Canceled: AD3C Monthly Meeting for Project/Core Discussions
Start Time:	Thur 6/25/2020 3:30:00 PM (UTC-05:00)
End Time:	Thur 6/25/2020 5:00:00 PM (UTC-05:00)
Required Attendees:	'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Mark Denison '; Sarah M. Dowdy
Optional Attendees:	Sara Davis; Kathy Keith; 'Diamond, Michael'; 'Graham, Rachel'; 'Bostwick, Bob'; 'Suto, Mark J.'; 'Evans, Carrie W.'; 'Swanstrom, Ronald I'; 'Chappell, Jim'

AD3C Zoom Meeting invitation

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International numbers available: https://uasystem.zoom.us/u/aiNDytfdU
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07.226.132.110 (Japan)
Meeting ID: 946 2553 1176
assword: **552.136**

IP: 94625531176@zoomcrc.com
assword: **552.136**

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina

Location: https://who.zoom.us/j/94806447981

Subject: [COVID-19] 36th WHO TC - Assays

From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Attendees:	'Fred Hayden'; 'kara.carter01@comcast.net'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; Chelsea Tompkins; Atefeh Garzan; 'Karyakarte, Shuklendu'; 'Morrison, Thomas'; 'Ahmed, Syed K.'; 'Bratton, Larry D.'; Sixue Zhang
Location:	https://uab.zoom.us/j/98568125080?pwd=dXkwNTNjRGdidUI1dVQwblh2aVdCdz09
Importance:	Normal
Subject:	AD3C Annual Meeting (VIRTUAL)
Start Time:	Thur 11/12/2020 10:00:00 AM (UTC-06:00)
End Time:	Thur 11/12/2020 4:00:00 PM (UTC-06:00)
Required Attendees:	'Fred Hayden'; 'kara.carter01@comcast.net'; 'Mike Bray'; 'Rick Keenan'; 'Tom Shenk'; 'Alana Centilli'; 'Alec Hirsch'; 'Amelia George'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Kathy Keith'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Nicole Haese'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Tameca Winston; 'Thomas Morrison'; 'Tia Hughes'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; Chelsea Tompkins
Optional Attendees:	Atefeh Garzan; 'Karyakarte, Shuklendu'; 'Morrison, Thomas'; 'Ahmed, Syed K.'; 'Bratton, Larry D.'; Sixue Zhang

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; fjc37@cam.ac.uk; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; alex@lji.org; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ZHOU, Tiequn;

	lschwartz36
Sent:	Mon 11/16/2020 7:39:55 AM (UTC-06:00)
Subject:	[COVID-19] 38th WHO TC - Assays

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; fjc37@cam.ac.uk; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; alex@lji.org; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ZHOU, Tiequn;

lschwartz36

Sent: Mon 11/16/2020 7:44:47 AM (UTC-06:00)

Subject: [COVID-19] 38th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwho.zoom.us%2Fj%2F98146173887&data=04%7C01%7Cpeshi%40utmb.edu%7C00b91a2591654d88896d08d88a35c59b%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637411310865683814%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=yh8%2BI3VM4Cb2SpfdKjvX1Yv2wmRbatK8rSR0ZTL43KY%3D&reserved=0

Meeting ID: 981 4617 3887
Passcode: **552.136**

Dial by your location
+1 669 219 2599 US (San Jose)
+1 669 900 9128 US (San Jose)
+1 720 928 9299 US (Denver)
+1 786 635 1003 US (Miami)
+1 971 247 1195 US (Portland)
+1 213 338 8477 US (Los Angeles)
+1 253 215 8782 US (Tacoma)
+1 267 831 0333 US (Philadelphia)
+1 301 715 8592 US (Washington D.C)
+1 312 626 6799 US (Chicago)
+1 346 248 7799 US (Houston)
+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 602 753 0140 US (Phoenix)
+1 646 518 9805 US (New York)
+1 646 558 8656 US (New York)
+1 651 372 8299 US (St. Paul)
Meeting ID: 981 4617 3887
Passcode: **552.136**
Find your local number:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwho.zoom.us%2Fu%2FaC3ISFHte&data=04%7C01%7Cpeshi%40utmb.edu%7C00b91a2591654d88896d08d88a35c59b%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637411310865683814%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=YbEYFq71Ap4RZet6rgIgiOQFrKSvLPP%2BnndjFQehmE4%3D&reserved=0

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster,

Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; william.lee; ASiyer@mgh.harvard.edu; MAFUNGA, Neddy

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Subject: WHO working group on COVID-19 assays

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster,

Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk

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Subject: WHO Working Group on COVID-19 Assays

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song

(mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont

Sent: Sun 6/6/2021 10:20:14 AM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and zoom information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 9 2:30PM CET (Geneva Time)

1. Theodora Hatziioannou (Rockefeller) - *Evolution of neutralizing antibody responses to SARS-CoV-2*
2. Larry Dumont (Vitalant Research)- *SARS-CoV-2 Antibody persistence in COVID-19 convalescent plasma donors: Dependency on assay format and applicability to serosurveillance*

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69.174.57.160 (Canada)
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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER,

Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont

Sent: Sun 6/13/2021 2:38:54 PM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and zoom information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 16 2:30PM CET (Geneva Time)

1. Amy Chung (U. Melbourne) - *Simultaneous evaluation of antibodies that inhibit SARS-CoV-2 RBD variants with a novel competitive multiplex assay*
2. David Goldblatt (UCL) - *Comparing immune responses between SARS-CoV-2 vaccines, correlates of protection and variant immunity*

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; Suthar, Mehul; rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; 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pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan@phe.gov.uk; Carol.Sabourin@hhs.gov; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu;

larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; sid.byrareddy@unmc.edu; awchung@unimelb.edu.au; Breeze.Cavell@phe.gov.uk; gbu3@cdc.gov; Jilian Sacks; Griffiths, Anthony; euiho.kim@ip-korea.org; sangchul.lee@ip-korea.org; Georgia Tomaras, Ph.D.

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Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; Vasan.Vasan@csiro.au; a.luttick@360biolabs.com; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; liyl@cde.org.cn; liub@cde.org.cn; tlying@fudan.edu.cn; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; baihe@nmpa.gov.cn; zlshi@wh.iov.cn; mafranco@javeriana.edu.co; rawcraig@yahoo.com; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; emmanuelle.charton@edqm.eu; BUDA Mihaela; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; munoz-fontela@bnitm.de; christian.drosten@charite.de; Barbara.Schnierle@pei.de; rafael.delgado@salud.madrid.org; cheryl@gisaid.org; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; christian.brechot@pasteur.fr; jokim@ivi.int; mksong@ivi.int; dboyle@path.org; tdelossantos@path.org; bleader@path.org; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'KNEZEVIC, Ivana'; SWAMINATHAN, Soumya; malik@hku.hk; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; dancohen@tauex.tau.ac.il; Youngmee Jee; alankhoo.imr@gmail.com; celine.gurry@cepi.net; y.m.vasiliev@spbniivs.ru; ramadany@sfda.gov.sa; linfa.wang@duke-nus.edu.sg; engeong.ooi@duke-nus.edu.sg; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon@korea.kr; limhy0919@korea.kr; angeliki.melidou@ecdc.europa.eu; Eeva Broberg; qiang.pan-hammarstrom@ki.se; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; supaporn.p@dmsc.mail.go.th; pilailuk.o@dmsc.mail.go.th; pawinee.k@redcross.or.th; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; fjc37@cam.ac.uk; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; r.tedder@imperial.ac.uk; katie.doores@kcl.ac.uk; Liz.Miller@lshtm.ac.uk; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; jma@sgul.ac.uk; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; teresa.lambe@ndm.ox.ac.uk; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; Jacqueline.Fryer@nibsc.org; Kevin.Bewley@phe.gov.uk; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; ahgriff@bu.edu; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; sarah.mudrak@duke.edu; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; jmcelrat@fredhutch.org; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; vyusibov@indianabiosciences.org; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; daniela@lji.org; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; william.lee@health.ny.gov; tcs38@psu.edu; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; msalit@stanford.edu; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; rbaric@email.unc.edu; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; SCHWARTZ, Lauren; thatziio@rockefeller.edu; Jiae Kim; Ruben.Donis@hhs.gov; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; cjmiller@UCDAVIS.EDU; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; fcassels@path.org; Carol.Sabourin@hhs.gov; Vidadi.Yusibov@hhs.gov; miturrizagomara@path.org; david.montefiori@duke.edu;

sujan@lji.org; Camille.Escadafal@finddx.org; g.pollakis@liverpool.ac.uk; w.a.paxton@liverpool.ac.uk; rahmed@emory.edu; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; Galloway, Summer (CDC/DDID/NCIRD/ID); Griffiths, Anthony; euiho.kim@ip-korea.org; sangchul.lee@ip-korea.org

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; a.luttick@360biolabs.com; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; ramadany@sfda.gov.sa; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; angeliki.melidou@ecdc.europa.eu; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; cjmiller@UCDAVIS.EDU; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris@cdph.ca.gov; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan; Carol.Sabourin@hhs.gov; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu;

larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; Byrareddy, Siddappa; Griffiths, Anthony; sangchul.lee@ip-korea.org; Important; euiho.kim@ip-korea.org

Sent: Sun 5/16/2021 10:11:16 AM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

Join Zoom Meeting
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213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)

64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
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To: 'Ralph Baric'[rbaric@email.unc.edu]; 'Mike Bray'[mikebray10@gmail.com]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Daniel Streblow[streblow@ohsu.edu]
Cc: Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Sara Davis[sadavis@peds.uab.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Wed 2/12/2020 11:35:07 AM (UTC-06:00)
Subject: Re: IMPORTANT: Logistics and Presentation Items for the AD3C Reverse Site Visit on February 11, 2020 in Rockville, MD
guest travel template[2].pdf

Hello all,

Thank you for your attendance at the reverse site visit. Please don't forget to send your signed form to us for reimbursement. Let us know if you have any question. It was so great to see you and I will be in touch!

Thank you,

Steph

From: Antiviral Drug Discovery and Development <ad3c@peds.uab.edu>
Date: Thursday, January 9, 2020 at 8:40 AM
To: 'Mark Heise' <mark_heisem@med.unc.edu>, 'Mark Denison' <mark.denison@vanderbilt.edu>, Pei-Yong Shi <peshi@utmb.edu>, 'Ralph Baric' <rbaric@email.unc.edu>, "msuto@southernresearch.org" <msuto@southernresearch.org>, "'kara.carter@evotec.com'" <kara.carter@evotec.com>, 'Mike Bray' <mikebray10@gmail.com>, 'Fred Hayden' <fgh@virginia.edu>
Cc: "Richard Whitley, M.D." <RWhitley@peds.uab.edu>, Mary Wyatt Bowers <MWBowers@peds.uab.edu>, Stephanie Moore <smoore@peds.uab.edu>, "'antoinette_baric@med.unc.edu'" <antoinette_baric@med.unc.edu>, 'Alana Centilli' <acentilli@southernresearch.org>
Subject: IMPORTANT: Logistics and Presentation Items for the AD3C Reverse Site Visit on February 11, 2020 in Rockville, MD

Greetings and Happy New Year:

It is time to move forward with final plans for the AD3C Reverse Site Visit, scheduled for **Tuesday, February 11, 2020** at the NIAID Building, 5601 Fishers Lane. Rockville, MD. **In preparation for this visit, please read the following instructions carefully:**

- At this time, **please purchase a plane ticket using a domestic carrier and select a seat in economy class**, so your ticket can be reimbursed. For those who will be staying overnight, we suggest that you stay at the Hilton Washington DC/Rockville Hotel, 1750 Rockville Pike, Rockville, MD 20852, Phone is 301-468-1100 and the website link is https://www3.hilton.com/en/hotels/maryland/hilton-washington-dc-rockville-hotel-and-executive-meeting-ctr-IADMRHF/index.html. It is a short walk to the NIAID or a quick cab/Uber ride.

- Please use the attached form to keep track of your travel expenses and speed up reimbursement after the trip. It is important for you to sign the form before sending it to us with your receipts.

- If you will be arriving in the area on the evening of Monday, February 10 and would like to have dinner, **please let us know** so we will have a head count for making a group reservation at a nice local restaurant.

- In order to produce a presentation that contains uniform content for each project, please send the following items to Stephanie Moore at smoore@peds.uab.edu no later than **February 3, 2020** to be compiled into one presentation. There can be **10 slides** maximum per project that will take 20-25 minutes at most to cover. I have attached a blank AD3C slide if you would like to use it. Below are the areas that Maureen Beanan has requested that we cover:

  a. Status (1-2 slides - utilize timeline structure perhaps?)
  b. Accomplishments (2-3 slides)
  c. Proposed for upcoming year(s) (1-2 slides)
  d. Significant publications (1 slide)

Here are additional details on the meeting location, and the meeting agenda provided by NIH for your use, shown below:

Meeting Location:
NIAID
5601 Fishers Lane
Rockville MD 20852

Building Access: It is very important that you arrive at the building by **8:30 am Eastern Time** to allow sufficient time to get through security. Domestic travelers will need a government issued ID (i.e. driver's license) to enter the building. We plan to meet as a group in the lobby, but if you are early/late, please call Maureen Beanan at 301-339-4753 when you arrive at the lobby security station and she or one of her colleagues will come down to escort you.

Parking: Parking is available in the garage at 5635 Fishers Lane, Rockville, MD 20852 – the road to the garage is the first left after turning on to Fisher's Lane. The garage will be at the end of a road. Walk back out to Fisher's Lane, turn left and walk one block, cross the street to reach our building, about a 3 minute walk.

Meeting schedule: 9:00 to 11:00 am Part I: (~2.0 hours, including time for questions)
(Audience: This part of the meeting is open to all NIAID staff, including CETR Program Staff and all other interested NIAID staff)

9:00 am NIAID CETR staff welcome participants and Introductions (5 minutes)

9:05 am CETR presentations:

- Brief overview of the Center including the goals, administrative structure, projects, and cores – please include a slide summarizing the progress of depositing the genome sequences into NCBI in this part of the presentation;
- Report on Year 1 activities for each project (~15-20 minutes per project)
- Summarize the status of the project at the end of Year 1 (1 slide)
- Describe the progress on each project during year 1 and plans for remaining 4 years

11:00 am to 12:00 pm Part II: Discussion with CETR Program staff (~0.5 - 1 hour)
Possible topics:

- Senior NIAID staff questions
- Issues that have arisen during year and proposed options

- CETR Program updates
- Annual Progress Report questions

Thank you for agreeing to participate in the AD3C Reverse Site Visit. If you need any additional items or information, please contact any of our Administrative Core group members and we will be happy to assist you.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

Guest Travel **Date**_____ **Person's Name**_____

Points of Travel

Date	From	To	Mode

Transportation		Private Car, Rental Car, Plane, Train etc.
- Private Car mileage (Not rental cars)	_____ miles @ _____	
- Private Car mileage (Not rental cars)	_____ miles @ _____	
-Airfare/Train fare (Coach class only. Attach ticket stub.)		
-Rental Car (Attach original receipts. Give justification for why rental car was used instead of public transportation)		
-Taxi/Van (Including tips. Attach original receipts for fare where applicable.)		
-Parking (Attach receipt if applicable.)		
	Total Transportation	

Meals (Attach original receipts. Cannot include any alcoholic beverages.)

Date	Breakfast($)	Lunch($)	Dinner($)	Day Total ($)

Total Meals ($) _____

Hotel Room (Attach original receipts. Basic single occupancy room rate only.)

Date(s)	Rate($)	Number of Nights	Total ($)

Total Hotel ($) _____

Miscellaneous

-Baggage Handling Tips (Receipts not required), etc.

Total Miscellaneous	

Total Reimbursement Requested _____

Certification: I hereby request reimbursement of the travel related expenses detailed above and do hereby certify that:
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Signature _____ Date_____

To: 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Amy Sims'[sims0018@ad.unc.edu]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Debra Warren'[dewarren@DOM.wustl.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'George Painter'[george.r.painter@emory.edu]; Avery, Gloria J.[gjavery@UTMB.EDU]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Javier Gomez'[Jcampos-gomez@southernresearch.org]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; Maaike Everts, Ph.D.[meverts@peds.uab.edu]; 'Maria Agostini'[Maria.I.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; Mark Prichard, PhD.[MPrichard@peds.uab.edu]; 'Mark Suto'[suto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Michelle Almajano'[Michelle.Almajano@gilead.com]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Tameca Winston[twinston@peds.uab.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Tomas Cihlar'[Tomas.Cihlar@gilead.com]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]; 'Sides, Kate'[ksides@southernresearch.org]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Tue 4/23/2019 8:53:30 AM (UTC-05:00)
Subject: RE: Monthly AD3C Teleconference for Project and Core Reporting
April 25 2019 AD3C Agenda.pdf

Hello To Everyone:

Please be reminded of the AD3C monthly call scheduled for **Thursday, April 25 at 3:30 pm Central Time.** Attached please find the meeting agenda that contains the dial-in information. If you would like to share any slides with the group, please send them to me by 12:00 pm on Thursday and I will send them via e-mail to the conference call participants.

With best regards and many thanks,

Sara Davis | Program Coordinator II
Direct Line: 205.996.7804 | sadavis@peds.uab.edu

-----Original Appointment-----
From: Antiviral Drug Discovery and Development Center-AD3C
Sent: Monday, January 14, 2019 9:27 AM
To: Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Amy Sims'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Bob Bostwick'; 'Carrie Evans'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Debra Warren'; 'Erica Bitten'; 'George Painter'; 'Gloria Avery'; 'Greg Bluemling'; 'Hope Angel'; 'Javier Gomez'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; Maaike Everts, Ph.D.; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; Mark Prichard, PhD.; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Michelle Almajano'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; 'Pei-Yong Shi'; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; Tameca Winston; 'Thomas Morrison'; 'Tim Sheahan'; 'Tomas Cihlar'; 'Toni Baric'; 'Victor DeFilippis'
Cc: 'Rasmussen, Lynn'; 'Bostwick, Bob'; 'Diamond, Michael'; Sides, Kate
Subject: Monthly AD3C Teleconference for Project and Core Reporting
When: Thursday, April 25, 2019 3:30 PM-5:00 PM (UTC-06:00) Central Time (US & Canada).
Where: Call in at 1-888-806-5025 and use the passcode of **552.136**

Here is the 2019 notice for the monthly conference call for the AD3C grant. Please contact me if you need anything or have questions.

Sara Davis
sadavis@peds.uab.edu

AD3C Teleconference Agenda
April 25, 2019, 3:30 p.m. CST

Meeting Number: (888) 806-5025 **Participant code: 420976**

1. Admin Core

   - Status subaward close out and new award set up along with consortium agreement addendum
   - Meeting after ICAR
   - Final RPPR

2. Project progress updates

   - Project 1 – Corona (MDenison, RBaric; Core B BBostwick; Core C APathak; GBluemling)
   - Project 2 – Alpha (DStreblow, MHeise, TMorrison; Core B BBostwick; Core C APathak; GBluemling)
   - Project 3 – Flavi (PYShi, JNelson, AHirsch, MDiamond; Core B BBostwick; Core C APathak; GBluemling)
   - Project 4 – Influenza (RWhitley, MPrichard, BTekwani; Core B BBostwick; Core C OMoukha-Chafiq)

To: Denison, Mark[mark.denison@vumc.org]; Ralph Baric[rbaric@email.unc.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; Daniel Streblow[streblow@ohsu.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Thomas.Morrison@ucdenver.edu[Thomas.Morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; Alec Hirsch[hirschal@ohsu.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Tekwani, Babu[btekwani@southernresearch.org]; Diamond, Michael[mdiamond@wustl.edu]; Jay Nelson[nelsonj@ohsu.edu]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Pathak, Ashish[apathak@southernresearch.org]; Suto, Mark J.[msuto@southernresearch.org]; Maaike Everts, Ph.D.[meverts@peds.uab.edu]; Sara Davis[sadavis@peds.uab.edu]
From: Evans, Carrie W.[cevans@southernresearch.org]
Sent: Fri 5/31/2019 3:49:03 PM (UTC-05:00)
Subject: Timelines (Microsoft Project, Gantt Chart)
Timeline worksheet.xlsx
Example Timeline.pdf

Dear AD3C Team,

As a follow up to our last AD3C team meeting, I have attached a spreadsheet which will capture all of the information I need to assist you with your Microsoft Project timeline. If you would like my assistance with drafting your timeline, please fill out the attached spreadsheet with all of your tasks, durations and dependencies. Once you return the attached to me, I will draft your timeline and sent it back to you for review. I have also attached an example timeline to give you an idea of the sort of information that we typically capture in a Gantt chart. For the purposes of this specific timeline, the milestone tasks should be Go/No Go decision points.

If you are going to draft your own Gantt Chart, I would greatly appreciate it if you would send me the Microsoft Project file once you have finalized your Gantt. I will need all Gantt Charts in order to compile them into a single file with all projects.

Please let me know if you need any additional information and/or if I can be of assistance!

Thanks,

Carrie

Carrie W. Evans, MS, PMP
Senior Manager of Operations
Drug Discovery Division
Southern Research
2000 9th Ave. South
Birmingham, AL 35205
Phone: 205-581-2528
Email: cevans@southernresearch.org

Task number	Task Name

Start Date	Finish Date	Is this task dependent on the completion of another task?	If yes, what task number?

Is this a milestone?

Task number	Task Name	Start Date	Finish Date
1	**High-through put screening**	4/22/19	8/26/19
2	HTS Screen	4/22/19	6/21/19
3	HTS Dose Response	6/22/19	7/26/19
4	Completion & selection of best reporter	4/22/19	7/26/19
5	Identification of optimized of reporter	7/27/19	7/27/19
6	Transfer of SAR assay to HTS	7/28/19	8/5/19
7	Validation in HTS driving SAR construct	8/6/19	8/26/19
8	**Chemistry**	8/26/19	12/27/19
9	Computational analysis of hits	8/27/19	9/2/19
10	Initate SAR Chemistry	9/3/19	12/4/19

Task number 1 and Task number 8, which are in bold are called summary tasks. The items bel
what will happenand how long each subtask will take. The start and end dates for summary t
the subtasks.

It is not a requirement that start or end dates are on weekdays.

Is this task dependent on the completion of another task?	If yes, what task number?	Is this a milestone?
No		No
No		No
Yes	2	No
No		No
No		Yes
Yes	5	No
Yes	6	No
No		No
Yes	7	No
Yes	9	No

ow these task break down in more details
asks have a duration that matches all of

Task number
Task Name
Start Date
Finish Date

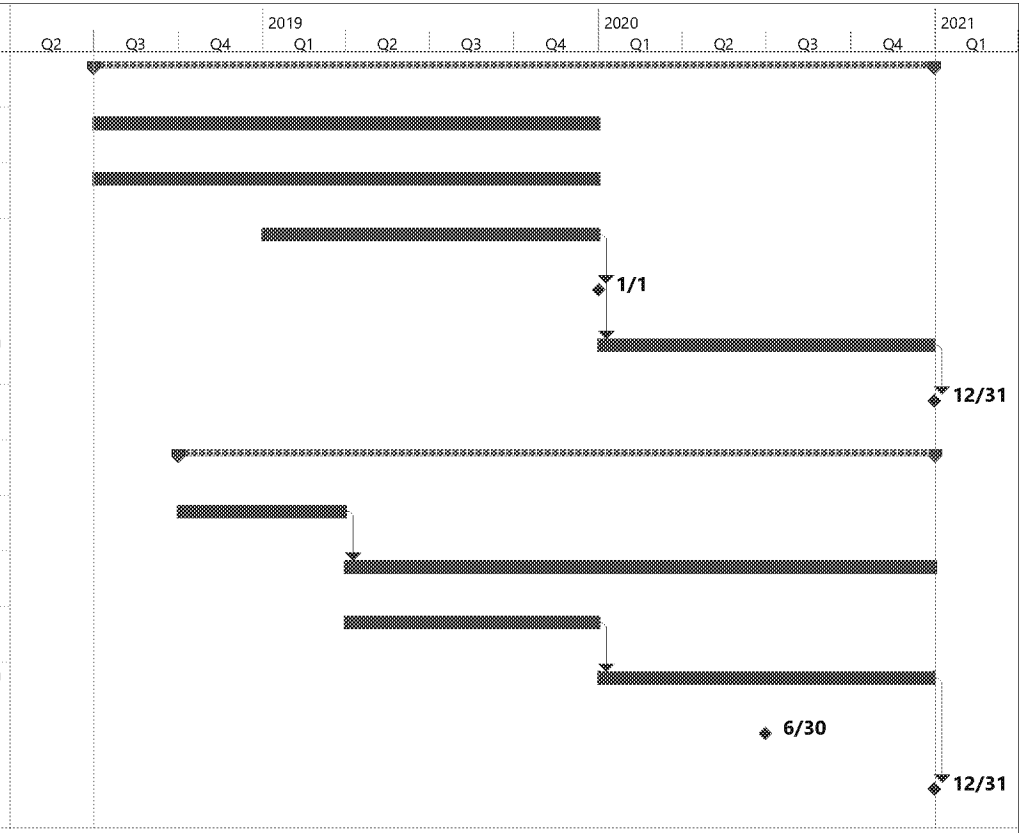
Is this task dependent on the completion of another task?
If yes, what task number?

Is this a milestone?

This will reflect the order the tasks.
This is the name of the action or task that will take place.
This is the start date of the particular task.
This is the end date of the particular task.

This links a task to certain work (a different task) that needs to be completed prior to a task being started.
Note the task number that is dependant on, so these task can be linked together.
A milestone mark secific points along a project timeline. These put focus on major progress points that indicate not only p
achieved success.

ID	Task Name	Start	Finish
1	**Continuation of Existing Efforts**	**Sun 7/1/18**	**Thu 12/31/20**
2	Continue Lead Optimization of Current Hits	Sun 7/1/18	Tue 12/31/19
3	SAR Driving Assays	Sun 7/1/18	Tue 12/31/19
4	Additional Studies (e.g., Full PK, Cyp, preclinical tox, panel profiling, met ID)	Tue 1/1/19	Tue 12/31/19
5	Identify a Lead Series for Non-GLP Toxicity Studies	Wed 1/1/20	Wed 1/1/20
6	Pre-IND Studies	Wed 1/1/20	Wed 12/30/20
7	ID Preclinical Candidate	Thu 12/31/20	Thu 12/31/20
8	**Option 1: 550K Compound Screen**	**Mon 10/1/18**	**Thu 12/31/20**
9	550K Compound High Throughput Screen	Mon 10/1/18	Sun 3/31/19
10	SAR Driving Assays	Mon 4/1/19	Thu 12/31/20
11	Analysis of Hits/Selection of Scaffolds/Synthesis/SAR	Mon 4/1/19	Tue 12/31/19
12	Lead optimization/Additional Studies as Above/Pre-IND Studies	Wed 1/1/20	Wed 12/30/20
13	Identify a Lead Series for Non-GLP Toxicity Studies	Tue 6/30/20	Tue 6/30/20
14	ID Preclinical Candidate	Thu 12/31/20	Thu 12/31/20



To: Evans, Carrie W.[cevans@southernresearch.org]; Denison, Mark[mark.denison@vumc.org]; Ralph Baric[rbaric@email.unc.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; Daniel Streblow[streblow@ohsu.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Thomas.Morrison@ucdenver.edu[Thomas.Morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; Alec Hirsch[hirschal@ohsu.edu]; Tekwani, Babu[btekwani@southernresearch.org]; Diamond, Michael[mdiamond@wustl.edu]; Jay Nelson[nelsonj@ohsu.edu]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Pathak, Ashish[apathak@southernresearch.org]; Suto, Mark J.[msuto@southernresearch.org]; Maaike Everts, Ph.D.[meverts@peds.uab.edu]; Sara Davis[sadavis@peds.uab.edu]
From: Richard Whitley, M.D.[RWhitley@peds.uab.edu]
Sent: Mon 6/3/2019 9:15:41 AM (UTC-05:00)
Subject: Re: Timelines (Microsoft Project, Gantt Chart)

Hi Carrie,

If ok with you I will come to SR and you, Mark, Babu and I can talk through this. It would need to be the end of next week

rich

From: "Evans, Carrie W." <cevans@southernresearch.org>
Date: Friday, May 31, 2019 at 9:08 PM
To: "Denison, Mark" <mark.denison@vumc.org>, Ralph Baric <rbaric@email.unc.edu>, "Pruijssers, Ardina" <ardina.pruijssers@vumc.org>, Dan Streblow <streblow@ohsu.edu>, Mark Heise <mark_heisem@med.unc.edu>, Thomas Morrison <Thomas.Morrison@ucdenver.edu>, "Sheahan, Timothy Patrick" <sheahan@email.unc.edu>, Alec Hirsch <hirschal@ohsu.edu>, Rich Whitley <RWhitley@peds.uab.edu>, "Tekwani, Babu" <btekwani@southernresearch.org>, "Diamond, Michael" <mdiamond@wustl.edu>, Jay Nelson <nelsonj@ohsu.edu>, Pei-Yong Shi <peshi@UTMB.EDU>
Cc: Ashish Pathak <apathak@southernresearch.org>, "Suto, Mark J." <msuto@southernresearch.org>, Maaike Everts <meverts@peds.uab.edu>, Sara Davis <sadavis@peds.uab.edu>
Subject: Timelines (Microsoft Project, Gantt Chart)

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Email: cevans@southernresearch.org

To: E.J.Snijder@lumc.nl[E.J.Snijder@lumc.nl]; rbaric@email.unc.edu[rbaric@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; diamond@wusm.wustl.edu[diamond@wusm.wustl.edu]; raul.andino@ucsf.edu[raul.andino@ucsf.edu]; randy.albrecht@mssm.edu[randy.albrecht@mssm.edu]; Paessler, Slobodan[SLPAESSL@utmb.edu]; bneuman@tamu[bneuman@tamu]
Cc: Moulton, Hong[Hong.Moulton@oregonstate.edu]
From: Stein, David Adam[Dave.Stein@oregonstate.edu]
Sent: Thur 3/12/2020 10:09:07 AM (UTC-05:00)
Subject: covid ppmo testing
SARS JVi 8-05.pdf

Hi Guys,
Just wondering if any of you have any suggestions for us regarding a research lab, preferably based in US, that may be interested to pursue testing of PPMO targeted against SARS2_CoV RNA. Of course, it would be necessary that the lab have BSL 3+ facilities.

From the attached paper you can see that PPMO worked well vs SARS1 in cell cultures (never got to try it in vivo). We make PPMO in our lab at OSU. PPMO are not available commercially.

We already have some testing of PPMO vs SARS2 in the works, but are interested to find a reserach lab that may wish to join in and possibly write a grant with us to pursue various project/possibilities. If you would like to discuss please let me know and perhaps we can have a quick phone call.

With Regards,
Dave

David Stein

Moulton Lab

Dept. of Biomedical Sciences

College of Veterinary Medicine

Oregon State University

Corvallis, OR 97331

541-231-1332 (dave cell)

dave.stein@oregonstate.edu

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0022-538X/05/$08.00+0 doi:10.1128/JVI.79.15.9665–9676.2005

Inhibition, Escape, and Attenuated Growth of Severe Acute Respiratory Syndrome Coronavirus Treated with Antisense Morpholino Oligomers†

Benjamin W. Neuman,[1]* David A. Stein,[4] Andrew D. Kroeker,[4] Michael J. Churchill,[2] Alice M. Kim,[1] Peter Kuhn,[2] Philip Dawson,[2,3] Hong M. Moulton,[4] Richard K. Bestwick,[4] Patrick L. Iversen,[4] and Michael J. Buchmeier[1]

The Scripps Research Institute, Division of Virology, Department of Neuropharmacology,[1] and Department of Cell Biology,[2] and Skaggs Institute for Chemical Biology,[3] 10550 North Torrey Pines Rd., La Jolla, California 92037, and AVI BioPharma Inc., 4575 SW Research Way, Corvallis, Oregon 97333[4]

Received 10 November 2004/Accepted 4 April 2005

The recently emerged severe acute respiratory syndrome coronavirus (SARS-CoV) is a potent pathogen of humans and is capable of rapid global spread. Peptide-conjugated antisense morpholino oligomers (P-PMO) were designed to bind by base pairing to specific sequences in the SARS-CoV (Tor2 strain) genome. The P-PMO were tested for their capacity to inhibit production of infectious virus as well as to probe the function of conserved viral RNA motifs and secondary structures. Several virus-targeted P-PMO and a random-sequence control P-PMO showed low inhibitory activity against SARS coronavirus. Certain other virus-targeted P-PMO reduced virus-induced cytopathology and cell-to-cell spread as a consequence of decreasing viral amplification. Active P-PMO were effective when administered at any time prior to peak viral synthesis and exerted sustained antiviral effects while present in culture medium. P-PMO showed low nonspecific inhibitory activity against translation of nontargeted RNA or growth of the arenavirus lymphocytic choriomeningitis virus. Two P-PMO targeting the viral transcription-regulatory sequence (TRS) region in the 5′ untranslated region were the most effective inhibitors tested. After several viral passages in the presence of a TRS-targeted P-PMO, partially drug-resistant SARS-CoV mutants arose which contained three contiguous base point mutations at the binding site of a TRS-targeted P-PMO. Those partially resistant viruses grew more slowly and formed smaller plaques than wild-type SARS-CoV. These results suggest PMO compounds have powerful therapeutic and investigative potential toward coronavirus infection.

The perception of coronaviruses as harmless seasonal pathogens was indelibly changed in 2002, with the emergence of severe acute respiratory syndrome, a severe, sometimes fatal respiratory disease. Thanks in part to the availability of severe acute respiratory syndrome coronavirus (SARS-CoV) bioinformatics and structural data, identification of potential SARS-CoV antiviral compounds has moved rapidly. For example, antiviral compounds which target the SARS-CoV superfamily 1 helicase and the 3C-related serine proteinase with 50% effective concentration (EC_{50}) values in the low micromolar range have been reported (1, 19, 20, 44). However, the second SARS-CoV-encoded proteinase, a papain-related cysteine proteinase, may prove to be a less suitable drug target, as a coronavirus molecular clone lacking one of the two known cleavage sites for this enzyme displayed only minor growth defects in cell culture (7).

Other confirmed and putative viral enzymes, including the polymerase, poly(U)-specific endoribonuclease homolog, *S*-adenosylmethionine-dependent ribose 2′-*O*-methyltransferase, and cyclic phosphodiesterase, are potential anti-SARS drug targets (34). Furthermore, not all proposed SARS-CoV inhibitors act by inhibiting viral enzymes. Compounds targeting the interaction of the viral spike protein with the ACE-2 receptor (20, 44, 45) or with the spike-mediated fusion event (3, 14, 22, 47) and showing micromolar-scale efficiency in cell culture have been reported. Several groups have also reported in vitro efficacy with small interfering RNAs (42, 48) targeted at suppression of viral gene expression.

Compounds designed to function by base pairing to specific nucleic acid sequences, collectively known as antisense agents, offer a potentially powerful and selective tool for manipulating host and pathogen gene expression. Antisense agents directed against single-stranded RNA are known to act by two general mechanisms: by causing damage to an RNA strand containing the complementary "target" sequence through priming of endogenous RNase H activity, or by steric interference with targeted RNA function. Phosphorodiamidate morpholino oligomers (PMO) act by the latter mechanism, duplexing to specific RNA sequence by Watson-Crick base-pairing and forming a steric block (37).

The most frequently successful strategies for PMO-based gene knockdown are inhibiting translation initiation (28) and mRNA splicing (9). We recently demonstrated the antiviral effects of one peptide-conjugated PMO (P-PMO) complemen-

* Corresponding author. Mailing address: The Scripps Research Institute, Division of Virology, Department of Neuropharmacology, 10550 North Torrey Pines Rd., La Jolla, CA 92037. Phone: 858-784-7162. Fax: 858-784-7369. E-mail: bneuman@scripps.edu.

† This is TSRI manuscript 16974-NP.

TABLE 1. PMO and oligonucleotide sequences

Name	Sequence (5′–3′)	Positions[a]	Sense[b]
FN-F1	AAGCCAACCAACCTCGATCT	27–46	+
FN-R1	CTTCAGGTGTAGGTTCTGGTTCTGGC	3240–3265	−
FN-R2	CACCGGTCAAGGTCACTACCACT	21525–21547	−
FN-R3	GCAGGAGAAGCATTGTCAATTT	25323–25344	−
FN-R4	CAGTAAGGATGGCTAGTGTGACT	26200–26222	−
FN-R5	CATAATCCAGGCTAGGAATAG	26473–26493	−
FN-R6	ATGAAACATCTGTTGTCACTTACT	27059–27082	−
FN-R7	TACCGTCAGCACAAGCAAAAGC	27462–27483	−
FN-R8	GCGCACCACCAGCTGGATCTTGAC	28006–28029	−
FN-R9	CGTCACCACCACGAACTCGTCG	28396–28417	−
AUG1	CTTTCGGTCACACCCGGACG	240–259	−
AUG2	GAACAAGGCTCTCCATCTTAC	260–280	−
AUG3	CCAAGAACAAGGCTCTCCATC	264–284	−
TRS1	GTTCGTTTAGAGAACAGATC	53–72	−
TRS2	TAAAGTTCGTTTAGAGAACAG	56–76	−
1ABFS	AAGACGGGCTGCACTTACAC	13408–13427	−
3UTR	GTATCGTAAACGGAATTGCG	29435–29454	−
S2M	GTACTCCGCGTGGCCTCGATG	29587–29607	−
3TERM	TTTTTGTCATTCTCCTAAGAAGC	29710–end	−
DSCR	AGTCTCGACTTGCTACCTCA	N/A[c]	N/A
FT	CTCCCTCATGGTGGCAGTTGA	N/A	N/A
SEQ-F1	TATTAGGTTTTTACCTACCC	2–21	+
SEQ-R2	GAAGAAGAACATTGCGGTATG	614–634	−
RVS-1	CTCCCTCATGGTGGCAGTTGA	1774–1795	−
RVS-2	GAGTTAAATAAAGAGTGTCTG	21637–21657	−
RVS-3	GATTAGCAACTCCTGAAGAGC	26016–26036	−
RVS-4	TTTTTTTTTTGTCATTCTCC	29718–end	−
5UTR-PCRF	ATCGGCTAGCATATTAGGTTTTTACCTACCCAGGAAAAG	2–30	+
5UTR-PCRR	ATCGGTCGACTGACACCAAGAACAAGGCTCTCCATCTTA	262–290	−

[a] SARS-CoV-Tor2, GenBank AY274119.
[b] Identical (+) or complementary (−) to the genomic plus-strand.
[c] NA, not applicable; non-SARS-CoV sequence.

tary to the AUG translation start site region of a murine coronavirus replicase polyprotein in vitro (29). We reasoned that the activity of P-PMO against coronaviruses might be improved by the rational targeting of RNA sequence elements and secondary structures critical for replication, transcription, and host factor interaction.

In this report, we demonstrate that antisense-mediated suppression of viral replication can be achieved by binding to conserved RNA elements implicated in viral RNA synthesis and translation. Nine P-PMO with sequences complementary to coding and noncoding regions of the SARS-CoV genome were used to probe the function of conserved RNA features during infection in cell culture. The most effective anti-SARS CoV P-PMO described in this report are over 100-fold more active than the anti-murine hepatitis virus coronavirus P-PMO described previously (26). Inhibition of viral yield exceeded 10^4-fold for compounds designed to bind the transcription regulatory sequence (TRS) region present in the viral genomic 5′ untranslated region (UTR). Corresponding effects on viral RNA level, cell-to-cell spread, and cytopathology were observed. Virus clones partially resistant to P-PMO were selected by multiple rounds of growth in the presence of P-PMO. Partially resistant clones selected with a TRS-directed P-PMO developed clustered point mutations at the P-PMO binding site proximal to the leader TRS and grew more slowly in cell culture than wild-type SARS-CoV. We conclude that P-PMO offer a highly specific antisense-based method for probing the function of specific RNA elements in intact RNA virus genomes in addition to their considerable therapeutic potential.

MATERIALS AND METHODS

Cells and viruses. Vero-E6 cells were cultured in Dulbecco's modified Eagle's medium containing 10% fetal bovine serum, 0.01 M HEPES, penicillin, and streptomycin for general growth and maintenance or in serum-free medium (VP-SFM; Invitrogen) supplemented with L-glutamine, penicillin, and streptomycin during P-PMO studies. SARS-CoV-Tor2 (24) was cultured on Vero-E6 cells. Arenavirus lymphocytic choriomeningitis virus-Armstrong was grown and titrated as previously described (4).

Plaque assay. For the SARS-CoV plaque assay, Vero-E6 cells were seeded in 12-well tissue culture plates at 2×10^5 cells per well and allowed to adhere overnight at 37°C and 5% CO_2. The culture medium was removed and replaced with 0.5 ml of inoculum. Cells were treated as specified, and a 2% fetal bovine serum, 0.7% agarose overlay was applied 1 h after inoculation. After 72 h, cells were fixed by immersion in 10% formaldehyde in phosphate-buffered saline for 24 h, agarose plugs were removed, and cells were stained with 0.1% crystal violet. Plaque size reduction assays were cultured and inoculated as above except that individual 0.7% agarose overlays were prepared for each treatment group. Agarose overlays for plaque size reduction assays were prepared with serum-free VP-SFM and P-PMO.

Virus growth and titer reduction assays. Vero-E6 cells were seeded at a density of 5×10^5 cells per 25-cm^2 tissue culture flask and allowed to adhere overnight at 37°C and 5% CO_2. Cells were pretreated with 1 ml VP-SFM containing treatment for 6 h, except where stated, as in time-of-addition and time-of-removal experiments. Cells were inoculated with SARS-CoV or lymphocytic choriomeningitis virus Armstrong at a multiplicity of ≈0.1 or ≈10 PFU/cell and placed at 37°C for 1 h. The inoculum was removed and replaced with fresh VP-SFM with or without P-PMO treatment. Cell culture medium was collected, stored, and replaced with fresh medium at the designated time points. The virus in cell culture supernatants was titrated by 50% tissue culture infectious dose

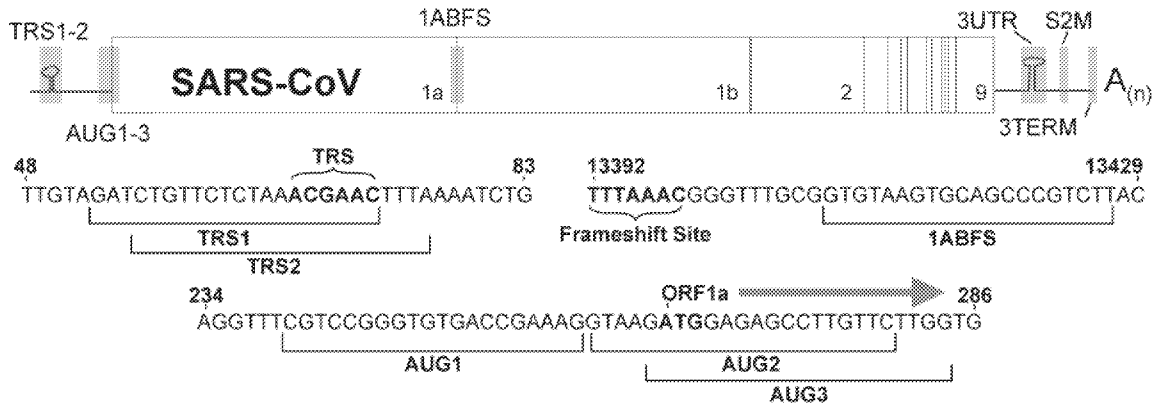

FIG. 1. P-PMO targeting schematic. Relative positions of P-PMO targets on the genomic plus-strand of SARS CoV are indicated by grey boxes. Enlarged regions of the genome indicate the specific target sequences of P-PMO directed against the TRS and AUG regions and the relative proximity of the 1ABFS P-PMO to the ribosomal frameshift site. Nucleotide positions refer to the published sequence of the SARS-CoV-Tor2 strain.

($TCID_{50}$) with threefold dilution steps analyzed according to the method of Reed and Muench or by plaque assay as described above.

PMO design, synthesis, and quality control. PMO were designed to be complementary to the viral plus-strand in several regions showing no sequence variation among sequenced SARS-CoV isolates. Table 1 describes all PMO and DNA oligonucleotide sequences. PMO were synthesized complementary to overlapping sequences in the vicinity of the replicase open reading frame (ORF) 1a initiation codon (AUG1; AUG2; and AUG3), the ORF 1a/1b frameshift signal pseudoknot (1ABFS), the consensus body and leader TRS (TRS1), leader TRS (TRS2), the S2M motif (S2M), the 3′-UTR pseudoknot (3UTR), and the 3′ genomic terminus (3TERM; Fig. 1). Random-sequence "nonsense" PMO (DSCR and FT) were included as controls.

PMO targets were screened with BLAST (http://www.ncbi.nlm.nih.gov/BLAST/) against known human mRNA sequences in order to preclude unintentional gene-silencing effects. PMO were covalently linked to peptide NH_2-RRRRRRRRRFFC-$CONH_2$ or NH_2-RRRRRFFRRRRC-$CONH_2$ designated R_9F_2 or $R_5F_2R_4$, respectively. Both types of peptide-conjugated PMO are henceforth referred to as P-PMO. PMO were synthesized at AVI BioPharma Inc. (Corvallis, OR) by a method described previously (38). The conjugation, purification, and analysis of P-PMO compounds were carried out at AVI BioPharma according to methods described elsewhere (25).

Coiled-coil design, synthesis, and quality control. We identified a 28-mer peptide from the S2 region of the SARS-CoV spike protein with the highest probability to form a coiled coil using the software program Coils 2.2 (by A. N. Lupas and J. M. Lupas). This peptide, designated SARS-HR2, was synthesized as previously described (18). Circular dichroism (CD) was performed on an Aviv 203-02 spectropolarimeter. Samples for CD contained 10 μM peptide in 5 mM sodium phosphate at pH 5, 6, and 7. Spectra were collected between 200 and 265 nm at 25°C in a 2-mm quartz cell; three spectra were acquired and averaged per sample before subtracting the background spectra.

Nonviral assays. The protein-coding sequence for firefly luciferase, without the ATG initiator-Met codon, was subcloned into the multiple cloning site of plasmid pCiNeo (Promega) at the SalI and NotI sites. The pCiNeo expression vector includes both cytomegalovirus and T7 promoters (for mammalian cellular and cell-free transcription of cloned inserts, respectively). Subsequently, complementary oligonucleotides SARSL+ and SARSL− were duplexed and subcloned into the NheI and SalI sites. This effectively replaced the start codon of the luciferase gene with sequence encoding bases −31 to +22 relative to the A of the AUG translation start-site codon of the SARS-CoV polyprotein (identical to the region shown in Fig. 1). This leader sequence includes the complete target sites for the AUG1, AUG2, and AUG3 antisense P-PMO. The −31 to +22 target region corresponds to genomic plus-strand nucleotides 235 to 287, as depicted in Fig. 1.

Three other constructs were made in a similar manner by inserting immediately upstream of the intact luciferase gene the DSCR P-PMO target sequence (5′-AGTCTCGACTTGCTACCTCATG-3′), the SARS TRS target sequence that corresponds to nucleotides 51 to 80 of the genomic plus-strand (5′-CTAG ATAGATCTGTT*CTC*TAAACGAACTTTAAAATG-3′), and the same SARS TRS target sequence that incorporates the three observed nucleotide polymorphisms described in the text (5′-CTAGATAGATCTGTT*AAA*TAAACGAACT TTAAAATG-3′). The luciferase gene for each of these three constructs contains a functional ATG initiator-Met codon. A final construct was made by performing PCR with oligonucleotides 5UTR-PCRF (including an NheI site and bases 2 to 30 of genomic plus-strand) and 5UTR-PCRR (including a SalI site and bases 290 to 262 of genomic plus-strand). The resulting 289-bp fragment was restricted with NheI and SalI and subcloned into pCiNeoluc. This construct utilizes the intact ATG initiator-Met codon within the subcloned SARS sequence (genomic plus-strand bases 266 to 268), as the ATG within the luciferase gene has been deleted.

For the luciferase-fusion constructs that include the TRS sequence, the TRS sequence with three mutations, and the SARS 5′UTR (genomic plus-strand bases 2 to 290), in vitro-transcribed 5′-capped RNA was produced with the mMESSAGE mMACHINE kit (Ambion) after plasmid linearization with NotI. For the SARS AUG and DSCR luciferase fusion constructs, the MegaScript T7 kit (Ambion) was used as described previously (29). In vitro translations were carried out on all constructs as described previously (29). Luciferase-induced light emission was read on a FLx800 microplate luminometer as described previously (29). Cellular efficacy studies were carried out using confluent Vero-E6 cells transiently transfected with target-leader/luciferase plasmids using Lipofectamine (Gibco BRL) according to the manufacturer's directions and assayed as above. The 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assay was used to measure cell viability as described previously (29).

Resistance studies. Virus was passaged 11 times on fresh Vero-E6 cells pretreated with 2 to 10 μM P-PMO. Biologically cloned viruses were cultured from individual, well-spaced plaques. Viral RNA was prepared from infected cells by Trizol lysis followed by an additional chloroform extraction. Reverse transcription-PCR was carried out according to the enzyme manufacturer's specifications (Invitrogen). The 5′-terminal region of the SARS-CoV genome was amplified using primers SEQ-F1 and SEQ-R2. PCR products were sequenced using primer SEQ-R2. Relative RNA load was determined by 25-cycle PCR of cDNA primed with oligonucleotides RVS1 through RVS4. PCR was primed with FN-F1 and the appropriate FN-R oligonucleotide to generate products of 104, 127, 156, 188, 212, 259, 299, and 353 bp, corresponding to viral subgenomic RNAs 2 through 9, respectively.

RESULTS

Design of antivirals. P-PMO were designed to target conserved viral sequences implicated in SARS-CoV RNA synthesis, translation, and/or host factor interaction (Fig. 1). The expression of the coronavirus replicase polyprotein is controlled at two points: the initiation of translation at open reading frame 1a, and the ribosomal frameshift which results in translation of the extended open reading frame 1ab. Three sequences were selected in the immediate vicinity of the AUG translation-initiation codon of the viral replicase polyprotein

open reading frame 1a (AUG1, AUG2, and AUG3) such that AUG2 and AUG3 overlapped the initiation codon and AUG1 was located in the 5′ untranslated region proximal to the translation start site. P-PMO 1ABFS was designed to disrupt the RNA secondary structure at the −1 ribosomal frameshift site that mediates translation of the remainder of the replicase polyprotein. The untranslated 5′-terminal 263 nucleotides of the SARS-CoV RNA also contain the ≈80-nucleotide leader sequence found at one terminus of each of the 5′- and 3′-coterminal subgenomic viral RNA species produced in the infected cell.

The transcription regulatory sequence (TRS) located in the 5′-UTR of the genome is believed to participate in discontinuous RNA synthesis (30–32, 39). The leader TRS was targeted with two P-PMO, each designed to mask the consensus TRS (5′-CGAAC-3′) and disrupt the stem-loop predicted to form in this region (40). TRS1 is complementary to the TRS in the leader RNA present on both genomic and subgenomic RNA species. TRS2 spans the junction between the leader and a portion of the 5′-UTR not present on subgenomic RNAs (39).

Studies of coronavirus defective-interfering RNAs have shown the genomic termini contain several conserved motifs, some of which act as discrete signals for RNA replication (6, 15). P-PMO compounds designed against targets in the 3′-untranslated region included 3UTR, targeting a portion of the conserved RNA stem-loop/pseudoknot found in most coronavirus genomes (10–13); S2M, targeting the stem-loop 2 motif region related to sequences in astroviruses and equine rhinovirus (17); and 3TERM, targeting the 3′ terminus of the genomic RNA, including the first five bases of the polyadenosine tail. Two nonsense P-PMO, DSCR and FT, were included to control for nonspecific P-PMO effects. The 5′ termini of P-PMO were conjugated to an arginine-rich delivery peptide (R_9F_2; 26, 29) or to a rearranged $R_5F_2R_4$ peptide, which confers equivalent delivery and efficacy properties (Moulton et al., unpublished data). The R_9F_2 and $R_5F_2R_4$ peptide conjugates were used interchangeably in the antiviral studies presented here. We did not observe detectable differences in sequence-specific or nonspecific effects between PMO conjugated to one or the other of the two delivery peptides.

Non-antisense antiviral compounds which targeted different stages of the viral growth cycle were included in some assays to provide a bridge for comparison of the results reported here with other studies reported in the literature. Among the control antivirals tested was a peptide identical to the carboxyl-terminal heptad repeat region of the SARS-CoV spike (HR2), which was designed to bind the spike protein during virus-cell fusion and arrest fusion at an intermediate stage. Amphipathic helices of the SARS and murine hepatitis virus coronaviruses form six-helix bundles that are believed to mimic the postfusion state of the spike glycoprotein. Several reports have demonstrated the antiviral properties of peptides based on amphipathic helices of coronavirus spike protein (3, 14, 22, 47).

We synthesized and purified a heptad repeat peptide derived from residues 1158 to 1185 of the SARS-CoV-Tor2 spike protein, designated SARS-HR2. The SARS-HR2 protein was selected to allow comparison of direct inhibition of SARS-CoV growth by different methods, e.g., fusion arrest versus antisense. The circular dichroism spectrum of SARS-HR2 (data not shown) displayed an equilibrium between disordered and helical structure, as previously reported for similar peptides (14).

P-PMO are effective and specific. As we have reported previously, the conjugated "delivery" peptides increase both the efficacy and toxicity of PMO in cell culture (29). $R_5F_2R_4$-conjugated PMO were tested for cytotoxicity by the MTT assay under the serum-free culture conditions used throughout this report. $R_5F_2R_4$-PMOs were nontoxic (defined as ≥90% cell viability after 24 h) at concentrations as high as 20 μM on Vero-E6 cells (data not shown). The level of toxicity of $R_5F_2R_4$-PMO was similar to that reported for R_9F_2-PMO previously (29). Based on this finding, treatment doses of P-PMO were limited to 20 μM. Hygromycin B, a broad-spectrum translation inhibitor active against most coronaviruses, was nontoxic to ≥80 μM (data not shown), in agreement with other published results (2).

P-PMO designed to inhibit initiation of translation of the SARS-CoV replicase polyprotein were tested in a rabbit reticulocyte lysate cell-free translation assay to determine which compound was most effective at inhibiting expression of a luciferase reporter. P-PMO were added to reticulocyte lysates programmed with in vitro-transcribed RNA in which translation of the luciferase gene was initiated at a small region derived from the SARS-CoV 5′-UTR containing the AUG1-3 P-PMO target sites. AUG1, AUG2, and AUG3 P-PMO generated comparable nanomolar-scale dose-dependent reduction of luciferase expression in this cell-free translation system (Fig. 2A). The FT P-PMO, described in our previous studies (29), was included here as a negative control.

DSCR P-PMO consistently generated low nonspecific activity in a variety of assays in this study. In order to demonstrate that the ineffectiveness of DSCR was not due to some innate defect in the compound itself, we compared the effects of DSCR and AUG1 P-PMO on inhibition of luciferase expression from a DSCR-target/luciferase construct (Fig. 2B). As expected, DSCR P-PMO specifically suppressed translation from the DSCR/luciferase transcripts. Nonspecific effects of AUG1 P-PMO against the DSCR/luciferase RNA were comparable to those of DSCR P-PMO against the SARS AUG-target/luciferase RNA described above. We therefore concluded that the DSCR and P-PMO AUG1 to AUG3 acted solely through antisense activity and displayed low nonspecific effects.

The three AUG P-PMO also displayed equivalent micromolar-scale effects on translation of the reporter gene in Vero cell cultures transiently transfected with the SARS/luciferase reporter plasmid used in the previous experiment (Fig. 2C). Synergistic effects can potentially be obtained when antiviral compounds with different targets are administered in combination (41). Nonoverlapping combinations of P-PMO were tested in the cell-free translation system in order to screen for additive synergy or anergy. The effects of combinations of AUG1 to AUG3 at a given total molarity did not differ significantly from the effects of an individual AUG P-PMO at the same total molarity (Fig. 2C), as might be expected for compounds targeting essentially identical targets by the same mechanism.

Reduction of SARS-CoV CPE and growth. In order to characterize the nine SARS-CoV-specific P-PMO, we tested them for several correlates of antiviral efficacy: prevention of cyto-

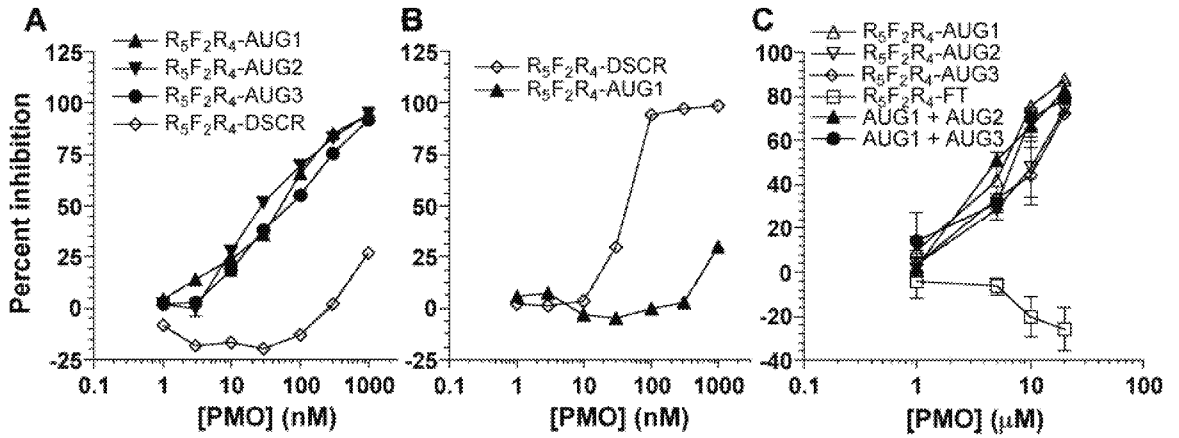

FIG. 2. Peptide-conjugated PMO specifically reduce cell-free and cell culture expression of plasmid-generated target sequences. (A) Cell-free translation assay demonstrates the inhibition of SARS AUG region/luciferase translation by AUG P-PMO relative to nonspecific activity of the DSCR control P-PMO. Data are expressed as percent inhibition relative to 12 untreated control values. (B) The converse assay, inhibiting translation from DSCR target/luciferase RNA specifically with the DSCR P-PMO demonstrates the lack of cross-reactivity of DSCR and AUG P-PMO in this system. (C) Luciferase expression from AUG region/luciferase mRNA generated from a transiently transfected plasmid in cell culture was inhibited by single-AUG P-PMO and combination AUG PMO treatments. Concentrations of combined P-PMO are expressed as the molarity of a 1:1 mixture of two nonoverlapping compounds. Error bars indicate standard error of the mean.

pathic effects, reduction of viral titer, and reduction of the spread of an established infection. SARS-CoV cytopathic effects (CPE) on Vero-E6 include vacuolation and extensive cell rounding by 24 h postinoculation in the case of high-multiplicity inoculation. We chose to compare cytopathic effects 72 h after high-multiplicity (≥10 PFU/cell) inoculation, by which time cells in untreated controls and those receiving ineffective treatments had displayed severe CPE for 24 to 48 h (Fig. 3A). Typical SARS-CoV-induced CPE was observed in infected cells treated with vehicle (water) only, DSCR, S2M, and 3TERM-P-PMO. The AUG1, AUG2, AUG3, 1ABFS, and 3UTR P-PMO consistently reduced CPE only after 20 μM treatment (AUG1 results are presented in Fig. 3A; the remaining data are not shown). Treatment with lower doses of AUG1 to AUG3 P-PMO appeared to reduce the severity of CPE in some experiments, as in the case shown in Fig. 3A. However, the protective effect of lower doses of the three AUG-targeted P-PMO was not observed consistently, and when present was always less pronounced than the protective effect of either TRS-targeted P-PMO. TRS1 and TRS2 strongly reduced CPE after ≥6 μM treatment (results for TRS1 are presented in Fig. 3A; TRS2 data are not shown). We thus concluded that TRS1 and TRS2 had at least a threefold greater antiviral activity compared to the AUG1 to AUG3, 1ABFS, or 3UTR P-PMO. The AUG3 P-PMO was not studied further since it was not found to differ from AUG2 or AUG1 in efficacy, toxicity, or CPE reduction.

Next, P-PMO were tested for the ability to reduce virus yield in pretreated cells. It is our observation that SARS-CoV growth plateaus by 24 h and remains high through 48 h following high-multiplicity inoculation (≥3 PFU/cell) or peaks ≈24 h later following low-multiplicity inoculation (≤0.1 PFU/cell). In order to compare P-PMO effects on log-phase viral growth, we compared infectious titers 24 h after low-multiplicity inoculation (Fig. 3B). The viral titer results were generally consistent with the cytoprotection results (Fig. 3A). The most effective P-PMO decreased viral titers to below the threshold of detection, 100 PFU/ml in the experiment shown in Fig. 3B. The 3UTR P-PMO had slight antiviral effects, while 1ABFS, AUG1, and AUG2 displayed equivalent moderate antiviral activity. TRS1 and TRS2 clearly exhibited robust antiviral activity in the low micromolar range. In repeated experiments, titers were consistently reduced by over 100-fold by treatment with ≥6 μM AUG1, AUG,2 and 1ABFS P-PMO or by ≥2 μM TRS1 and TRS2 PMO.

We next sought to further characterize the highly effective TRS2 P-PMO by performing time course studies in which this compound was added or removed at different times. Antivirals affecting a particular stage of the viral growth cycle, such as entry (early) or assembly (late), would likely be effective on different time scales, whereas inhibitors of ongoing processes such as replication and translation could be active at any point prior to the peak of viral growth. In order to investigate this hypothesis, we tested the effects of time of addition on the control heptad repeat peptide SARS-HR2, designed to inhibit virus-cell fusion after receptor binding and some conformational changes have occurred. SARS-HR2 was active when administered 1 h before inoculation or in combination with the inoculum. SARS-HR2 did not alter the titer of infectious virus present in the supernatant 24 h postinoculation when SARS-HR2 was administered 1 h postinoculation or later, indicating that an early event was targeted, and consistent with the predicted target of the membrane fusion process (data not shown). The TRS2 P-PMO significantly reduced viral titer when added up to 4 h after high-multiplicity infection and 8 h after low-multiplicity infection (data not shown), consistent with the effects expected from inhibition at a later stage in the viral life cycle. However, this result also indicated a requirement that TRS2 P-PMO be present early in the infection process for maximal antiviral effect.

In order to determine the duration and reversibility of TRS2 P-PMO-mediated antiviral effects, the TRS2 P-PMO was removed from the cell culture medium at various intervals and viral titer was assessed at several time points (Fig. 3C). Re-

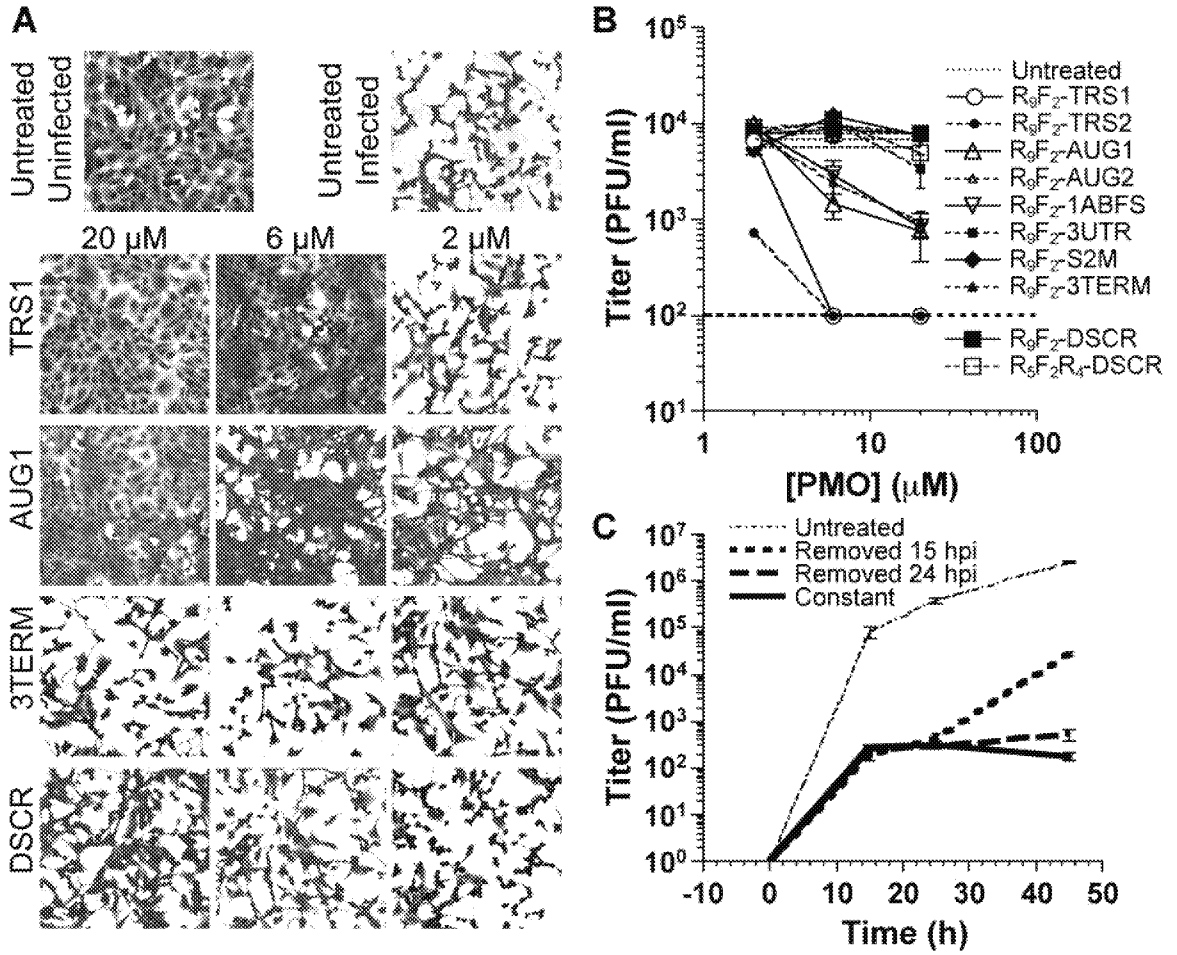

FIG. 3. Peptide-conjugated PMO reduce SARS-CoV cytopathology and titer. Qualitative changes in cell morphology and density were gauged against untreated infected (upper right) and untreated uninfected (upper left) controls. (A) Representative images of cells pretreated for 6 h with selected R_9F_2-conjugated PMO and fixed 72 h after inoculation. (B) Dose-response of titer reduction. Triplicate wells of Vero-E6 cells were pretreated with P-PMO or vehicle-only at 6 h before inoculation with SARS-CoV at a multiplicity of 0.1 PFU/cell. Virus yield was quantified 24 h after. The limit of detection for the assay shown was 100 PFU/ml. Error bars indicate standard error of the mean. (C) Cells were pretreated with 20 μM TRS2 R_9F_2-PMO or mock treated 6 h before inoculation. Culture medium was collected at 15 h and 24 h and replaced with medium containing P-PMO or medium alone as indicated. Virus yield was measured at 15 h, 24 h, and 48 h.

moval of TRS2 P-PMO as late as 15 h after infection resulted in increased viral amplification as measured at 24 and 48 h. This result suggests either rapid neutralization of the P-PMO or saturation of the TRS2 P-PMO molecules at the site of activity for a period of time. Taken together, these results demonstrate that the constant presence of TRS2 P-PMO is required to maintain maximum antiviral activity.

Preventing spread of an existing infection. Pathways leading to the establishment or spread of an infection can differ for some viruses. In murine hepatitis virus, initial cell entry of virus has rigorous receptor specificity requirements, but infection can subsequently be spread to receptor-null cells by contact with infected cells (8). Consequently, despite the positive results for the AUG1 to AUG3, 1ABFS, and TRS1 and TRS2 P-PMO, we hypothesized that successful inhibition of SARS-CoV-induced CPE and infectious titer might not necessarily predict effective treatment of an existing infection. The effects on viral persistence and spread of an existing infection were measured in a plaque size reduction assay. In this assay, cells were treated with P-PMO 1 h after inoculation with a standardized amount of SARS-CoV. The progress of the initial infection was quantified by measuring the diameter of the resulting viral plaques 72 h after inoculation.

The observed effects on viral spread (Fig. 4A-C) closely resembled the titer reduction results (Fig. 3B). DSCR, 3UTR, S2M, and 3TERM P-PMO were ineffective. The dose-response curves of the AUG1 and AUG2 P-PMO were essentially equivalent and showed slightly more potency than the 1ABFS P-PMO. The TRS1 and TRS2 P-PMO were again the most effective. Treatment with ≥6 μM TRS1 or TRS2 P-PMO completely prevented the formation of visible plaques.

We compared the effects of the AUG1 P-PMO against DSCR P-PMO, SARS-HR2 peptide, and hygromycin B on the spread of SARS-CoV infection (Fig. 4C). The slopes of the dose-response curves for hygromycin B and the AUG1 P-PMO were similar, indicating similar kinetics of activity, although the AUG1 P-PMO was approximately 10-fold more potent than hygromycin B. The slope of the dose-response curve for SARS-

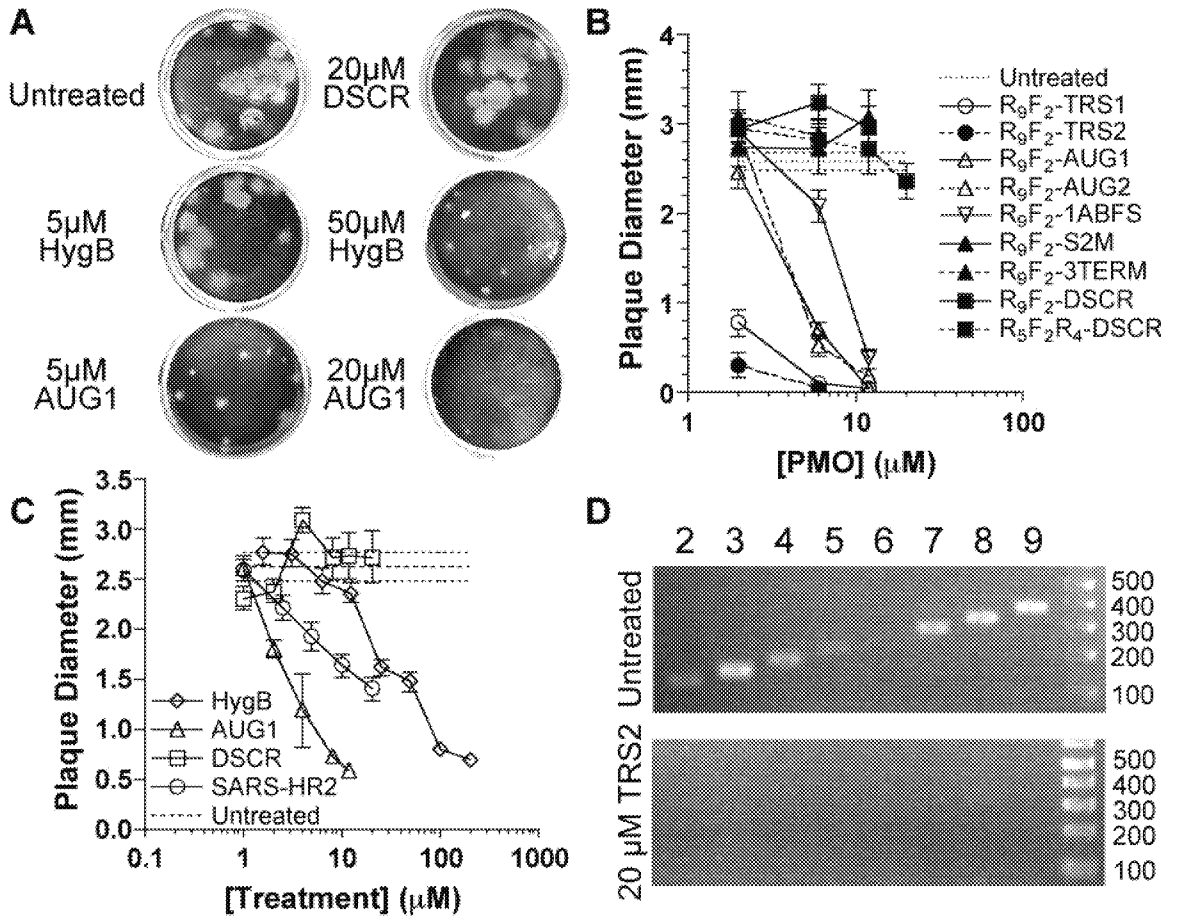

FIG. 4. Peptide-conjugated PMO and coiled-coil peptides inhibit the propagation of SARS-CoV infection. Plaque diameter on treated and mock-treated cells was visualized (A) and measured (B) 72 h after inoculation under the same experimental conditions as described for Fig. 3A. (C) Comparison of 72-h plaque diameter on cells treated with $R_5F_2R_4$-AUG1 P-PMO, $R_5F_2R_4$-DSCR P-PMO, hygromycin B (HygB), or coiled-coil SARS-HR2 and on mock-treated cells (untreated). Error bars indicate standard error of the mean. (D) Reverse transcription-25-cycle PCR comparison of viral subgenomic RNA 2 to 9 levels in an equivalent number of mock-treated or 20 μM TRS2 P-PMO-treated cells 24 h after inoculation. Sizes in bp are indicated to the right. Amplicons of 104, 127, 156, 188, 212, 259, 299, and 353 bp were expected, corresponding to viral subgenomic RNAs 2 through 9, respectively.

HR2 was less steep, indicating that relatively more SARS-HR2 was required to produce incremental inhibitory effects compared to P-PMO or hygromycin B. Possible explanations for this difference in dose-response ratio include peptide lability, the brief availability of the transition state amenable to competitive SARS-HR2 binding during the fusion process compared to continuous inhibition by hygromycin B or P-PMO, and the potential for up to three SARS-HR2 peptides to bind each prefusion intermediate of the spike homotrimer compared to the presumed binding of one P-PMO molecule per viral RNA molecule.

We reasoned that the observed inhibition of viral growth and propagation might correspond to a decrease in the viral RNA level, whether through inhibition of replicase expression, interference with discontinuous RNA synthesis at the leader TRS, or an alternatiove mechanism. Coronaviruses produce a nested set of subgenome-length RNA species in infected cells. Most coronavirus subgenomic RNAs are produced in molar excess of the genomic RNA, though genomic RNA and trace amounts of subgenomic RNAs are typically packaged in the virion (reviewed in reference 33). Therefore, we investigated genomic and subgenomic RNA production 24 h after low-multiplicity inoculation, as an indicator of ongoing infection. The 24-h time point was selected as a time when several rounds of replication would have occurred but virus-induced cell lysis would be negligible.

Reverse transcription-PCR products specific for each of eight subgenomic RNA species were strongly amplified from mock-treated cells and cells treated with mildly effective P-PMO (Fig. 4D and data not shown). Equal volumes of reverse transcription-PCR products from an equivalent number of 20 μM TRS2 P-PMO-treated cells were faint (i.e., subgenomic RNA 8 and possibly 9) or undetectable (subgenomic RNAs 2 to 7; Fig. 4D). Genomic RNA synthesis was likewise qualitatively reduced by 20 μM TRS2 P-PMO (data not shown), though whether this resulted directly from steric hindrance of target RNA or indirectly through inhibition of replicase polyprotein expression was not determined. This result suggests P-PMO effects on SARS-CoV growth, CPE, and spread correlate with a qualitative decrease of viral RNA level.

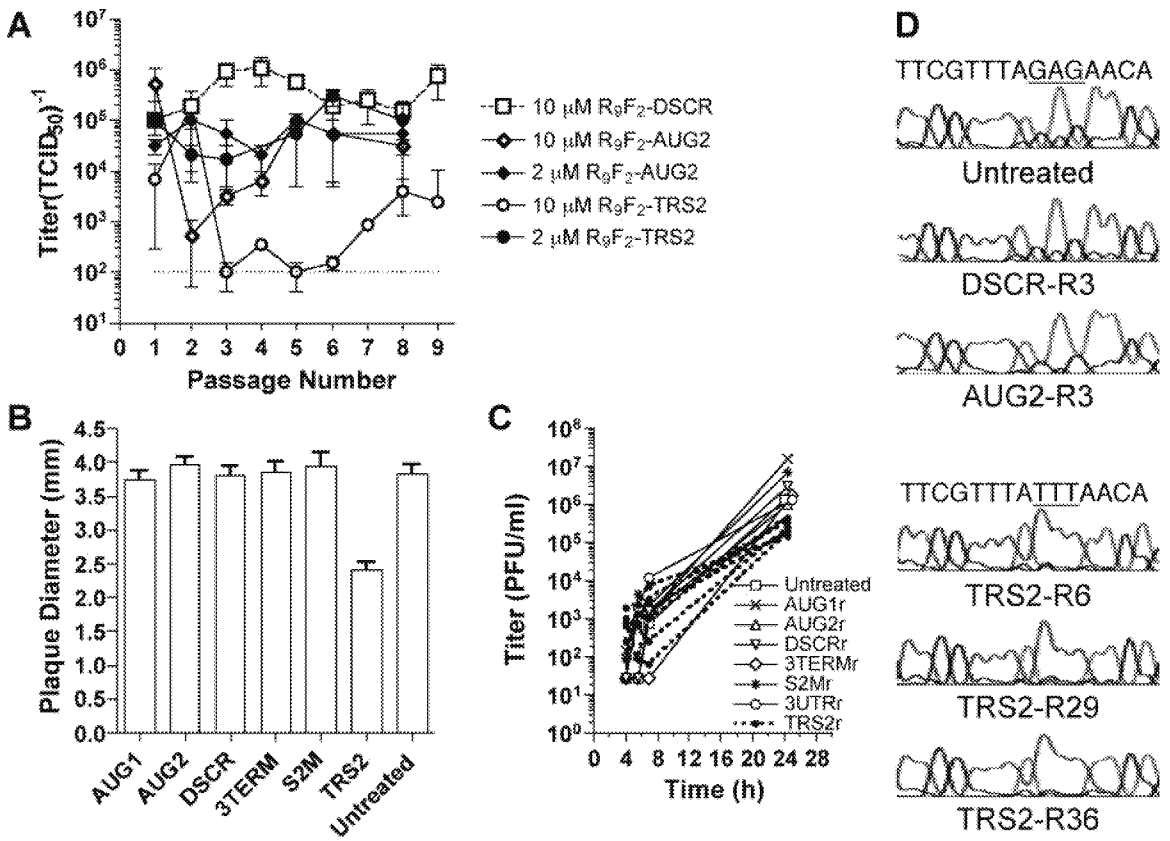

FIG. 5. Characterization of P-PMO-resistant SARS-CoV. SARS-CoV was serially passaged on cells pretreated with 2 μM or 10 μM R_9F_2-PMO or mock-treated cells. (A) Virus yield over the first nine passages was quantified 24 h after inoculation at an initial multiplicity of ≈10 PFU/cell. (B) The diameters of 50 plaques were measured after 11 viral passages on untreated or 10 μM P-PMO-treated cells. (C) Growth kinetics of P-PMO-resistant plaque-purified SARS-CoV on untreated Vero-E6 cells are shown. Biologically cloned virus was cultured from plaque-purified stocks selected after 11 passages on untreated cells or cells treated with AUG1, AUG2, S2M, 3TERM, 3UTR, TRS2, or DSCR P-PMO. Growth curves for five median-growth partially TRS2-resistant SARS-CoV biological clones are shown. $TCID_{50}$ titrations were calculated for four fourfold replicates. Error bars indicate standard error of the mean. (D) The 5′-terminal regions of P-PMO-resistant and mock-treated clones were amplified and sequenced in the antigenomic orientation. A portion of the TRS2 P-PMO target region is shown, with the mutations in TRS2-resistant clones underlined.

Specificity of P-PMO. The most effective anti-SARS-CoV P-PMO was found to be TRS2. Therefore TRS2 was tested for effects on an unrelated virus, the arenavirus lymphocytic choriomeningitis virus, that grows well in Vero-E6 cells under the same culture conditions under which the SARS-CoV experiments were carried out. Cells treated with 2 to 20 μM TRS2 were inoculated at a multiplicity of about 0.1 PFU/cell, and cell culture supernatants were harvested and titrated by plaque assay. Virus amplification at 24 h was not significantly altered in cells treated for 6 h with TRS2 P-PMO at any concentration compared to untreated controls (data not shown). Although the cellular functions required for arenavirus and coronavirus replication are likely not identical, we interpret this result as a further confirmation that the effectiveness of P-PMO against SARS-CoV was antisense mediated.

Partial resistance to P-PMO. The error-prone replication of RNA viruses presents a rapid model for viral evolution and drug resistance studies. In order to assess the propensity for SARS-CoV to develop resistance to antisense P-PMO, a stock cultured from a plaque-purified biological clone of SARS-CoV was serially passaged on cells treated with 0.5, 2, or 10 μM P-PMO. The term biological clone as used here designates an isolate derived from a single viral plaque. We chose to administer submaximal doses of P-PMO in order to allow the generation of P-PMO-resistant mutant strains. SARS-CoV was passaged blindly 11 times in cells pretreated with P-PMO. Viral growth was assessed, as an indicator of resistance, after each of the first nine passages (Fig. 5A).

The 3TERM and DSCR P-PMO did not inhibit SARS-CoV growth at any concentration or passage number. The AUG1, AUG2, and 3UTR P-PMO inhibited SARS-CoV growth for one to three passages after 10 μM treatment only. Treatment with 10 μM TRS2 P-PMO strongly inhibited SARS-CoV growth in each of the 11 passages tested. However, an increase in titer indicative of partial resistance was observed by passage 7. The peak titer of the TRS2 P-PMO-resistant virus population, during the 11 passages performed, was at least 100-fold below the titer of mock-treated cells, indicating acquisition of partial but not total resistance.

Viral plaques reflect the progress of a single infected cell's progression through multiple waves of viral entry, replication, and spread, and altered plaque diameter or morphology can be

indicative of perturbation to some stage of the virus replication cycle. To determine whether partially or totally P-PMO-resistant virus clones displayed altered amplification characteristics in the absence of P-PMO selection, plaque morphology and size were examined (Fig. 5B). Plaque morphology was found to be unaffected, though TRS2-selected biological clones displayed a smaller plaque morphology compared to that of wild-type SARS-CoV. Eight to 41 plaque-purified viruses were selected from each treatment pool. All AUG1, AUG2, DSCR, 3UTR, S2M, and 3TERM P-PMO-selected viruses caused typical CPE on Vero-E6 cells. Sixteen of 41 TRS2 P-PMO-selected clones caused negligible CPE on cells 72 h after inoculation, while the remaining clones caused reduced CPE.

One-step growth curves were performed for a selection of the P-PMO-selected SARS-CoV biological clones. TRS2 P-PMO-selected clones displayed delayed growth kinetics compared to untreated SARS-CoV and other P-PMO-selected clones (Fig. 5C). The titers of untreated and non-TRS P-PMO-treated SARS-CoV biological clones displayed in Fig. 5C represent typical titers observed 24 h after high-multiplicity inoculation. Continuous TRS2 P-PMO treatment, as shown in Fig. 3C, suppressed viral titers to approximately 100 PFU/ml, a decrease of ≈4 to 5 $\log_{10}$ from peak titers of ≈6 to 7 $\log_{10}$ observed in Fig. 3C, 5A, and 5C.

Reverse transcription-PCR amplicons from 14 TRS2-P-PMO-resistant SARS-CoV clones and one each of AUG1, AUG2, DSCR, 3UTR, S2M, and 3TERM and mock-treated clones were sequenced to determine whether the observed phenotypes correlated with specific genetic variations (Fig. 5D). Three consensus sequences were obtained for each biological clone, reflecting the dominant genotype over the first ≈600 bases proximal to the 5′ terminus of the genomic plus-strand. The sequences fell into two categories: TRS2-resistant clones each carried an identical set of mutations. Clones resulting from selection with the other P-PMO and mock treatment-selected clones were all identical. The 21 sequences that were obtained differed at three points: a silent mutation, C543T, and a block of three contiguous base changes of CTC to AAA at positions 62 to 64 proximal to the leader TRS (within the target region of TRS2-P-PMO) appeared in only the 14 TRS2-resistant clones, whereas a mutation, T281C, resulting in a leucine-to-proline shift at the sixth codon of ORF1a was present in only the AUG1, AUG2, DSCR, 3UTR, S2M, and 3TERM P-PMO-selected and vehicle-treated clones. Since the point mutation at position 281 relative to the original SARS-Tor2 sequence was found in both selected and mock-selected clones, we interpret this change as having likely evolved during serial passage in Vero-E6 cells prior to P-PMO selection. All TRS2-resistant clones identified likely derived from a single escape mutant. Mutations were not observed in the AUG1 or AUG2 P-PMO target regions of clones resistant to either of these P-PMO. We cannot at present rule out the possibility of compensating downstream mutations in AUG P-PMO-resistant biological clones.

Thermal melting curve data for peptide-conjugated PMO/RNA duplexes with variable mismatches led us to speculate that the three mutations at the TRS2-P-PMO target site reduce the effective binding affinity as measured by melting temperature (T_m) by ≈25 to 30°C (H. Moulton et al., manuscript in preparation) (36). We are unable at present to predict the precise number of mutations required to completely abrogate P-PMO efficacy. However, we tested the hypothesis that decreased affinity of the TRS2 P-PMO for the mutated target site could explain the decreased sensitivity of TRS2-selected SARS-CoV biological clones to TRS2 P-PMO.

P-PMO binding affinity was compared using a reporter construct in which the luciferase reporter gene was placed immediately downstream of either the wild-type SARS-CoV TRS region or the same region with the CTC→AAA mutations observed in TRS2 P-PMO-selected SARS-CoV clones (Fig. 6A). TRS2 P-PMO was approximately 10-fold less active against the three-mismatch TRS target compared to the wild-type target (EC_{50} of 500 nM and 50 nM, respectively). EC_{50}, as used here, refers to the amount of compound required to reduce luciferase luminescence by 50% compared to untreated controls. The decreased TRS2 P-PMO sensitivity of TRS2-selected strains was therefore consistent with the apparent reduction in stability of the P-PMO/target RNA duplex in TRS2-resistant biological clones. A similar observation was recently reported for human immunodeficiency virus type 1 escape variants resistant to small interfering RNAs (43).

While the experiments described above addressed the specificity and efficacy of P-PMO, we also wished to explore which molecular events of the viral life cycle the TRS2 P-PMO was affecting. In order to examine the effects of TRS2 PMO on inhibition of viral translation, a luciferase reporter construct was designed in which the entire SARS-CoV 5′-UTR was placed upstream of the reporter. The new reporter construct was designed so that luciferase expression would be initiated at the authentic SARS-CoV ORF 1a AUG codon. Contrary to our expectation, the TRS2 P-PMO outperformed AUG1 P-PMO by severalfold in translation inhibition (EC_{50}s of 35 nM and 185 nM, respectively; Fig. 6B). The TRS2 target site (bases 55 to 75) is sufficiently distant from both the 5′ terminus and the site of translation initiation to make it unlikely that interference with any of the discrete events of preinitiation at the terminus (e.g., 43S complex loading onto mRNA) or initiation at the initiator AUG (e.g., 48S-complex formation and/or joining of 48S and 60S ribosomal subunits) forms the basis for the observed effect. We therefore concluded, pending further testing, that TRS2 P-PMO inhibits SARS-CoV amplification primarily by interfering with the 43S preinitiation complex scanning process.

DISCUSSION

The results of this study demonstrate that P-PMO specific to the SARS-CoV genome can reduce production of infectious virus and thereby protect cells from virus-induced CPE as well as slow the cell-to-cell spread of infection. P-PMO acted by a sequence-specific mechanism, with low nonspecific activity on off-target cellular and viral functions. SARS-CoV overcame the antiviral activity of P-PMO directed against a number of sites on the viral genome, while resistance to P-PMO targeting the leader TRS element developed only after several host cell passages. The precise mechanism and timing of TRS2-associated nucleotide changes is unclear. We note, however, that the 5′-UTR typically displays relatively low sequence variability among coronaviruses of one species (one notable exception being a TRS-proximal polymorphism in murine hepatitis virus

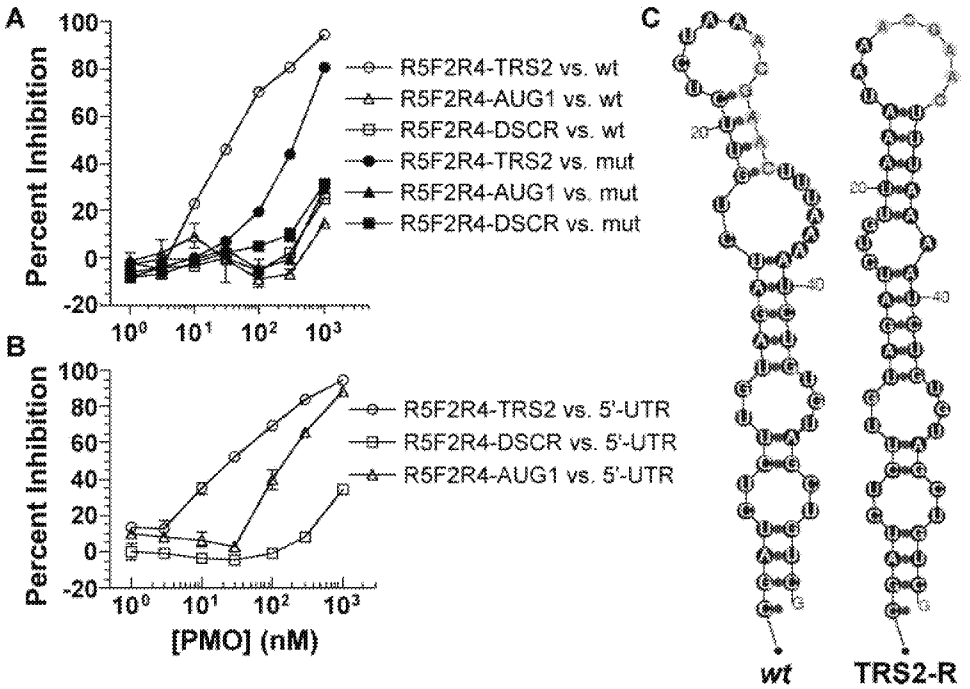

FIG. 6. Mechanisms of P-PMO efficacy and partial resistance. (A) Binding of P-PMO to the TRS region (nucleotide positions 51 to 79) was assessed in a cell-free translation inhibition assay. The relative binding strength of P-PMO to the wild-type SARS-CoV target (wt) and the three-mispair target (mut) is expressed as percent inhibition of luciferase expression. Zero percent inhibition was determined by the average level of luciferase expression from untreated control translations programmed with both wild-type and mutant mRNAs. (B) Comparison of inhibition of luciferase expression downstream of the entire SARS-CoV 5′-UTR sequence by three P-PMO. Error bars indicate standard error of the mean. (C) Low-energy secondary structures of the TRS hairpin of wild-type SARS-CoV (wt) and TRS2 P-PMO-selected SARS-CoV (TRS2-R) were generated using Mfold (49). The core TRS is near the top of the stem and shown in white circles; flanking sequences are depicted inside black circles. Nucleotides are numbered from the beginning of the predicted stem-loop.

JHM) (46), and the observed TRS2-associated polymorphism is not represented among SARS-CoV sequences currently available in the GenBank database. SARS-CoV resistant to TRS P-PMO displayed reduced cytopathology and cell-to-cell spread. Mutations at the TRS 2 P-PMO target site confirm that P-PMO act directly on the viral RNA, as similarly shown for in situ-generated RNA complementary to human immunodeficiency virus type 1 *env* (23) and small interfering RNAs directed against human immunodeficiency virus type 1 (43). Decreased P-PMO-target affinity to altered target sequence almost certainly explains the observed loss of P-PMO sensitivity in resistant isolates.

The CTC→AAA mutations found in all TRS2-P-PMO-resistant SARS-CoV clones occur outside the region occupied by the consensus TRS (5′-CGAAC-3′) (Fig. 6C), but within the TRS2 P-PMO target region. No mutations were observed in resistant isolates cloned from cultures treated with other P-PMO. The presence of short complementary regions surrounding the TRS is a conserved feature among the *Nidovirales* and is called stem-loop II (5) or the leader TRS hairpin (40). Mfold secondary-structure predictions (49) indicate that the TRS2-resistant SARS-CoV could form a destabilized alternate hairpin conformation (boldface), **TTAAA**-TAA*ACGAAC*-**TTTAA**, surrounding the TRS (italic). The lowest-energy fold of the TRS hairpin with the AAA mutation has a calculated ΔG of −4.1 kcal/mol, compared to −7.0 kcal/mol for the wild-type CTC sequence.

Our analysis yields no compelling rationale that would favor the incorporation of the particular set of mutations observed. Finding a clustered three-nucleotide substitution in a coronavirus after 11 passages would generally be considered a rare event, and further study will be required to clarify the mechanism involved. Moreover, it is unclear whether these point mutations arose from a low-probability chance event or whether the particular set of mutations observed represent a preferred solution to the selective pressures toward optimal replication and drug resistance. So, while it would appear that antisense may designate a site for mutation, the present data are insufficient to suggest the type of mutation most likely to be incorporated.

Levels of P-PMO efficacy appeared to group with respect to the nature of the viral target sequence. This was most striking in the case of the AUG1 P-PMO, targeted to the 3′ end of the 5′-UTR, the AUG2 and AUG3 P-PMO, which directly masked the ORF 1a translation initiation codon, and the 1ABFS P-PMO, targeted over 13 kb downstream. All four of these P-PMO were conceived as inhibitors of replicase translation, with targets designed to interfere with ribosome scanning, translation initiation, or the ribosomal frameshift event by which the coronaviruses produce the enzymatic products of ORFs 1a and 1b. Results for the 3UTR P-PMO, though modest, were interesting because the effects of 3UTR cannot be readily attributed to inhibition of translation and therefore likely derive from some effect on viral RNA synthesis. The selection of the 3UTR

P-PMO target was perhaps unfortunate, as a study from the Masters group that appeared during the course of our studies showed that the loop and upper stem regions of the stem-loop/pseudoknot structure in the 3′-UTR targeted by the 3UTR P-PMO were tolerant of extensive mutations and deletions (10). Our results appear to confirm that result. The relative lack of activity of the three compounds targeted near the 3′ terminus of the genome may indicate that the processing minus-strand polymerase complex displaces bound P-PMO or that P-PMO compete inefficiently with viral and host proteins for binding in this region (16, 21, 27, 35).

The most effective P-PMO targeted the transcription regulatory sequence. Two different P-PMO, TRS1 and TRS2, showed the highest levels of antiviral activity compared to all other P-PMO used in this study. The 20-mer TRS1 and 21-mer TRS2 vary by only a few nucleotides, as shown in Fig. 1, but are predicted to vary considerably in the targets to which they can bind. The TRS1 target includes the consensus TRS core sequence ACGAAC and 14 bases in the viral 5′ direction. TRS2 covers the TRS core, four bases in the 3′ direction, and 11 bases on the 5′ side. This difference is predicted to allow binding of TRS1 to full-length genomic RNA and all eight of the subgenomic mRNAs (27). Out of the eight SARS subgenomic RNAs, five have start codons either adjacent to or within two bases of the TRS core (27). The 3′ end of the TRS core is also the 3′ end of the TRS1 target. TRS1 was therefore expected to have a more profound antiviral effect due to its potential for translational inhibition via duplexing to a region immediately upstream of the AUG translation start sites of at least five discrete viral RNAs combined with its potential ability to block discontinuous transcription of all subgenomic minus-strand RNAs. The TRS2 P-PMO spans the flanking sequence on both sides of the TRS core more extensively than TRS1 P-PMO and may therefore be more effective at inhibiting discontinuous transcription. The observation that TRS2 is more efficacious than TRS1 suggests that targeting the genomic RNA exclusively is a more efficient antiviral strategy with this class of antisense compound.

The SARS-CoV was able to partially escape inhibition by the TRS2 P-PMO within four viral passages. The forced generation of resistance suggests antisense agents as a powerful means of investigating virus structure and function and as a complement to traditional reverse-genetic studies. Furthermore, the observation that the TRS2-resistant SARS-CoV showed a reduced level of cytopathology opens the possibility for a new approach to the generation of attenuated viral strains. The results presented here indicate that the selection of therapeutic antisense antiviral targets will present the greatest opportunity for success when informed by detailed molecular understanding of the physical and temporal requirements for virus amplification.

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To: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]; 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Babu Tekwani'[btekwani@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; Chad Petit[cpetit@uab.edu]; 'Clare O'Regan'[coregan@wustl.edu]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'Fahim Ahmad'[fahmad@southernresearch.org]; 'George Painter'[george.r.painter@emory.edu]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; 'Maria Agostini'[Maria.l.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Suto'[suto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; 'Ron Swanstrom'[risunc@med.unc.edu]; 'Shuntai Zhou'[shuntaiz@email.unc.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]; 'Amelia.s.george@vumc.org'[Amelia.s.george@vumc.org]; 'Hughes, Tia M'[tia.m.hughes@vumc.org]; 'kak@uab.edu'[kak@uab.edu]; Jessica Eagar[JEagar@uab.edu]; Tameca Winston[twinston@peds.uab.edu]; 'Nicole Haese'[haese@ohsu.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Sat 4/4/2020 12:39:28 PM (UTC-05:00)
Subject: AD3C Project/Core Teleconference Call
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Modeling SARS v6[1].pptx

Hello all AD3C members,

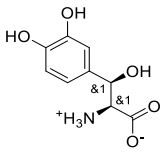
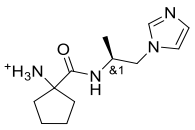
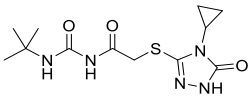
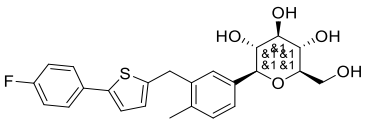
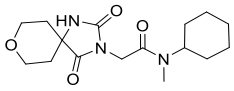
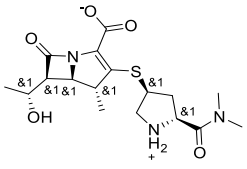
Hoping this email finds you safe and well. Although we did cancel last week's call, we would like to follow up with everyone and have a check-in. Further, we would like to update and obtain feedback from everyone on some of the COVID-19 work. Attached please find the virtual screens that we received from SR's Med Chem group:
1. Virtual screen of 102K library against exonuclease site of SARS nsP14 crystal structure.
2. Virtual screen of 122K library against conserved binding site of SARS/COVID-19 main protease crystal structures
3. Repurposing of drugs/compounds from literature according to cheminformatics analysis (not included in current HTS library).

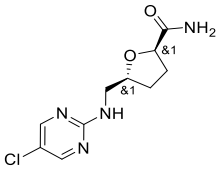
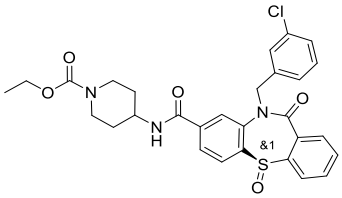
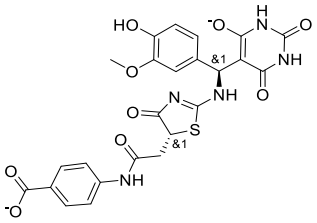
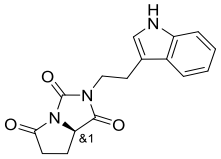
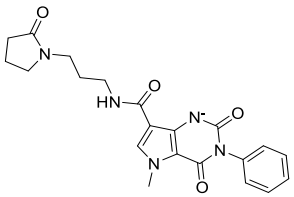
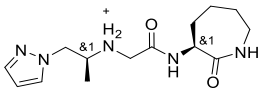
A presentation is attached for further details. In total, 52 compounds were sorted and initially 38 compounds will be accessed for SARS/COVID-19 SAR assays (See excel file for details). Some of these will be purchased from commercial sources in coming days.

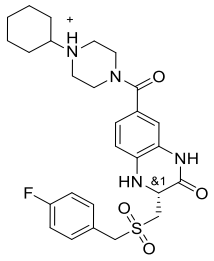
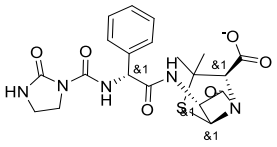
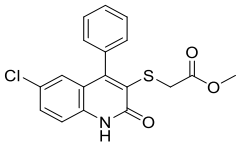
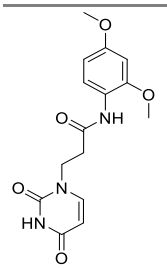
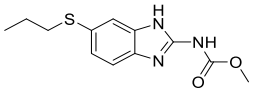
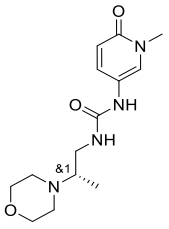
A doodle poll may be found here in order to schedule in such a tight turn around:
https://doodle.com/poll/emrk69gb327hqa9a
Please do this at your earliest convenience. Hope you all have a nice weekend and stay safe and well.

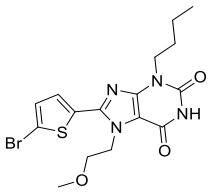
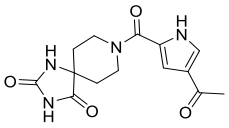
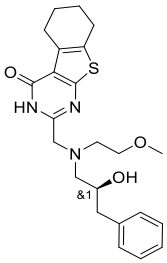
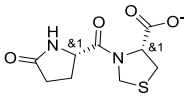
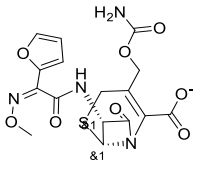
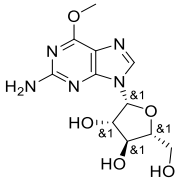
Thank you all,

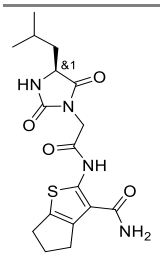
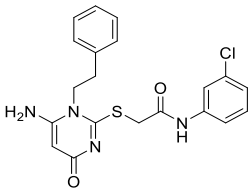
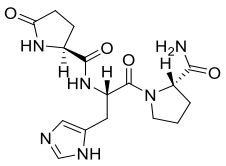
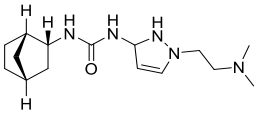
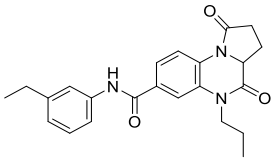
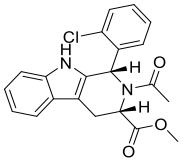
Stephanie
Cell: 205-563-8565

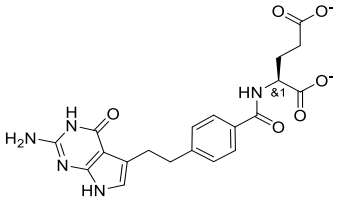
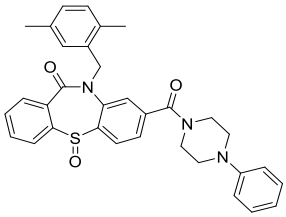
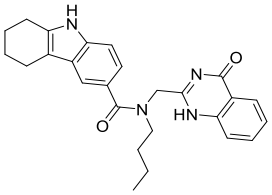
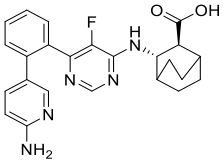
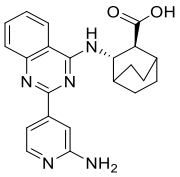
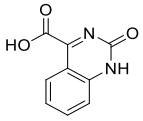
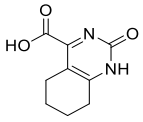
Structure	VS Scores (kcal/mol)
	-14.3 SARS nsP14
	-9.7 SARS nsP14
	-9.4 SARS nsP14
	-9.4 SARS nsP14
	-9.3 SARS nsP14
	-9.3 SARS nsP14

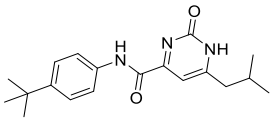
	-8.8	SARS nsP14
	-8.7	SARS nsP14
	-8.6	SARS nsP14
	-8.6	SARS nsP14
	-8.5	SARS nsP14
	-8.5	SARS nsP14

	-8.5 SARS nsP14
	-8.5 SARS nsP14
	-8.4 SARS nsP14
	-8.3 SARS nsP14
	-8.3 SARS nsP14
	-8.2 SARS nsP14

	-8.2	SARS nsP14
	-8.1	SARS nsP14
	-7.9	SARS nsP14
	-7.9	SARS nsP14
	-7.8	SARS nsP14
	-7.7	SARS nsP14

	-7.6 SARS nsP14
	-9.6 COVID-19 3CLpro
	-9.5 COVID-19 3CLpro
	-9.3 COVID-19 3CLpro
	-8.7 COVID-19 3CLpro
	-8.3 COVID-19 3CLpro

	N/A
	N/A
	N/A
	N/A
	N/A
	N/A
	N/A



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Library	Supplier ID
Selleckchem FDA	Droxidopa S3041
Enamine Antivirus	Z3019991808
Enamine Diversity	Z97433880
Selleckchem FDA	Canagliflozin S2760
ChemDiv Antivirus	S453-0072
Selleckchem FDA	Meropenem S1381

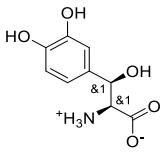
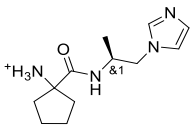
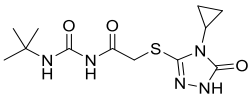
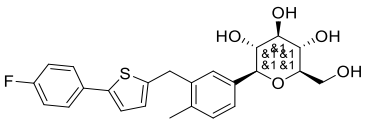
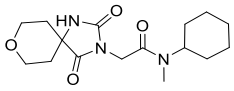
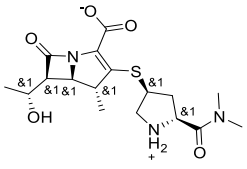
Enamine Antivirus	Z1416552092
ChemDiv Antivirus	K788-8341
ChemDiv chelatorMMPs	C202-2026
ChemDiv Diversity	Y042-2141
ChemDiv Antivirus	F216-0094
Enamine Antivirus	Z1139745046

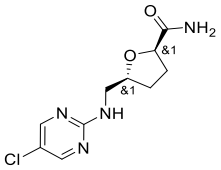
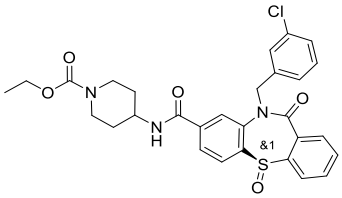
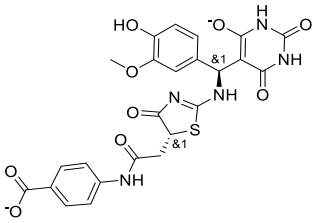
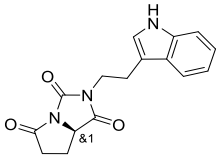
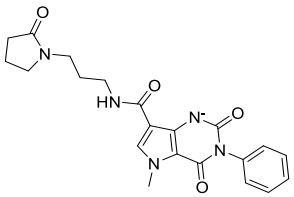
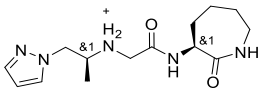
ChemDiv Antivirus	K977-0236
Selleckchem FDA	Azlocillin S3195
ChemDiv Antivirus	5236-0086
ChemDiv Diversity	D459-0057
Selleckchem FDA	Albendazole S1836
Enamine Antivirus	Z3019991258

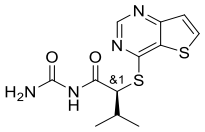
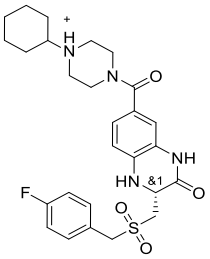
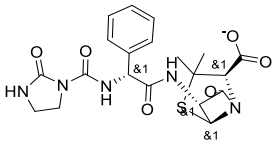
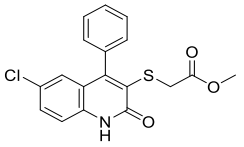
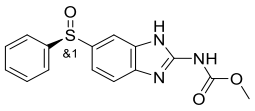
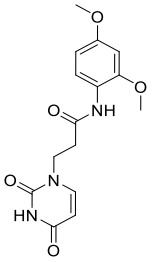
Enamine Diversity	Z50140169
Enamine Diversity	Z225729962
ChemDiv Antivirus	V016-3656
Selleckchem FDA	Pidotimod S3106
Selleckchem FDA	Cefuroxime S4620
Selleckchem FDA	Nelarabine S1213

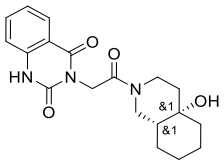
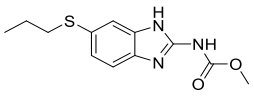
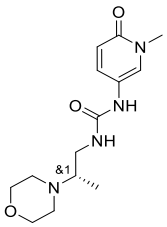
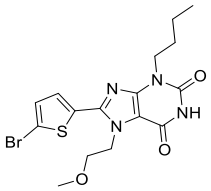
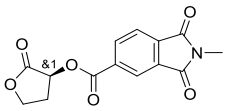
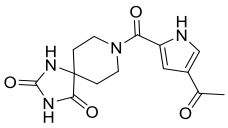
Enamine Diversity	T5286232
ChemDiv Diversity	8014-2830
Selleckchem FDA	Protirelin S4680
Enamine Antivirus	Z1278200544
ChemDiv Peptidomimetics	P071-0707
ChemDiv Peptidomimetics	D715-0085

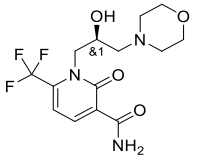
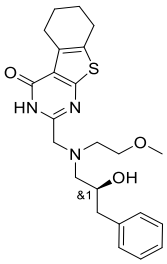
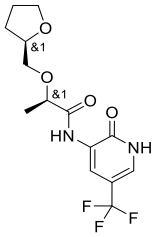
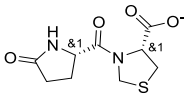
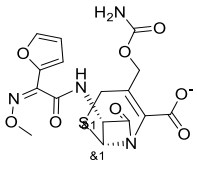
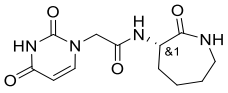
SR Repurposition Antifolate, Selleckchem FDA	Pemetrexed S1135
SR Repurposition HIV CCR5	SRI-37517, ChemDiv C529-0936
SR Repurposition HIV CCR5	SRI-38150, Enamine Z28492461
SR Repurposition Influenza PB2	SRI-44448
SR Repurposition Influenza PB2	SRI-44449
SR Repurposition CHIKV nsP3	SRI-43750
SR Repurposition CHIKV nsP3	SRI-43945

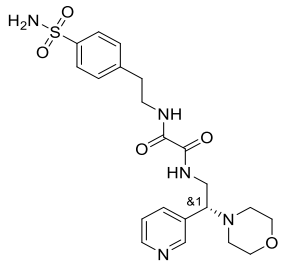
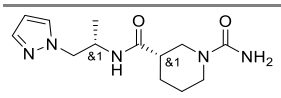
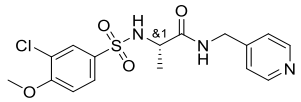
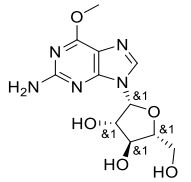
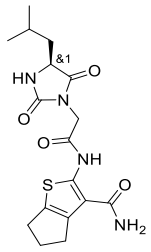
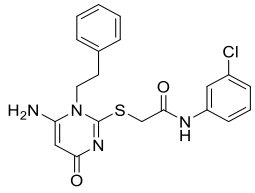
Structure	VS Scores (kcal/mol)
	-14.3 SARS nsP14
	-9.7 SARS nsP14
	-9.4 SARS nsP14
	-9.4 SARS nsP14
	-9.3 SARS nsP14
	-9.3 SARS nsP14

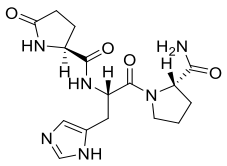
	-8.8	SARS nsP14
	-8.7	SARS nsP14
	-8.6	SARS nsP14
	-8.6	SARS nsP14
	-8.5	SARS nsP14
	-8.5	SARS nsP14

	-8.5 SARS nsP14
	-8.5 SARS nsP14
	-8.5 SARS nsP14
	-8.4 SARS nsP14
	-8.4 SARS nsP14
	-8.3 SARS nsP14

	-8.3 SARS nsP14
	-8.3 SARS nsP14
	-8.2 SARS nsP14
	-8.2 SARS nsP14
	-8.1 SARS nsP14
	-8.1 SARS nsP14

	-8.0	SARS nsP14
	-7.9	SARS nsP14
	-7.9	SARS nsP14
	-7.9	SARS nsP14
	-7.8	SARS nsP14
	-7.8	SARS nsP14

	-7.8 SARS nsP14
	-7.8 SARS nsP14
	-7.7 SARS nsP14
	-7.7 SARS nsP14
	-7.6 SARS nsP14
	-9.6 COVID-19 3CLpro



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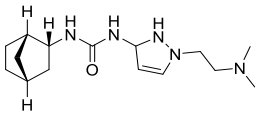

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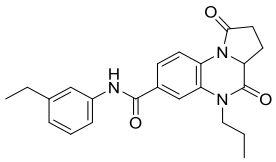

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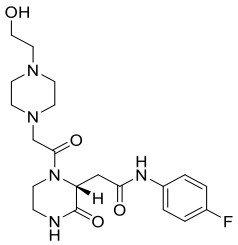

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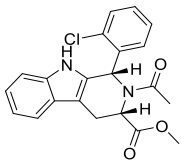

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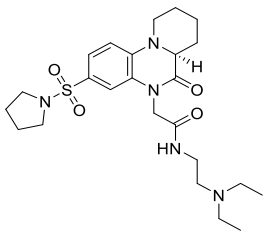

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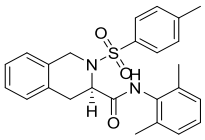

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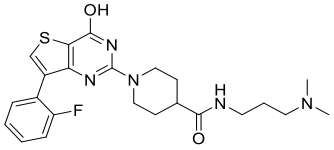

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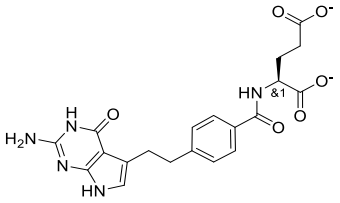

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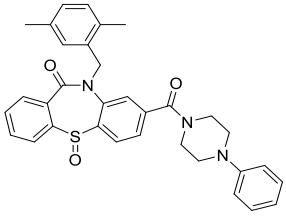

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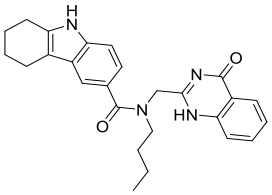

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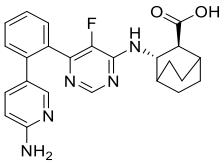

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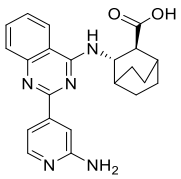

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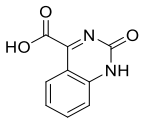

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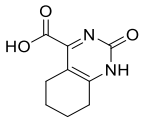

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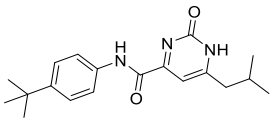

N/A

Library	Supplier ID
Selleckchem FDA	Droxidopa S3041
Enamine Antivirus	Z3019991808
Enamine Diversity	Z97433880
Selleckchem FDA	Canagliflozin S2760
ChemDiv Antivirus	S453-0072
Selleckchem FDA	Meropenem S1381

Enamine Antivirus	Z1416552092
ChemDiv Antivirus	K788-8341
ChemDiv chelatorMMPs	C202-2026
ChemDiv Diversity	Y042-2141
ChemDiv Antivirus	F216-0094
Enamine Antivirus	Z1139745046

Enamine Diversity	Z194686656
ChemDiv Antivirus	K977-0236
Selleckchem FDA	Azlocillin S3195
ChemDiv Antivirus	5236-0086
Selleckchem FDA	Oxfendazole S1830
ChemDiv Diversity	D459-0057

ChemDiv Diversity	Y043-6144
Selleckchem FDA	Albendazole S1836
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Enamine Antivirus	Z3019991279
ChemDiv Antivirus	V016-3656
Enamine Antivirus	Z872068520
Selleckchem FDA	Pidotimod S3106
Selleckchem FDA	Cefuroxime S4620
Enamine Antivirus	Z3019991087

ChemDiv Antivirus	E155-0016
Enamine Antivirus	Z403696376
ChemDiv chelatorMMPs	Y050-1228
Selleckchem FDA	Nelarabine S1213
Enamine Diversity	T5286232
ChemDiv Diversity	8014-2830

Selleckchem FDA	Protirelin S4680
Enamine Antivirus	Z1278200544
ChemDiv Peptidomimetics	P071-0707
ChemDiv Peptidomimetics	D718-0742
ChemDiv Peptidomimetics	D715-0085
ChemDiv Peptidomimetics	G672-0298

ChemDiv Peptidomimetics	G791-0830
ChemDiv Peptidomimetics	Z250-1144

SR Repurposition Antifolate, Selleckchem FDA	Pemetrexed S1135
SR Repurposition HIV CCR5	SRI-37517, ChemDiv C529-0936
SR Repurposition HIV CCR5	SRI-38150, Enamine Z28492461
SR Repurposition Influenza PB2	SRI-44448

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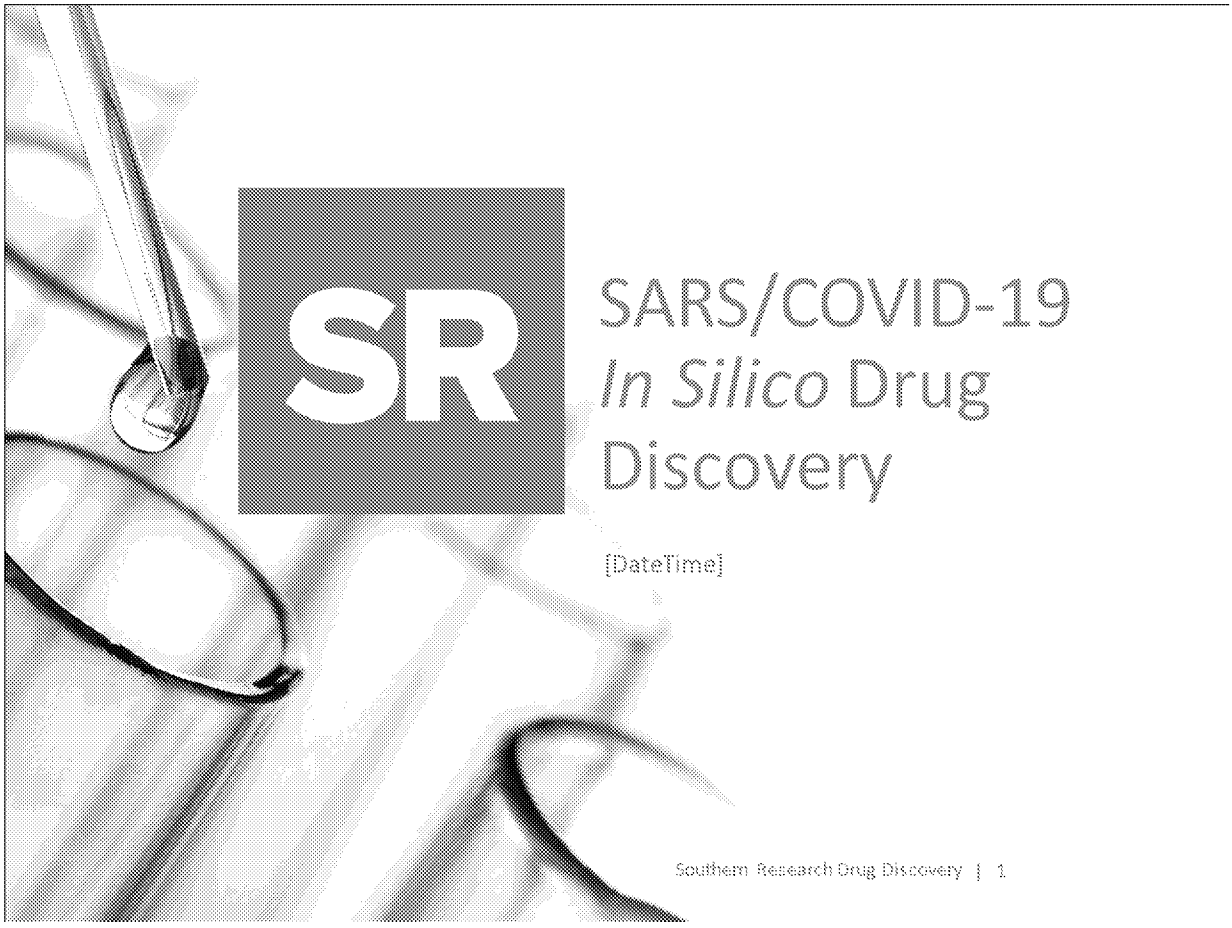

9/27/2021

Southern Research Engineering

Outline

- Virtual screen of SARS nsP14
- Virtual screen of SARS/COVID-19 main protease
- Other strategies for virtual screen

9/27/2021

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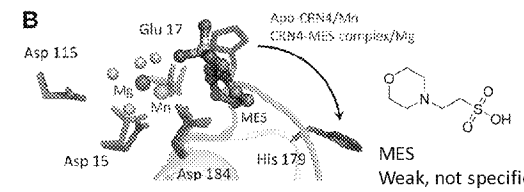
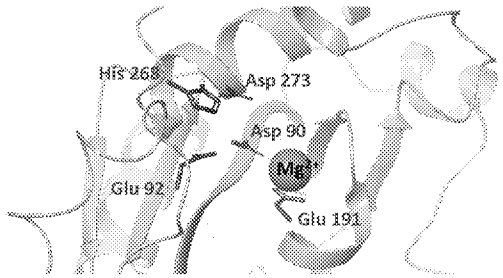
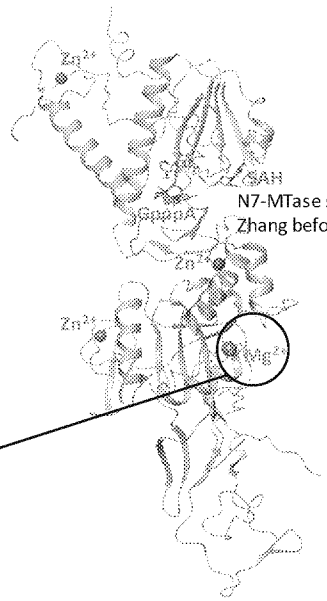
Virtual Screen (VS) Site at SARS nsP14



Inhibitor MES co-crystalized at DEDDh exonuclease site of *C. elegans* CRN-4 (Figure 6B, Huang, KW; *et. al. J. Med. Chem.* 2016, 59: 8019)





N7-MTase site (VS by Dr. Wei Zhang before)

SARS nsP14 crystal (PDB ID 5C8S)

❖ DEEDh exonuclease site in SARS nsP14 (equivalent to DEDDh family) is used for new VS

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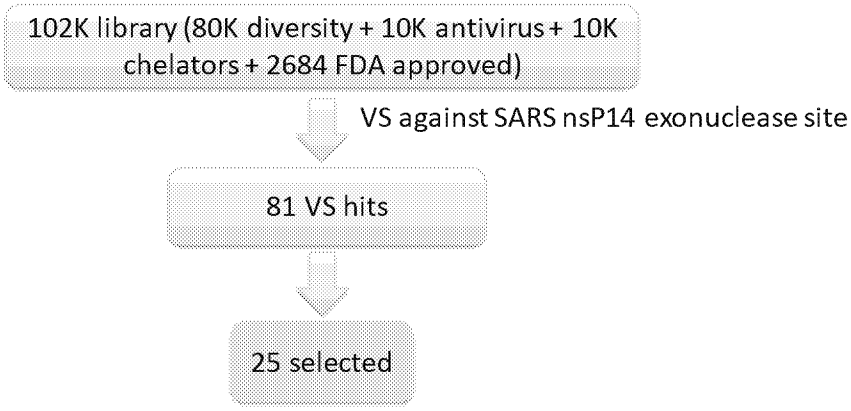
Summary of VS Result of nsP14



- Challenge: bring specificity at the metal ion binding site

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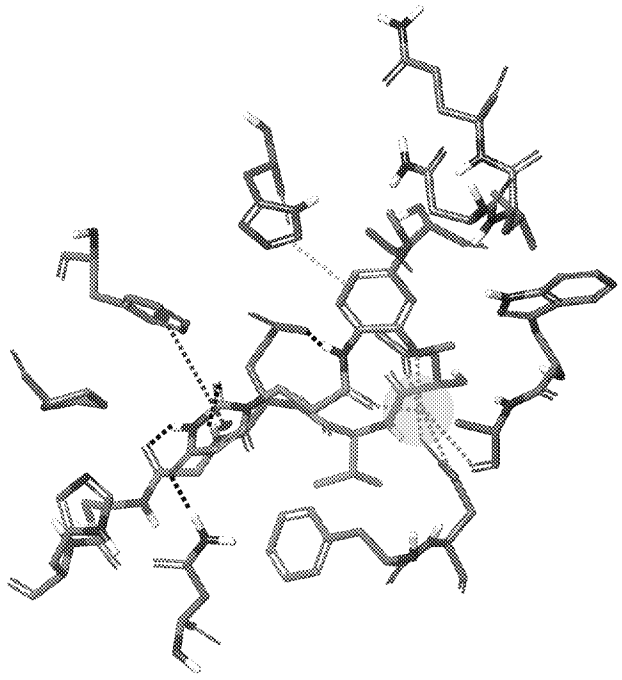
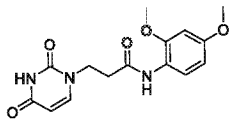
Examples From Diversity Set for nsP14



VS pose at SARS nsP14 exonuclease site



ChemDiv D459-0057 (left figure)
Score: -8.3

- Hydrogen bond
- Coordinate bond
- Hydrophobic contact
- π-π stacking

Purple residues: DEEDh motif
Pink sphere: Mg^{2+}

*Score in kcal/mol, more negative, the better

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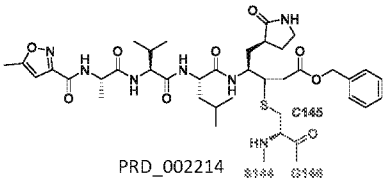
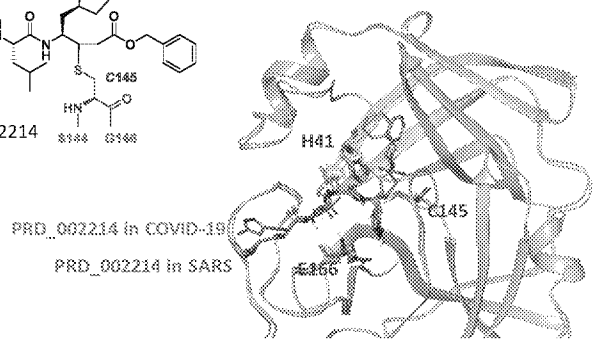
SARS & COVID-19 Main Protease





Overlay of SARS and COVID-19 co-crystals of 3CLpro/PRD_002214

- **SARS main protease (nsP5 3CLpro) crystal structure** (PDB ID 2AMQ) and COVID-19 3CLpro crystal structure (PDB ID 6LU7, published in Feb.) has 97% sequence similarity and identical active site
- Since active sites are identical, VS results of COVID-19 protease will be applicable to SARS protease

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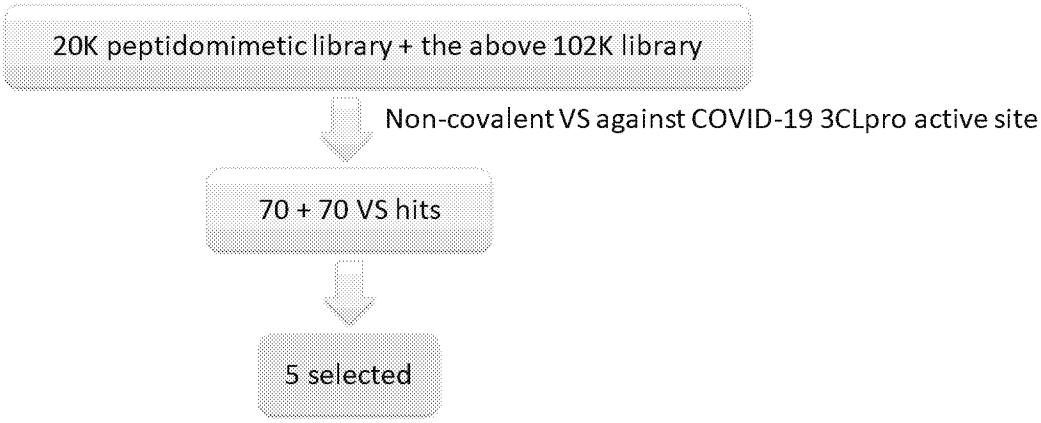
Summary of VS Result of 3CLpro



- Challenge: non-covalent inhibitors may not be as potent as covalent inhibitors

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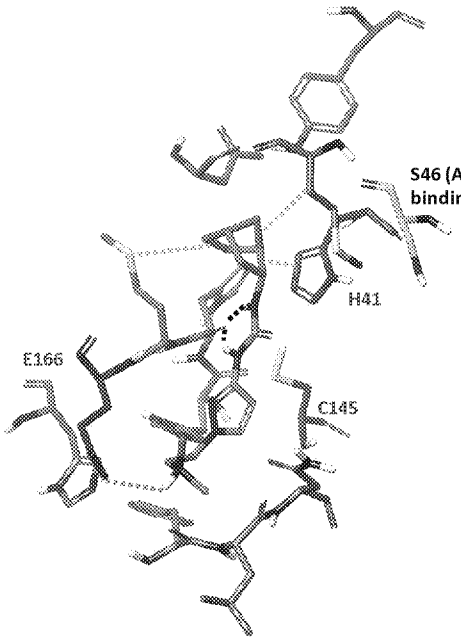
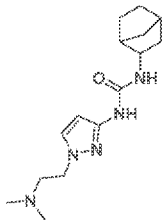
Example Hit for SARS/COVID-19 3CLpro



VS pose at COVID-19 protease active site



Enamine antivirus library Z1278200544
Score: -9.3

- Hydrogen bond
- Salt bridge
- Hydrophobic contact
- π-π stacking

Purple residues: active site
Cyan residue: variant in SARS

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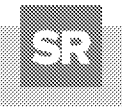
Other VS Strategies

- ❖ Receptor-based VS
  - Protease inhibitor library against SARS/COVID-19 nsP5 3CLpro crystal
  - SARS nsP3 papain-like protease crystal
  - SARS nsP3 macrodomain crystal
  - Other crystal structures of interest
- ❖ Ligand-based VS
  - Machine learning model built on in-house SARS HTS data and literature COVID-19 data



Solving the world's hardest problems.

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Back-up Slides
Additional Information

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Additional Details of VS Strategies

- VS protease inhibitor library against SARS/COVID-19 nsP5 3CLpro crystal
  - 227 cmpds from Selleckchem and 108 cmpds from TargetMol
- VS against SARS nsP3 papain-like protease crystal (not macrodomain)
  - COVID-19 has 91% sequence similarity and identical binding site according to homology model
- VS against SARS nsP3 macrodomain crystal
  - COVID-19 has 83% sequence similarity and identical binding site according to homology model
  - An conserved ribose binding site across alphaviruses and coronaviruses
  - Knowledge gained from in-house CHIKV nsP3 fragment VS/co-crystalization can be applied here
- Ligand-based VS of 775K in-house compounds against an in-house built COVID-19 pharmacophore model
  - A.I./machine learning model built with COVID-19 actives in literature and SARS data from SR HTS
  - As a pilot run, 8 in-house compounds have been selected for re-purpose

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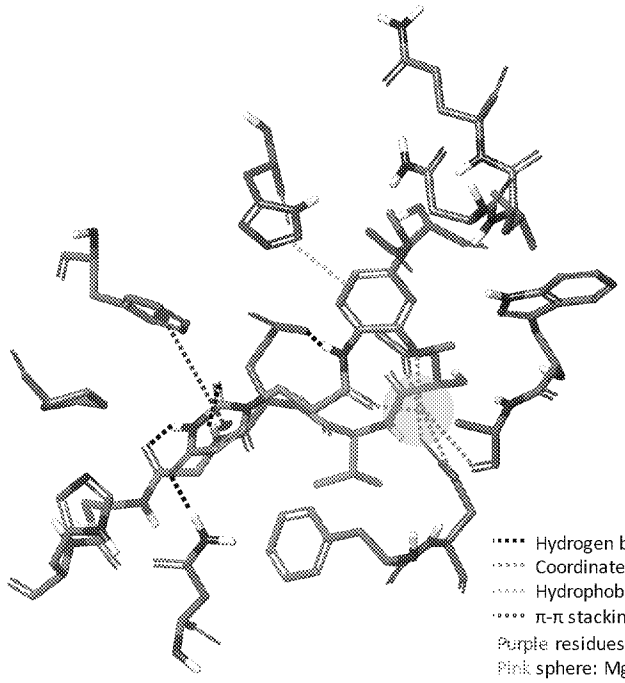
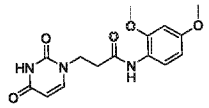
Examples From Diversity Set for nsP14

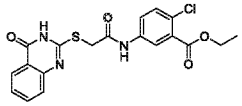


Hydrogen bond
Coordinate bond
Hydrophobic contact
π-π stacking
Purple residues: DEEDh motif
Pink sphere: Mg^{2+}

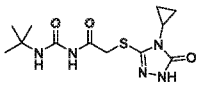
VS pose at SARS nsP14 exonuclease site



ChemDiv D459-0057 (left figure)
Score: -8.3



ChemBridge 7729713
Score: -8.4



Enamine Z97433880
Score: -9.4

*Score in kcal/mol, more negative, the better

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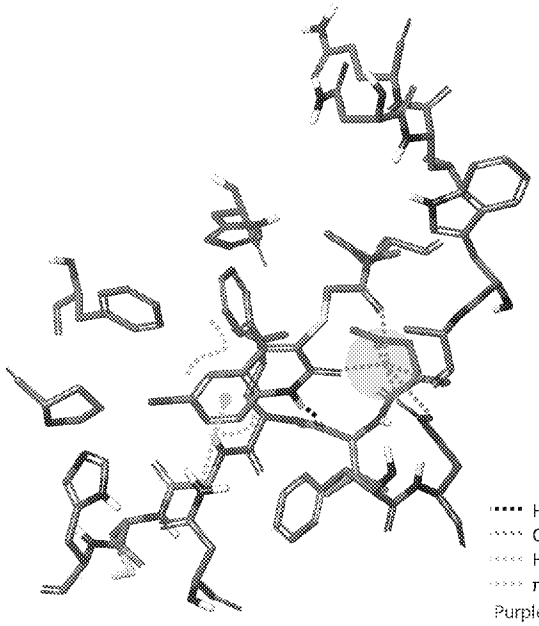
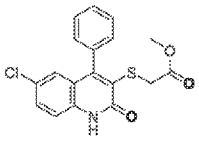
Examples From Antivirus Set for nsP14

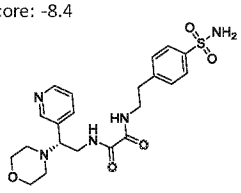


VS pose at SARS nsP14 exonuclease site

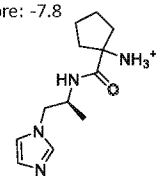
Hydrogen bond
Coordinate bond
Hydrophobic contact
π-asparagine interaction
Purple residues: DEEDh motif
Pink sphere: Mg^{2+}



ChemDiv 5236-0086 (left figure)
Score: -8.4



ChemDiv E155-0016
Score: -7.8



Enamine Z3019991808
Score: -9.7

[Date (free)] Southern Research Drug Discovery 14

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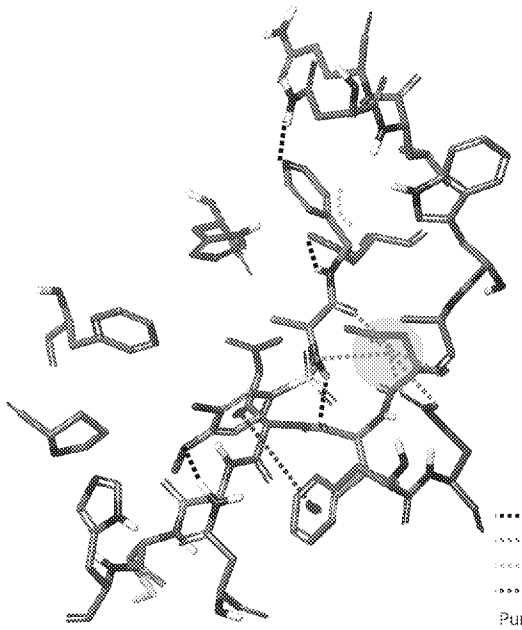
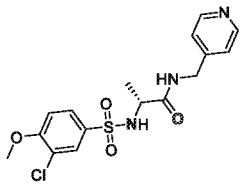
Example From Chelator Set for nsP14



Hydrogen bond
Coordinate bond
Hydrophobic contact
π-π stacking
Purple residues: DEEDh motif
Pink sphere: Mg^{2+}

V5 pose at SARS nsP14 exonuclease site



ChemDiv Y050-1228 (left figure)
Score: -7.7

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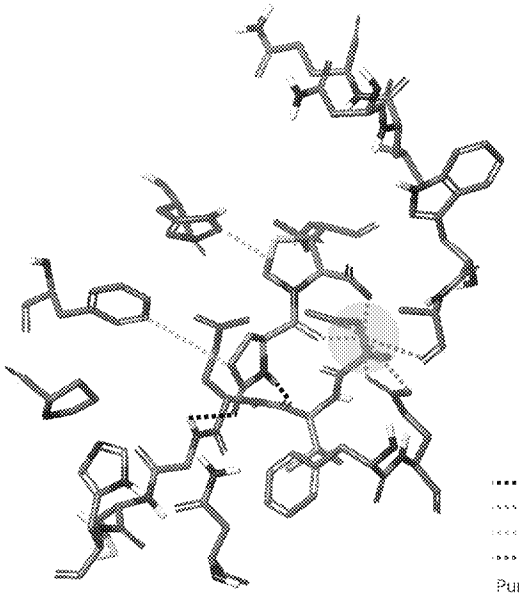
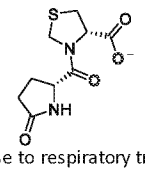
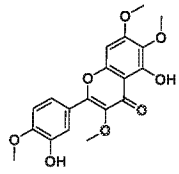
Examples from FDA Set for nsP14



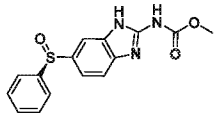
VS pose at SARS nsP14 exonuclease site



Selleckchem S3106 (left figure)
Score: -7.9
Pidotimod: stimulate immune response to respiratory tract infection such as pneumonia. Also used to treat HPV and hepatitis C. May be easy to co-crystalize with SARS nsp14 due to high solubility (80-150 mM)



Selleckchem S9288
Score: -7.6
Casticin: enhance antimalaria activity of artemisinin



Selleckchem S1830
Score: -8.3
Oxfendazole: kill parasite in veterinary practice

Hydrogen bond
Coordinate bond
Hydrophobic contact
π-π stacking
Purple residues: DEEDh motif
Pink sphere: Mg^{2+}

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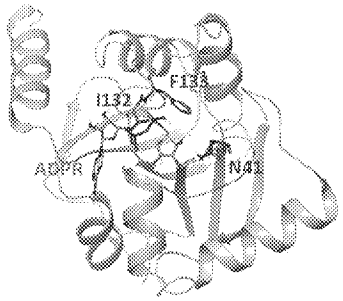
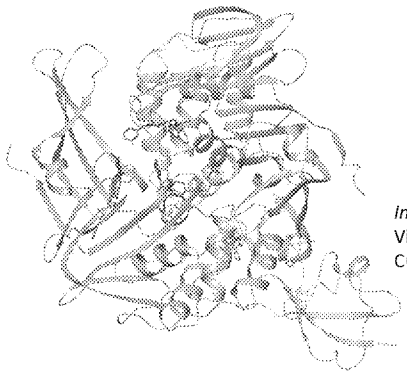
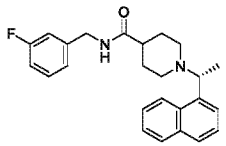
Other SARS Proteins Crystal Structures



SARS macrodomain (PDB ID 2FAV)
Egloff, M. P.; *et. al. J. Virol.* 2006, 80: 8493



SARS papain-like protease (PDB ID 4OW0)
Baez-Santos, Y. M.; *et. al. J. Med. Chem.* 2014, 57: 2393



In vitro enzymatic IC_{50} = 0.15±0.01 μM
Virus replication IC_{50} = 5.4±0.6 μM
CC_{50} > 100 μM

- In addition, SARS nsP7-10, 12, 13, 15, 16, and spike protein also have crystal structures

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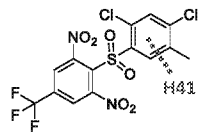
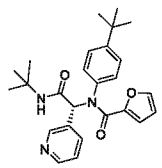
Examples of Literature SARS inhibitors



Co-crystalized non-covalent inhibitor reported in a VS in literature
In vitro enzymatic IC_{50} = 0.3±0.05 μM
Lu, I. L.; *et. al. J. Med. Chem.* 2006, 49: 5154



Another co-crystalized non-covalent inhibitor reported in literature
In vitro enzymatic IC_{50} = 1.5 μM
Virus replication IC_{50} = 12.9 μM
Jacobs, J.; *et. al. J. Med. Chem.* 2013, 56: 534

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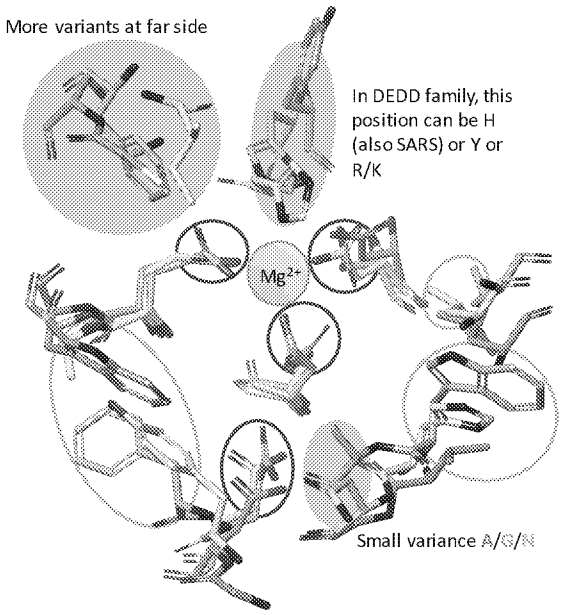
SARS and Human Exonuclease



- Gray: SARS nsP14 crystal structure (PDB ID 5C8S)
- Blue: human WRN crystal (2FBT), inhibition has developmental toxicity, not wanted
- Green: mouse TREX1 crystal (3B60), human TREX1 is a host protein utilized by HIV, inhibition may be acceptable for antivirus purpose

DEDD motif in human and DEED in SARS

Hydrophobic region

Sequence variants

❖ SARS and human exonuclease are highly conserved around the DEDD core, but have more variants at far side for specificity

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To: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]; 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Babu Tekwani'[btekwani@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; Chad Petit[cpetit@uab.edu]; 'Clare O'Regan'[coregan@wustl.edu]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'Fahim Ahmad'[fahmad@southernresearch.org]; 'George Painter'[george.r.painter@emory.edu]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; 'Maria Agostini'[Maria.l.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Suto'[suto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; 'Ron Swanstrom'[risunc@med.unc.edu]; 'Shuntai Zhou'[shuntaiz@email.unc.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]; 'Amelia.s.george@vumc.org'[Amelia.s.george@vumc.org]; 'Hughes, Tia M'[tia.m.hughes@vumc.org]; 'kak@uab.edu'[kak@uab.edu]; Jessica Eagar[JEagar@uab.edu]; Tameca Winston[twinston@peds.uab.edu]; 'Nicole Haese'[haese@ohsu.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Mon 4/6/2020 2:53:35 PM (UTC-05:00)
Subject: Re: AD3C Project/Core Teleconference Call

Hello all,
We have much to discuss, as we forwarded the information from SR to go over, I wanted to also include the general meeting agenda below. Thank you,
Stephanie

AD3C Teleconference Agenda
April 6, 2020 4:00 p.m. Central Time

Join from PC, Mac, Linux, iOS or Android: https://uasystem.zoom.us/j/ **552.136**

Or iPhone one-tap:
US: +13126266799,, 552.136 or +16465588656,, 552.136

Or Telephone:
Dial US: +1 312 626 6799 or +1 646 558 8656
Meeting ID: 552.136

A. Admin Core
- Y2 funding
- Administrative Supplement Project 1 submitted and Gates ReFRAME screening against SARS-CoV-2

B. Project Progress Updates
- Project 1 – Corona (MDenison, RBaric; Core B BBostwick; Core C APathak; GBluemling)
- Project 2 – Alpha (DStreblow, MHeise, TMorrison; Core B BBostwick; Core C APathak; GBluemling)
- Project 3 – Flavi (PYShi, JNelson, AHirsch, MDiamond; Core B BBostwick; Core C APathak; GBluemling)
- Project 4 – Influenza (RWhitley, BTekwani; Core B BBostwick; Core C OMoukha-Chafiq)

From: Stephanie Moore <smoore@peds.uab.edu>
Date: Saturday, April 4, 2020 at 12:39 PM
To: Antiviral Drug Discovery and Development <ad3c@peds.uab.edu>, 'Alana Centilli' <acentilli@southernresearch.org>, 'Alec Hirsch' <hirschal@ohsu.edu>, 'Ardina Pruijssers' <ardina.pruijssers@vumc.org>, 'Ashish Pathak' <apathak@southernresearch.org>, 'Babu Tekwani' <btekwani@southernresearch.org>, 'Bob Bostwick' <bostwick@southernresearch.org>, 'Carrie Evans' <evans@southernresearch.org>, Chad Petit <cpetit@uab.edu>, 'Clare O'Regan' <coregan@wustl.edu>, 'Corinne Augelli-Szafran' <caugelli-szafran@southernresearch.org>, 'Daniel Streblow' <streblow@ohsu.edu>, 'Erica Bitten' <erica.bitten@emory.edu>, 'Fahim Ahmad' <fahmad@southernresearch.org>, 'George Painter' <george.r.painter@emory.edu>, 'Greg Bluemling' <gblueml@emory.edu>, 'Hope Angel' <angelh@ohsu.edu>, 'Jay Nelson' <nelsonj@ohsu.edu>, 'Jessica Smith' <smijessi@ohsu.edu>, 'Jim Chappell' <jim.chappell@Vanderbilt.edu>, 'Lynn Rasmussen' <rasmussen@southernresearch.org>, 'Maria Agostini' <Maria.l.agostini@vanderbilt.edu>, 'Mark Denison' <mark.denison@vanderbilt.edu>, 'Mark Heise' <mark_heisem@med.unc.edu>, 'Mark Suto' <suto@southernresearch.org>, Mary Wyatt Bowers <MWBowers@peds.uab.edu>, 'Mason Wu' <mwu@southernresearch.org>, 'Michael Diamond' <diamond@borcim.wustl.edu>, 'Miranda Nebane' <nebane@southernresearch.org>, 'Nichole Tower' <tower@southernresearch.org>, 'Omar Moukha-Chafiq' <omoukha-chafiq@southernresearch.org>, Pei-Yong Shi <peshi@utmb.edu>, 'Rachel Graham' <rlgraham@email.unc.edu>, 'Ralph Baric' <rbaric@email.unc.edu>, "Richard Whitley, M.D." <RWhitley@peds.uab.edu>, 'Ron Swanstrom' <risunc@med.unc.edu>, 'Shuntai Zhou' <shuntaiz@email.unc.edu>, 'Thomas Morrison' <thomas.morrison@ucdenver.edu>, 'Tim Sheahan' <sheahan@email.unc.edu>, 'Toni Baric' <antoinette_baric@med.unc.edu>, 'Victor DeFilippis' <defilipp@ohsu.edu>, "'Amelia.s.george@vumc.org'" <Amelia.s.george@vumc.org>, "'Hughes, Tia M'" <tia.m.hughes@vumc.org>, "'kak@uab.edu'" <kak@uab.edu>, Jessica Eagar <JEagar@uab.edu>, Tameca Winston <twinston@peds.uab.edu>, 'Nicole Haese' <haese@ohsu.edu>
Subject: AD3C Project/Core Teleconference Call

Hello all AD3C members,

Hoping this email finds you safe and well. Although we did cancel last week's call, we would like to follow up with everyone and have a check-in. Further, we would like to update and obtain feedback from everyone on some of the COVID-19 work. Attached please find the virtual screens that we received from SR's Med Chem group:
1. Virtual screen of 102K library against exonuclease site of SARS nsP14 crystal structure.
2. Virtual screen of 122K library against conserved binding site of SARS/COVID-19 main protease crystal structures
3. Repurposing of drugs/compounds from literature according to cheminformatics analysis (not included in current HTS library).

A presentation is attached for further details. In total, 52 compounds were sorted and initially 38 compounds will be accessed for SARS/COVID-19 SAR assays (See excel file for details). Some of these will be purchased from commercial sources in coming days.

A doodle poll may be found here in order to schedule in such a tight turn around:
https://doodle.com/poll/emrk69gb327hqa9a
Please do this at your earliest convenience. Hope you all have a nice weekend and stay safe and well.

Thank you all,

Stephanie
Cell: 205-563-8565

To: 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Amy Sims'[sims0018@ad.unc.edu]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'George Painter'[george.r.painter@emory.edu]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; 'Maria Agostini'[Maria.l.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Suto'[suto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]; 'Sides, Kate'[ksides@southernresearch.org]; 'Babu Tekwani'[btekwani@southernresearch.org]; 'fahmad@southernresearch.org'[fahmad@southernresearch.org]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Tue 8/13/2019 9:20:56 AM (UTC-05:00)
Subject: RE: Monthly AD3C Teleconference for Project and Core Reporting
Aug 15 2019 AD3C Agenda.pdf

Here is the agenda for the meeting on Thursday, August 15 at 3:30 pm Central Time. Please send any materials to share to me by 12:00 noon Central Time that day and I will distribute to the group.

Thanks,

Sara Davis | Program Coordinator II
Direct Line: 205.996.7804 | sadavis@peds.uab.edu

-----Original Appointment-----
From: Antiviral Drug Discovery and Development Center-AD3C
Sent: Monday, January 14, 2019 9:27 AM
To: Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Amy Sims'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Bob Bostwick'; 'Carrie Evans'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; 'Pei-Yong Shi'; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Sides, Kate'; Babu Tekwani; 'fahmad@southernresearch.org'
Cc: 'Suto, Mark J.'; 'Evans, Carrie W.'; 'Morrison, Thomas'; 'Bostwick, Bob'; 'Rasmussen, Lynn'; 'Tower, Nichole A.'
Subject: Monthly AD3C Teleconference for Project and Core Reporting
When: Thursday, August 15, 2019 3:30 PM-5:00 PM (UTC-06:00) Central Time (US & Canada).
Where: Call in at 1-888-806-5025 and use the passcode of **552.136**

Hello to Everyone:

Due to several scheduling issues, we are moving the August 2019 AD3C monthly call from August 22nd to Thursday, August 15th at 3:30 pm Central Time. We hope you are able to join the call. If you have slides to share, please send them to me by 12:00 pm Central Time on that day and I will distribute to the group.

With kind regards,

Sara Davis
sadavis@peds.uab.edu

AD3C Teleconference Agenda
August 15, 2019, 3:30 p.m. CST

Meeting Number: (888) 806-5025 **Participant code: 420976**

1. Admin Core

   - Subaward status consortium agreement addendum
   - Annual meeting information

2. Project progress updates

   - Project 1 – Corona (MDenison, RBaric; Core B BBostwick; Core C APathak; GBluemling)
   - Project 2 – Alpha (DStreblow, MHeise, TMorrison; Core B BBostwick; Core C APathak; GBluemling)
   - Project 3 – Flavi (PYShi, JNelson, AHirsch, MDiamond; Core B BBostwick; Core C APathak; GBluemling)
   - Project 4 – Influenza (RWhitley, BTekwani; Core B BBostwick; Core C OMoukha-Chafiq)

To: Denison, Mark[mark.denison@vumc.org]; Baric, Ralph S[rbaric@email.unc.edu]; Daniel Streblow[streblow@ohsu.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Babu Tekwani'[btekwani@southernresearch.org]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Pathak, Ashish[apathak@southernresearch.org]; Augelli-Szafran, Corinne[caugelli-szafran@southernresearch.org]; Mark Suto[msuto@southernresearch.org]; Bostwick, Bob[bbostwick@southernresearch.org]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Thur 6/25/2020 4:35:47 PM (UTC-05:00)
Subject: FW: [EXT] FW: USU B01 SouthernResearchInstitute-Augelli-Szafran May-20
USU B01 SouthernResearchInstitute-Augelli-Szafran May-20.pdf

Hello all,
Attached please find the WEEV data that was discussed on the call today.
Thank you,
Stephanie

From: "Pathak, Ashish" <apathak@southernresearch.org>
Date: Thursday, June 25, 2020 at 4:12 PM
To: Stephanie Moore <smoore@peds.uab.edu>
Subject: [EXT] FW: USU B01 SouthernResearchInstitute-Augelli-Szafran May-20

Hi Stephanie,

Here is the data received from NIAID activity against WEEV. Can you forward this data to all PI's? Thanks

Ashish

From: Pathak, Ashish
Sent: Monday, June 15, 2020 8:03 AM
To: Daniel Streblow <streblow@ohsu.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Stephanie Moore <smoore@peds.uab.edu>
Cc: Richard Whitley, M.D. <RWhitley@peds.uab.edu>
Subject: FW: USU B01 SouthernResearchInstitute-Augelli-Szafran May-20

Data from NIAID on WEEV. EEEV data pending. Thanks

Ashish

Ashish K. Pathak, Ph.D.
Principal Scientist
Chemistry Department | Drug Discovery Division
Southern Research | 2000 Ninth Ave South, Birmingham AL 35205
Tel: 205-581-2542 | Email: apathak@southernresearch.org

From: Augelli-Szafran, Corinne <caugelli-szafran@southernresearch.org>
Sent: Friday, June 12, 2020 4:31 PM
To: Pathak, Ashish <apathak@southernresearch.org>
Subject: FW: USU B01 SouthernResearchInstitute-Augelli-Szafran May-20

Hi Ashish – Please see attached and share with the team. Thank you.
Corinne

From: Justin Julander <justin.julander@usu.edu>
Sent: Friday, June 12, 2020 4:25 PM
To: Augelli-Szafran, Corinne <caugelli-szafran@southernresearch.org>
Cc: Davis, Mindy (NIH/NIAID) [E] <mindy.davis@nih.gov>
Subject: USU B01 SouthernResearchInstitute-Augelli-Szafran May-20

Please find the attached report for the compounds you submitted for screening under the NIH B01 contract.
Best Regards,
Justin

Justin Julander
Research Associate Professor
Institute for Antiviral Research
Utah State University
5600 Old Main Hill
Logan, UT. 84322-5600
Ph: 435-797-7215
Fax: 435-797-3959

In-Vitro Antiviral Screening Report

Task Order Number:	B01

Organization:	Southern Research Institute
Submitter Name:	Corinne Augelli-Szafran
Email:	caugelli-Szafran@southernresearch.org
Test Site:	USU
Investigator:	Julander
Test Date *(m/dd/yy)* :	05/08/20
Report Date *(Mmm-yy)* :	May-20

Virus Screened:	Western Equine Encephalitis
Virus Strain:	California
Cell Line:	Vero 76
Vehicle:	DMSO
Drug Conc. Range:	0.032-100 µM
Control Conc. Range:	0.0000032-0.01 µg/ml
Experiment Number:	WEEV-064

Control Drug Name	Control Assay Order	Control Assay Name	EC50	EC90	CC50	SI50	SI90
Infergen	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		0.0000068	>0.01		>1500
Infergen	Secondary	Neutral Red (Cytopathic effect/Toxicity)	0.0000059		>0.01	>1700	

EC50 - compound concentration that reduces viral replication by 50%

EC90 - compound concentration that reduces viral replication by 90%

CC50 - compound concentration that reduces cell viability by 50%

SI50 - CC50/EC50

SI90 - CC50/EC90

Compounds with SI values >10 are considered active and merit further investigati

Notes

Screening Results

ARB No.	Date Received m/dd/yy	Compound Name/ID	Drug Assay Order	Drug Assay Name	EC50	EC90	CC50	SI50	SI90
20-000011	5/5/2020	SRI-00042718	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		14	>100		>7.1
20-000011	5/5/2020	SRI-00042718	Secondary	Neutral Red (Cytopathic effect/Toxicity)	20		>100	>5	
20-000012	5/5/2020	SRI-00040507	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		4.3	>100		>23
20-000012	5/5/2020	SRI-00040507	Secondary	Neutral Red (Cytopathic effect/Toxicity)	4.5		>100	>22	
20-000015	5/5/2020	SRI-00044087	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		1.8	>100		>56
20-000015	5/5/2020	SRI-00044087	Secondary	Neutral Red (Cytopathic effect/Toxicity)	4.7		>100	>21	
20-000017	5/5/2020	SRI-00041627	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		>9.3	9.3		0
20-000017	5/5/2020	SRI-00041627	Secondary	Neutral Red (Cytopathic effect/Toxicity)	>9.3		9.3	0	
20-000018	5/5/2020	SRI-00043799	Secondary	Visual (Virus yield reduction)/Neutral Red (Toxicity)		0.79	>100		>130
20-000018	5/5/2020	SRI-00043799	Secondary	Neutral Red (Cytopathic effect/Toxicity)	7		>100	>14	

To: galter@partners.org[galter@partners.org]; maria.baca-estrada@canada.ca[maria.baca-estrada@canada.ca]; baihe@nmpa.gov.cn[baihe@nmpa.gov.cn]; rbaric@email.unc.edu[rbaric@email.unc.edu]; cheryl@gisaid.org[cheryl@gisaid.org]; Valentina Bernasconi[valentina.bernasconi@cepi.net]; shinjini.bhatnagar@thsti.res.in[shinjini.bhatnagar@thsti.res.in]; karin.bok@nih.gov[karin.bok@nih.gov]; dboyle@path.org[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; christian.brechot[christian.brechot@pasteur.fr]; Christine.bruce@phe.gov.uk[Christine.bruce@phe.gov.uk]; zuz4@cdc.gov[zuz4@cdc.gov]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; Marco.Cavaleri@ema.europa.eu[Marco.Cavaleri@ema.europa.eu]; MONALISA.CHATTERJI@gatesfoundation.org[MONALISA.CHATTERJI@gatesfoundation.org]; MAY.CHU@CUANSCHUTZ.EDU[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; costaa@who.int[costaa@who.int]; htq4@cdc.gov[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; tdelossantos@path.org[tdelossantos@path.org]; emmie.dewit@nih.gov[emmie.dewit@nih.gov]; marciela.degrace@nih.gov[marciela.degrace@nih.gov]; rafael.delgado@salud.madrid.org[rafael.delgado@salud.madrid.org]; mit666666@pitt.edu[mit666666@pitt.edu]; William Dowling[william.dowling@cepi.net]; christian.drosten@charite.de[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; darryl.falzarano@usask.ca[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; clint.florence@nih.gov[clint.florence@nih.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Simon.Funnell@phe.gov.uk[Simon.Funnell@phe.gov.uk]; Luc.Gagnon@nexelis.com[Luc.Gagnon@nexelis.com]; Mayra.Garcia@fda.hhs.gov[Mayra.Garcia@fda.hhs.gov]; bhx1@cdc.gov[bhx1@cdc.gov]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; barney.graham@nih.gov[barney.graham@nih.gov]; ahgriff@bu.edu[ahgriff@bu.edu]; Elwyn Griffiths[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; GSELL, Pierre[gsellp@who.int]; ilj2@cdc.gov[ilj2@cdc.gov]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; rzh7@cdc.gov[rzh7@cdc.gov]; henaorestrepoa@who.int[henaorestrepoa@who.int]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; paul.hodgson@usask.ca[paul.hodgson@usask.ca]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; Johan Holst[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; tkh4@cdc.gov[tkh4@cdc.gov]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Cassandra.Kelly@finddx.org[Cassandra.Kelly@finddx.org]; Jacqueline.Kirchner@gatesfoundation.org[Jacqueline.Kirchner@gatesfoundation.org]; knezevici[knezevici@who.int]; m.koopmans@erasmusmc.nl[m.koopmans@erasmusmc.nl]; Gerald.Kovacs@hhs.gov[Gerald.Kovacs@hhs.gov]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; Phil Krause[philip.krause@fda.hhs.gov]; skrebs@hivresearch.org[skrebs@hivresearch.org]; Greg.Kulnis@nexelis.com[Greg.Kulnis@nexelis.com]; Arun Kumar[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; teresa.lambe@ndm.ox.ac.uk[teresa.lambe@ndm.ox.ac.uk]; janet.lathey[janet.lathey@nih.gov]; bleader@path.org[bleader@path.org]; leejooyeon@korea.kr[leejooyeon@korea.kr]; MSLEVER@dstl.gov.uk[MSLEVER@dstl.gov.uk]; liyl@cde.org.cn[liyl@cde.org.cn]; changguili@aliyun.com[changguili@aliyun.com]; lyhchengdu@163.com[lyhchengdu@163.com]; limhy0919@korea.kr[limhy0919@korea.kr]; James.Little@hhs.gov[James.Little@hhs.gov]; liub@cde.org.cn[liub@cde.org.cn]; Tracy.MacGill@fda.hhs.gov[Tracy.MacGill@fda.hhs.gov]; Karen Makar[Karen.Makar@gatesfoundation.org]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; adrian.mcdermott@nih.gov[adrian.mcdermott@nih.gov]; jmcelrat@fredhutch.org[jmcelrat@fredhutch.org]; gmedigeshi@thsti.res.in[gmedigeshi@thsti.res.in]; jwm1@pitt.edu[jwm1@pitt.edu]; philip.minor2@gmail.com[philip.minor2@gmail.com]; kmodjarrad@eidresearch.org[kmodjarrad@eidresearch.org]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; omorgan@who.int[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; sarah.mudrak@duke.edu[sarah.mudrak@duke.edu]; munoz-fontela@bnitm.de[munoz-fontela@bnitm.de]; vincent.munster@nih.gov[vincent.munster@nih.gov]; Todd.Myers@fda.hhs.gov[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ@mail.mil[aysegul.nalca.civ@mail.mil]; scott.napper@usask.ca[scott.napper@usask.ca]; MNELSON@dstl.gov.uk[MNELSON@dstl.gov.uk]; pilailuk.o@dmsc.mail.go.th[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; golinger@MRIGLOBAL.ORG[golinger@MRIGLOBAL.ORG]; jokim@ivi.int[jokim@ivi.int]; Mark.Page@nibsc.org[Mark.Page@nibsc.org]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; map1@cdc.gov[map1@cdc.gov]; xdv3@cdc.gov[xdv3@cdc.gov]; Keith.Peden@fda.hhs.gov[Keith.Peden@fda.hhs.gov]; sheila.a.peel2.civ@mail.mil[sheila.a.peel2.civ@mail.mil]; malik@hku.hk[malik@hku.hk]; perkinsm@who.int[perkinsm@who.int]; supaporn.p@dmsc.mail.go.th[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ@mail.mil[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR@dstl.gov.uk[JLPRIOR@dstl.gov.uk]; arimoin@g.ucla.edu[arimoin@g.ucla.edu]; lauriex@who.int[lauriex@who.int]; Nicola.Rose@nibsc.org[Nicola.Rose@nibsc.org]; msalit@stanford.edu[msalit@stanford.edu]; erica@lji.org[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; schendel@lji.org[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; PScott@eidresearch.org[PScott@eidresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; Ragini.Shivji@ema.europa.eu[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; mksong@ivi.int[mksong@ivi.int]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; swaminathans@who.int[swaminathans@who.int]; nax3@cdc.gov[nax3@cdc.gov]; tracey.thue@usask.ca[tracey.thue@usask.ca]; georgia.tomaras@duke.edu[georgia.tomaras@duke.edu]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; john.c.trefry.civ@mail.mil[john.c.trefry.civ@mail.mil]; luk_vandenberghe@meei.harvard.edu[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; Vasan.Vasan@csiro.au[Vasan.Vasan@csiro.au]; y.m.vasiliev@spbniivs.ru[y.m.vasiliev@spbniivs.ru]; David Vaughn[David.Vaughn@gatesfoundation.org]; linfa.wang@duke-

nus.edu.sg[linfa.wang@duke-nus.edu.sg]; wangjz@nifdc.org.cn[wangjz@nifdc.org.cn]; wangyc@nifdc.org.cn[wangyc@nifdc.org.cn]; Jerry.Weir@fda.hhs.gov[Jerry.Weir@fda.hhs.gov]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; dj56wood@gmail.com[dj56wood@gmail.com]; xumiaobj@126.com[xumiaobj@126.com]; Solomon Abebe Yimer[solomon.yimer@cepi.net]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; vyusibov@indianabiosciences.org[vyusibov@indianabiosciences.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; PNorris@vitalant.org[PNorris@vitalant.org]; Lisa@amicitiam.com[Lisa@amicitiam.com]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; rolandsutter@gmail.com[rolandsutter@gmail.com]
From: William Dowling[william.dowling@cepi.net]
Sent: Tue 8/4/2020 1:22:58 PM (UTC-05:00)
Subject: WHO Viruses reagents and assays working group - No meeting this week

Hello all
There will be no meeting of WHO Viruses reagents and assays working group this week (Wed, Aug. 5). We will return next week on Aug 12 at 2:30 PM CET.
Thanks
Bill

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Amelia George'[Amelia.s.george@vumc.org]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Babu Tekwani'[btekwani@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; Chad Petit[cpetit@uab.edu]; 'Clare O'Regan'[coregan@wustl.edu]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'Fahim Ahmad'[fahmad@southernresearch.org]; 'George Painter'[george.r.painter@emory.edu]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Kathy Keith'[kak@uab.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; 'Maria Agostini'[Maria.l.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Suto'[suto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Nicole Haese'[haese@ohsu.edu]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; 'Ron Swanstrom'[risunc@med.unc.edu]; 'Shuntai Zhou'[shuntaiz@email.unc.edu]; Stephanie Moore[smoore@peds.uab.edu]; Tameca Winston[twinston@peds.uab.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tia Hughes'[tia.m.hughes@vumc.org]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]
Cc: Sara Davis[sadavis@peds.uab.edu]; Kathy Keith[KKeith@peds.uab.edu]; 'Diamond, Michael'[mdiamond@wustl.edu]; 'Graham, Rachel'[rlgraham@ad.unc.edu]; 'Bostwick, Bob'[bbostwick@southernresearch.org]; 'Suto, Mark J.'[msuto@southernresearch.org]; 'Evans, Carrie W.'[cevans@southernresearch.org]; 'Swanstrom, Ronald I'[ron_swanstrom@med.unc.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Mon 7/20/2020 9:47:26 AM (UTC-05:00)
Subject: IMPORTANT: AD3C Monthly Meeting Date Change for July Meeting
7.30.20 AD3C Agenda.pdf

Hello to Everyone:

I am writing to you today to let you know that the Administrative Group needs to change the date of the July monthly AD3C Zoom call from July 23 to **Thursday, July 30 at the same time, 3:30 pm Central Time.** We apologize for any difficulties that this change might cause for you, and hope that you will be able to join us. The agenda for the call is attached, and I will send an Outlook Calendar notice with the new date this morning. Thank you.

With kind regards,

Sara Davis
Program Coordinator II
Collaborative Antiviral Study Group/Pediatrics/Infectious Diseases
sadavis@peds.uab.edu
Direct Line Telephone: 205-638-2536

AD3C Teleconference Agenda
July 30, 2020 3:30 p.m. Central Time

Join from PC, Mac, Linux, iOS or
Android: https://uasystem.zoom.us/j/94625531176?pwd=ZnFiYWNBNEpUYXdFdHlxVzhzWTBMQT09
Password: 767262
Meeting ID: 946 2553 1176

Or Telephone:
Dial (for higher quality, dial a number based on your current location):
US: +1 646 558 8656 or +1 301 715 8592 or +1 312 626 6799 or +1 669 900 6833 or +1 253 215 8782 or +1 346 248 7799
Meeting ID: 946 2553 1176

SIP: 94625531176@zoomcrc.com
Password: 767262

AD3C Meeting Agenda

A. Admin Core

- If you have data to share with the group, we can use the "share screen" feature for you to present. Please let Stephanie know if you have questions.
- Subawards are completed, thanks everyone.
- Standing reminder to please make sure that there are MTAs in place between all institutions.

B. Project Progress Updates

- Project 1 – Corona (MDenison, RBaric; Core B BBostwick; Core C APathak; GBluemling)
- Project 2 – Alpha (DStreblow, MHeise, TMorrison; Core B BBostwick; Core C APathak; GBluemling)
- Project 3 – Flavi (PYShi, JNelson, AHirsch, MDiamond; Core B BBostwick; Core C APathak; GBluemling)
- Project 4 – Influenza (RWhitley, BTekwani; Core B BBostwick; Core C OMoukha-Chafiq)

To: galter@partners.org[galter@partners.org]; maria.baca-estrada@canada.ca[maria.baca-estrada@canada.ca]; baihe@nmpa.gov.cn[baihe@nmpa.gov.cn]; rbaric@email.unc.edu[rbaric@email.unc.edu]; cheryl@gisaid.org[cheryl@gisaid.org]; Valentina Bernasconi[valentina.bernasconi@cepi.net]; shinjini.bhatnagar@thsti.res.in[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok[karin.bok@nih.gov]; dboyle@path.org[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; christian.brechot[christian.brechot@pasteur.fr]; Christine.bruce@phe.gov.uk[Christine.bruce@phe.gov.uk]; zuz4@cdc.gov[zuz4@cdc.gov]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; Marco.Cavaleri[Marco.Cavaleri@ema.europa.eu]; MONALISA.CHATTERJI@gatesfoundation.org[MONALISA.CHATTERJI@gatesfoundation.org]; MAY.CHU@CUANSCHUTZ.EDU[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; costaa@who.int[costaa@who.int]; htq4@cdc.gov[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; tdelossantos@path.org[tdelossantos@path.org]; emmie.dewit@nih.gov[emmie.dewit@nih.gov]; marciela.degrace@nih.gov[marciela.degrace@nih.gov]; rafael.delgado@salud.madrid.org[rafael.delgado@salud.madrid.org]; mit666666@pitt.edu[mit666666@pitt.edu]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; William Dowling[william.dowling@cepi.net]; christian.drosten@charite.de[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; darryl.falzarano@usask.ca[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; clint.florence@nih.gov[clint.florence@nih.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Simon.Funnell@phe.gov.uk[Simon.Funnell@phe.gov.uk]; Luc.Gagnon@nexelis.com[Luc.Gagnon@nexelis.com]; Mayra.Garcia@fda.hhs.gov[Mayra.Garcia@fda.hhs.gov]; bhx1@cdc.gov[bhx1@cdc.gov]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; barney.graham@nih.gov[barney.graham@nih.gov]; ahgriff@bu.edu[ahgriff@bu.edu]; d.goldblatt@ucl.ac.uk[d.goldblatt@ucl.ac.uk]; Elwyn Griffiths[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; GSELL, Pierre[gsellp@who.int]; ilj2@cdc.gov[ilj2@cdc.gov]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; rzh7@cdc.gov[rzh7@cdc.gov]; henaorestrepoa@who.int[henaorestrepoa@who.int]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; paul.hodgson@usask.ca[paul.hodgson@usask.ca]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; Johan Holst[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; tkh4@cdc.gov[tkh4@cdc.gov]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Cassandra.Kelly@finddx.org[Cassandra.Kelly@finddx.org]; Jacqueline.Kirchner@gatesfoundation.org[Jacqueline.Kirchner@gatesfoundation.org]; knezevici[knezevici@who.int]; m.koopmans@erasmusmc.nl[m.koopmans@erasmusmc.nl]; Gerald.Kovacs@hhs.gov[Gerald.Kovacs@hhs.gov]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; Phil Krause[philip.krause@fda.hhs.gov]; skrebs@hivresearch.org[skrebs@hivresearch.org]; Greg.Kulnis@nexelis.com[Greg.Kulnis@nexelis.com]; Arun Kumar[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; teresa.lambe@ndm.ox.ac.uk[teresa.lambe@ndm.ox.ac.uk]; janet.lathey[janet.lathey@nih.gov]; bleader@path.org[bleader@path.org]; leejooyeon@korea.kr[leejooyeon@korea.kr]; MSLEVER@dstl.gov.uk[MSLEVER@dstl.gov.uk]; liyl@cde.org.cn[liyl@cde.org.cn]; changguili@aliyun.com[changguili@aliyun.com]; lyhchengdu@163.com[lyhchengdu@163.com]; limhy0919@korea.kr[limhy0919@korea.kr]; James.Little@hhs.gov[James.Little@hhs.gov]; liub@cde.org.cn[liub@cde.org.cn]; Tracy.MacGill@fda.hhs.gov[Tracy.MacGill@fda.hhs.gov]; Karen Makar[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; adrian.mcdermott@nih.gov[adrian.mcdermott@nih.gov]; jmcelrat@fredhutch.org[jmcelrat@fredhutch.org]; gmedigeshi@thsti.res.in[gmedigeshi@thsti.res.in]; jwm1@pitt.edu[jwm1@pitt.edu]; philip.minor2@gmail.com[philip.minor2@gmail.com]; kmodjarrad@eidresearch.org[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; omorgan@who.int[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; sarah.mudrak@duke.edu[sarah.mudrak@duke.edu]; munoz-fontela@bnitm.de[munoz-fontela@bnitm.de]; vincent.munster@nih.gov[vincent.munster@nih.gov]; Todd.Myers@fda.hhs.gov[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ@mail.mil[aysegul.nalca.civ@mail.mil]; scott.napper@usask.ca[scott.napper@usask.ca]; MNELSON@dstl.gov.uk[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o@dmsc.mail.go.th[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; golinger@MRIGLOBAL.ORG[golinger@MRIGLOBAL.ORG]; jokim@ivi.int[jokim@ivi.int]; Mark.Page@nibsc.org[Mark.Page@nibsc.org]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; map1@cdc.gov[map1@cdc.gov]; xdv3@cdc.gov[xdv3@cdc.gov]; Keith.Peden@fda.hhs.gov[Keith.Peden@fda.hhs.gov]; sheila.a.peel2.civ@mail.mil[sheila.a.peel2.civ@mail.mil]; malik@hku.hk[malik@hku.hk]; perkinsm@who.int[perkinsm@who.int]; supaporn.p@dmsc.mail.go.th[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ@mail.mil[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR@dstl.gov.uk[JLPRIOR@dstl.gov.uk]; arimoin@g.ucla.edu[arimoin@g.ucla.edu]; lauriex@who.int[lauriex@who.int]; Nicola.Rose@nibsc.org[Nicola.Rose@nibsc.org]; msalit@stanford.edu[msalit@stanford.edu]; erica@lji.org[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; schendel@lji.org[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; PScott@eidresearch.org[PScott@eidresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; Ragini.Shivji@ema.europa.eu[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; mksong@ivi.int[mksong@ivi.int]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; swaminathans@who.int[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; nax3@cdc.gov[nax3@cdc.gov]; tracey.thue@usask.ca[tracey.thue@usask.ca]; georgia.tomaras@duke.edu[georgia.tomaras@duke.edu]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; john.c.trefry.civ@mail.mil[john.c.trefry.civ@mail.mil];

luk_vandenberghe@meei.harvard.edu[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan.Vasan@csiro.au[Vasan.Vasan@csiro.au]; y.m.vasiliev@spbniivs.ru[y.m.vasiliev@spbniivs.ru]; David Vaughn[David.Vaughn@gatesfoundation.org]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; wangjz@nifdc.org.cn[wangjz@nifdc.org.cn]; wangyc@nifdc.org.cn[wangyc@nifdc.org.cn]; Jerry.Weir@fda.hhs.gov[Jerry.Weir@fda.hhs.gov]; alex@lji.org[alex@lji.org]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; dj56wood@gmail.com[dj56wood@gmail.com]; xumiaobj@126.com[xumiaobj@126.com]; Solomon Abebe Yimer[solomon.yimer@cepi.net]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; vyusibov@indianabiosciences.org[vyusibov@indianabiosciences.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]
From: William Dowling[william.dowling@cepi.net]
Sent: Wed 9/9/2020 8:52:48 AM (UTC-05:00)
Subject: RE: cell paper about very potent highly stable human domain

Dear all,
Here is the paper mentioned by Dimiter on our call today. I tried to send an email with the file , but the email bounced back from most due to the file size. Please just use the link.
Thanks
Bill

From: Dimitrov, Dimiter Stanchev <mit666666@pitt.edu>
Sent: Wednesday, September 9, 2020 9:29 AM
To: William Dowling <william.dowling@cepi.net>
Subject: cell paper about very potent highly stable human domain

Hi Bill,

I put it on the chat in the last second, here it is
https://www.cell.com/cell/fulltext/S0092-8674(20)31148-X

also attached the file just in case.

It is human domain fused to Fc and every stable – for 3 months at 37C no change in activity.
Was thinking even could be used as reference reagent, you mentioned there is also another candidate.

Best
Mitko
(Dimiter Dimitrov)

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; fjc37@cam.ac.uk; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; alex@lji.org; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ZHOU, Tiequn;

lschwartz36; Kristina Peachman; Important; Racine, Trina; Liz Miller; Liz Miller

Sent: Tue 11/17/2020 5:49:14 AM (UTC-06:00)

Subject: [COVID-19] 38th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting
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Meeting ID: 981 4617 3887
Passcode: **552.136**

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+1 786 635 1003 US (Miami)
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+1 253 215 8782 US (Tacoma)
+1 267 831 0333 US (Philadelphia)
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+1 312 626 6799 US (Chicago)
+1 346 248 7799 US (Houston)
+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 602 753 0140 US (Phoenix)
+1 646 518 9805 US (New York)
+1 646 558 8656 US (New York)
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Meeting ID: 981 4617 3887
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To: galter@partners.org[galter@partners.org]; maria.baca-estrada@canada.ca[maria.baca-estrada@canada.ca]; baihe@nmpa.gov.cn[baihe@nmpa.gov.cn]; rbaric@email.unc.edu[rbaric@email.unc.edu]; cheryl@gisaid.org[cheryl@gisaid.org]; Valentina Bernasconi[valentina.bernasconi@cepi.net]; shinjini.bhatnagar@thsti.res.in[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Bok, Karin (NIH/VRC) [E][karin.bok@nih.gov]; dboyle@path.org[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; brangelp@who.int[brangelp@who.int]; christian.brechot[christian.brechot@pasteur.fr]; Christine.bruce@phe.gov.uk[Christine.bruce@phe.gov.uk]; zuz4@cdc.gov[zuz4@cdc.gov]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Marco.Cavaleri[Marco.Cavaleri@ema.europa.eu]; MONALISA.CHATTERJI@gatesfoundation.org[MONALISA.CHATTERJI@gatesfoundation.org]; MAY.CHU@CUANSCHUTZ.EDU[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; costaa@who.int[costaa@who.int]; htq4@cdc.gov[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; tdelossantos@path.org[tdelossantos@path.org]; emmie.dewit@nih.gov[emmie.dewit@nih.gov]; marciela.degrace@nih.gov[marciela.degrace@nih.gov]; rafael.delgado@salud.madrid.org[rafael.delgado@salud.madrid.org]; mit666666@pitt.edu[mit666666@pitt.edu]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; William Dowling[william.dowling@cepi.net]; christian.drosten@charite.de[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; darryl.falzarano@usask.ca[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; clint.florence@nih.gov[clint.florence@nih.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Simon.Funnell@phe.gov.uk[Simon.Funnell@phe.gov.uk]; Luc Gagnon[luc.gagnon@nexelis.com]; Mayra.Garcia@fda.hhs.gov[Mayra.Garcia@fda.hhs.gov]; bhx1@cdc.gov[bhx1@cdc.gov]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; d.goldblatt@ucl.ac.uk[d.goldblatt@ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; barney.graham@nih.gov[barney.graham@nih.gov]; ahgriff@bu.edu[ahgriff@bu.edu]; Elwyn Griffiths[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; GSELL, Pierre[gsellp@who.int]; Celine Gurry[celine.gurry@cepi.net]; ilj2@cdc.gov[ilj2@cdc.gov]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; rzh7@cdc.gov[rzh7@cdc.gov]; henaorestrepoa@who.int[henaorestrepoa@who.int]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; paul.hodgson@usask.ca[paul.hodgson@usask.ca]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; Johan Holst[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; tkh4@cdc.gov[tkh4@cdc.gov]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Cassandra.Kelly@finddx.org[Cassandra.Kelly@finddx.org]; Jacqueline.Kirchner@gatesfoundation.org[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; m.koopmans@erasmusmc.nl[m.koopmans@erasmusmc.nl]; Gerald.Kovacs@hhs.gov[Gerald.Kovacs@hhs.gov]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; Phil Krause[philip.krause@fda.hhs.gov]; skrebs@hivresearch.org[skrebs@hivresearch.org]; Greg Kulnis[greg.kulnis@nexelis.com]; Arun Kumar[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; teresa.lambe@ndm.ox.ac.uk[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; bleader@path.org[bleader@path.org]; leejooyeon@korea.kr[leejooyeon@korea.kr]; MSLEVER@dstl.gov.uk[MSLEVER@dstl.gov.uk]; liyl@cde.org.cn[liyl@cde.org.cn]; changguili@aliyun.com[changguili@aliyun.com]; lyhchengdu@163.com[lyhchengdu@163.com]; limhy0919@korea.kr[limhy0919@korea.kr]; James.Little@hhs.gov[James.Little@hhs.gov]; liub@cde.org.cn[liub@cde.org.cn]; Tracy.MacGill@fda.hhs.gov[Tracy.MacGill@fda.hhs.gov]; Karen Makar[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; adrian.mcdermott@nih.gov[adrian.mcdermott@nih.gov]; jmcelrat@fredhutch.org[jmcelrat@fredhutch.org]; Guruprasad[gmedigeshi@thsti.res.in]; jwm1@pitt.edu[jwm1@pitt.edu]; philip.minor2@gmail.com[philip.minor2@gmail.com]; kmodjarrad@eidresearch.org[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; omorgan@who.int[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; sarah.mudrak@duke.edu[sarah.mudrak@duke.edu]; munoz-fontela@bnitm.de[munoz-fontela@bnitm.de]; vincent.munster@nih.gov[vincent.munster@nih.gov]; Todd.Myers@fda.hhs.gov[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ@mail.mil[aysegul.nalca.civ@mail.mil]; scott.napper@usask.ca[scott.napper@usask.ca]; MNELSON@dstl.gov.uk[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o@dmsc.mail.go.th[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; golinger@MRIGLOBAL.ORG[golinger@MRIGLOBAL.ORG]; jokim@ivi.int[jokim@ivi.int]; Mark Page[mark.page@nibsc.org]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; map1@cdc.gov[map1@cdc.gov]; xdv3@cdc.gov[xdv3@cdc.gov]; Keith.Peden@fda.hhs.gov[Keith.Peden@fda.hhs.gov]; sheila.a.peel2.civ@mail.mil[sheila.a.peel2.civ@mail.mil]; malik@hku.hk[malik@hku.hk]; perkinsm@who.int[perkinsm@who.int]; supaporn.p@dmsc.mail.go.th[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ@mail.mil[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR@dstl.gov.uk[JLPRIOR@dstl.gov.uk]; arimoin@g.ucla.edu[arimoin@g.ucla.edu]; lauriex@who.int[lauriex@who.int]; Nicola.Rose@nibsc.org[Nicola.Rose@nibsc.org]; msalit@stanford.edu[msalit@stanford.edu]; erica@lji.org[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; schendel@lji.org[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; PScott@eidresearch.org[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Ragini.Shivji[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; yoos@who.int[yoos@who.int]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; mksong@ivi.int[mksong@ivi.int]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; subissil@who.int[subissil@who.int]; swaminathans@who.int[swaminathans@who.int];

r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; nax3@cdc.gov[nax3@cdc.gov]; tracey.thue@usask.ca[tracey.thue@usask.ca]; georgia.tomaras@duke.edu[georgia.tomaras@duke.edu]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; john.c.trefry.civ@mail.mil[john.c.trefry.civ@mail.mil]; luk_vandenberghe@meei.harvard.edu[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan.Vasan@csiro.au[Vasan.Vasan@csiro.au]; y.m.vasiliev@spbniivs.ru[y.m.vasiliev@spbniivs.ru]; David Vaughn[David.Vaughn@gatesfoundation.org]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; wangjz@nifdc.org.cn[wangjz@nifdc.org.cn]; wangyc@nifdc.org.cn[wangyc@nifdc.org.cn]; Jerry.Weir@fda.hhs.gov[Jerry.Weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; dj56wood@gmail.com[dj56wood@gmail.com]; xumiaobj@126.com[xumiaobj@126.com]; Solomon Abebe Yimer[solomon.yimer@cepi.net]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; vyusibov@indianabiosciences.org[vyusibov@indianabiosciences.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; zhout@who.int[zhout@who.int]
From: William Dowling[william.dowling@cepi.net]
Sent: Tue 11/24/2020 6:27:49 AM (UTC-06:00)
Subject: Agenda for WHO working group on COVID-19 assays

Hello all

Here is the agenda for tomorrow's meeting of the WHO working group on COVID-19 assays:

1. David Eyre form Oxford University will talk about the paper "Antibodies to SARS-CoV-2 are associated with protection against reinfection " doi: https://doi.org/10.1101/2020.11.18.20234369
2. Updates:
    a. Simon Funnell - update on the working group on SARS-COV-2 propagation
    b. Mark page- update on the work towards an International Standard
    c. Any other updates from the group
3. Discussion on future topics

Best regards
Bill

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: 'Ralph Baric'[rbaric@email.unc.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'mikebray10@gmail.com'[mikebray10@gmail.com]; 'kara.carter@evotec.com'[kara.carter@evotec.com]; 'Fred Hayden'[fgh@virginia.edu]; 'rickkeenan@gmail.com'[rickkeenan@gmail.com]; 'shenk@Princeton.EDU'[shenk@Princeton.EDU]
Cc: 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'tgriffin@Princeton.EDU'[tgriffin@Princeton.EDU]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Wed 9/18/2019 1:44:37 PM (UTC-05:00)
Subject: Scheduling Dr. Whitley's AD3C Year 1 Reverse Site Visit in February 2020

Hello To Everyone:

You are receiving this message because you are either a member of the Antiviral Drug Discovery and Development Center External Advisory Board, or you are a Project Leader for this CETR grant. It is time to reach out and schedule the Reverse Site Visit for **Year 1** of the grant.

Dr. Maureen Beanan, our NIH/NIAID Program Officer for the grant, has written to Dr. Whitley and shared possible dates for this meeting. Because our group is holding our Annual Meeting later than usual this year (November 15-16), I have created a Doodle Poll with possible dates for the Reverse Site Visit in February of 2020. The January dates have already been scheduled by other CETR groups.

The meeting will be held in Rockville, MD at the NIAID Building on Fishers Lane, from 9 am to around 12 noon Eastern Time on the selected day.

Here is the link to the Doodle Poll: https://doodle.com/poll/eviskabvb2576e2k

Please take a moment and indicate which dates might work for your schedule, and I will be back in touch as soon as we have found the best date for all.

Thank you very much for your assistance and your attention to my request.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

To: Stephanie Moore[smoore@peds.uab.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Alec Hirsch[hirschal@ohsu.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; Tekwani, Babu[btekwani@southernresearch.org]; Bostwick, Bob[bbostwick@southernresearch.org]; Daniel Streblow[streblow@ohsu.edu]; 'George Painter'[george.r.painter@emory.edu]; Jay Nelson[nelsonj@ohsu.edu]; Chappell, Jim[jim.chappell@Vanderbilt.Edu]; Denison, Mark[mark.denison@Vanderbilt.Edu]; Denison, Mark[mark.denison@vumc.org]; Heise, Mark T[mark_heisem@med.unc.edu]; Diamond, Michael[mdiamond@wustl.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Ralph Baric'[rbaric@email.unc.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]; 'Morrison, Thomas'[THOMAS.MORRISON@CUANSCHUTZ.EDU]
Cc: Augelli-Szafran, Corinne[caugelli-szafran@southernresearch.org]; Pathak, Ashish[apathak@southernresearch.org]; Moukha-Chafiq, Omar[omoukha-chafiq@southernresearch.org]
From: Evans, Carrie W.[cevans@southernresearch.org]
Sent: Wed 12/9/2020 5:10:28 PM (UTC-06:00)
Subject: Cross Virus Data

Hi AD3C Team,

I have uploaded the AD3C cross virus data spreadsheet to ShareFile at the link below. This spreadsheet shows the data that has been generated for compounds across multiple viruses to date. The Chemistry Core will continue to submit active compounds for screening against other viruses, and we will update this spreadsheet as we generate additional data.

https://southernresearch.sharefile.com/d-s3d089a933d6843dda6d8d3e80db15f97

Please let me know if you need any additional information and/or have any problems accessing ShareFile!

Thanks,

Carrie

Carrie W. Evans, MS, PMP
Senior Manager of Operations
Drug Discovery Division &
Drug Development Division
Southern Research
2000 9th Ave. South
Birmingham, AL 35205
Phone: 205-581-2528
Email: cevans@southernresearch.org

To: 'Ralph Baric'[rbaric@email.unc.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'mikebray10@gmail.com'[mikebray10@gmail.com]; 'kara.carter@evotec.com'[kara.carter@evotec.com]; 'Fred Hayden'[fgh@virginia.edu]; 'rickkeenan@gmail.com'[rickkeenan@gmail.com]; 'shenk@Princeton.EDU'[shenk@Princeton.EDU]
Cc: 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'tgriffin@Princeton.EDU'[tgriffin@Princeton.EDU]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Wed 9/18/2019 1:57:33 PM (UTC-05:00)
Subject: RE: Scheduling Dr. Whitley's AD3C Year 1 Reverse Site Visit in February 2020

A quick note of correction: The 2019 AD3C Annual Meeting will be held on November 13-14, 2019 (Wednesday and Thursday), not November 15-16 as I wrote in the message that you just received. I apologize if I created any confusion for you.

Sara Davis | Program Coordinator II
Direct Line: 205.996.7804 | sadavis@peds.uab.edu

From: Antiviral Drug Discovery and Development Center-AD3C
Sent: Wednesday, September 18, 2019 1:45 PM
To: 'Ralph Baric' <rbaric@email.unc.edu>; 'Mark Heise' <mark_heisem@med.unc.edu>; 'Mark Denison' <mark.denison@vanderbilt.edu>; 'Pei-Yong Shi' <peshi@utmb.edu>; 'mikebray10@gmail.com' <mikebray10@gmail.com>; 'kara.carter@evotec.com' <kara.carter@evotec.com>; 'Fred Hayden' <fgh@virginia.edu>; 'rickkeenan@gmail.com' <rickkeenan@gmail.com>; 'shenk@Princeton.EDU' <shenk@Princeton.EDU>
Cc: 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'tgriffin@Princeton.EDU' <tgriffin@Princeton.EDU>; Mary Wyatt Bowers <MWBowers@peds.uab.edu>
Subject: Scheduling Dr. Whitley's AD3C Year 1 Reverse Site Visit in February 2020

Hello To Everyone:

You are receiving this message because you are either a member of the Antiviral Drug Discovery and Development Center External Advisory Board, or you are a Project Leader for this CETR grant. It is time to reach out and schedule the Reverse Site Visit for **Year 1** of the grant.

Dr. Maureen Beanan, our NIH/NIAID Program Officer for the grant, has written to Dr. Whitley and shared possible dates for this meeting. Because our group is holding our Annual Meeting later than usual this year (November 15-16), I have created a Doodle Poll with possible dates for the Reverse Site Visit in February of 2020. The January dates have already been scheduled by other CETR groups.

The meeting will be held in Rockville, MD at the NIAID Building on Fishers Lane, from 9 am to around 12 noon Eastern Time on the selected day.

Here is the link to the Doodle Poll: https://doodle.com/poll/eviskabvb2576e2k

Please take a moment and indicate which dates might work for your schedule, and I will be back in touch as soon as we have found the best date for all.

Thank you very much for your assistance and your attention to my request.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

To: galter (galter@partners.org)[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; GSELL, Pierre[gsellp@who.int]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Cassandra Kelly (Cassandra.Kelly@finddx.org)[Cassandra.Kelly@finddx.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; jmcelrat (jmcelrat@fredhutch.org)[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ

(margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Nick.Gilbert@ed.ac.uk[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma@sgul.ac.uk[jma@sgul.ac.uk]
Cc: Alter, Galit[GALTER@mgh.harvard.edu]; Sujan Shresta[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 12/7/2020 12:29:19 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for our group call on Wednesday December 9, 2020 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Drs. Galit Alter and Dan Barouch from the Ragon Institute of MGH, MIT and Harvard, "T cell and antibody functional correlates of severe COVID-19"
2. Dr. Qiang Pan-Hammarström from the Karolinska Institutet, "Persistence of SARS-CoV-2 specific B- and T-cell responses in convalescent COVID-19 patients 6-8 months after the infection"

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, December 6, 2020 11:29 AM
To: SCHWARTZ, Lauren; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; Iad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net;

christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; GSELL, Pierre; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra.Kelly@finddx.org; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk
Cc: Alter, Galit; Sujan Shresta
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, December 9, 2020 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

SCHWARTZ, Lauren is inviting you to a scheduled Zoom meeting.

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To: galter (galter@partners.org)[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; jmcelrat (jmcelrat@fredhutch.org)[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ

(margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Nick.Gilbert@ed.ac.uk[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma@sgul.ac.uk[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 12/15/2020 10:01:28 AM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for our group call on Wednesday December 16, 2020 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Remarks from Ana María Henao Restrepo
2. Mark Page and Giada Mattiuzzo NIBSC - *Harmonisation and increased comparability of SARS-COV-2 serological assays by WHO International standard*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, December 13, 2020 10:09 AM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net;

christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit (msalit@stanford.edu); erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; SCHWARTZ, Lauren; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); stanley-perlman@uiowa.edu
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, December 16, 2020 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

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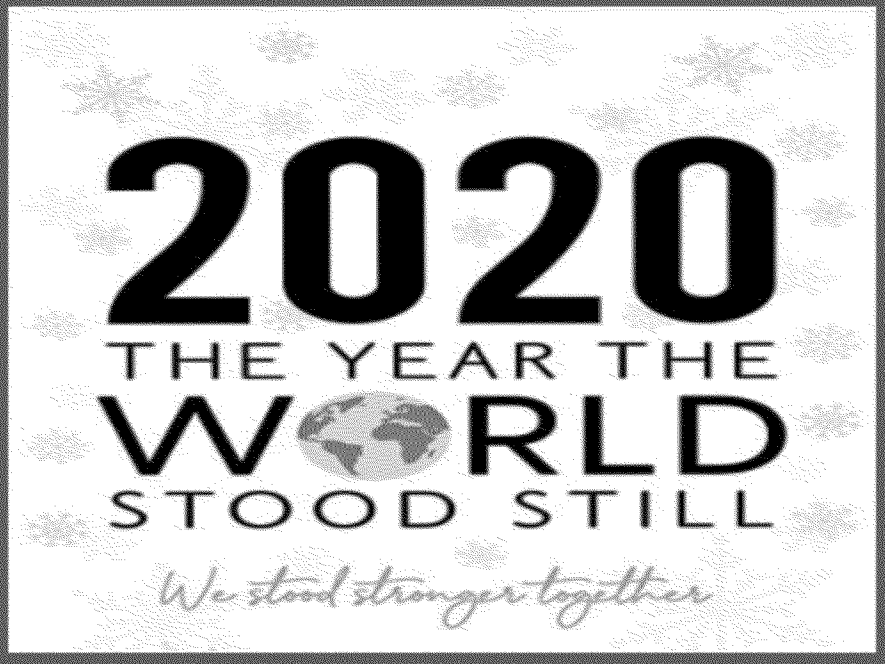
To: galter (galter@partners.org)[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; jmcelrat (jmcelrat@fredhutch.org)[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ

(margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; SCHWARTZ, Lauren[schwartzl@who.int]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma@sgul.ac.uk[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 12/23/2020 2:12:03 PM (UTC-06:00)
Subject: Thank You and Happy Holidays to the WHO Working Group on COVID-19 Assays

There is no better time than the holid



Thank you to everyone who has helpe

One of the real joys this holiday seas
thank you and wish you the very be

R&DBlueprint
Powering research
to prevent epidemics

To: 'Ralph Baric'[rbaric@email.unc.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'mikebray10@gmail.com'[mikebray10@gmail.com]; 'kara.carter@evotec.com'[kara.carter@evotec.com]; 'Fred Hayden'[fgh@virginia.edu]; 'rickkeenan@gmail.com'[rickkeenan@gmail.com]; 'shenk@Princeton.EDU'[shenk@Princeton.EDU]
Cc: 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'tgriffin@Princeton.EDU'[tgriffin@Princeton.EDU]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Thur 9/19/2019 10:40:01 AM (UTC-05:00)
Subject: RE: Scheduling Dr. Whitley's AD3C Year 1 Reverse Site Visit in February 2020

Greetings!

First, a huge thank you to everyone for replying to the scheduling poll in such a speedy fashion! Before your schedules fill up, I am going to have you lock in **Tuesday, February 11, 2020** on your calendars. That date works for Maureen Beanan and the NIH/NIAID stuff as well. That will require travel on Monday, February 10, because the meeting will take place on Tuesday morning.

Additional details and instructions on crafting the presentation for the site visit will be discussed at the Annual Meeting on November 13-14 here in Birmingham, AL.

We appreciate your participation and look forward to seeing you soon.

With kind regards,

Sara Davis | Program Coordinator II
Direct Line: 205.996.7804 | sadavis@peds.uab.edu

From: Antiviral Drug Discovery and Development Center-AD3C
Sent: Wednesday, September 18, 2019 1:45 PM
To: 'Ralph Baric' <rbaric@email.unc.edu>; 'Mark Heise' <mark_heisem@med.unc.edu>; 'Mark Denison' <mark.denison@vanderbilt.edu>; 'Pei-Yong Shi' <peshi@utmb.edu>; 'mikebray10@gmail.com' <mikebray10@gmail.com>; 'kara.carter@evotec.com' <kara.carter@evotec.com>; 'Fred Hayden' <fgh@virginia.edu>; 'rickkeenan@gmail.com' <rickkeenan@gmail.com>; 'shenk@Princeton.EDU' <shenk@Princeton.EDU>
Cc: 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'tgriffin@Princeton.EDU' <tgriffin@Princeton.EDU>; Mary Wyatt Bowers <MWBowers@peds.uab.edu>
Subject: Scheduling Dr. Whitley's AD3C Year 1 Reverse Site Visit in February 2020

Hello To Everyone:

You are receiving this message because you are either a member of the Antiviral Drug Discovery and Development Center External Advisory Board, or you are a Project Leader for this CETR grant. It is time to reach out and schedule the Reverse Site Visit for **Year 1** of the grant.

Dr. Maureen Beanan, our NIH/NIAID Program Officer for the grant, has written to Dr. Whitley and shared possible dates for this meeting. Because our group is holding our Annual Meeting later than usual this year (November 15-16), I have created a Doodle Poll with possible dates for the Reverse Site Visit in February of 2020. The January dates have already been scheduled by other CETR groups.

The meeting will be held in Rockville, MD at the NIAID Building on Fishers Lane, from 9 am to around 12 noon Eastern Time on the selected day.

Here is the link to the Doodle Poll: https://doodle.com/poll/eviskabvb2576e2k

Please take a moment and indicate which dates might work for your schedule, and I will be back in touch as soon as we have found the best date for all.

Thank you very much for your assistance and your attention to my request.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

To: galter (galter@partners.org)[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; jmcelrat (jmcelrat@fredhutch.org)[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ

(margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma@sgul.ac.uk[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]
Cc: IRAHETA, Raul[irahetar@who.int]; pennym@nicd.ac.za[pennym@nicd.ac.za]; alex.sigal@ahri.org[alex.sigal@ahri.org]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 1/5/2021 2:50:23 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for our group call on Wednesday January 6, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Kevin McCarthy and Paul Duprex (University of Pittsburgh)- *Natural deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape*
2. Discussion on the UK variant

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, January 3, 2021 8:32 PM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; Iad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net;

christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; SCHWARTZ, Lauren; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu

Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, January 6, 2021 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
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Meeting ID: 361 256 8290

To: galter (galter@partners.org)[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; jma[jma@sgul.ac.uk]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; jmcelrat (jmcelrat@fredhutch.org)[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov];

Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]
Cc: alex@lji.org[alex@lji.org]; Joe Campo[jcampo@antigendiscovery.com]; Angela Yee[ayee@antigendiscovery.com]; Xiaowu Liang[xliang@antigendiscovery.com]; Arlo Randall[arandall@antigendiscovery.com]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 1/11/2021 5:43:28 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for our group call on Wednesday January 13, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Alessandro Sette (LJI) - *Comprehensive analysis of T cell immunodominance and immunoprevalence of SARS-CoV-2 epitopes in COVID-19 cases*
2. Joe Campo (Antigen Discovery Inc) - *A Multi-Coronavirus Protein Microarray for Mapping SARS-CoV-2 Antibody Epitopes and Characterizing Immune Responses to Infection and Vaccination*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, January 10, 2021 2:22 PM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in;

pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; Iad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; ASiyer@mgh.harvard.edu; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Jilian.Sacks@finddx.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov

Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, January 13, 2021 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

Join Zoom Meeting
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+41225910005,,3612568290# Switzerland
+41225910156,,3612568290# Switzerland

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+41 22 591 00 05 Switzerland
+41 22 591 01 56 Switzerland

+41 31 528 09 88 Switzerland
+41 43 210 70 42 Switzerland
+41 43 210 71 08 Switzerland
+1 253 215 8782 US (Tacoma)
+1 720 928 9299 US (Denver)
+1 971 247 1195 US (Portland)
+1 213 338 8477 US (Los Angeles)
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+1 669 900 9128 US (San Jose)
+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 646 518 9805 US (New York)
+1 646 558 8656 US (New York)
+1 651 372 8299 US (Minnesota)
+1 786 635 1003 US (Miami)
+1 267 831 0333 US (Philadelphia)
+1 301 715 8592 US (Washington D.C)
+1 312 626 6799 US (Chicago)
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To: jboyer@inovio.com[jboyer@inovio.com]; acope@iavi.org[acope@iavi.org]; adanalioser@gmail.com[adanalioser@gmail.com]; akbulut@medicine.ankara.edu.tr[akbulut@medicine.ankara.edu.tr]; Alessandra.Vitelli@reithera.com[Alessandra.Vitelli@reithera.com]; Stefania.Capone@reithera.com[Stefania.Capone@reithera.com]; annied@epivax.com[annied@epivax.com]; Anthony.Macaluso (Anthony.Macaluso@tonixpharma.com)[Anthony.Macaluso@tonixpharma.com]; boulayi@medicago.com[boulayi@medicago.com]; brian.zabel@lakepharma.com[brian.zabel@lakepharma.com]; C.M.Smales@kent.ac.uk[C.M.Smales@kent.ac.uk]; christoph.rademacher@mpikg.mpg.de[christoph.rademacher@mpikg.mpg.de]; CKeech@Novavax.com[CKeech@Novavax.com]; coleman (coleman@codagenix.com)[coleman@codagenix.com]; rajeev.dhere@seruminstitute.com[rajeev.dhere@seruminstitute.com]; CVHerst@flowpharma.com[CVHerst@flowpharma.com]; cyrus.yang@sbc-biotech.com[cyrus.yang@sbc-biotech.com]; d.watterson@uq.edu.au[d.watterson@uq.edu.au]; dapengzhoulab@tongji.edu.cn[dapengzhoulab@tongji.edu.cn]; dguyongellin@osivax.com[dguyongellin@osivax.com]; diane.vanhoorick@etherna.be[diane.vanhoorick@etherna.be]; dong.shen@rnaimmune.com[dong.shen@rnaimmune.com]; Thien Do (dothuanthien@vabiotech.com.vn)[dothuanthien@vabiotech.com.vn]; dsz@imbcams.com.cn[dsz@imbcams.com.cn]; dulin@zhifeishengwu.com[dulin@zhifeishengwu.com]; dailp@biols.ac.cn[dailp@biols.ac.cn]; ercument.karasulu@ege.edu.tr[ercument.karasulu@ege.edu.tr]; fguirakhoo (fguirakhoo@geovax.com)[fguirakhoo@geovax.com]; farshad@covaxx.com[farshad@covaxx.com]; fguirakhoo@unitedneuroscience.com[fguirakhoo@unitedneuroscience.com]; fred@imophoron.com[fred@imophoron.com]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; greanggrai.h@bionet-asia.com[greanggrai.h@bionet-asia.com]; guido.grandi@unitn.it[guido.grandi@unitn.it]; 秀樹 長谷川 (hasegawa@nih.go.jp)[hasegawa@nih.go.jp]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; hironorinakagami@gmail.com[hironorinakagami@gmail.com]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Holger.Martinius@neovii.com[Holger.Martinius@neovii.com]; hotez (hotez@bcm.edu)[hotez@bcm.edu]; huyl@sinovac.com[huyl@sinovac.com]; james.hayward (james.hayward@adnas.com)[james.hayward@adnas.com]; James.Huleatt@sanofi.com[James.Huleatt@sanofi.com]; jarininger@lathambiopharm.com[jarininger@lathambiopharm.com]; jeff@stabilitech.com[jeff@stabilitech.com]; jennifer@immunoprecise.com[jennifer@immunoprecise.com]; yabdiche@immunoprecise.com[yabdiche@immunoprecise.com]; Ilse Roodink (iroodink@immunoprecise.com)[iroodink@immunoprecise.com]; JHendri1@its.jnj.com[JHendri1@its.jnj.com]; jkalil@usp.br[jkalil@usp.br]; jlh66@cam.ac.uk[jlh66@cam.ac.uk]; jprice (jprice@greffex.com)[jprice@greffex.com]; jwolf (jwolf@heatbio.com)[jwolf@heatbio.com]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Kapil Maithal (Kapil.Maithal@zyduscadila.com)[Kapil.Maithal@zyduscadila.com]; khirullin@mail.ru[khirullin@mail.ru]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; kovac@axon-neuroscience.eu[kovac@axon-neuroscience.eu]; michelle.hoffmann@axon-neuroscience.eu[michelle.hoffmann@axon-neuroscience.eu]; kozhemyakina@biocad.ru[kozhemyakina@biocad.ru]; lei.li@flinders.edu.au[lei.li@flinders.edu.au]; lindy.durrant@nottingham.ac.uk[lindy.durrant@nottingham.ac.uk]; linjinzhong@fudan.edu.cn[linjinzhong@fudan.edu.cn]; luistataje@farvet.com[luistataje@farvet.com]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; maksyutov_ra@vector.nsc.ru[maksyutov_ra@vector.nsc.ru]; martin.reers@biologicale.com[martin.reers@biologicale.com]; Matthias.Schnell@jefferson.edu[Matthias.Schnell@jefferson.edu]; mehmet.ozturk@ibg.edu.tr[mehmet.ozturk@ibg.edu.tr]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; mgursel@metu.edu.tr[mgursel@metu.edu.tr]; morishit@cgt.med.osaka-u.ac.jp[morishit@cgt.med.osaka-u.ac.jp]; nakagami@gts.med.osaka-u.ac.jp[nakagami@gts.med.osaka-u.ac.jp]; MStanford@imv-inc.com[MStanford@imv-inc.com]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; nadirkocak@yahoo.com[nadirkocak@yahoo.com]; naomi.van.vlies@intravacc.nl[naomi.van.vlies@intravacc.nl]; nesrin.ozoren@boun.edu.tr[nesrin.ozoren@boun.edu.tr]; nhj1114@mogam.re.kr[nhj1114@mogam.re.kr]; Olaf-Oliver.Wolz@curevac.com[Olaf-Oliver.Wolz@curevac.com]; Hodgson, Paul[paul.hodgson@usask.ca]; pdeshpande@indimmune.com[pdeshpande@indimmune.com]; phil.yang@nantworks.com[phil.yang@nantworks.com]; prasadsd (prasadsd@bharatbiotech.com)[prasadsd@bharatbiotech.com]; qinjian_zhao (qinjian_zhao@xmu.edu.cn)[qinjian_zhao@xmu.edu.cn]; Liang Qu (Jenny) (quliang@sinopharm.com)[quliang@sinopharm.com]; Ricardo.Gazzinelli@umassmed.edu[Ricardo.Gazzinelli@umassmed.edu]; Webby, Richard[richard.webby@stjude.org]; roland.tschismarov@themisbio.com[roland.tschismarov@themisbio.com]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Rolando.pajon@modernatx.com[Rolando.pajon@modernatx.com]; Rong.Xu@sabin.org[Rong.Xu@sabin.org]; roy.duncan@dal.ca[roy.duncan@dal.ca]; Senta.Walton@usz.ch[Senta.Walton@usz.ch]; Shailesh.DEWASTHALY@valneva.com[Shailesh.DEWASTHALY@valneva.com]; somchaiya@gpo.or.th[somchaiya@gpo.or.th]; songqiaoqiao@ystwt.com[songqiaoqiao@ystwt.com]; steven.gong@cloverbiopharma.com[steven.gong@cloverbiopharma.com]; stucker (stucker@vaxart.com)[stucker@vaxart.com]; sunL@antibodychina.com[sunL@antibodychina.com]; tapia@mpi-magdeburg.mpg.de[tapia@mpi-magdeburg.mpg.de]; tedross@uga.edu[tedross@uga.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; THeiland@immunomix.com[THeiland@immunomix.com]; Ugur.Sahin@biontech.de[Ugur.Sahin@biontech.de]; vgarg (vgarg@altimmune.com)[vgarg@altimmune.com]; wdj@adaptvac.com[wdj@adaptvac.com]; wdj@expres2ionbio.com[wdj@expres2ionbio.com]; Xiao-Jian.Yao@umanitoba.ca[Xiao-Jian.Yao@umanitoba.ca]; xuefeng.yu@cansinotech.com[xuefeng.yu@cansinotech.com]; zengming@biominhai.com[zengming@biominhai.com]; Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll

(Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley

(OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]
Cc: William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; gnorheim@vaccibody.com[gnorheim@vaccibody.com]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; KNEZEVIC, Ivana[knezevici@who.int]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; peter.rigsby@nibsc.org[peter.rigsby@nibsc.org]; Alex Sigal[alex.sigal@ahri.org]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Fri 1/15/2021 1:58:17 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers

Dear All,

Please find below the agenda for our group call with vaccine developers on Wednesday January 20, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays with vaccine developers

1. WHO standards for COVID-19 - I. Knezevic (WHO)
2. Roles and Importance of Standards in Assays – G. Mattiuzzo (NIBSC)
3. Calibration of secondary standards to WHO International Standards – P. Rigsby (NIBSC)
4. Discussion on standards
5. Update on 501Y.V2 variants – Alex Sigal (AHRI)

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Monday, December 21, 2020 10:47 AM
To: SCHWARTZ, Lauren; jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso@tonixpharma.com; boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman@codagenix.com; rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; dothuanthien@vabiotech.com.vn; dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo@geovax.com; farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary.Kobinger@crchudequebec.ulaval.ca; greanggrai.h@bionet-

asia.com; guido.grandi@unitn.it; hasegawa@nih.go.jp; hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; hotez@bcm.edu; huyl@sinovac.com; james.hayward@adnas.com; James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; iroodink@immunoprecise.com; JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice@greffex.com; jwolf@heatbio.com; kandeil_a@hotmail.com; Kapil.Maithal@zyduscadila.com; khirullin@mail.ru; kmodjarrad@eidresearch.org; kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe@meei.harvard.edu; maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban@cnb.csic.es; mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; muhammad.munir@lancaster.ac.uk; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; paul.hodgson@usask.ca; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd@bharatbiotech.com; qinjian_zhao@xmu.edu.cn; quliang@sinopharm.com; Ricardo.Gazzinelli@umassmed.edu; Richard.Webby@STJUDE.ORG; roland.tschismarov@themisbio.com; christiane.gerke@pasteur.fr; Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker@vaxart.com; sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; teresa.lambe@ndm.ox.ac.uk; THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg@altimmune.com; wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; SCHWARTZ, Lauren; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu

Subject: WHO Working Group on COVID-19 Assays with Vaccine Developers
When: Wednesday, January 20, 2021 5:30 AM-7:00 AM (UTC-08:00) Pacific Time (US & Canada).
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Agenda to follow.

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To: jboyer@inovio.com[jboyer@inovio.com]; acope@iavi.org[acope@iavi.org]; adanalioser@gmail.com[adanalioser@gmail.com]; akbulut@medicine.ankara.edu.tr[akbulut@medicine.ankara.edu.tr]; Alessandra.Vitelli@reithera.com[Alessandra.Vitelli@reithera.com]; Stefania.Capone@reithera.com[Stefania.Capone@reithera.com]; annied@epivax.com[annied@epivax.com]; Anthony.Macaluso (Anthony.Macaluso@tonixpharma.com)[Anthony.Macaluso@tonixpharma.com]; boulayi@medicago.com[boulayi@medicago.com]; brian.zabel@lakepharma.com[brian.zabel@lakepharma.com]; C.M.Smales@kent.ac.uk[C.M.Smales@kent.ac.uk]; christoph.rademacher@mpikg.mpg.de[christoph.rademacher@mpikg.mpg.de]; CKeech@Novavax.com[CKeech@Novavax.com]; coleman (coleman@codagenix.com)[coleman@codagenix.com]; rajeev.dhere@seruminstitute.com[rajeev.dhere@seruminstitute.com]; CVHerst@flowpharma.com[CVHerst@flowpharma.com]; cyrus.yang@sbc-biotech.com[cyrus.yang@sbc-biotech.com]; d.watterson@uq.edu.au[d.watterson@uq.edu.au]; dapengzhoulab@tongji.edu.cn[dapengzhoulab@tongji.edu.cn]; dguyongellin@osivax.com[dguyongellin@osivax.com]; diane.vanhoorick@etherna.be[diane.vanhoorick@etherna.be]; dong.shen@rnaimmune.com[dong.shen@rnaimmune.com]; Thien Do (dothuanthien@vabiotech.com.vn)[dothuanthien@vabiotech.com.vn]; dsz@imbcams.com.cn[dsz@imbcams.com.cn]; dulin@zhifeishengwu.com[dulin@zhifeishengwu.com]; dailp@biols.ac.cn[dailp@biols.ac.cn]; ercument.karasulu@ege.edu.tr[ercument.karasulu@ege.edu.tr]; fguirakhoo (fguirakhoo@geovax.com)[fguirakhoo@geovax.com]; farshad@covaxx.com[farshad@covaxx.com]; fguirakhoo@unitedneuroscience.com[fguirakhoo@unitedneuroscience.com]; fred@imophoron.com[fred@imophoron.com]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; greanggrai.h@bionet-asia.com[greanggrai.h@bionet-asia.com]; guido.grandi@unitn.it[guido.grandi@unitn.it]; 秀樹 長谷川 (hasegawa@nih.go.jp)[hasegawa@nih.go.jp]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; hironorinakagami@gmail.com[hironorinakagami@gmail.com]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Holger.Martinius@neovii.com[Holger.Martinius@neovii.com]; hotez (hotez@bcm.edu)[hotez@bcm.edu]; huyl@sinovac.com[huyl@sinovac.com]; james.hayward (james.hayward@adnas.com)[james.hayward@adnas.com]; James.Huleatt@sanofi.com[James.Huleatt@sanofi.com]; jarininger@lathambiopharm.com[jarininger@lathambiopharm.com]; jeff@stabilitech.com[jeff@stabilitech.com]; jennifer@immunoprecise.com[jennifer@immunoprecise.com]; yabdiche@immunoprecise.com[yabdiche@immunoprecise.com]; Ilse Roodink (iroodink@immunoprecise.com)[iroodink@immunoprecise.com]; JHendri1@its.jnj.com[JHendri1@its.jnj.com]; jkalil@usp.br[jkalil@usp.br]; jlh66@cam.ac.uk[jlh66@cam.ac.uk]; jprice (jprice@greffex.com)[jprice@greffex.com]; jwolf (jwolf@heatbio.com)[jwolf@heatbio.com]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Kapil Maithal (Kapil.Maithal@zyduscadila.com)[Kapil.Maithal@zyduscadila.com]; khirullin@mail.ru[khirullin@mail.ru]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; kovac@axon-neuroscience.eu[kovac@axon-neuroscience.eu]; michelle.hoffmann@axon-neuroscience.eu[michelle.hoffmann@axon-neuroscience.eu]; kozhemyakina@biocad.ru[kozhemyakina@biocad.ru]; lei.li@flinders.edu.au[lei.li@flinders.edu.au]; lindy.durrant@nottingham.ac.uk[lindy.durrant@nottingham.ac.uk]; linjinzhong@fudan.edu.cn[linjinzhong@fudan.edu.cn]; luistataje@farvet.com[luistataje@farvet.com]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; maksyutov_ra@vector.nsc.ru[maksyutov_ra@vector.nsc.ru]; martin.reers@biologicale.com[martin.reers@biologicale.com]; Matthias.Schnell@jefferson.edu[Matthias.Schnell@jefferson.edu]; mehmet.ozturk@ibg.edu.tr[mehmet.ozturk@ibg.edu.tr]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; mgursel@metu.edu.tr[mgursel@metu.edu.tr]; morishit@cgt.med.osaka-u.ac.jp[morishit@cgt.med.osaka-u.ac.jp]; nakagami@gts.med.osaka-u.ac.jp[nakagami@gts.med.osaka-u.ac.jp]; MStanford@imv-inc.com[MStanford@imv-inc.com]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; nadirkocak@yahoo.com[nadirkocak@yahoo.com]; naomi.van.vlies@intravacc.nl[naomi.van.vlies@intravacc.nl]; nesrin.ozoren@boun.edu.tr[nesrin.ozoren@boun.edu.tr]; nhj1114@mogam.re.kr[nhj1114@mogam.re.kr]; Olaf-Oliver.Wolz@curevac.com[Olaf-Oliver.Wolz@curevac.com]; Hodgson, Paul[paul.hodgson@usask.ca]; pdeshpande@indimmune.com[pdeshpande@indimmune.com]; phil.yang@nantworks.com[phil.yang@nantworks.com]; prasadsd (prasadsd@bharatbiotech.com)[prasadsd@bharatbiotech.com]; qinjian_zhao (qinjian_zhao@xmu.edu.cn)[qinjian_zhao@xmu.edu.cn]; Liang Qu (Jenny) (quliang@sinopharm.com)[quliang@sinopharm.com]; Ricardo.Gazzinelli@umassmed.edu[Ricardo.Gazzinelli@umassmed.edu]; Webby, Richard[richard.webby@stjude.org]; roland.tschismarov@themisbio.com[roland.tschismarov@themisbio.com]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Rolando.pajon@modernatx.com[Rolando.pajon@modernatx.com]; Rong.Xu@sabin.org[Rong.Xu@sabin.org]; roy.duncan@dal.ca[roy.duncan@dal.ca]; Senta.Walton@usz.ch[Senta.Walton@usz.ch]; Shailesh.DEWASTHALY@valneva.com[Shailesh.DEWASTHALY@valneva.com]; somchaiya@gpo.or.th[somchaiya@gpo.or.th]; songqiaoqiao@ystwt.com[songqiaoqiao@ystwt.com]; steven.gong@cloverbiopharma.com[steven.gong@cloverbiopharma.com]; stucker (stucker@vaxart.com)[stucker@vaxart.com]; sunL@antibodychina.com[sunL@antibodychina.com]; tapia@mpi-magdeburg.mpg.de[tapia@mpi-magdeburg.mpg.de]; tedross@uga.edu[tedross@uga.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; THeiland@immunomix.com[THeiland@immunomix.com]; Ugur.Sahin@biontech.de[Ugur.Sahin@biontech.de]; vgarg (vgarg@altimmune.com)[vgarg@altimmune.com]; wdj@adaptvac.com[wdj@adaptvac.com]; wdj@expres2ionbio.com[wdj@expres2ionbio.com]; Xiao-Jian.Yao@umanitoba.ca[Xiao-Jian.Yao@umanitoba.ca]; xuefeng.yu@cansinotech.com[xuefeng.yu@cansinotech.com]; zengming@biominhai.com[zengming@biominhai.com]; Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll

(Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley

(OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]
Cc: William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; gnorheim@vaccibody.com[gnorheim@vaccibody.com]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; KNEZEVIC, Ivana[knezevici@who.int]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; peter.rigsby@nibsc.org[peter.rigsby@nibsc.org]; Alex Sigal[alex.sigal@ahri.org]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Rong.Xu@sabin.org[Rong.Xu@sabin.org]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Matthias.Schnell@jefferson.edu[Matthias.Schnell@jefferson.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Alter, Galit[galter@partners.org]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 1/18/2021 4:51:31 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers

Hi All,

Before the call on Wednesday, if you have specific questions you can email Bill Dowling, Mark Page, and myself (click here for email). We will try and address these questions on the call.

Best,
Lauren

From: SCHWARTZ, Lauren
Sent: Friday, January 15, 2021 11:58 AM
To: 'jboyer@inovio.com' <jboyer@inovio.com>; 'acope@iavi.org' <acope@iavi.org>; 'adanalioser@gmail.com' <adanalioser@gmail.com>; 'akbulut@medicine.ankara.edu.tr' <akbulut@medicine.ankara.edu.tr>; 'Alessandra.Vitelli@reithera.com' <Alessandra.Vitelli@reithera.com>; 'Stefania.Capone@reithera.com' <Stefania.Capone@reithera.com>; 'annied@epivax.com' <annied@epivax.com>; 'Anthony.Macaluso@tonixpharma.com'

<Anthony.Macaluso@tonixpharma.com>; 'boulayi@medicago.com' <boulayi@medicago.com>; 'brian.zabel@lakepharma.com' <brian.zabel@lakepharma.com>; 'C.M.Smales@kent.ac.uk' <C.M.Smales@kent.ac.uk>; 'christoph.rademacher@mpikg.mpg.de' <christoph.rademacher@mpikg.mpg.de>; 'CKeech@Novavax.com' <CKeech@Novavax.com>; 'coleman@codagenix.com' <coleman@codagenix.com>; 'rajeev.dhere@seruminstitute.com' <rajeev.dhere@seruminstitute.com>; 'CVHerst@flowpharma.com' <CVHerst@flowpharma.com>; 'cyrus.yang@sbc-biotech.com' <cyrus.yang@sbc-biotech.com>; 'd.watterson@uq.edu.au' <d.watterson@uq.edu.au>; 'dapengzhoulab@tongji.edu.cn' <dapengzhoulab@tongji.edu.cn>; 'dguyongellin@osivax.com' <dguyongellin@osivax.com>; 'diane.vanhoorick@etherna.be' <diane.vanhoorick@etherna.be>; 'dong.shen@rnaimmune.com' <dong.shen@rnaimmune.com>; 'dothuanthien@vabiotech.com.vn' <dothuanthien@vabiotech.com.vn>; 'dsz@imbcams.com.cn' <dsz@imbcams.com.cn>; 'dulin@zhifeishengwu.com' <dulin@zhifeishengwu.com>; 'dailp@biols.ac.cn' <dailp@biols.ac.cn>; 'ercument.karasulu@ege.edu.tr' <ercument.karasulu@ege.edu.tr>; 'fguirakhoo@geovax.com' <fguirakhoo@geovax.com>; 'farshad@covaxx.com' <farshad@covaxx.com>; 'fguirakhoo@unitedneuroscience.com' <fguirakhoo@unitedneuroscience.com>; 'fred@imophoron.com' <fred@imophoron.com>; 'Gary.Kobinger@crchudequebec.ulaval.ca' <Gary.Kobinger@crchudequebec.ulaval.ca>; 'greanggrai.h@bionet-asia.com' <greanggrai.h@bionet-asia.com>; 'guido.grandi@unitn.it' <guido.grandi@unitn.it>; 'hasegawa@nih.go.jp' <hasegawa@nih.go.jp>; 'hendrikjan.thibaut@kuleuven.be' <hendrikjan.thibaut@kuleuven.be>; 'hironorinakagami@gmail.com' <hironorinakagami@gmail.com>; 'hlchen@hku.hk' <hlchen@hku.hk>; 'Holger.Martinius@neovii.com' <Holger.Martinius@neovii.com>; 'hotez@bcm.edu' <hotez@bcm.edu>; 'huyl@sinovac.com' <huyl@sinovac.com>; 'james.hayward@adnas.com' <james.hayward@adnas.com>; 'James.Huleatt@sanofi.com' <James.Huleatt@sanofi.com>; 'jarininger@lathambiopharm.com' <jarininger@lathambiopharm.com>; 'jeff@stabilitech.com' <jeff@stabilitech.com>; 'jennifer@immunoprecise.com' <jennifer@immunoprecise.com>; 'yabdiche@immunoprecise.com' <yabdiche@immunoprecise.com>; 'iroodink@immunoprecise.com' <iroodink@immunoprecise.com>; 'JHendri1@its.jnj.com' <JHendri1@its.jnj.com>; 'jkalil@usp.br' <jkalil@usp.br>; 'jlh66@cam.ac.uk' <jlh66@cam.ac.uk>; 'jprice@greffex.com' <jprice@greffex.com>; 'jwolf@heatbio.com' <jwolf@heatbio.com>; 'kandeil_a@hotmail.com' <kandeil_a@hotmail.com>; 'Kapil.Maithal@zyduscadila.com' <Kapil.Maithal@zyduscadila.com>; 'khirullin@mail.ru' <khirullin@mail.ru>; 'kmodjarrad@eidresearch.org' <kmodjarrad@eidresearch.org>; 'kovac@axon-neuroscience.eu' <kovac@axon-neuroscience.eu>; 'michelle.hoffmann@axon-neuroscience.eu' <michelle.hoffmann@axon-neuroscience.eu>; 'kozhemyakina@biocad.ru' <kozhemyakina@biocad.ru>; 'lei.li@flinders.edu.au' <lei.li@flinders.edu.au>; 'lindy.durrant@nottingham.ac.uk' <lindy.durrant@nottingham.ac.uk>; 'linjinzhong@fudan.edu.cn' <linjinzhong@fudan.edu.cn>; 'luistataje@farvet.com' <luistataje@farvet.com>; 'luk_vandenberghe@meei.harvard.edu' <luk_vandenberghe@meei.harvard.edu>; 'maksyutov_ra@vector.nsc.ru' <maksyutov_ra@vector.nsc.ru>; 'martin.reers@biologicale.com' <martin.reers@biologicale.com>; 'Matthias.Schnell@jefferson.edu' <Matthias.Schnell@jefferson.edu>; 'mehmet.ozturk@ibg.edu.tr' <mehmet.ozturk@ibg.edu.tr>; 'mesteban@cnb.csic.es' <mesteban@cnb.csic.es>; 'mgursel@metu.edu.tr' <mgursel@metu.edu.tr>; 'morishit@cgt.med.osaka-u.ac.jp' <morishit@cgt.med.osaka-u.ac.jp>; 'nakagami@gts.med.osaka-u.ac.jp' <nakagami@gts.med.osaka-u.ac.jp>; 'MStanford@imv-inc.com' <MStanford@imv-inc.com>; 'muhammad.munir@lancaster.ac.uk' <muhammad.munir@lancaster.ac.uk>; 'nadirkocak@yahoo.com' <nadirkocak@yahoo.com>; 'naomi.van.vlies@intravacc.nl' <naomi.van.vlies@intravacc.nl>; 'nesrin.ozoren@boun.edu.tr' <nesrin.ozoren@boun.edu.tr>; 'nhj1114@mogam.re.kr' <nhj1114@mogam.re.kr>; 'Olaf-Oliver.Wolz@curevac.com' <Olaf-Oliver.Wolz@curevac.com>; 'paul.hodgson@usask.ca' <paul.hodgson@usask.ca>; 'pdeshpande@indimmune.com' <pdeshpande@indimmune.com>; 'phil.yang@nantworks.com' <phil.yang@nantworks.com>; 'prasadsd@bharatbiotech.com' <prasadsd@bharatbiotech.com>; 'qinjian_zhao@xmu.edu.cn' <qinjian_zhao@xmu.edu.cn>; 'quliang@sinopharm.com' <quliang@sinopharm.com>; 'Ricardo.Gazzinelli@umassmed.edu' <Ricardo.Gazzinelli@umassmed.edu>; 'Richard.Webby@STJUDE.ORG' <Richard.Webby@STJUDE.ORG>; 'roland.tschismarov@themisbio.com' <roland.tschismarov@themisbio.com>; 'christiane.gerke@pasteur.fr' <christiane.gerke@pasteur.fr>; 'Rolando.pajon@modernatx.com' <Rolando.pajon@modernatx.com>; 'Rong.Xu@sabin.org' <Rong.Xu@sabin.org>; 'roy.duncan@dal.ca' <roy.duncan@dal.ca>; 'Senta.Walton@usz.ch' <Senta.Walton@usz.ch>; 'Shailesh.DEWASTHALY@valneva.com' <Shailesh.DEWASTHALY@valneva.com>; 'somchaiya@gpo.or.th' <somchaiya@gpo.or.th>; 'songqiaoqiao@ystwt.com' <songqiaoqiao@ystwt.com>; 'steven.gong@cloverbiopharma.com' <steven.gong@cloverbiopharma.com>; 'stucker@vaxart.com' <stucker@vaxart.com>; 'sunL@antibodychina.com' <sunL@antibodychina.com>; 'tapia@mpi-magdeburg.mpg.de' <tapia@mpi-magdeburg.mpg.de>; 'tedross@uga.edu' <tedross@uga.edu>; 'teresa.lambe@ndm.ox.ac.uk' <teresa.lambe@ndm.ox.ac.uk>; 'THeiland@immunomix.com' <THeiland@immunomix.com>; 'Ugur.Sahin@biontech.de' <Ugur.Sahin@biontech.de>; 'vgarg@altimmune.com' <vgarg@altimmune.com>; 'wdj@adaptvac.com' <wdj@adaptvac.com>; 'wdj@expres2ionbio.com' <wdj@expres2ionbio.com>; 'Xiao-Jian.Yao@umanitoba.ca' <Xiao-Jian.Yao@umanitoba.ca>; 'xuefeng.yu@cansinotech.com' <xuefeng.yu@cansinotech.com>; 'zengming@biominhai.com' <zengming@biominhai.com>; 'galter@partners.org' <galter@partners.org>; 'maria.baca-estrada@canada.ca' <maria.baca-estrada@canada.ca>; 'baihe@nmpa.gov.cn' <baihe@nmpa.gov.cn>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'cheryl@gisaid.org' <cheryl@gisaid.org>; 'valentina.bernasconi@cepi.net' <valentina.bernasconi@cepi.net>; 'shinjini.bhatnagar@thsti.res.in' <shinjini.bhatnagar@thsti.res.in>; 'pbieniasz@mail.rockefeller.edu' <pbieniasz@mail.rockefeller.edu>; 'karin.bok@nih.gov' <karin.bok@nih.gov>; 'dboyle@path.org' <dboyle@path.org>; 'brooke.bozick@nih.gov' <brooke.bozick@nih.gov>; BRANGEL, Polina <brangelp@who.int>;

'christian.brechot@pasteur.fr' <christian.brechot@pasteur.fr>; 'Christine.bruce@phe.gov.uk' <Christine.bruce@phe.gov.uk>; 'zuz4@cdc.gov' <zuz4@cdc.gov>; 'Miles.Carroll@phe.gov.uk' <Miles.Carroll@phe.gov.uk>; 'fjc37@cam.ac.uk' <fjc37@cam.ac.uk>; 'Marco.Cavaleri@ema.europa.eu' <Marco.Cavaleri@ema.europa.eu>; 'MONALISA.CHATTERJI@gatesfoundation.org' <MONALISA.CHATTERJI@gatesfoundation.org>; 'MAY.CHU@CUANSCHUTZ.EDU' <MAY.CHU@CUANSCHUTZ.EDU>; 'carolyn.clark@cepi.net' <carolyn.clark@cepi.net>; 'kizzmekia.corbett@nih.gov' <kizzmekia.corbett@nih.gov>; COSTA, Alejandro Javier <costaa@who.int>; 'htq4@cdc.gov' <htq4@cdc.gov>; 'shane@lji.org' <shane@lji.org>; 'ian.crozier@nih.gov' <ian.crozier@nih.gov>; 'Iad7@cdc.gov' <Iad7@cdc.gov>; 'Lisa@amicitiam.com' <Lisa@amicitiam.com>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'tdelossantos@path.org' <tdelossantos@path.org>; 'emmie.dewit@nih.gov' <emmie.dewit@nih.gov>; 'marciela.degrace@nih.gov' <marciela.degrace@nih.gov>; 'rafael.delgado@salud.madrid.org' <rafael.delgado@salud.madrid.org>; 'mit666666@pitt.edu' <mit666666@pitt.edu>; 'katie.doores@kcl.ac.uk' <katie.doores@kcl.ac.uk>; 'william.dowling@cepi.net' <william.dowling@cepi.net>; 'christian.drosten@charite.de' <christian.drosten@charite.de>; 'epstein@ecohealthalliance.org' <epstein@ecohealthalliance.org>; 'Karl.Erlandson@hhs.gov' <Karl.Erlandson@hhs.gov>; 'darryl.falzarano@usask.ca' <darryl.falzarano@usask.ca>; 'jason.fernandes@canada.ca' <jason.fernandes@canada.ca>; 'clint.florence@nih.gov' <clint.florence@nih.gov>; 'MFrieman@som.umaryland.edu' <MFrieman@som.umaryland.edu>; 'Simon.Funnell@phe.gov.uk' <Simon.Funnell@phe.gov.uk>; 'Luc.Gagnon@nexelis.com' <Luc.Gagnon@nexelis.com>; 'Mayra.Garcia@fda.hhs.gov' <Mayra.Garcia@fda.hhs.gov>; 'bhx1@cdc.gov' <bhx1@cdc.gov>; 'Volker.gerdts@usask.ca' <Volker.gerdts@usask.ca>; 'd.goldblatt@ucl.ac.uk' <d.goldblatt@ucl.ac.uk>; 'guy.gorochov@sorbonne-universite.fr' <guy.gorochov@sorbonne-universite.fr>; 'barney.graham@nih.gov' <barney.graham@nih.gov>; 'ahgriff@bu.edu' <ahgriff@bu.edu>; 'elwyn.griffiths@cepi.net' <elwyn.griffiths@cepi.net>; 'gregory.d.gromowski.civ@mail.mil' <gregory.d.gromowski.civ@mail.mil>; 'celine.gurry@cepi.net' <celine.gurry@cepi.net>; 'ilj2@cdc.gov' <ilj2@cdc.gov>; 'b.haagmans@erasmusmc.nl' <b.haagmans@erasmusmc.nl>; 'rzh7@cdc.gov' <rzh7@cdc.gov>; HENAO RESTREPO, Ana Maria <henaorestrepoa@who.int>; 'lisa.hensley@nih.gov' <lisa.hensley@nih.gov>; 'Michael.holbrook@nih.gov' <Michael.holbrook@nih.gov>; 'johan.holst@cepi.net' <johan.holst@cepi.net>; 'rawcraig@yahoo.com' <rawcraig@yahoo.com>; 'tkh4@cdc.gov' <tkh4@cdc.gov>; 'REIRELAND@mail.dstl.gov.uk' <REIRELAND@mail.dstl.gov.uk>; 'Lakshmi.Jayashankar@hhs.gov' <Lakshmi.Jayashankar@hhs.gov>; 'djernigan@cdc.gov' <djernigan@cdc.gov>; 'johnsonreed@niaid.nih.gov' <johnsonreed@niaid.nih.gov>; 'ydm9@cdc.gov' <ydm9@cdc.gov>; 'Jacqueline.Kirchner@gatesfoundation.org' <Jacqueline.Kirchner@gatesfoundation.org>; KNEZEVIC, Ivana <knezevici@who.int>; 'm.koopmans@erasmusmc.nl' <m.koopmans@erasmusmc.nl>; 'Gerald.Kovacs@hhs.gov' <Gerald.Kovacs@hhs.gov>; 'florian.krammer@mssm.edu' <florian.krammer@mssm.edu>; 'Philip.Krause@fda.hhs.gov' <Philip.Krause@fda.hhs.gov>; 'skrebs@hivresearch.org' <skrebs@hivresearch.org>; 'Greg.Kulnis@nexelis.com' <Greg.Kulnis@nexelis.com>; 'arun.kumar@cepi.net' <arun.kumar@cepi.net>; 'pawinee.k@redcross.or.th' <pawinee.k@redcross.or.th>; 'janet.lathey@nih.gov' <janet.lathey@nih.gov>; 'bleader@path.org' <bleader@path.org>; 'leejooyeon@korea.kr' <leejooyeon@korea.kr>; 'MSLEVER@dstl.gov.uk' <MSLEVER@dstl.gov.uk>; 'liyl@cde.org.cn' <liyl@cde.org.cn>; 'changguili@aliyun.com' <changguili@aliyun.com>; 'lyhchengdu@163.com' <lyhchengdu@163.com>; 'limhy0919@korea.kr' <limhy0919@korea.kr>; 'James.Little@hhs.gov' <James.Little@hhs.gov>; 'liub@cde.org.cn' <liub@cde.org.cn>; 'Tracy.MacGill@fda.hhs.gov' <Tracy.MacGill@fda.hhs.gov>; 'Karen.Makar@gatesfoundation.org' <Karen.Makar@gatesfoundation.org>; 'Mary.Matheson@phe.gov.uk' <Mary.Matheson@phe.gov.uk>; 'Giada.Mattiuzzo@nibsc.org' <Giada.Mattiuzzo@nibsc.org>; 'jmclellan@austin.utexas.edu' <jmclellan@austin.utexas.edu>; 'adrian.mcdermott@nih.gov' <adrian.mcdermott@nih.gov>; 'jmcelrat@fredhutch.org' <jmcelrat@fredhutch.org>; 'gmedigeshi@thsti.res.in' <gmedigeshi@thsti.res.in>; 'jwm1@pitt.edu' <jwm1@pitt.edu>; 'philip.minor2@gmail.com' <philip.minor2@gmail.com>; 'david.montefiori@duke.edu' <david.montefiori@duke.edu>; 'kaitlyn.dambach@nih.gov' <kaitlyn.dambach@nih.gov>; MORGAN, Oliver <omorgan@who.int>; 'Clare.Morris@nibsc.org' <Clare.Morris@nibsc.org>; 'sarah.mudrak@duke.edu' <sarah.mudrak@duke.edu>; 'munoz-fontela@bnitm.de' <munoz-fontela@bnitm.de>; 'vincent.munster@nih.gov' <vincent.munster@nih.gov>; 'Todd.Myers@fda.hhs.gov' <Todd.Myers@fda.hhs.gov>; 'aysegul.nalca.civ@mail.mil' <aysegul.nalca.civ@mail.mil>; 'scott.napper@usask.ca' <scott.napper@usask.ca>; 'MNELSON@dstl.gov.uk' <MNELSON@dstl.gov.uk>; 'PNorris@vitalant.org' <PNorris@vitalant.org>; 'pilailuk.o@dmsc.mail.go.th' <pilailuk.o@dmsc.mail.go.th>; 'n.okba@erasmusmc.nl' <n.okba@erasmusmc.nl>; 'golinger@MRIGLOBAL.ORG' <golinger@MRIGLOBAL.ORG>; 'jokim@ivi.int' <jokim@ivi.int>; 'Mark.Page@nibsc.org' <Mark.Page@nibsc.org>; 'gustavo.f.palacios.civ@mail.mil' <gustavo.f.palacios.civ@mail.mil>; 'map1@cdc.gov' <map1@cdc.gov>; 'xdv3@cdc.gov' <xdv3@cdc.gov>; 'Keith.Peden@fda.hhs.gov' <Keith.Peden@fda.hhs.gov>; 'sheila.a.peel2.civ@mail.mil' <sheila.a.peel2.civ@mail.mil>; 'malik@hku.hk' <malik@hku.hk>; PERKINS, Mark <perkinsm@who.int>; 'supaporn.p@dmsc.mail.go.th' <supaporn.p@dmsc.mail.go.th>; 'margaret.l.pitt.civ@mail.mil' <margaret.l.pitt.civ@mail.mil>; 'mireille.plamondon@canada.ca' <mireille.plamondon@canada.ca>; 'JLPRIOR@dstl.gov.uk' <JLPRIOR@dstl.gov.uk>; 'arimoin@g.ucla.edu' <arimoin@g.ucla.edu>; RIVEROS BALTA, Ximena <lauriex@who.int>; 'Nicola.Rose@nibsc.org' <Nicola.Rose@nibsc.org>; 'msalit@stanford.edu' <msalit@stanford.edu>; 'erica@lji.org' <erica@lji.org>; SATHIYAMOORTHY, Vaseeharan <moorthyv@who.int>; 'schendel@lji.org' <schendel@lji.org>; 'connie.schmaljohn@nih.gov' <connie.schmaljohn@nih.gov>; 'Barbara.Schnierle@pei.de' <Barbara.Schnierle@pei.de>; 'PScott@eidresearch.org' <PScott@eidresearch.org>; 'alex@lji.org' <alex@lji.org>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; 'Ragini.Shivji@ema.europa.eu'

<Ragini.Shivji@ema.europa.eu>; 'amy.c.shurtleff@cepi.net' <amy.c.shurtleff@cepi.net>; YOO, Si Hyung <yoos@who.int>; 'Ashley.Smith1@hhs.gov' <Ashley.Smith1@hhs.gov>; 'mksong@ivi.int' <mksong@ivi.int>; 'erik.stemmy@nih.gov' <erik.stemmy@nih.gov>; SUBISSI, Lorenzo <subissil@who.int>; SWAMINATHAN, Soumya <swaminathans@who.int>; 'r.tedder@imperial.ac.uk' <r.tedder@imperial.ac.uk>; 'nax3@cdc.gov' <nax3@cdc.gov>; 'tracey.thue@usask.ca' <tracey.thue@usask.ca>; 'georgia.tomaras@duke.edu' <georgia.tomaras@duke.edu>; 'Julia.Tree@phe.gov.uk' <Julia.Tree@phe.gov.uk>; 'john.c.trefry.civ@mail.mil' <john.c.trefry.civ@mail.mil>; 'sylvie.van-der-werf@pasteur.fr' <sylvie.van-der-werf@pasteur.fr>; 'eric.vangieson@darpa.mil' <eric.vangieson@darpa.mil>; 'Vasan.Vasan@csiro.au' <Vasan.Vasan@csiro.au>; 'y.m.vasiliev@spbniivs.ru' <y.m.vasiliev@spbniivs.ru>; 'David.Vaughn@gatesfoundation.org' <David.Vaughn@gatesfoundation.org>; 'linfa.wang@duke-nus.edu.sg' <linfa.wang@duke-nus.edu.sg>; 'wangjz@nifdc.org.cn' <wangjz@nifdc.org.cn>; 'wangyc@nifdc.org.cn' <wangyc@nifdc.org.cn>; 'Jerry.Weir@fda.hhs.gov' <Jerry.Weir@fda.hhs.gov>; 'gweiss@uci.edu' <gweiss@uci.edu>; 'daniela@lji.org' <daniela@lji.org>; 'wilsonp@uchicago.edu' <wilsonp@uchicago.edu>; 'larry.wolfraim@nih.gov' <larry.wolfraim@nih.gov>; 'dj56wood@gmail.com' <dj56wood@gmail.com>; 'xumiaobj@126.com' <xumiaobj@126.com>; 'solomon.yimer@cepi.net' <solomon.yimer@cepi.net>; 'tlying@fudan.edu.cn' <tlying@fudan.edu.cn>; 'vyusibov@indianabiosciences.org' <vyusibov@indianabiosciences.org>; 'zlshi@wh.iov.cn' <zlshi@wh.iov.cn>; ZHOU, Tiequn <ZhouT@who.int>; 'william.lee@health.ny.gov' <william.lee@health.ny.gov>; 'ASiyer@mgh.harvard.edu' <ASiyer@mgh.harvard.edu>; 'Nick.Gilbert@ed.ac.uk' <Nick.Gilbert@ed.ac.uk>; 'Jilian.Sacks@finddx.org' <Jilian.Sacks@finddx.org>; 'jma@sgul.ac.uk' <jma@sgul.ac.uk>; 'sujan@lji.org' <sujan@lji.org>; 'dbarouch@bidmc.harvard.edu' <dbarouch@bidmc.harvard.edu>; 'qiang.pan-hammarstrom@ki.se' <qiang.pan-hammarstrom@ki.se>; 'tomwhite42450@gmail.com' <tomwhite42450@gmail.com>; 'Liz.Miller@lshtm.ac.uk' <Liz.Miller@lshtm.ac.uk>; 'emmanuelle.charton@edqm.eu' <emmanuelle.charton@edqm.eu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>
Cc: william.dowling@cepi.net; 'gnorheim@vaccibody.com' <gnorheim@vaccibody.com>; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu) <Eeva.Broberg@ecdc.europa.eu>; SALAMI, Kolawole <salamik@who.int>; 'diane.descamps@aphp.fr' <diane.descamps@aphp.fr>; 'SGalloway@cdc.gov' <SGalloway@cdc.gov>; 'lny1@cdc.gov' <lny1@cdc.gov>; 'gll9@cdc.gov' <gll9@cdc.gov>; 'mbo2@cdc.gov' <mbo2@cdc.gov>; 'sot1@cdc.gov' <sot1@cdc.gov>; KNEZEVIC, Ivana <knezevici@who.int>; Giada.Mattiuzzo@nibsc.org; 'peter.rigsby@nibsc.org' <peter.rigsby@nibsc.org>; 'Alex Sigal' <alex.sigal@ahri.org>
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers

Dear All,

Please find below the agenda for our group call with vaccine developers on Wednesday January 20, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays with vaccine developers

1. WHO standards for COVID-19 - I. Knezevic (WHO)
2. Roles and Importance of Standards in Assays – G. Mattiuzzo (NIBSC)
3. Calibration of secondary standards to WHO International Standards – P. Rigsby (NIBSC)
4. Discussion on standards
5. Update on 501Y.V2 variants – Alex Sigal (AHRI)

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Monday, December 21, 2020 10:47 AM
To: SCHWARTZ, Lauren; jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso@tonixpharma.com; boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman@codagenix.com; rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; dothuanthien@vabiotech.com.vn; dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo@geovax.com; farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary.Kobinger@crchudequebec.ulaval.ca; greanggrai.h@bionet-asia.com; guido.grandi@unitn.it; hasegawa@nih.go.jp; hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; hotez@bcm.edu; huyl@sinovac.com; james.hayward@adnas.com;

James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; iroodink@immunoprecise.com; JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice@greffex.com; jwolf@heatbio.com; kandeil_a@hotmail.com; Kapil.Maithal@zyduscadila.com; khirullin@mail.ru; kmodjarrad@eidresearch.org; kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe@meei.harvard.edu; maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban@cnb.csic.es; mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; muhammad.munir@lancaster.ac.uk; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; paul.hodgson@usask.ca; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd@bharatbiotech.com; qinjian_zhao@xmu.edu.cn; quliang@sinopharm.com; Ricardo.Gazzinelli@umassmed.edu; Richard.Webby@STJUDE.ORG; roland.tschismarov@themisbio.com; christiane.gerke@pasteur.fr; Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker@vaxart.com; sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; teresa.lambe@ndm.ox.ac.uk; THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg@altimmune.com; wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; SCHWARTZ, Lauren; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu

Subject: WHO Working Group on COVID-19 Assays with Vaccine Developers

When: Wednesday, January 20, 2021 5:30 AM-7:00 AM (UTC-08:00) Pacific Time (US & Canada).

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To: jboyer@inovio.com[jboyer@inovio.com]; acope@iavi.org[acope@iavi.org]; adanalioser@gmail.com[adanalioser@gmail.com]; akbulut@medicine.ankara.edu.tr[akbulut@medicine.ankara.edu.tr]; Alessandra.Vitelli@reithera.com[Alessandra.Vitelli@reithera.com]; Stefania.Capone@reithera.com[Stefania.Capone@reithera.com]; annied@epivax.com[annied@epivax.com]; Anthony.Macaluso (Anthony.Macaluso@tonixpharma.com)[Anthony.Macaluso@tonixpharma.com]; boulayi@medicago.com[boulayi@medicago.com]; brian.zabel@lakepharma.com[brian.zabel@lakepharma.com]; C.M.Smales@kent.ac.uk[C.M.Smales@kent.ac.uk]; christoph.rademacher@mpikg.mpg.de[christoph.rademacher@mpikg.mpg.de]; CKeech@Novavax.com[CKeech@Novavax.com]; coleman (coleman@codagenix.com)[coleman@codagenix.com]; rajeev.dhere@seruminstitute.com[rajeev.dhere@seruminstitute.com]; CVHerst@flowpharma.com[CVHerst@flowpharma.com]; cyrus.yang@sbc-biotech.com[cyrus.yang@sbc-biotech.com]; d.watterson@uq.edu.au[d.watterson@uq.edu.au]; dapengzhoulab@tongji.edu.cn[dapengzhoulab@tongji.edu.cn]; dguyongellin@osivax.com[dguyongellin@osivax.com]; diane.vanhoorick@etherna.be[diane.vanhoorick@etherna.be]; dong.shen@rnaimmune.com[dong.shen@rnaimmune.com]; Thien Do (dothuanthien@vabiotech.com.vn)[dothuanthien@vabiotech.com.vn]; dsz@imbcams.com.cn[dsz@imbcams.com.cn]; dulin@zhifeishengwu.com[dulin@zhifeishengwu.com]; dailp@biols.ac.cn[dailp@biols.ac.cn]; ercument.karasulu@ege.edu.tr[ercument.karasulu@ege.edu.tr]; fguirakhoo (fguirakhoo@geovax.com)[fguirakhoo@geovax.com]; farshad@covaxx.com[farshad@covaxx.com]; fguirakhoo@unitedneuroscience.com[fguirakhoo@unitedneuroscience.com]; fred@imophoron.com[fred@imophoron.com]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; greanggrai.h@bionet-asia.com[greanggrai.h@bionet-asia.com]; guido.grandi@unitn.it[guido.grandi@unitn.it]; 秀樹 長谷川 (hasegawa@nih.go.jp)[hasegawa@nih.go.jp]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; hironorinakagami@gmail.com[hironorinakagami@gmail.com]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Holger.Martinius@neovii.com[Holger.Martinius@neovii.com]; hotez (hotez@bcm.edu)[hotez@bcm.edu]; huyl@sinovac.com[huyl@sinovac.com]; james.hayward (james.hayward@adnas.com)[james.hayward@adnas.com]; James.Huleatt@sanofi.com[James.Huleatt@sanofi.com]; jarininger@lathambiopharm.com[jarininger@lathambiopharm.com]; jeff@stabilitech.com[jeff@stabilitech.com]; jennifer@immunoprecise.com[jennifer@immunoprecise.com]; yabdiche@immunoprecise.com[yabdiche@immunoprecise.com]; Ilse Roodink (iroodink@immunoprecise.com)[iroodink@immunoprecise.com]; JHendri1@its.jnj.com[JHendri1@its.jnj.com]; jkalil@usp.br[jkalil@usp.br]; jlh66@cam.ac.uk[jlh66@cam.ac.uk]; jprice (jprice@greffex.com)[jprice@greffex.com]; jwolf (jwolf@heatbio.com)[jwolf@heatbio.com]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Kapil Maithal (Kapil.Maithal@zyduscadila.com)[Kapil.Maithal@zyduscadila.com]; khirullin@mail.ru[khirullin@mail.ru]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; kovac@axon-neuroscience.eu[kovac@axon-neuroscience.eu]; michelle.hoffmann@axon-neuroscience.eu[michelle.hoffmann@axon-neuroscience.eu]; kozhemyakina@biocad.ru[kozhemyakina@biocad.ru]; lei.li@flinders.edu.au[lei.li@flinders.edu.au]; lindy.durrant@nottingham.ac.uk[lindy.durrant@nottingham.ac.uk]; linjinzhong@fudan.edu.cn[linjinzhong@fudan.edu.cn]; luistataje@farvet.com[luistataje@farvet.com]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; maksyutov_ra@vector.nsc.ru[maksyutov_ra@vector.nsc.ru]; martin.reers@biologicale.com[martin.reers@biologicale.com]; Matthias.Schnell@jefferson.edu[Matthias.Schnell@jefferson.edu]; mehmet.ozturk@ibg.edu.tr[mehmet.ozturk@ibg.edu.tr]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; mgursel@metu.edu.tr[mgursel@metu.edu.tr]; morishit@cgt.med.osaka-u.ac.jp[morishit@cgt.med.osaka-u.ac.jp]; nakagami@gts.med.osaka-u.ac.jp[nakagami@gts.med.osaka-u.ac.jp]; MStanford@imv-inc.com[MStanford@imv-inc.com]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; nadirkocak@yahoo.com[nadirkocak@yahoo.com]; naomi.van.vlies@intravacc.nl[naomi.van.vlies@intravacc.nl]; nesrin.ozoren@boun.edu.tr[nesrin.ozoren@boun.edu.tr]; nhj1114@mogam.re.kr[nhj1114@mogam.re.kr]; Olaf-Oliver.Wolz@curevac.com[Olaf-Oliver.Wolz@curevac.com]; Hodgson, Paul[paul.hodgson@usask.ca]; pdeshpande@indimmune.com[pdeshpande@indimmune.com]; phil.yang@nantworks.com[phil.yang@nantworks.com]; prasadsd (prasadsd@bharatbiotech.com)[prasadsd@bharatbiotech.com]; qinjian_zhao (qinjian_zhao@xmu.edu.cn)[qinjian_zhao@xmu.edu.cn]; Liang Qu (Jenny) (quliang@sinopharm.com)[quliang@sinopharm.com]; Ricardo.Gazzinelli@umassmed.edu[Ricardo.Gazzinelli@umassmed.edu]; Webby, Richard[richard.webby@stjude.org]; roland.tschismarov@themisbio.com[roland.tschismarov@themisbio.com]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Rolando.pajon@modernatx.com[Rolando.pajon@modernatx.com]; Rong.Xu@sabin.org[Rong.Xu@sabin.org]; roy.duncan@dal.ca[roy.duncan@dal.ca]; Senta.Walton@usz.ch[Senta.Walton@usz.ch]; Shailesh.DEWASTHALY@valneva.com[Shailesh.DEWASTHALY@valneva.com]; somchaiya@gpo.or.th[somchaiya@gpo.or.th]; songqiaoqiao@ystwt.com[songqiaoqiao@ystwt.com]; steven.gong@cloverbiopharma.com[steven.gong@cloverbiopharma.com]; stucker (stucker@vaxart.com)[stucker@vaxart.com]; sunL@antibodychina.com[sunL@antibodychina.com]; tapia@mpi-magdeburg.mpg.de[tapia@mpi-magdeburg.mpg.de]; tedross@uga.edu[tedross@uga.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; THeiland@immunomix.com[THeiland@immunomix.com]; Ugur.Sahin@biontech.de[Ugur.Sahin@biontech.de]; vgarg (vgarg@altimmune.com)[vgarg@altimmune.com]; wdj@adaptvac.com[wdj@adaptvac.com]; wdj@expres2ionbio.com[wdj@expres2ionbio.com]; Xiao-Jian.Yao@umanitoba.ca[Xiao-Jian.Yao@umanitoba.ca]; xuefeng.yu@cansinotech.com[xuefeng.yu@cansinotech.com]; zengming@biominhai.com[zengming@biominhai.com]; Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll

(Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; david.montefiori@duke.edu[david.montefiori@duke.edu]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Smith, Ashley

(OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; jma[jma@sgul.ac.uk]; sujan@lji.org[sujan@lji.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Perlman, Stanley[stanley-perlman@uiowa.edu]
Cc: William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; gnorheim@vaccibody.com[gnorheim@vaccibody.com]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; KNEZEVIC, Ivana[knezevici@who.int]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; peter.rigsby@nibsc.org[peter.rigsby@nibsc.org]; Alex Sigal[alex.sigal@ahri.org]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Rong.Xu@sabin.org[Rong.Xu@sabin.org]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Matthias.Schnell@jefferson.edu[Matthias.Schnell@jefferson.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Alter, Galit[galter@partners.org]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; BRANGEL, Polina[brangelp@who.int]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Thur 1/21/2021 6:31:04 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers
MEDRXIV-2021-250224v1-Sigal.pdf
3-Calibration to WHO International Standards.pptx
1-Introduction.WHO standards.IK.18_Jan_2021.pptx
2-Roles_and_Importance_of_Standards_in_Assays.pptx
Chat_Assays Call with Vaccine Developers_20Jan2021.docx

Dear All,

Many thanks for joining the discussion on Wednesday. See attached the presentations on standards, a summary of some of the questions from the zoom chat, and the pre-print from Alex Sigal.

Best,
Lauren

From: SCHWARTZ, Lauren
Sent: Monday, January 18, 2021 2:52 PM

To: jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso@tonixpharma.com; boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman@codagenix.com; rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; dothuanthien@vabiotech.com.vn; dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo@geovax.com; farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary.Kobinger@crchudequebec.ulaval.ca; greanggrai.h@bionet-asia.com; guido.grandi@unitn.it; hasegawa@nih.go.jp; hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; hotez@bcm.edu; huyl@sinovac.com; james.hayward@adnas.com; James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; iroodink@immunoprecise.com; JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice@greffex.com; jwolf@heatbio.com; kandeil_a@hotmail.com; Kapil.Maithal@zyduscadila.com; khirullin@mail.ru; kmodjarrad@eidresearch.org; kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe@meei.harvard.edu; maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban@cnb.csic.es; mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; muhammad.munir@lancaster.ac.uk; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; paul.hodgson@usask.ca; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd@bharatbiotech.com; qinjian_zhao@xmu.edu.cn; quliang@sinopharm.com; Ricardo.Gazzinelli@umassmed.edu; Richard.Webby@STJUDE.ORG; roland.tschismarov@themisbio.com; christiane.gerke@pasteur.fr; Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker@vaxart.com; sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; teresa.lambe@ndm.ox.ac.uk; THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg@altimmune.com; wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina <brangelp@who.int>; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier <costaa@who.int>; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria <henaorestrepoa@who.int>; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana <knezevici@who.int>; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver <omorgan@who.int>; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark <perkinsm@who.int>; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena <lauriex@who.int>; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan <moorthyv@who.int>; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung <yoos@who.int>;

Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo <subissil@who.int>; SWAMINATHAN, Soumya <swaminathans@who.int>; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn <ZhouT@who.int>; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu
Cc: william.dowling@cepi.net; gnorheim@vaccibody.com; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu) <Eeva.Broberg@ecdc.europa.eu>; SALAMI, Kolawole <salamik@who.int>; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; KNEZEVIC, Ivana <knezevici@who.int>; Giada.Mattiuzzo@nibsc.org; peter.rigsby@nibsc.org; Alex Sigal <alex.sigal@ahri.org>; celine.gurry@cepi.net; carolyn.clark@cepi.net; vincent.munster@nih.gov; lisa.hensley@nih.gov; kizzmekia.corbett@nih.gov; kaitlyn.dambach@nih.gov; marciela.degrace@nih.gov; erik.stemmy@nih.gov; ian.crozier@nih.gov; larry.wolfraim@nih.gov; janet.lathey@nih.gov; brooke.bozick@nih.gov; karin.bok@nih.gov; Rong.Xu@sabin.org; solomon.yimer@cepi.net; adrian.mcdermott@nih.gov; emmie.dewit@nih.gov; johnsonreed@niaid.nih.gov; elwyn.griffiths@cepi.net; connie.schmaljohn@nih.gov; johan.holst@cepi.net; clint.florence@nih.gov; Michael.holbrook@nih.gov; ASiyer@mgh.harvard.edu; valentina.bernasconi@cepi.net; Matthias.Schnell@jefferson.edu; Graham, Barney (NIH/VRC) [E] <bgraham@mail.nih.gov>; galter@partners.org; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu) <Eeva.Broberg@ecdc.europa.eu>
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers

Hi All,

Before the call on Wednesday, if you have specific questions you can email Bill Dowling, Mark Page, and myself (click here for email). We will try and address these questions on the call.

Best,
Lauren

From: SCHWARTZ, Lauren
Sent: Friday, January 15, 2021 11:58 AM
To: 'jboyer@inovio.com' <jboyer@inovio.com>; 'acope@iavi.org' <acope@iavi.org>; 'adanalioser@gmail.com' <adanalioser@gmail.com>; 'akbulut@medicine.ankara.edu.tr' <akbulut@medicine.ankara.edu.tr>; 'Alessandra.Vitelli@reithera.com' <Alessandra.Vitelli@reithera.com>; 'Stefania.Capone@reithera.com' <Stefania.Capone@reithera.com>; 'annied@epivax.com' <annied@epivax.com>; 'Anthony.Macaluso@tonixpharma.com' <Anthony.Macaluso@tonixpharma.com>; 'boulayi@medicago.com' <boulayi@medicago.com>; 'brian.zabel@lakepharma.com' <brian.zabel@lakepharma.com>; 'C.M.Smales@kent.ac.uk' <C.M.Smales@kent.ac.uk>; 'christoph.rademacher@mpikg.mpg.de' <christoph.rademacher@mpikg.mpg.de>; 'CKeech@Novavax.com' <CKeech@Novavax.com>; 'coleman@codagenix.com' <coleman@codagenix.com>; 'rajeev.dhere@seruminstitute.com' <rajeev.dhere@seruminstitute.com>; 'CVHerst@flowpharma.com' <CVHerst@flowpharma.com>; 'cyrus.yang@sbc-biotech.com' <cyrus.yang@sbc-biotech.com>; 'd.watterson@uq.edu.au' <d.watterson@uq.edu.au>; 'dapengzhoulab@tongji.edu.cn' <dapengzhoulab@tongji.edu.cn>; 'dguyongellin@osivax.com' <dguyongellin@osivax.com>; 'diane.vanhoorick@etherna.be' <diane.vanhoorick@etherna.be>; 'dong.shen@rnaimmune.com' <dong.shen@rnaimmune.com>; 'dothuanthien@vabiotech.com.vn' <dothuanthien@vabiotech.com.vn>; 'dsz@imbcams.com.cn' <dsz@imbcams.com.cn>; 'dulin@zhifeishengwu.com' <dulin@zhifeishengwu.com>; 'dailp@biols.ac.cn' <dailp@biols.ac.cn>; 'ercument.karasulu@ege.edu.tr' <ercument.karasulu@ege.edu.tr>; 'fguirakhoo@geovax.com' <fguirakhoo@geovax.com>; 'farshad@covaxx.com' <farshad@covaxx.com>; 'fguirakhoo@unitedneuroscience.com' <fguirakhoo@unitedneuroscience.com>; 'fred@imophoron.com' <fred@imophoron.com>; 'Gary.Kobinger@crchudequebec.ulaval.ca' <Gary.Kobinger@crchudequebec.ulaval.ca>; 'greanggrai.h@bionet-asia.com' <greanggrai.h@bionet-asia.com>; 'guido.grandi@unitn.it' <guido.grandi@unitn.it>; 'hasegawa@nih.go.jp' <hasegawa@nih.go.jp>; 'hendrikjan.thibaut@kuleuven.be' <hendrikjan.thibaut@kuleuven.be>; 'hironorinakagami@gmail.com' <hironorinakagami@gmail.com>; 'hlchen@hku.hk' <hlchen@hku.hk>; 'Holger.Martinius@neovii.com' <Holger.Martinius@neovii.com>; 'hotez@bcm.edu' <hotez@bcm.edu>; 'huyl@sinovac.com' <huyl@sinovac.com>; 'james.hayward@adnas.com' <james.hayward@adnas.com>; 'James.Huleatt@sanofi.com' <James.Huleatt@sanofi.com>; 'jarininger@lathambiopharm.com' <jarininger@lathambiopharm.com>; 'jeff@stabilitech.com' <jeff@stabilitech.com>; 'jennifer@immunoprecise.com' <jennifer@immunoprecise.com>; 'yabdiche@immunoprecise.com'

<yabdiche@immunoprecise.com>; 'iroodink@immunoprecise.com' <iroodink@immunoprecise.com>; 'JHendri1@its.jnj.com' <JHendri1@its.jnj.com>; 'jkalil@usp.br' <jkalil@usp.br>; 'jlh66@cam.ac.uk' <jlh66@cam.ac.uk>; 'jprice@greffex.com' <jprice@greffex.com>; 'jwolf@heatbio.com' <jwolf@heatbio.com>; 'kandeil_a@hotmail.com' <kandeil_a@hotmail.com>; 'Kapil.Maithal@zyduscadila.com' <Kapil.Maithal@zyduscadila.com>; 'khirullin@mail.ru' <khirullin@mail.ru>; 'kmodjarrad@eidresearch.org' <kmodjarrad@eidresearch.org>; 'kovac@axon-neuroscience.eu' <kovac@axon-neuroscience.eu>; 'michelle.hoffmann@axon-neuroscience.eu' <michelle.hoffmann@axon-neuroscience.eu>; 'kozhemyakina@biocad.ru' <kozhemyakina@biocad.ru>; 'lei.li@flinders.edu.au' <lei.li@flinders.edu.au>; 'lindy.durrant@nottingham.ac.uk' <lindy.durrant@nottingham.ac.uk>; 'linjinzhong@fudan.edu.cn' <linjinzhong@fudan.edu.cn>; 'luistataje@farvet.com' <luistataje@farvet.com>; 'luk_vandenberghe@meei.harvard.edu' <luk_vandenberghe@meei.harvard.edu>; 'maksyutov_ra@vector.nsc.ru' <maksyutov_ra@vector.nsc.ru>; 'martin.reers@biologicale.com' <martin.reers@biologicale.com>; 'Matthias.Schnell@jefferson.edu' <Matthias.Schnell@jefferson.edu>; 'mehmet.ozturk@ibg.edu.tr' <mehmet.ozturk@ibg.edu.tr>; 'mesteban@cnb.csic.es' <mesteban@cnb.csic.es>; 'mgursel@metu.edu.tr' <mgursel@metu.edu.tr>; 'morishit@cgt.med.osaka-u.ac.jp' <morishit@cgt.med.osaka-u.ac.jp>; 'nakagami@gts.med.osaka-u.ac.jp' <nakagami@gts.med.osaka-u.ac.jp>; 'MStanford@imv-inc.com' <MStanford@imv-inc.com>; 'muhammad.munir@lancaster.ac.uk' <muhammad.munir@lancaster.ac.uk>; 'nadirkocak@yahoo.com' <nadirkocak@yahoo.com>; 'naomi.van.vlies@intravacc.nl' <naomi.van.vlies@intravacc.nl>; 'nesrin.ozoren@boun.edu.tr' <nesrin.ozoren@boun.edu.tr>; 'nhj1114@mogam.re.kr' <nhj1114@mogam.re.kr>; 'Olaf-Oliver.Wolz@curevac.com' <Olaf-Oliver.Wolz@curevac.com>; 'paul.hodgson@usask.ca' <paul.hodgson@usask.ca>; 'pdeshpande@indimmune.com' <pdeshpande@indimmune.com>; 'phil.yang@nantworks.com' <phil.yang@nantworks.com>; 'prasadsd@bharatbiotech.com' <prasadsd@bharatbiotech.com>; 'qinjian_zhao@xmu.edu.cn' <qinjian_zhao@xmu.edu.cn>; 'quliang@sinopharm.com' <quliang@sinopharm.com>; 'Ricardo.Gazzinelli@umassmed.edu' <Ricardo.Gazzinelli@umassmed.edu>; 'Richard.Webby@STJUDE.ORG' <Richard.Webby@STJUDE.ORG>; 'roland.tschismarov@themisbio.com' <roland.tschismarov@themisbio.com>; 'christiane.gerke@pasteur.fr' <christiane.gerke@pasteur.fr>; 'Rolando.pajon@modernatx.com' <Rolando.pajon@modernatx.com>; 'Rong.Xu@sabin.org' <Rong.Xu@sabin.org>; 'roy.duncan@dal.ca' <roy.duncan@dal.ca>; 'Senta.Walton@usz.ch' <Senta.Walton@usz.ch>; 'Shailesh.DEWASTHALY@valneva.com' <Shailesh.DEWASTHALY@valneva.com>; 'somchaiya@gpo.or.th' <somchaiya@gpo.or.th>; 'songqiaoqiao@ystwt.com' <songqiaoqiao@ystwt.com>; 'steven.gong@cloverbiopharma.com' <steven.gong@cloverbiopharma.com>; 'stucker@vaxart.com' <stucker@vaxart.com>; 'sunL@antibodychina.com' <sunL@antibodychina.com>; 'tapia@mpi-magdeburg.mpg.de' <tapia@mpi-magdeburg.mpg.de>; 'tedross@uga.edu' <tedross@uga.edu>; 'teresa.lambe@ndm.ox.ac.uk' <teresa.lambe@ndm.ox.ac.uk>; 'THeiland@immunomix.com' <THeiland@immunomix.com>; 'Ugur.Sahin@biontech.de' <Ugur.Sahin@biontech.de>; 'vgarg@altimmune.com' <vgarg@altimmune.com>; 'wdj@adaptvac.com' <wdj@adaptvac.com>; 'wdj@expres2ionbio.com' <wdj@expres2ionbio.com>; 'Xiao-Jian.Yao@umanitoba.ca' <Xiao-Jian.Yao@umanitoba.ca>; 'xuefeng.yu@cansinotech.com' <xuefeng.yu@cansinotech.com>; 'zengming@biominhai.com' <zengming@biominhai.com>; 'galter@partners.org' <galter@partners.org>; 'maria.baca-estrada@canada.ca' <maria.baca-estrada@canada.ca>; 'baihe@nmpa.gov.cn' <baihe@nmpa.gov.cn>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'cheryl@gisaid.org' <cheryl@gisaid.org>; 'valentina.bernasconi@cepi.net' <valentina.bernasconi@cepi.net>; 'shinjini.bhatnagar@thsti.res.in' <shinjini.bhatnagar@thsti.res.in>; 'pbieniasz@mail.rockefeller.edu' <pbieniasz@mail.rockefeller.edu>; 'karin.bok@nih.gov' <karin.bok@nih.gov>; 'dboyle@path.org' <dboyle@path.org>; 'brooke.bozick@nih.gov' <brooke.bozick@nih.gov>; BRANGEL, Polina <brangelp@who.int>; 'christian.brechot@pasteur.fr' <christian.brechot@pasteur.fr>; 'Christine.bruce@phe.gov.uk' <Christine.bruce@phe.gov.uk>; 'zuz4@cdc.gov' <zuz4@cdc.gov>; 'Miles.Carroll@phe.gov.uk' <Miles.Carroll@phe.gov.uk>; 'fjc37@cam.ac.uk' <fjc37@cam.ac.uk>; 'Marco.Cavaleri@ema.europa.eu' <Marco.Cavaleri@ema.europa.eu>; 'MONALISA.CHATTERJI@gatesfoundation.org' <MONALISA.CHATTERJI@gatesfoundation.org>; 'MAY.CHU@CUANSCHUTZ.EDU' <MAY.CHU@CUANSCHUTZ.EDU>; 'carolyn.clark@cepi.net' <carolyn.clark@cepi.net>; 'kizzmekia.corbett@nih.gov' <kizzmekia.corbett@nih.gov>; COSTA, Alejandro Javier <costaa@who.int>; 'htq4@cdc.gov' <htq4@cdc.gov>; 'shane@lji.org' <shane@lji.org>; 'ian.crozier@nih.gov' <ian.crozier@nih.gov>; 'lad7@cdc.gov' <lad7@cdc.gov>; 'Lisa@amicitiam.com' <Lisa@amicitiam.com>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'tdelossantos@path.org' <tdelossantos@path.org>; 'emmie.dewit@nih.gov' <emmie.dewit@nih.gov>; 'marciela.degrace@nih.gov' <marciela.degrace@nih.gov>; 'rafael.delgado@salud.madrid.org' <rafael.delgado@salud.madrid.org>; 'mit666666@pitt.edu' <mit666666@pitt.edu>; 'katie.doores@kcl.ac.uk' <katie.doores@kcl.ac.uk>; 'william.dowling@cepi.net' <william.dowling@cepi.net>; 'christian.drosten@charite.de' <christian.drosten@charite.de>; 'epstein@ecohealthalliance.org' <epstein@ecohealthalliance.org>; 'Karl.Erlandson@hhs.gov' <Karl.Erlandson@hhs.gov>; 'darryl.falzarano@usask.ca' <darryl.falzarano@usask.ca>; 'jason.fernandes@canada.ca' <jason.fernandes@canada.ca>; 'clint.florence@nih.gov' <clint.florence@nih.gov>; 'MFrieman@som.umaryland.edu' <MFrieman@som.umaryland.edu>; 'Simon.Funnell@phe.gov.uk' <Simon.Funnell@phe.gov.uk>; 'Luc.Gagnon@nexelis.com' <Luc.Gagnon@nexelis.com>; 'Mayra.Garcia@fda.hhs.gov' <Mayra.Garcia@fda.hhs.gov>; 'bhx1@cdc.gov' <bhx1@cdc.gov>; 'Volker.gerdts@usask.ca' <Volker.gerdts@usask.ca>; 'd.goldblatt@ucl.ac.uk' <d.goldblatt@ucl.ac.uk>; 'guy.gorochov@sorbonne-universite.fr' <guy.gorochov@sorbonne-universite.fr>; 'barney.graham@nih.gov' <barney.graham@nih.gov>; 'ahgriff@bu.edu' <ahgriff@bu.edu>; 'elwyn.griffiths@cepi.net' <elwyn.griffiths@cepi.net>; 'gregory.d.gromowski.civ@mail.mil' <gregory.d.gromowski.civ@mail.mil>; 'celine.gurry@cepi.net'

<celine.gurry@cepi.net>; 'ilj2@cdc.gov' <ilj2@cdc.gov>; 'b.haagmans@erasmusmc.nl' <b.haagmans@erasmusmc.nl>; 'rzh7@cdc.gov' <rzh7@cdc.gov>; HENAO RESTREPO, Ana Maria <henaorestrepoa@who.int>; 'lisa.hensley@nih.gov' <lisa.hensley@nih.gov>; 'Michael.holbrook@nih.gov' <Michael.holbrook@nih.gov>; 'johan.holst@cepi.net' <johan.holst@cepi.net>; 'rawcraig@yahoo.com' <rawcraig@yahoo.com>; 'tkh4@cdc.gov' <tkh4@cdc.gov>; 'REIRELAND@mail.dstl.gov.uk' <REIRELAND@mail.dstl.gov.uk>; 'Lakshmi.Jayashankar@hhs.gov' <Lakshmi.Jayashankar@hhs.gov>; 'djernigan@cdc.gov' <djernigan@cdc.gov>; 'johnsonreed@niaid.nih.gov' <johnsonreed@niaid.nih.gov>; 'ydm9@cdc.gov' <ydm9@cdc.gov>; 'Jacqueline.Kirchner@gatesfoundation.org' <Jacqueline.Kirchner@gatesfoundation.org>; KNEZEVIC, Ivana <knezevici@who.int>; 'm.koopmans@erasmusmc.nl' <m.koopmans@erasmusmc.nl>; 'Gerald.Kovacs@hhs.gov' <Gerald.Kovacs@hhs.gov>; 'florian.krammer@mssm.edu' <florian.krammer@mssm.edu>; 'Philip.Krause@fda.hhs.gov' <Philip.Krause@fda.hhs.gov>; 'skrebs@hivresearch.org' <skrebs@hivresearch.org>; 'Greg.Kulnis@nexelis.com' <Greg.Kulnis@nexelis.com>; 'arun.kumar@cepi.net' <arun.kumar@cepi.net>; 'pawinee.k@redcross.or.th' <pawinee.k@redcross.or.th>; 'janet.lathey@nih.gov' <janet.lathey@nih.gov>; 'bleader@path.org' <bleader@path.org>; 'leejooyeon@korea.kr' <leejooyeon@korea.kr>; 'MSLEVER@dstl.gov.uk' <MSLEVER@dstl.gov.uk>; 'liyl@cde.org.cn' <liyl@cde.org.cn>; 'changguili@aliyun.com' <changguili@aliyun.com>; 'lyhchengdu@163.com' <lyhchengdu@163.com>; 'limhy0919@korea.kr' <limhy0919@korea.kr>; 'James.Little@hhs.gov' <James.Little@hhs.gov>; 'liub@cde.org.cn' <liub@cde.org.cn>; 'Tracy.MacGill@fda.hhs.gov' <Tracy.MacGill@fda.hhs.gov>; 'Karen.Makar@gatesfoundation.org' <Karen.Makar@gatesfoundation.org>; 'Mary.Matheson@phe.gov.uk' <Mary.Matheson@phe.gov.uk>; 'Giada.Mattiuzzo@nibsc.org' <Giada.Mattiuzzo@nibsc.org>; 'jmclellan@austin.utexas.edu' <jmclellan@austin.utexas.edu>; 'adrian.mcdermott@nih.gov' <adrian.mcdermott@nih.gov>; 'jmcelrat@fredhutch.org' <jmcelrat@fredhutch.org>; 'gmedigeshi@thsti.res.in' <gmedigeshi@thsti.res.in>; 'jwm1@pitt.edu' <jwm1@pitt.edu>; 'philip.minor2@gmail.com' <philip.minor2@gmail.com>; 'david.montefiori@duke.edu' <david.montefiori@duke.edu>; 'kaitlyn.dambach@nih.gov' <kaitlyn.dambach@nih.gov>; MORGAN, Oliver <omorgan@who.int>; 'Clare.Morris@nibsc.org' <Clare.Morris@nibsc.org>; 'sarah.mudrak@duke.edu' <sarah.mudrak@duke.edu>; 'munoz-fontela@bnitm.de' <munoz-fontela@bnitm.de>; 'vincent.munster@nih.gov' <vincent.munster@nih.gov>; 'Todd.Myers@fda.hhs.gov' <Todd.Myers@fda.hhs.gov>; 'aysegul.nalca.civ@mail.mil' <aysegul.nalca.civ@mail.mil>; 'scott.napper@usask.ca' <scott.napper@usask.ca>; 'MNELSON@dstl.gov.uk' <MNELSON@dstl.gov.uk>; 'PNorris@vitalant.org' <PNorris@vitalant.org>; 'pilailuk.o@dmsc.mail.go.th' <pilailuk.o@dmsc.mail.go.th>; 'n.okba@erasmusmc.nl' <n.okba@erasmusmc.nl>; 'golinger@MRIGLOBAL.ORG' <golinger@MRIGLOBAL.ORG>; 'jokim@ivi.int' <jokim@ivi.int>; 'Mark.Page@nibsc.org' <Mark.Page@nibsc.org>; 'gustavo.f.palacios.civ@mail.mil' <gustavo.f.palacios.civ@mail.mil>; 'map1@cdc.gov' <map1@cdc.gov>; 'xdv3@cdc.gov' <xdv3@cdc.gov>; 'Keith.Peden@fda.hhs.gov' <Keith.Peden@fda.hhs.gov>; 'sheila.a.peel2.civ@mail.mil' <sheila.a.peel2.civ@mail.mil>; 'malik@hku.hk' <malik@hku.hk>; PERKINS, Mark <perkinsm@who.int>; 'supaporn.p@dmsc.mail.go.th' <supaporn.p@dmsc.mail.go.th>; 'margaret.l.pitt.civ@mail.mil' <margaret.l.pitt.civ@mail.mil>; 'mireille.plamondon@canada.ca' <mireille.plamondon@canada.ca>; 'JLPRIOR@dstl.gov.uk' <JLPRIOR@dstl.gov.uk>; 'arimoin@g.ucla.edu' <arimoin@g.ucla.edu>; RIVEROS BALTA, Ximena <lauriex@who.int>; 'Nicola.Rose@nibsc.org' <Nicola.Rose@nibsc.org>; 'msalit@stanford.edu' <msalit@stanford.edu>; 'erica@lji.org' <erica@lji.org>; SATHIYAMOORTHY, Vaseeharan <moorthyv@who.int>; 'schendel@lji.org' <schendel@lji.org>; 'connie.schmaljohn@nih.gov' <connie.schmaljohn@nih.gov>; 'Barbara.Schnierle@pei.de' <Barbara.Schnierle@pei.de>; 'PScott@eidresearch.org' <PScott@eidresearch.org>; 'alex@lji.org' <alex@lji.org>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; 'Ragini.Shivji@ema.europa.eu' <Ragini.Shivji@ema.europa.eu>; 'amy.c.shurtleff@cepi.net' <amy.c.shurtleff@cepi.net>; YOO, Si Hyung <yoos@who.int>; 'Ashley.Smith1@hhs.gov' <Ashley.Smith1@hhs.gov>; 'mksong@ivi.int' <mksong@ivi.int>; 'erik.stemmy@nih.gov' <erik.stemmy@nih.gov>; SUBISSI, Lorenzo <subissil@who.int>; SWAMINATHAN, Soumya <swaminathans@who.int>; 'r.tedder@imperial.ac.uk' <r.tedder@imperial.ac.uk>; 'nax3@cdc.gov' <nax3@cdc.gov>; 'tracey.thue@usask.ca' <tracey.thue@usask.ca>; 'georgia.tomaras@duke.edu' <georgia.tomaras@duke.edu>; 'Julia.Tree@phe.gov.uk' <Julia.Tree@phe.gov.uk>; 'john.c.trefry.civ@mail.mil' <john.c.trefry.civ@mail.mil>; 'sylvie.van-der-werf@pasteur.fr' <sylvie.van-der-werf@pasteur.fr>; 'eric.vangieson@darpa.mil' <eric.vangieson@darpa.mil>; 'Vasan.Vasan@csiro.au' <Vasan.Vasan@csiro.au>; 'y.m.vasiliev@spbniivs.ru' <y.m.vasiliev@spbniivs.ru>; 'David.Vaughn@gatesfoundation.org' <David.Vaughn@gatesfoundation.org>; 'linfa.wang@duke-nus.edu.sg' <linfa.wang@duke-nus.edu.sg>; 'wangjz@nifdc.org.cn' <wangjz@nifdc.org.cn>; 'wangyc@nifdc.org.cn' <wangyc@nifdc.org.cn>; 'Jerry.Weir@fda.hhs.gov' <Jerry.Weir@fda.hhs.gov>; 'gweiss@uci.edu' <gweiss@uci.edu>; 'daniela@lji.org' <daniela@lji.org>; 'wilsonp@uchicago.edu' <wilsonp@uchicago.edu>; 'larry.wolfraim@nih.gov' <larry.wolfraim@nih.gov>; 'dj56wood@gmail.com' <dj56wood@gmail.com>; 'xumiaobj@126.com' <xumiaobj@126.com>; 'solomon.yimer@cepi.net' <solomon.yimer@cepi.net>; 'tlying@fudan.edu.cn' <tlying@fudan.edu.cn>; 'vyusibov@indianabiosciences.org' <vyusibov@indianabiosciences.org>; 'zlshi@wh.iov.cn' <zlshi@wh.iov.cn>; ZHOU, Tiequn <ZhouT@who.int>; 'william.lee@health.ny.gov' <william.lee@health.ny.gov>; 'ASiyer@mgh.harvard.edu' <ASiyer@mgh.harvard.edu>; 'Nick.Gilbert@ed.ac.uk' <Nick.Gilbert@ed.ac.uk>; 'Jilian.Sacks@finddx.org' <Jilian.Sacks@finddx.org>; 'jma@sgul.ac.uk' <jma@sgul.ac.uk>; 'sujan@lji.org' <sujan@lji.org>; 'dbarouch@bidmc.harvard.edu' <dbarouch@bidmc.harvard.edu>; 'qiang.pan-hammarstrom@ki.se' <qiang.pan-hammarstrom@ki.se>; 'tomwhite42450@gmail.com' <tomwhite42450@gmail.com>; 'Liz.Miller@lshtm.ac.uk' <Liz.Miller@lshtm.ac.uk>; 'emmanuelle.charton@edqm.eu' <emmanuelle.charton@edqm.eu>; 'stanley-perlman@uiowa.edu' <stanley-

perlman@uiowa.edu>
Cc: william.dowling@cepi.net; 'gnorheim@vaccibody.com' <gnorheim@vaccibody.com>; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu) <Eeva.Broberg@ecdc.europa.eu>; SALAMI, Kolawole <salamik@who.int>; 'diane.descamps@aphp.fr' <diane.descamps@aphp.fr>; 'SGalloway@cdc.gov' <SGalloway@cdc.gov>; 'lny1@cdc.gov' <lny1@cdc.gov>; 'gll9@cdc.gov' <gll9@cdc.gov>; 'mbo2@cdc.gov' <mbo2@cdc.gov>; 'sot1@cdc.gov' <sot1@cdc.gov>; KNEZEVIC, Ivana <knezevici@who.int>; Giada.Mattiuzzo@nibsc.org; 'peter.rigsby@nibsc.org' <peter.rigsby@nibsc.org>; 'Alex Sigal' <alex.sigal@ahri.org>
Subject: RE: WHO Working Group on COVID-19 Assays with Vaccine Developers

Dear All,

Please find below the agenda for our group call with vaccine developers on Wednesday January 20, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays with vaccine developers

1. WHO standards for COVID-19 - I. Knezevic (WHO)
2. Roles and Importance of Standards in Assays – G. Mattiuzzo (NIBSC)
3. Calibration of secondary standards to WHO International Standards – P. Rigsby (NIBSC)
4. Discussion on standards
5. Update on 501Y.V2 variants – Alex Sigal (AHRI)

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Monday, December 21, 2020 10:47 AM
To: SCHWARTZ, Lauren; jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso@tonixpharma.com; boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman@codagenix.com; rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; dothuanthien@vabiotech.com.vn; dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo@geovax.com; farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary.Kobinger@crchudequebec.ulaval.ca; greanggrai.h@bionet-asia.com; guido.grandi@unitn.it; hasegawa@nih.go.jp; hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; hotez@bcm.edu; huyl@sinovac.com; james.hayward@adnas.com; James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; iroodink@immunoprecise.com; JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice@greffex.com; jwolf@heatbio.com; kandeil_a@hotmail.com; Kapil.Maithal@zyduscadila.com; khirullin@mail.ru; kmodjarrad@eidresearch.org; kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe@meei.harvard.edu; maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban@cnb.csic.es; mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; muhammad.munir@lancaster.ac.uk; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; paul.hodgson@usask.ca; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd@bharatbiotech.com; qinjian_zhao@xmu.edu.cn; quliang@sinopharm.com; Ricardo.Gazzinelli@umassmed.edu; Richard.Webby@STJUDE.ORG; roland.tschismarov@themisbio.com; christiane.gerke@pasteur.fr; Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker@vaxart.com; sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; teresa.lambe@ndm.ox.ac.uk; THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg@altimmune.com; wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk;

fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; SCHWARTZ, Lauren; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu

Subject: WHO Working Group on COVID-19 Assays with Vaccine Developers
When: Wednesday, January 20, 2021 5:30 AM-7:00 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
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Escape of SARS-CoV-2 501Y.V2 variants from neutralization by convalescent plasma

Sandile Cele[1,2], Inbal Gazy[2,3,4], Laurelle Jackson[1], Shi-Hsia Hwa[1,5], Houriiyah Tegally[3], Gila Lustig[6], Jennifer Giandhari[3], Sureshnee Pillay[3], Eduan Wilkinson[3], Yeshnee Naidoo[3], Farina Karim[1,2], Yashica Ganga[1], Khadija Khan[1], Alejandro B. Balazs[7], Bernadett I. Gosnell[8], Willem Hanekom[1,5], Mahomed-Yunus S. Moosa[8], NGS-SA[§], COMMIT-KZN Team[§§], Richard J. Lessells[2,3,6], Tulio de Oliveira[2,3,6,9*], Alex Sigal[1,2,10*]

[1]Africa Health Research Institute, Durban 4001, South Africa. [2]School of Laboratory Medicine and Medical Sciences, University of KwaZulu-Natal, Durban 4001, South Africa. [3]KwaZulu-Natal Research Innovation and Sequencing Platform, Durban 4001, South Africa. [4]Department of Biochemistry and Molecular Biology, The Institute for Medical Research Israel-Canada, Hadassah Medical School, The Hebrew University of Jerusalem, 91120, Jerusalem, Israel. [5]Division of Infection and Immunity, University College London, London WC1E 6BT, UK. [6]Centre for the AIDS Programme of Research in South Africa, Durban 4001, South Africa. [7]Ragon Institute of MGH, Harvard, and MIT, Cambridge, USA. [8]Department of Infectious Diseases, Nelson R. Mandela School of Clinical Medicine, University of KwaZulu-Natal, Durban 4001, South Africa. [9]Department of Global Health, University of Washington, Seattle, USA. [10]Max Planck Institute for Infection Biology, Berlin 10117, Germany.

* Corresponding authors. Email: deoliveira@ukzn.ac.za, alex.sigal@ahri.org

Abstract

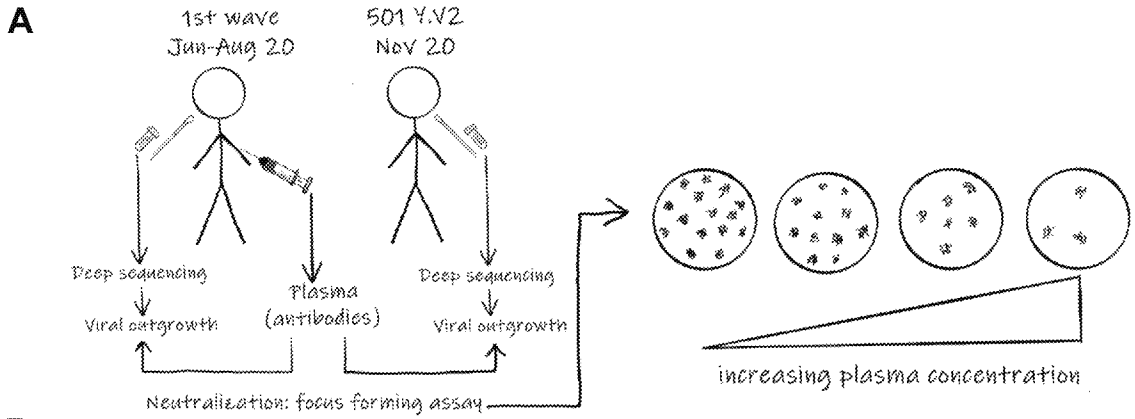
New SARS-CoV-2 variants with mutations in the spike glycoprotein have arisen independently at multiple locations and may have functional significance. The combination of mutations in the 501Y.V2 variant first detected in South Africa include the N501Y, K417N, and E484K mutations in the receptor binding domain (RBD) as well as mutations in the N-terminal domain (NTD). Here we address whether the 501Y.V2 variant could escape the neutralizing antibody response elicited by natural infection with earlier variants. We were the first to outgrow two variants of 501Y.V2 from South Africa, designated 501Y.V2.HV001 and 501Y.V2.HVdF002. We examined the neutralizing effect of convalescent plasma collected from six adults hospitalized with COVID-19 using a microneutralization assay with live (authentic) virus. Whole genome sequencing of the infecting virus of the plasma donors confirmed the absence of the spike mutations which characterize 501Y.V2. We infected with 501Y.V2.HV001 and 501Y.V2.HVdF002 and compared plasma neutralization to first wave virus which contained the D614G mutation but no RBD or NTD mutations. We observed that neutralization of the 501Y.V2 variants was strongly attenuated, with IC_{50} 6 to 200-fold higher relative to first wave virus. The degree of attenuation varied between participants and included a knockout of neutralization activity. This observation indicates that 501Y.V2 may escape the neutralizing antibody response elicited by prior natural infection. It raises a concern of potential reduced protection against re-infection and by vaccines designed to target the spike protein of earlier SARS-CoV-2 variants.

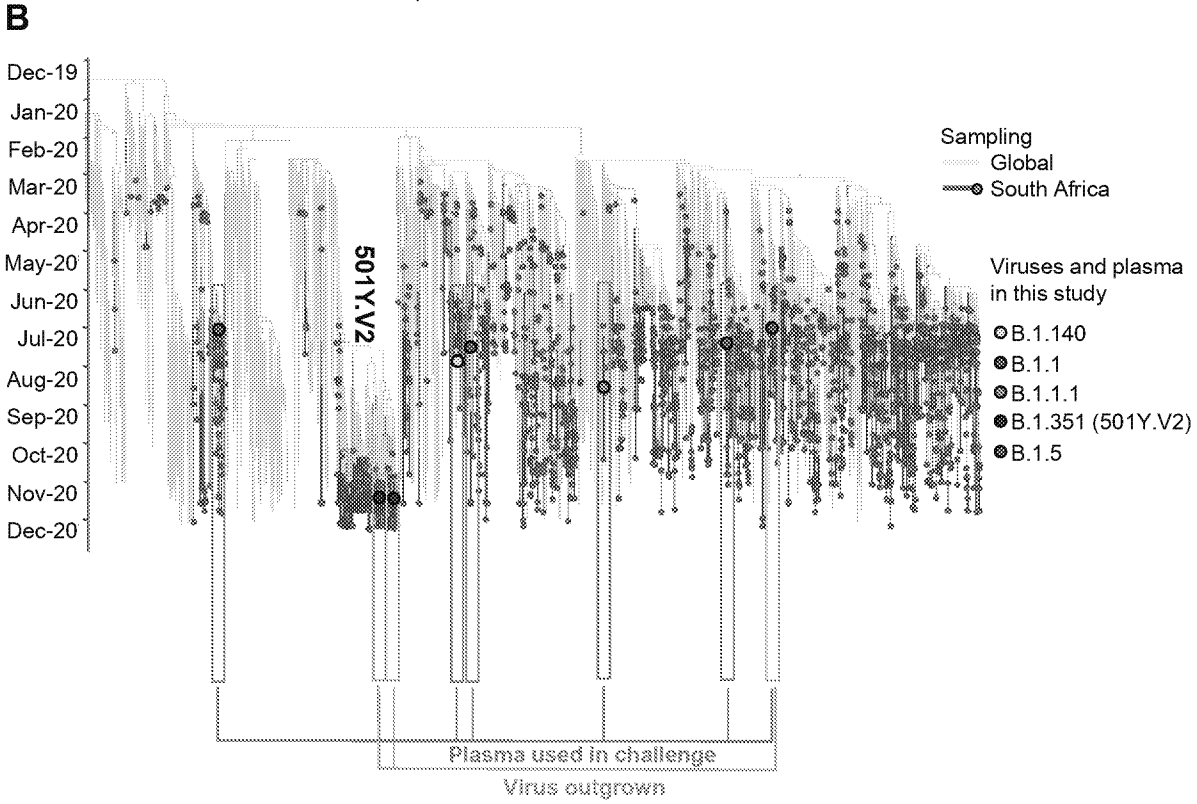
Through genomic surveillance of the severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), a number of new variants have recently been identified with multiple mutations in the spike glycoprotein [1, 2, 3]. We recently described the emergence of the N501Y.V2 variant in South Africa, characterised by the K417N, E484K, and N501Y mutations in the spike receptor binding domain (RBD) as well as four substitutions and a deletion in the N-terminal domain (NTD) [1]. This variant was first detected in October 2020, and has rapidly become the dominant variant in several parts of the country at a time of a rapid resurgence in infections.

The RBD is the main target of neutralizing antibodies (NAbs) elicited by SARS-CoV-2 infection, with the remaining activity directed at the NTD [4, 5, 6]. All three amino acid residues in the RBD that carry mutations in 501Y.V2 interact directly with the human angiotensin-converting enzyme 2 (hACE2) receptor and form part of the epitopes for hACE2-blocking NAbs [7]. The E484 residue specifically is a hotspot for binding of highly potent NAbs [7]. In a number of separate *in vitro* studies using monoclonal antibodies (mAbs), mutations at E484 have emerged as immune escape mutations, often conferring broad cross-resistance to panels of mAbs [8, 9, 10, 11]. E484K also emerged during passage with convalescent plasma, leading to substantial drops in neutralization with convalescent plasma samples [12, 13]. Using a deep mutation scanning approach to determine the effect of individual mutations on neutralization by polyclonal serum, mutations at E484 were associated with the largest drops in neutralization [14].

Here, using a microneutralization assay with authentic virus, we address the question of whether 501Y.V2 variants can escape the neutralizing response elicited by natural infection with previous variants. We outgrew and compared the neutralization of two SARS-CoV-2 501Y.V2 variants to a previously circulating variant derived from South Africa which does not have the 501Y.V2 defining mutations.

For neutralization, we used plasma samples from our ongoing longitudinal cohort study that tracks COVID-19 cases enrolled at two hospitals in Durban, South Africa [15]. We sampled participants weekly for the first month post-enrollment, and at each timepoint a blood draw and combined nasopharyngeal/oropharyngeal swab was performed to obtain both the plasma and the infecting virus.





	Outgrown viral variants			Infecting variant sequences of blood plasma donors					
Lineage	B.1.1	501Y.V2 (B.1.351)		B.1.1	B.1.1	B.1.5	B.1.5	B.1.140	B.1.1.1
Sequence ID	K002868	K005321	K005325	K002868	K004289	K004285	K004291	K004295	K004302
Plasma ID	039-13-0013			039-13-0013	039-02-0014	039-13-0015	039-13-0033	039-02-0017	039-13-0062
Isolate designation	CoV2.V003	501Y.V2. HVdF002	501Y.V2. HV001						
Spike mutations	D614G A688V	D80A D215G K417N E484K N501Y D614G A701V	L18F D80A D215G K417N E484K N501Y D614G A701V	D614G A688V	D614G	D614G	D614G	D614G	D614G
Spike indels		242-244del	242-244del						

Figure 1: Study design and sequences of SARS-CoV-2 variants. (A) We obtained convalescent plasma and detected the matching infecting variant in the first SARS-CoV-2 infection wave in South Africa. A blood draw and nasopharyngeal/oropharyngeal was performed on study participants. First wave virus was outgrown from one of the participants and compared to two viruses outgrown from the second wave, which were 501Y.V2 variants. A focus forming microneutralization assay was used to quantify neutralization. (B) Phylogenetic tree and mutations of variant sequences. Variants which infected the study participants who were plasma donors only for this study are marked in blue. Sequences of variants which were outgrown are marked in yellow. Participant 039-13-0013 was both a plasma donor and the donor from whom the first wave virus was outgrown. Y-axis denotes time of sampling for viral sequencing. Table shows mutations present in Spike for the 501Y.V2 variants and the first wave virus used in the study. See Table S2 for a complete list of mutations in the viral genomes.

We chose plasma from participants from the first infection wave where the infecting virus was successfully sequenced (Table S1) and where RBD binding was detected by ELISA. These viruses were from a variety of B.1 lineages circulating in South Africa and contained the D614G mutation but none of the spike mutations defining 501Y.V2 (Figure 1, see Table S2 for whole genome mutations). Plasma samples were from blood drawn approximately 1 month post-symptom onset (Table S1), shown to be close to the antibody response peak [16, 17].

We outgrew first wave virus (Materials and methods) from a sample obtained from a cohort participant (039-13-0013) in July 2020, and second wave 501Y.V2 virus from two samples obtained in November 2020 through our genomic surveillance program. We used a microneutralization live virus focus forming assay (FFA) [18]. This relies on a methylcellulose overlay to limit cell-free viral spread, resulting in a local infection focus then detected by an anti-SARS-CoV-2 Spike antibody (Materials and methods). Re-sequencing of the first 501Y.V2 variant after outgrowth revealed no changes in the RBD or NTD but a deletion in the furin cleavage site (Table S3) commonly observed after *in vitro* culture in Vero E6 cells [19, 20]. We designated this variant 501Y.V2.HVdF002. HV represents the outgrowth protocol which included initial outgrowth in a human H1299 cell line derivative overexpressing the ACE2 receptor, followed by a cell-to-cell infection of Vero E6 cells (Materials and methods). dF represents the deletion of the furin cleavage site. Deletion of the furin cleavage site may not affect neutralization [19]. However, we proceeded to test an additional 501Y.V2 variant. This variant, which we designated 501Y.V2.HV001, had an additional mutation, L18F, in the NTD prior to outgrowth and showed no changes in spike sequence after outgrowth.

We mixed the virus with serially diluted participant plasma, then added the mixture to Vero E6 cells and counted infection foci after 28 hours (Figure 2A, Materials and methods). There was a clear visual difference in the number of foci as a function of plasma dilution. 501Y.V2.HV001 also showed dramatically larger foci (Figure 2A).

We normalized the number of foci to the number of foci in the absence of plasma on the same plate to obtain the transmission index (Tx, [21]). In this context, it is the number of foci in the presence of plasma inhibition divided by the number of foci in the absence of plasma. This controls for experiment variability between plates and experiments. The data from the FFA approximated a normal distribution (Figure S1) and we therefore used parametric statistics to describe it. We observed neutralization of the first wave virus which varied between plasma samples (Figure 2B). To obtain the IC_{50}, we fitted the data for each participant to a sigmoidal function [22] with IC_{50} as the only free parameter (Materials and methods). Fitted IC_{50} values (Figure 2D) varied between 4×10^{-3} for participant 039-13-0013 to 1×10^{-4} for participants 039-13-0033 and 039-02-0015, consistent with the previously observed heterogeneity in neutralization between individuals [16, 17].

We next determined neutralization of 501Y.V2. A decline in plasma neutralization was clearly observed (Figure 2A). T501Y.V2.HV001 also showed attenuated neutralization likely greater than that of 501Y.V2.HVdF002 (Figure S2), ruling out the *in vitro* generated deletion in the furin cleavage site as being responsible for escape. We combined the data for both 501Y.V2 variants. Fitted IC_{50} values varied between 1×10^{-3} (1:100 dilution) for plasma from participant 039-13-0033 to a complete knock-out of activity for plasma from participant 039-13-0013 (Figure 2D). The 501Y.V2 to first wave IC_{50} ratio ranged from 6 to 200-fold (Figure 2D). Averaging across all participants highlighted the dramatic decrease in sensitivity to neutralization of authentic 501Y.V2 variants (Figure 2E).

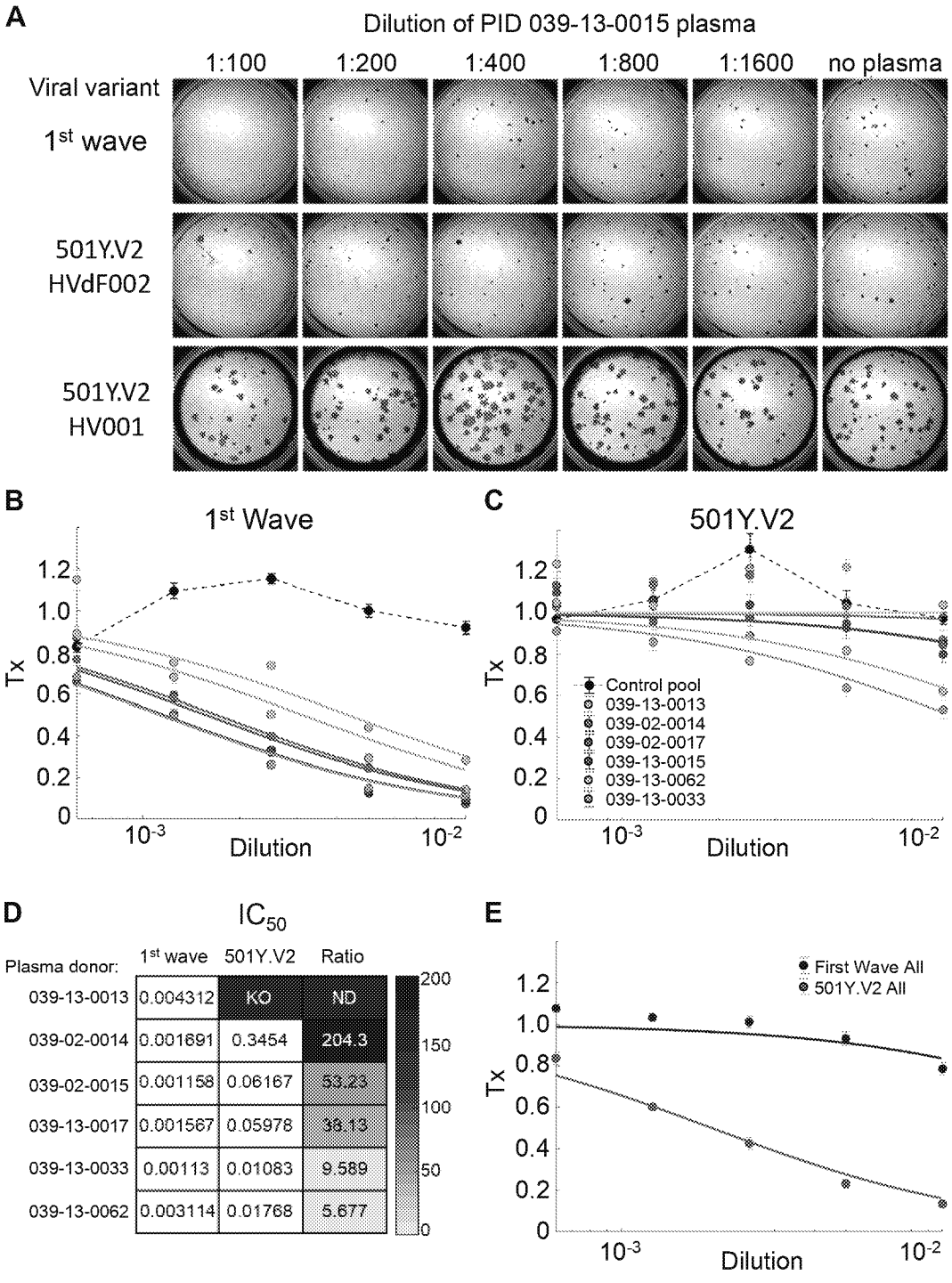


Figure 2: Neutralization of first wave and 501Y.V2 variants by convalescent plasma from first wave infections. (A) A representative focus forming assay using plasma from participant 039-13-0015. Plasma neutralization of (B) first wave virus and (C) the combined results from the two 501Y.V2 variants. Colored circles represent means and standard errors from 8 independent neutralization experiments using plasma from 6 convalescent participants who were infected by first wave variants in the first peak of the pandemic in South Africa. Correspondingly colored lines are fits of the sigmoidal equation with IC_{50} as the fitted parameter. Black points represent a pool of plasma from three uninfected controls. The transmission index (Tx) is the number of foci in the presence of the plasma dilution normalized by the number of foci in the absence of plasma. (D) Plasma IC_{50} values and ratios for first wave and 501Y.V2 variants. Knockout (KO) was scored as $IC_{50} > 1$. ND, not defined. (E) Mean and standard error across all plasma donors.

As we have entered the second year of the SARS-CoV-2 pandemic with high levels of transmission in many parts of the world, variants with mutations at key residues in the spike glycoprotein have emerged. Here we present clear evidence using authentic SARS-CoV-2 that the 501Y.V2 variant first detected in South Africa is associated with reduced neutralization by plasma collected from patients infected in the first wave with SARS-CoV-2 variants without the 501Y.V2 defining RBD and NTD mutations. While our findings are based on plasma samples from six convalescent study participants, the relative consistency of the effect argues that the potential to escape neutralizing antibodies elicited by prior SARS-CoV-2 infection may be widespread.

The reduced neutralization is most likely related to the mutations in the spike RBD and NTD that characterize the 501Y.V2 variant. While the E484K mutation has the clearest association with immune escape, the other mutations in the RBD (K417N, N501Y) are also located within residues targeted by some class 1 and class 2 NAbs [7]. Information about the significance of NTD mutations is also emerging. NAbs targeting this site have been shown to be potent neutralizers of SARS-CoV-2 [5, 6]. The deletion at residues 242-244 is just outside an antigenic supersite loop (residues 245-264) and L18 also falls within the antigenic supersite. Furthermore, mutations at L18 and D80 have been selected during passage with mAbs [5]. Our second variant contains the L18F mutation. This may be associated with the trend to lower neutralization sensitivity relative to the first 501Y.V2 variant (Figure S2). This variant also has strikingly larger foci (Figure 2A).

The reasons for the rapid emergence and fixation of potential immune escape mutations in South Africa remain unclear. The 501Y.V2 variant was first detected in the Eastern Cape Province of South Africa, in Nelson Mandela Bay, an urban municipality with a population of just over one million. While we have no SARS-CoV-2 seroprevalence data from this area, there were 1909 excess natural deaths (approximately 1600 per million population) by the end of the first wave in mid-September (https://www.samrc.ac.za/reports/report-weekly-deaths-south-africa). In the context of a young population (over 80 percent of the population under 50 years), this data would suggest a high attack rate from the first wave. While circumstantial, this provides some support to a hypothesis of high levels of population immunity driving the selection of variants with capacity to evade natural immunity. This area also has high HIV prevalence, and has amongst the lowest proportions of people with HIV who have viral suppression (http://www.hivdata.org.za/). We have not observed evidence of chronic SARS-CoV-2 infection in people living with HIV in our longitudinal cohort [15]. However, most cohort participants had sustained virological suppression with antiretroviral therapy (ART). We did observe altered immune dynamics after SARS-CoV-2 infection in HIV viremic participants relative to those who were virologically suppressed, and we are currently enrolling additional participants to examine SARS-CoV-2 clearance in the HIV viremic subset.

The implications of these results for re-infection and vaccine efficacy are still unclear. Our findings emphasize the need to understand whether the 501Y.V2 variant, and other similar variants, are associated with an increased rate of re-infection. Vaccines such as the Oxford/Astra Zeneca ChAdOx1 [23] and the Pfizer-BioNTech BNT162b2 [24] elicit neutralization titers in a similar range to the convalescent plasma in this study. However, these vaccines may elicit a broader antibody response and protective T cell immunity [25]. Protective T cell immunity also likely occurs following natural infection. Furthermore, it is unclear what degree of neutralization mediates protection, and infection may be particularly sensitive to inhibition at exposure [26].

In conclusion, we present data suggesting that the 501Y.V2 variant first detected in South Africa is able to escape the neutralizing antibody response elicited by natural infection with earlier variants. We expect data in the next weeks from phase 3 vaccine trials being conducted in South Africa. If the variant does have an effect on vaccine efficacy, then there may be a signal in the data from these clinical trials.

Material and methods

Ethical statement

Nasopharyngeal/oropharyngeal swab samples and plasma samples were obtained from six hospitalized adults with PCR-confirmed SARS-CoV-2 infection enrolled in a prospective cohort study approved by the Biomedical Research Ethics Committee (BREC) at the University of KwaZulu-Natal (reference BREC/00001275/2020). The 501Y.V2 variants were obtained from residual nasopharyngeal/oropharyngeal samples used for routine SARS-CoV-2 diagnostic testing by the National Health Laboratory Service, through our SARS-CoV-2 genomic surveillance program (BREC approval reference BREC/00001510/2020).

Whole genome sequencing, genome assembly and phylogenetic analysis

cDNA synthesis was performed on the extracted RNA using random primers followed by gene specific multiplex PCR using the ARTIC V3 protocol. Briefly, extracted RNA was converted to cDNA using the Superscript IV First Strand synthesis system (Life Technologies, Carlsbad, CA) and random hexamer primers. SARS-CoV-2 whole genome amplification was performed by multiplex PCR using primers designed on Primal Scheme (http://primal.zibraproject.org/) to generate 400bp amplicons with an overlap of 70bp that covers the 30Kb SARS-CoV-2 genome. PCR products were cleaned up using AmpureXP purification beads (Beckman Coulter, High Wycombe, UK) and quantified using the Qubit dsDNA High Sensitivity assay on the Qubit 4.0 instrument (Life Technologies Carlsbad, CA). We then used the Illumina® Nextera Flex DNA Library Prep kit according to the manufacturer's protocol to prepare indexed paired end libraries of genomic DNA. Sequencing libraries were normalized to 4nM, pooled and denatured with 0.2N sodium acetate. 12pM sample library was spiked with 1% PhiX (PhiX Control v3 adapter-ligated library used as a control). We sequenced libraries on a 500-cycle v2 MiSeq Reagent Kit on the Illumina MiSeq instrument (Illumina, San Diego, CA). We have previously published full details of the amplification and sequencing protocol [27].

We assembled paired-end fastq reads using Genome Detective 1.126 (https://www.genomedetective.com) and the Coronavirus Typing Tool [28]. We polished the initial assembly obtained from Genome Detective by aligning mapped reads to the references and filtering out low-quality mutations using bcftools 1.7-2 mpileup method. Mutations were confirmed visually with bam files using Geneious software (Biomatters Ltd, Auckland, New Zealand). All of the sequences were deposited in GISAID (https://www.gisaid.org/). We retrieved all South African SARS-CoV-2 genotypes from the GISAID database as of 11 January 2021 (N=2704). We initially analyzed South African genotypes against the global reference dataset (N=2592) using a custom pipeline based on a local version of NextStrain. The pipeline contains several python scripts that manage the analysis workflow. It performs alignment of genotypes in MAFFT [29], phylogenetic tree inference in IQ-Tree20, tree dating and ancestral state construction and annotation (https://github.com/nextstrain/ncov).

Cells

Vero E6 cells (ATCC CRL-1586, obtained from Cellonex) were propagated in complete DMEM with 10% fetal bovine serum (Hylone) containing 1% each of HEPES, sodium pyruvate, L-glutamine, and non-essential amino acids (Sigma-Aldrich). Cells were passaged every 3-4 days. H1299 cells were propagated in complete RPMI with 10% fetal bovine serum containing 1% each of HEPES, sodium pyruvate, L-glutamine, and non-essential amino acids and and passaged every second day.

H1299-E3 cell line for first passage SARS-CoV-2 outgrowth

The H1299-H2AZ clone with nuclear labelled YFP [30] was constructed to overexpress ACE2 as follows: VSVG-pseudotyped lentivirus containing the human ACE2 was generated by co-transfecting 293T cells with the pHAGE2-EF1alnt-ACE2-WT plasmid along with the lentiviral helper plasmids HDM-VSVG,

HDM-Hgpm2, HDM-tat1b and pRC-CMV-Rev1b using TransIT-LT1 (Mirus) transfection reagent. Supernatant containing the lentivirus was harvested two days after infection, filtered through a 0.45μm filter (Corning) and used to spinfect H1299-H2AZ at 1000 rcf for 2 hours at room temperature in the presence of 5 μg/mL polybrene (Sigma-Aldrich). ACE-2 transduced H1299-H2AZ cells were then subcloned at the single cell density in 96-well plates (Eppendorf) in conditioned media derived from confluent cells. After 3 weeks, wells were trypsinized (Sigma-Aldrich) and plated in two replicate plates, where the first plate was used to determine infectivity and the second was stock. The first plate was screened for the fraction of mCherry positive cells per cell clone upon infection with SARS-CoV-2 mCherry expressing Spike pseudotyped lentiviral vector 1610-pHAGE2/EF1a Int-mCherry3-W produced by transfecting as above. Screening was performed using a Metamorph-controlled (Molecular Devices, Sunnyvale, CA) Nikon TiE motorized microscope (Nikon Corporation, Tokyo, Japan) with a 20x, 0.75 NA phase objective, 561 laser line, and 607 nm emission filter (Semrock, Rochester, NY). Images were captured using an 888 EMCCD camera (Andor). Temperature (37°C), humidity and CO2 (5%) were controlled using an environmental chamber (OKO Labs, Naples, Italy). The clone with the highest fraction of mCherry expression was expanded from the stock plate and denoted H1299-E3. This clone was used in the outgrowth.

Viral Outgrowth

All live virus work was performed in Biosafety level 3 containment using AHRI Institutional Biosafety Committee approved protocols for SARS-CoV-2. For first wave virus, a T25 flask (Corning) was seeded with Vero E6 cells at 2×10^5 cells/ml and incubated for 18-20 hours. After 1 DPBS wash, the sub-confluent cell monolayer was inoculated with 500μL universal transport medium (UTM) diluted 1:1 with growth medium and filtered through a 0.45μM filter. Cells were incubated for 1 hour. Flask was then filled with 7mL of complete growth medium and checked daily for cytopathic effect (CPE). Four days post infection, supernatants of the infected culture were collected, centrifuged at 300 rcf for 3 minutes to remove cell debris, and filtered using a 0.45μM filter. Viral supernatant was aliquoted and stored at -80°C. For 501Y.V2 variants, we used H1299-ACE2-E3 cells for initial isolation followed by passage into Vero E6 cells. H1299-ACE2-E3 cells were seeded at 1.5×10^5 cells/ml and incubated for 18-20 hours. After 1 DPBS wash, the sub-confluent cell monolayer was inoculated with 500μL universal transport medium (UTM) diluted 1:1 with growth medium and filtered through a 0.45μM filter. Cells were incubated for 1 hour. Wells were then filled with 3mL of complete growth medium. 8 days post-infection, cells were trypsinized, centrifuged at 300 rcf for 3 minutes and resuspended in 4mL growth medium. 1mL was added to Vero E6 cells that had been seeded at t 2×10^5 cells/ml 18-20 hours earlier in a T25 flask (approximately 1:8 donor-to-target cell dilution ratio) for cell-to-cell infection. Coculture of H1299-ACE2-E3 and Vero E6 cells was incubated for 1 hour and flask was then filled with 7mL of complete growth medium and incubated for 6 days. Viral supernatant was aliquoted and stored at -80°C or further passaged in Vero E6 cells as above.

Microneutralization using focus forming assay

Vero E6 cells were plated in an 96 well plate (Eppendorf) at 30,000 cells per well 1 day pre-infection. Plasma was separated from EDTA-anticoagulated blood by centrifugation at 500 rcf for 10 minutes and stored at -80°C. Aliquots of plasma samples were heat-inactivated at 56°C for 30 minutes, and clarified by centrifugation at 10,000 rcf for 5 minutes, where the clear middle layer was used for experiments. Inactivated plasma was stored in single use aliquots to prevent freeze-thaw cycles. For experiments, plasma was serially diluted two-fold from 1:100 to 1:1600. Virus stocks were used at approximately 50 focus-forming units (FFU) per microwell and added to diluted plasma; antibody-virus mixtures were incubated for 1 hour at 37°C, 5% CO2 . Cells were infected with 100μL of the virus-antibody mixtures, to allow adsorption of virus. Subsequently, 100μL of a 1x RPMI 1640 (Sigma-Aldrich R6504), 1.5% carboxymethylcellulose (Sigma-Aldrich C4888) overlay was added to the wells without removing the inoculum. Cells were fixed at 28 hours post-infection using 4% paraformaldehyde (Sigma-Aldrich) for 20 minutes. For staining of foci, a rabbit anti-Spike monoclonal antibody (mAb BS-R2B12, GenScript

A02058) was used at 0.5μg/mL as the primary detection antibody. Antibody was resuspended in a permiabilization buffer containing 0.1% saponin (Sigma-Aldrich), 0.1% BSA (Sigma-Aldrich), and 0.05% tween (Sigma-Aldrich) in PBS. Plates were incubated with primary antibody overnight at 4°C, then washed with wash buffer containing 0.05% tween in PBS. Secondary goat anti-rabbit horseradish peroxidase (Abcam ab205718) was added at 1 μg/mL and incubated for 2 hours at room temperature with shaking. The TrueBlue peroxidase substrate (SeraCare 5510-0030) was then added at 50μL per well and incubated for 20 minutes at room temperature. Plates were then dried for 2 hours and imaged using a Metamorph-controlled Nikon TiE motorized microscope with a 2x objective. Automated image analysis was performed using a Matlab2019b (Mathworks) custom script, where focus detection was automated and did not involve user curation. Image segmentation steps were stretching the image from minimum to maximum intensity, local Laplacian filtering, image complementation, thresholding and binarization. For the second 501Y.V2 variant, a dilation/erosion step was introduced to prevent the large foci from fragmenting into smaller objects.

Statistics and fitting

All statistics and fitting were performed using Matlab2019b. Neutralization data was fit to

$$Tx = 1/1 + (D/IC_{50}).$$

Here Tx is the number of foci normalized to the number of foci in the absence of plasma on the same plate at dilution D. Fit to a normal distribution using Matlab2019b function normplot, which compared the distribution of the Tx data to the normal distribution (see https://www.mathworks.com/help/stats/normplot.html).

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Shareef Abrahams[1], Luiz Carlos Junior Alcantara[2], Arghavan Alisoltani-Dehkordi[3,4], Mushal Allam[5], Jinal N Bhiman[5,6], Mary-Ann Davies[7,8], Deelan Doolabh[9], Susan Engelbrecht[10], Vagner Fonseca[11], Marta Giovanetti[2], Allison J Glass[6,12], Adam Godzik[4], Dominique Goedhals[13], Diana Hardie[14], Marvin Hsiao[14], Arash Iranzadeh[4], Arshad Ismail[5], Stephen Korsman[14], Sergei L Kosakovsky Pond[15], Oluwakemi Laguda-Akingba[1,16], Jose Lourenco[17], Gert Marais[14], Darren Martin[9,18], Caroline Maslo[19], Koleka Mlisana[20,21], Thabo Mohale[5], Nokukhanya Msomi[22], Innocent Mudau[9], Francesco Petruccione[23,24], Wolfgang Preiser[10], Emmanuel James San[11], Bryan Trevor Sewell[25], Lynn Tyers[9], Gert Van Zyl[10], Anne von Gottberg[5,6], Sibongile Walaza[5,26], Steven Weaver[15], Constantinos Kurt Wibmer[5], Carolyn Williamson[9,14,21], Denis York[27].

[1]National Health Laboratory Service, Port Elizabeth, South Africa. [2]Laboratorio de Flavivirus, Fundacao Oswaldo Cruz, Rio de Janeiro, Brazil. [3]Division of Medical Virology, Department of Pathology, University of Cape Town, Cape Town, South Africa. [4]Division of Biomedical Sciences, University of California Riverside School of Medicine, Riverside, California, USA. [5]National Institute for Communicable Diseases of the National Health Laboratory Service, Johannesburg, South Africa. [6]School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa. [7]Centre for Infectious Disease Epidemiology and Research, University of Cape Town, Cape Town, South Africa. [8]Western Cape Government: Health, Cape Town, South Africa. [9]Division of Medical Virology, Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa. [10]Division of Medical Virology at NHLS Tygerberg Hospital and Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town, South Africa. [11]KwaZulu-Natal Research Innovation and

Sequencing Platform (KRISP), Department of Laboratory Medicine and Medical Sciences, University of KwaZulu-Natal, Durban, South Africa. [12]Department of Molecular Pathology, Lancet Laboratories, Johannesburg, South Africa. [13]Division of Virology at NHLS Universitas Academic Laboratories, University of The Free State, Bloemfontein, South Africa. [14]Division of Medical Virology at NHLS Groote Schuur Hospital, University of Cape Town, Cape Town, South Africa. [15]Institute for Genomics and Evolutionary Medicine, Temple University, Philadelphia, Pennsylvania, USA. [16]Department of Laboratory Medicine and Pathology, Faculty of Health Sciences, Walter Sisulu University, Mthatha, South Africa. [17]Department of Zoology, University of Oxford, Oxford, United Kingdom. [18]Computational Biology Division, Department of Integrative Biomedical Sciences, University of Cape Town, Cape Town, South Africa. [19]Department of Quality Leadership, Netcare Hospitals, Johannesburg, South Africa. [20]National Health Laboratory Service, Johannesburg, South Africa. [21]Centre for the AIDS Programme of Research in South Africa (CAPRISA), Durban, South Africa. [22]Discipline of Virology, University of KwaZulu-Natal, School of Laboratory Medicine and Medical Sciences and National Health Laboratory Service, Durban, South Africa. [23]Centre for Quantum Technology, University of KwaZulu-Natal, Durban, South Africa [24]National Institute for Theoretical Physics (NITheP), KwaZulu-Natal, South Africa. [25]Structural Biology Research Unit, Department of Integrative Biomedical Sciences, University of Cape Town, Rondebosch, South Africa. [26]School of Public Health, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa. [27]Molecular Diagnostics Services, Durban, South Africa.

§ § COMMIT-KZN Team

Moherndran Archary[1], Kaylesh J. Dullabh[2], Philip Goulder[3,4], Guy Harling[3,5], Rohen Harrichandparsad[6], Kobus Herbst[3,7], Prakash Jeena[1], Thandeka Khoza[3], Nigel Klein[3,8], Henrik Kløverpris[3,9,10], Alasdair Leslie[3,9], Rajhmun Madansein[2], Mohlopheni Marakalala[3,9], Matilda Mazibuko[3], Mosa Moshabela[11], Ntombifuthi Mthabela[3], Kogie Naidoo[12], Zaza Ndhlovu[3,13], Thumbi Ndung'u[3,9,14,15], Kennedy Nyamande[16], Nesri Padayatchi[12], Vinod Patel[17], Theresa Smit[3], Adrie Steyn[3,18], Emily Wong[3,18].

[1]Department of Paediatrics and Child Health, University of KwaZulu-Natal, Durban, South Africa. [2]Department of Cardiothoracic Surgery, University of KwaZulu-Natal, Durban, South Africa. [3]Africa Health Research Institute, Durban, South Africa. [4]Department of Paediatrics, Oxford, UK. [5]Institute for Global Health, University College London, UK. [6]Department of Neurosurgery, University of KwaZulu-Natal, Durban, South Africa. [7]South African Population Research Infrastructure Network, Durban, South Africa. [8]Institute of Child Health, University College London, UK. [9]Division of Infection and Immunity, University College London, London, UK. [10]Department of Immunology and Microbiology, University of Copenhagen, Copenhagen, Denmark. [11]College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa. [12]Centre for the AIDS Programme of Research in South Africa, Durban, South Africa. [13]Ragon Institute of MGH, MIT and Harvard, Boston, USA. [14]HIV Pathogenesis Programme, The Doris Duke Medical Research Institute, University of KwaZulu-Natal, Durban, South Africa. [15]Max Planck Institute for Infection Biology, Berlin, Germany. [16]Department of Pulmonology and Critical Care, University of KwaZulu-Natal, Durban, South Africa. [17]Department of Neurology, University of KwaZulu-Natal, Durban, South Africa. [18]Division of Infectious Diseases, University of Alabama at Birmingham.

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Ann Davies, Lynn Tyers, Innocent Mudau, Denis York, Caroline Maslo, Dominique Goedhals, Shareef Abrahams, Oluwakemi Laguda-Akingba, Arghavan Alisoltani-Dehkordi, Adam Godzik, Constantinos Kurt Wibmer, Bryan Trevor Sewell, José Lourenço, Luiz Carlos Junior Alcantara, Sergei L Kosakovsky Pond, Steven Weaver, Darren Martin, Richard J Lessells, Jinal N Bhiman, Carolyn Williamson, and Tulio de Oliveira. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (sars-cov-2) lineage with multiple spike mutations in south africa. *medRxiv*, page 2020.12.21.20248640, 2020. doi: 10.1101/2020.12.21.20248640. URL `https://www.medrxiv.org/content/medrxiv/early/2020/12/22/2020.12.21.20248640.full.pdf`.

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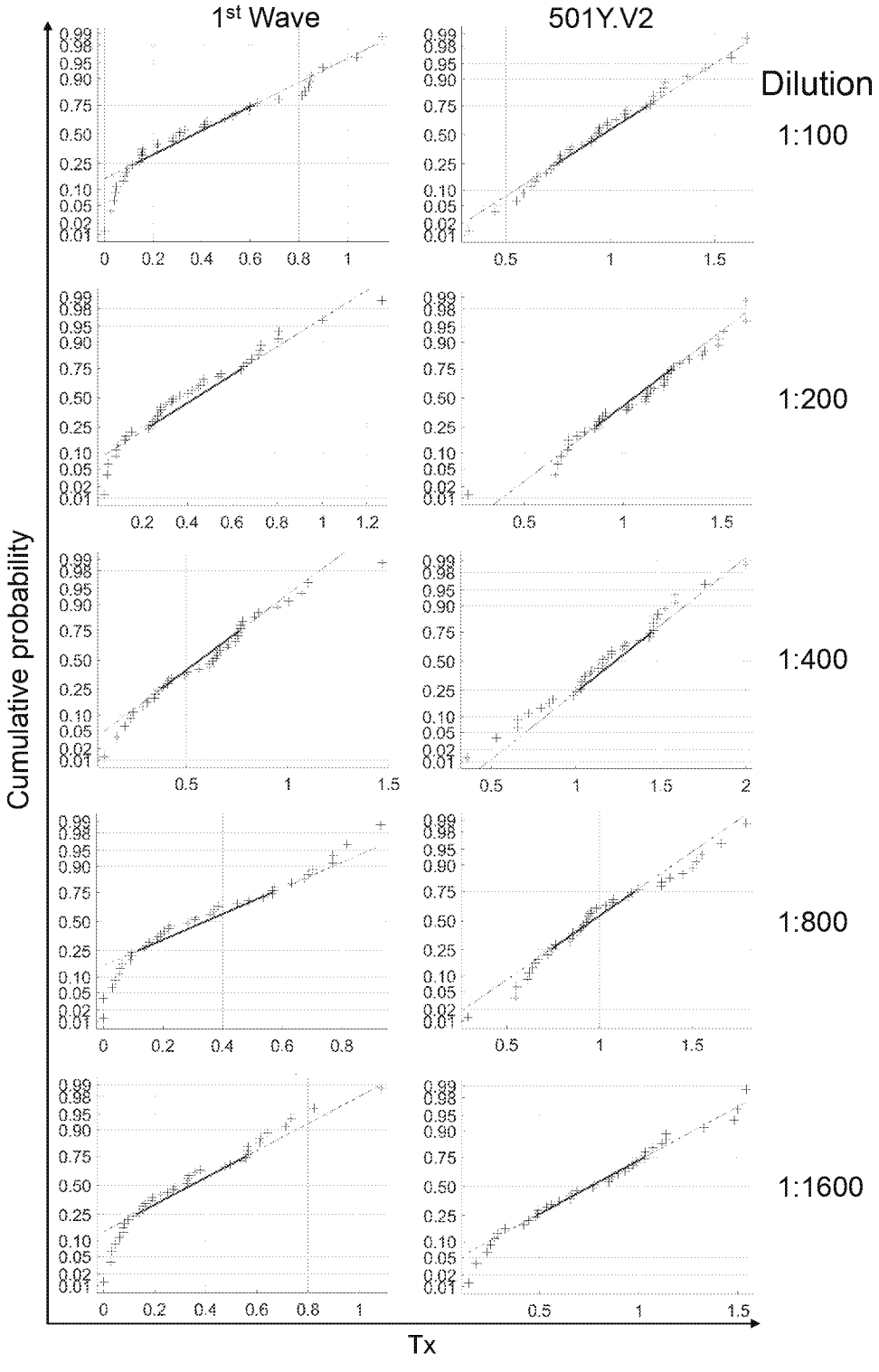


Figure S 1: Fit of combined data for each plasma dilution to a normal distribution. The Matlab2019b function normplot was used to assess the fit of the data (blue crosses) to a normal distribution (solid red line). Lack of pronounced curvature of the data in the range of the solid line indicates that a the data is a reasonably good fit to a normal distribution. see https://www.mathworks.com/help/stats/normplot.html for additional information.

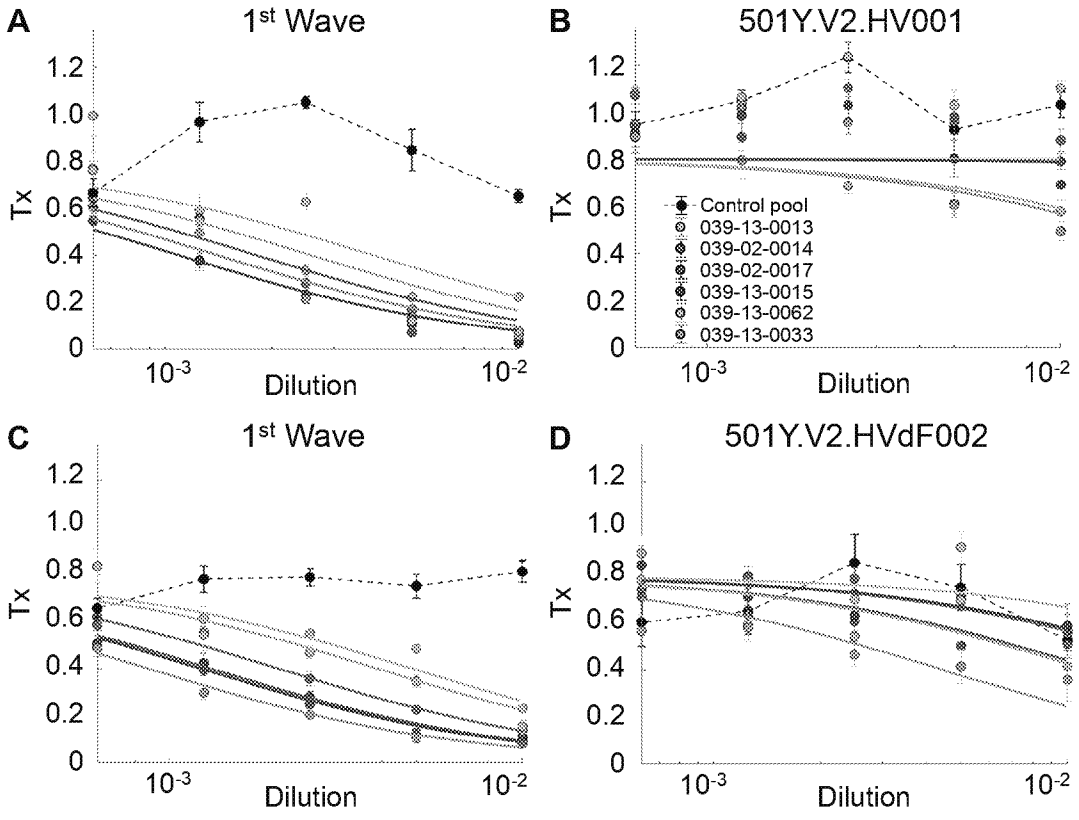


Figure S 2: Neutralization of first wave and 501Y.V2 by convalescent plasma from first wave infections separated by variant. Four sets of independent experiments were performed per 501Y.V2 - first wave pair, where the matched first wave variant results are shown to the left of the 501Y.V2 neutralization results. 501Y.V2 variant 2 contained the L18F mutation in addition to the mutations of variant 1 , and did not have the furin cleavage site deletion from outgrowth in Vero E6 cells. Colored points represent means and standard errors from 4 independent experiments for each 501Y.V2 variant/first wave pair of neutralization activity of plasma from 6 convalescent participants infected by first wave viruses. Corresponding lines are fits of the sigmoidal equation with IC_{50} as the fitted parameter. Black points represent a pool of plasma from three uninfected controls. The transmission index (Tx) is the number of foci in the presence of the plasma dilution normalized by the number of foci in the absence of plasma.

Table S 1: Plasma donor characteristics

Cohort ID	Sex	Age	Supplemental oxygen	Date of symptom onset	Days between symptom onset and diagnostic swab	Days between symptom onset and plasma collection
039-02-0014	F	66	No	01-Jul-2020	13	27
039-02-0017	F	66	Yes	21-Jul-2020	7	28
039-13-0013	F	54	No	29-Jun-2020	3	30
039-13-0015	F	42	No	21-Jun-2020	12	26
039-13-0033	F	37	No	24-Jun-2020	23	30
039-13-0062	M	67	No	06-Aug-2020	12	26

Table S 2: Mutation profile for the genomes of the outgrown viruses and for the infecting viruses of convalescent plasma donors

	Outgrown virus			Infecting virus from plasma donors					
Lineage	B.1.1	B.1.351 (510Y.V2)	B.1.351 (501Y.V2)	B.1.1	B.1.1	B.1.5	B.1.5	B.1.140	B.1.1.1
Sequence ID Accession ID Cohort ID	K002868 EPI_ISL_602622 039-13-0013	K005321 EPI_ISL_678570 -	K005325 EPI_ISL_678615 -	K002868 EPI_ISL_602622 039-13-0013	K004289 EPI_ISL_660170 039-02-0014	K004285 EPI_ISL_660167 039-13-0015	K004291 EPI_ISL_660172 039-13-0033	K004295 EPI_ISL_660167 039-02-0017	K004302 EPI_ISL_660181 039-13-0062
Spike amino acid substitutions	S:D614G S:A688V	S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:L18F S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:D614G S:A688V	S:D614G	S:D614G	S:D614G	S:D614G	S:D614G
Spike deletions		S:242-244del	S:242-244del						
Other amino acid substitutions	N:L139F N:R203K N:G204R ORF14:G50N ORF1a:D1481N ORF1b:P314L	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R ORF1b:P314L ORF3a:Q57H ORF3a:S171L	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R ORF1b:P314L ORF3a:Q57H ORF3a:W131L ORF3a:S171L ORF7a:V93F	N:L139F N:R203K N:G204R ORF14:G50N ORF1a:D1481N ORF1b:P314L	E:L73P N:R203K N:G204R ORF14:G50N ORF1b:P314L ORF1b:T1522I	E:L73P ORF1a:D3728N ORF1b:P314L	N:T148A ORF10:A28V ORF1a:K2511R ORF1a:V3858I ORF1b:P314L	ORF1a:F1178S ORF1b:P314L	N:R203K N:G204R ORF14:G50N ORF1a:T1246I ORF1a:G3278S ORF1b:P314L
Other deletions		orf1ab:3675-3677del	orf1ab:3675-3677del						

Lineage classification was performed by Pangolin software application version v2.1.7 (https://cov-lineages.org/pangolin.html).
Accession ID refers to GISAID EpiCoV™ database (www.gisaid.org)
Amino acid mutation nomenclature includes open reading frame, wild-type amino acid, ORF position and amino-acid mutation (e.g. S:D80A, Spike D to A substitution at position 80). del refers to deletion between stated positions. Amino acid mutations are annotated based on mature protein region of coding sequence (CDS) of SARS-CoV-2 reference sequence NC_045512.2.

Table S 3: Mutation profile for the genomes of the outgrown 501Y.V2 viruses, showing the original genome produced from the nasopharyngeal swab specimen and the genomes generated following passage in VeroE6 cells

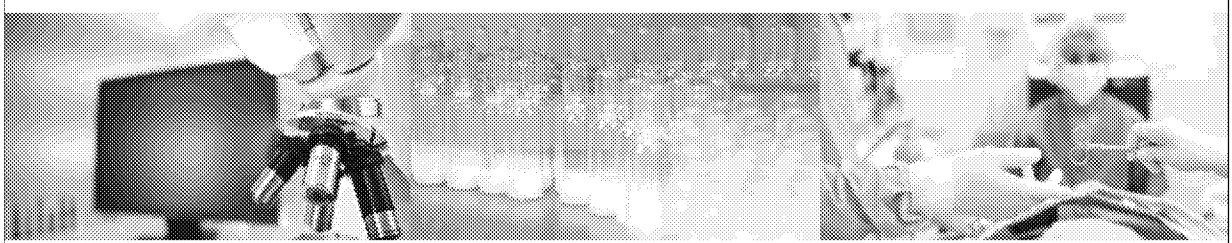
	Outgrown 501Y.V2 Original	**Outgrown 501Y.V2 After passage 2**	**Outgrown 501Y.V2 After passage 3**	**Outgrown 501Y.V2 Original**	**Outgrown 501Y.V2 After passage 3**
Sequence ID	K005321	K007776	K007624	K005325	K007621
Spike amino acid substitutions	S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:L18F S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V	S:L18F S:D80A S:D215G S:K417N S:E484K S:N501Y S:D614G S:A701V
Spike deletions	S:242-244del	S:242-244del **S:677-681del**	S:242-244del **S:677-681del**	S:242-244del	S:242-244del
Other amino acid substitutions	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R ORF1b:P314L ORF3a:Q57H ORF3a:S171L	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R **ORF1a:Q3878R** ORF1b:P314L ORF3a:Q57H ORF3a:S171L	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R **ORF1a:Q3878R** ORF1b:P314L ORF3a:Q57H ORF3a:S171L	E:P71L N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R ORF1b:P314L ORF3a:Q57H ORF3a:W131L ORF3a:S171L ORF7a:V93F	E:P71L **N:R32H** N:T205I ORF14:L52F ORF1a:T265I ORF1a:K1655N ORF1a:K3353R **ORF1a:N4358K** ORF1b:P314L ORF3a:Q57H ORF3a:W131L ORF3a:S171L ORF7a:V93F **ORF9b:A29T**
Other deletions	orf1ab:3675-3677del	orf1ab:3675-3677del	orf1ab:3675-3677del	orf1ab:3675-3677del	orf1ab:3675-3677del

Amino acid mutation nomenclature includes open reading frame, wild-type amino acid, ORF position and amino-acid mutation (e.g. S:D80A, Spike D to A substitution at position 80). del refers to deletion between stated positions. Amino acid mutations are annotated based on mature protein region of coding sequence (CDS) of SARS-CoV-2 reference sequence NC_045512.2. Substitutions and deletions in bold are those emerging during passage

NIBSC

Calibration of secondary standards to WHO International Standards

Peter Rigsby, Analytical & Biological Sciences, NIBSC



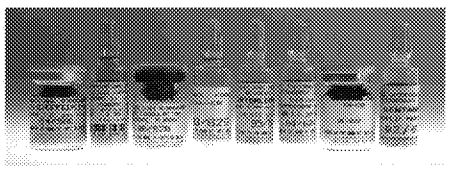
Medicines & Healthcare products Regulatory Agency

WHO International Standards (IS)

- World Health Organization International Standards: highest order standards used to enable biological & immunological assay results to be expressed in the same way worldwide
- WHO Expert Committee on Biological Standardization (ECBS) establishes and assigns a value to an IS
- "An international collaborative study must be carried out before any candidate biological reference standard can be considered for establishment by the WHO ECBS" *(WHO Technical Report Series, No. 932, 2006)*

WHO International Standards (IS)

- Most IS define International Units (IU) of biological activity
  - Arbitrary units representing content of ampoule or vial; no uncertainty assigned
  - Often not dependent on assay method used
- Often lyophilized, giving highly stable preparations



- Not intended for routine use
  - Secondary standards calibrated directly against (and traceable to) the relevant IS are required

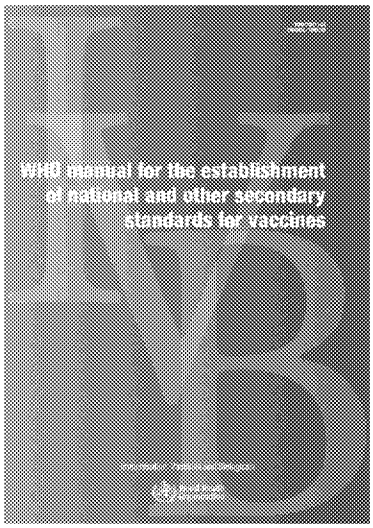
Guidance documents

World Health Organization

Post ECBS version

ENGLISH ONLY

MANUAL FOR THE PREPARATION OF SECONDARY REFERENCE MATERIALS FOR IN VITRO DIAGNOSTIC ASSAYS DESIGNED FOR INFECTIOUS DISEASE NUCLEIC ACID OR ANTIGEN DETECTION: CALIBRATION TO WHO INTERNATIONAL STANDARDS



Key properties of different standards

	WHO International Standard	Secondary standard	Tertiary standard
Alternate names	Highest order, International calibrator	Regional or national working reference materials, working reagents, manufacturer's working calibrator	Working reagents, in-house calibrators, in-house controls, manufacturer's product calibrator
Calibration	Established by WHO international collaborative study	Calibrated against the WHO International Standard	Calibrated against the secondary standard
Unitage	IU/mL	IU/mL	IU/mL
Traceability	N/A	Yes	Yes
Uncertainty of measurement	No	Yes (assay specific)	Yes (assay specific)
Final format	Lyophilised (generally)	Lyophilised or liquid	Liquid (generally)
Usage	Calibration of secondary standards, initial validation of new assay/platform	Calibration of tertiary standards, working reagent, limited use as run control or calibrator	Working reagent, run control, calibrator
Establishment of standard	International agreement through WHO international collaborative study including laboratories worldwide, different assays, different types of test laboratories (approximately 15-30 participants)	May be calibrated in several ways: • In parallel with a study to establish the International Standard • Regional or national collaborative study similar to the WHO collaborative study but with fewer participants from regional laboratories • Small study by a single or limited number of laboratories with a single or limited number of different assays/platforms	Assay-specific study, normally by a single laboratory for use with a specific test/platform Small study by a single or limited number of laboratories with a single or limited number of different assays/platforms

(WHO Technical Report Series, No. 1004, Annex 6, 2017)

Calibration principles

- Test secondary standard multiple times on different occasions in parallel with the WHO IS under exact same test conditions
- Assess validity of individual assays e.g. linearity and parallelism
- Estimate potency (IU/mL) for secondary standard in all valid assays
- Combine estimates and assign combined estimate as potency

Notes on calibration

- Use optimal test system (e.g. commercial assay, validated laboratory test)
- Use only qualified operators, equipment etc.
- No general guidance regarding number of assay runs to perform
  - Decision will depend on various factors
  - E.g. sufficient testing may be performed to give Uncertainty of Measurement (UoM) that is negligible in comparison to the expected precision of the routine assay

7

Assuming appropriate assay conditions, UoM can be expressed as 95% Confidence Interval (CI) for combined estimate. In such cases, this will account for imprecision but not any inherent bias so care should be taken with assay design etc.

Calibration example

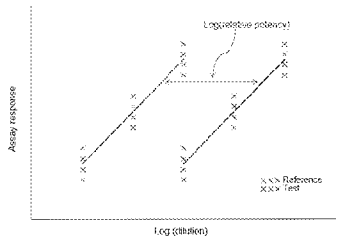
- Samples tested:
  - WHO IS for anti-SARS-CoV-2 immunoglobulin (20/136)
    Potency 250 IU/ampoule for neutralising antibody assays
    Reconstituted to concentration of 1000 IU/mL
  - In-House Standard (IHS)
- Aim: Calibrate IHS in IU/mL using IS
- Samples initially tested in 3 independent assay runs

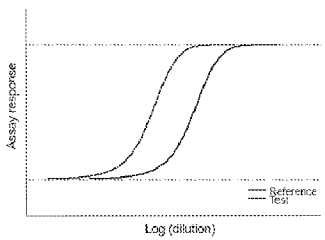
Calibration example – assay 1

IS 20/136 1000 IU/mL				IHS 20 IU/mL (assumed)			
Dilution	Responses			Dilution	Responses		
1/60	30	80	360	1/1	40	30	30
1/180	70800	92400	2510	1/3	580	2730	71600
1/540	142000	280000	64700	1/9	280000	200000	524000
1/1620	465000	844000	581000	1/27	863000	701000	924000
1/4860	953000	941000	843000	1/81	1170000	1490000	971000
1/14580	1060000	1680000	1340000	1/243	1560000	1920000	1600000
1/43740	870000	1480000	1290000	1/729	1210000	1410000	1310000

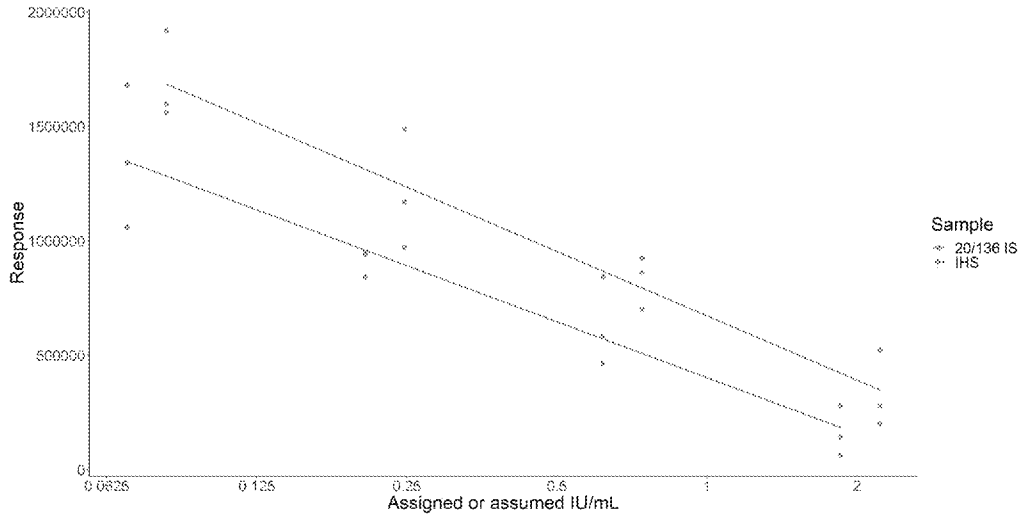
Data analysis

- Objectives of dose-response data analysis:
  - Assess assay validity e.g. linearity/parallelism for linear model
  - Estimate potency of IHS relative to WHO IS
- Various possible analysis methods, including:
  - Parallel line (parallel curve) analysis [recommended]
  - Interpolation from fitted dose-response curve for WHO IS
- Software options will depend on analysis method:
  - Specialised software for bioassay analysis
  - General statistical software packages, Excel





Calibration example – assay 1



Calibration example – assay 1 analysis

- Analysis output for assay 1:

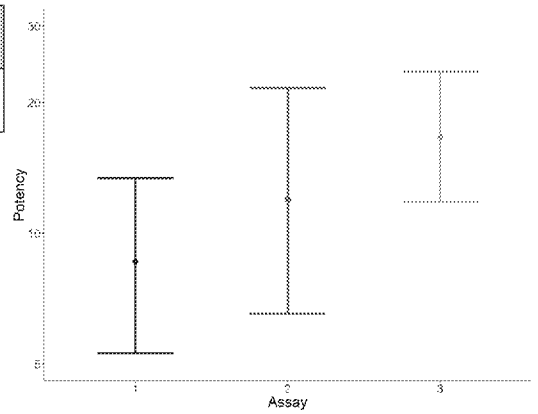
Source	Df	Sum of Sq	Mean Sq	F-ratio	P-Value
Treatments	7	5.63597E+12	8.05139E+11	21.549	<0.001 ***
Preparations	1	3.77329E+11	3.77329E+11	10.099	0.006 **
Regression	1	5.20746E+12	5.20746E+12	139.372	<0.001 ***
Non-parallelism	1	2.53490E+10	2.53490E+10	0.678	0.422
Non-linearity	4	2.58375E+10	6.45937E+09	0.173	0.949
Residual error	16	5.97818E+11	3.73637E+10		
Total	23	6.23379E+12	2.71034E+11		

IHS Potency (IU/mL)		
Estimate	95% LCL	95% UCL
8.60	5.29	13.40

Calibration example – combined estimate

- Combined estimate (IU/mL) from assays 1-3:

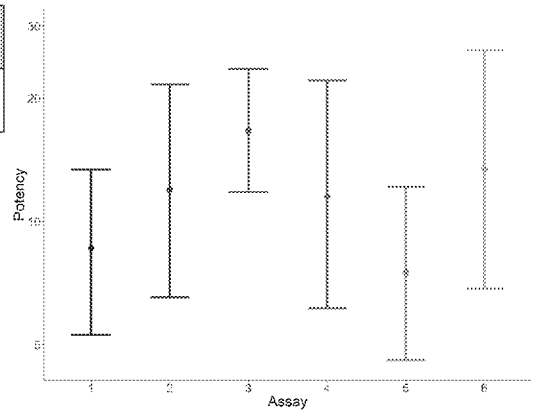
Estimate	95% LCL	95% UCL	LCL as %	UCL as %
12.3	8.5	17.9	68.9%	145.2%



Calibration example – after additional assays

- Combined estimate (IU/mL) from assays 1-6:

Estimate	95% LCL	95% UCL	LCL as %	UCL as %
11.5	9.2	14.4	79.9%	125.1%

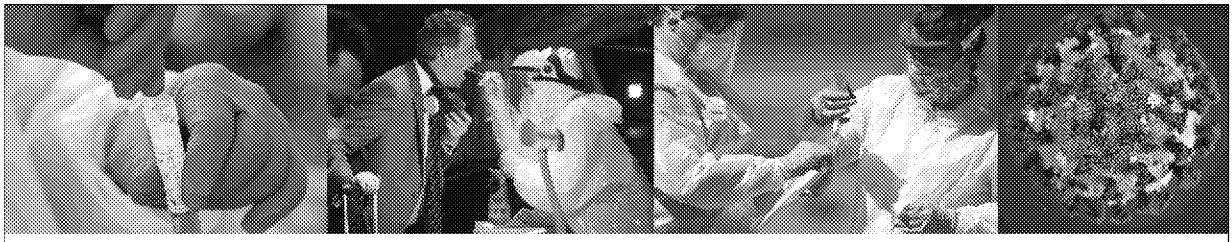


Calibration example – conclusions

- Assigned value to internal standard = 11.5 IU/mL
- Assay currently states µg/mL unitage for internal standard
  - Neat concentration used is 5 µg/mL
  - Calibration exercise estimated neat concentration as 11.5 IU/mL
  - Any existing results reported in µg/mL (from this assay platform, using this internal standard) can now be converted to IU/mL

Summary

- Expression of assay results in International Units (IU) requires use of the WHO International Standard (IS) directly, or the use of a secondary standard calibrated using the IS
- A calibration exercise can be performed to assign an IU value to the secondary standard
- Existing assay results already reported relative to a secondary standard (in µg, EU, relative titre etc.), can then be reported as IU
  - In most cases, existing assay analysis methods are unaffected



WHO standards for COVID-19: update from WHO ECBS

Dr Ivana Knezevic, Norms and Standards for Biologicals (WHO/MHP/HPS)

20 Jan 2021, WG on COVID-19 assays

WHO norms and standards for biologicals

https://www.who.int/groups/expert-committee-on-biological-standardization

Global written standards

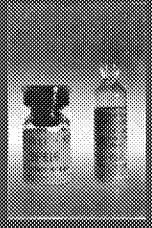
Total 103 docs (Recommendations/ Guidelines)
General docs that apply to vaccines & biologicals: 10
General documents that apply to all vaccines: 12
Vaccine specific: 71
BTP specific: 9

Scientific evidence

1) Standardization of assays
2) Further development and refinement of QC tests
3) Scientific basis for setting specifications

WHO Expert Committee on Biological Standardization

Global measurement standards



Measurement standards: essential elements for development, licensing and lot release

Main outcomes of 73rd ECBS meeting in 2020

World Health Organization

1. ECBS meeting on 9-10 Dec 2020 (focused on COVID-19): published on WHO web site: https://www.who.int/groups/expert-committee-on-biological-standardization

- Executive Summary posted on WHO web site on 16 Dec 2020:

https://www.who.int/groups/expert-committee-on-biological-standardization

3 new WHO International reference preparations established

Standards for use in public health emergencies		
SARS-CoV-2 RNA for NAT-based assays	7.40 $\log_{10}$ IU/ampoule	First WHO International Standard
Anti-SARS-CoV-2 immunoglobulin	250 IU/ampoule (neutralizing antibody activity)	First WHO International Standard
Anti-SARS-CoV-2 immunoglobulin panel	[no assigned units]	First WHO International Reference Panel

- Proposal to develop a standard for SARS-CoV-2 antigens to support the development, assessment and comparability of antigen-based rapid diagnostic tests.

- Update on written standards provided

Measurement standards for COVID-19

World Health Organization

Aim: to facilitate the development, validation and assessment of molecular and antibody assays. This will facilitate the comparability of results from different assays/labs and help harmonize the evaluation of diagnostics, vaccines and other products. Expression of the results of neutralization assays in the International Units would also contribute to the establishment of the correlates of protection.

Timeline: Feb to Dec 2020 is the absolute record for developing and establishing WHO International Standards in 9 months instead of 2-3 years.

Antibody standards during the COVID-19 pandemic: research reagents and WHO International Standards: joint effort by CEPI, NIBSC and WHO

WHO International Antibody Standards:

- **help interpreting results from vaccine CTs by providing the basis for the expression of the antibody titers in the International Units, particularly results from efficacy trials for various vaccine candidates. For instance, correlate of protection can be defined as IU/mL.**
- **IS permits datasets across a range of assays to be compared by reference to the IU. This is especially important with the large number of vaccine candidates**

Uptake of WHO Ab standards – way forward

World Health Organization

1. Why WHO Ab standards have not been used as expected?

- Lack of information on the existence of these standards
- Misunderstandings regarding the intended use
- Labour intense calibration of secondary standards
- Lack of expertise for the use of standards and for the assays in CTs
- Other reasons?

2. Need for secondary standards calibrated against WHO IS

- Several initiatives ongoing
- How many vaccine developers plan to express results of neutralization assays in IU?

How can we help users of standards to express CT results in the International Units?

World Health Organization

1. ECBS – Executive Summary and report in WHO TRS
2. Collaborative study report provides lots of information about the standards but also about the assays
3. Instruction for use
4. WHO EUL: "Considerations for the Assessment of COVID-19 Vaccines for Listing by WHO" (https://extranet.who.int/pqweb/sites/default/files/documents/Considerations_COVID-19_vaccines_for_listing_by_WHO_v1.0.pdf)
   - 4.1. The assays used for immunogenicity evaluation should be validated for their intended purpose and calibrated against WHO international standards, where available (section 3.2)
   - 4.2. Assay results should be reported in international units wherever possible (section 3.3.8)
5. Webinars
6. Case studies with the examples
7. Manual for secondary standards for vaccines – Update and/or specific advice for COVID-19 standards
8. Other opportunities?

Medicines & Healthcare products Regulatory Agency

NIBSC

Roles and Importance of Standards in Assays

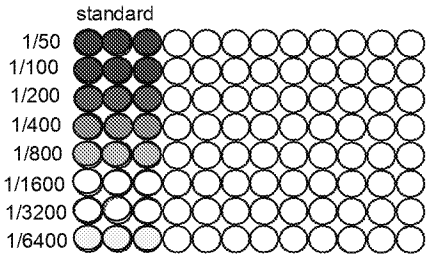
Giada Mattiuzzo

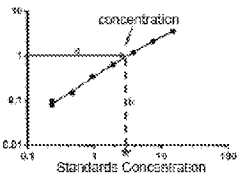
20th January 2021

Standards in assays

- 44 laboratories participated to the CS establishment of WHO IS for anti-SARS-CoV-2 immunoglobulin;
- 8 laboratories did not use an assay internal standard – results reported based on dilution factor
- Difficult to compare with other assays

- Internal calibrator/standard;
- run control;
- working reagent
- Secondary or tertiary reagent





2

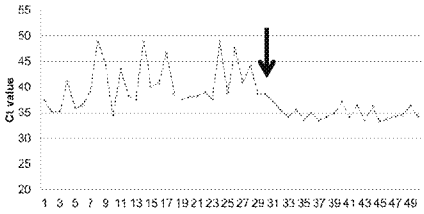
Most commercial assays have a calibrant

External controls

Allow to check for performance drifting of the assay over time/between operators

Monitoring data from diagnostic lab starting using NIBSC Working Reagent for Norovirus GII (↓)

Kindly provided by NIBSC Diagnostics Group, IDD

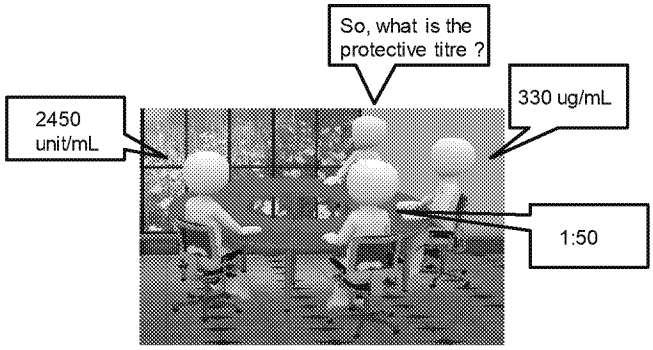


Examples are: national standards, commercially available secondary reagents

Can be used to compare assay between laboratory

Primary calibrant

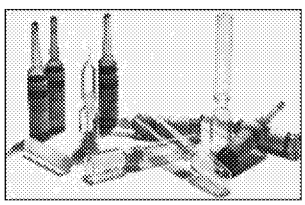
- WHO International Standard – established by the WHO ECBS
- Define the common language to expressed potency of the samples



Common language already reduces the difference between labs

Why International units? A bit of history

- 1890's First Biological: Diphtheria antitoxin
  No reliably produced. Lot to lot variation as biological activity differed from physical property
- Paul Ehrlich: STANDARD ANTITOXIN PREPARATION – calibrated in Units and used to calibrate future batches
- Henry Dale applied concept to insulin and other biologics (1920s) and on International level – appearance of International Units (IUs) as measure of strength or activity of a product

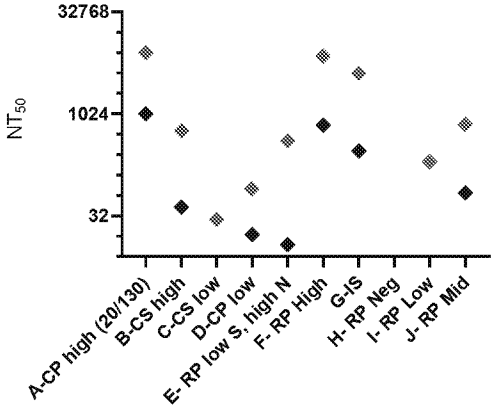


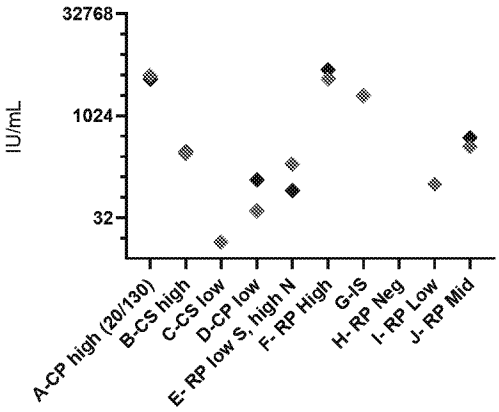
https://www.who.int/bloodproducts/ref_materials/en/

This is to answer the popular question on what's the conversion factor to ng/mL

A recent example: SARS-CoV-2 antibody

Foci reduction neutralisation assay





Binding antibody assay- Spike ELISA

output	lab	A-20/130	B-CS High	C- CS Low	D- CP low	E-low S,high N	F-High	G-IS	H- neg	I - low	J- mid
Dil fact	22b	10159	5081	-	100	1270	12800.0	18102.0	-	635	2851
AU/mL	37a	3464	1764	-	42	510	5284	7215	-	340	1812
ug/mL	9a	25.2	13.3	0.4	0.8	4.5	47.4	55.4	-	2.6	13.3
ratio S/CO	38	18.7	13.9	-	-	4.1	21.4	23.7	-	3.1	11.9

output	lab	A-20/130	B-CS High	C- CS Low	D- CP low	E-low S,high N	F-High	G-IS	H- neg	I - low	J- mid
IU/mL	22b	457	284	-	8	114	949	1000	-	47	154
	37a	480	244	-	6	71	732	1000	-	47	251
	9a	463	246	8	13	85	836	1000	-	47	230
	38	787	585	-	-	175	900	1000	-	131	503

7

2000 fold difference when expressed with different unitage vs less than 5 fold when expressed relative to IU

Unitage assign to the International Standard

- WHO IS established by WHO ECBS on 10th December 2020;
- Available in NIBSC catalogue on 18th December 2020;
- On 18th January 2021, approximately 50 end users have acquired the IS (tot shipped ampoules 162)

Medicines & Healthcare products Regulatory Agency

WHO International Standard
First WHO International Standard for anti-SARS-CoV-2 immunoglobulin (human)
NIBSC code: 20/136
Instructions for use
(Version 2.0, Dated 17/12/2020)

1. INTENDED USE

The First WHO International Standard for anti-SARS-CoV-2 immunoglobulin is the freeze-dried equivalent of 0.25 mL of pooled plasma obtained from eleven individuals recovered from SARS-CoV-2 infection. The preparation has been evaluated in a WHO International Collaborative study (1). The intended use of the International Standard is for the calibration and harmonisation of serological assays detecting anti-SARS-CoV-2 neutralising antibodies. The preparation can also be used as an internal reference reagent for the harmonisation of binding antibody assays. The preparation has been solvent-detergent treated to minimise the risk of the presence of enveloped viruses (2).

2. CAUTION

This preparation is not for administration to humans or animals in the human food chain

The preparation contains material of human origin, and either the final product or the source materials, from which it is derived, have been tested and found negative for HBsAg, anti-HIV and HCV RNA. As with all materials of biological origin, this preparation should be regarded as potentially hazardous to health. It should be used and discarded according to your own laboratory's safety procedures. Such safety procedures should include the wearing of protective gloves and avoiding the generation of aerosols. Care should be exercised in opening ampoules or vials, to avoid cuts.

3. UNITAGE

The assigned potency of the WHO International Standard for SARS-CoV-2 is 250 IU/ampoule for neutralising antibody activity. After reconstitution in 0.25 mL of distilled water, the final concentration of the preparation is 1000 IU/mL.

For binding antibody assays, an arbitrary unitage of 1000 binding antibody units (BAU)/mL can be used to assist the comparison of assays detecting the same class of immunoglobulins with the same specificity (e.g. anti-RBD IgG, anti-N IgM, etc.)

CEPI

First WHO International Reference Panel for anti-SARS-CoV-2 immunoglobulin (20/268)

Reference Panel will comprise 4 pools of COVID-19 convalescent plasma and a negative; freeze-dried equivalent of 0.25 mL

High (NIBSC code 20/150)

Mid (NIBSC code 20/148)

Low S, high N (NIBSC code 20/144)

Low (NIBSC code 20/140)

Negative (NIBSC code 20/142)

Representative data

	High 20/150	Mid 20/148	low S, high N 20/144	low 20/140	
Neut Ab	1473	210	95	44	IU/mL
anti-RBD IgG	817	205	66	45	BAU/mL
anti-S1 IgG	766	246	50	46	BAU/mL
anti-Spike IgG	832	241	86	53	BAU/mL
anti-N IgG	713	295	146	12	BAU/mL

The candidate Reference Panel samples were ranked similarly in almost all the assays used with very few exceptions

No unitage will be assigned for the Reference Panel, but representative data from CS include in IFU

CEPI

Reseach Reagent 20/130

- Made available end April 2020 for the development of assay for the detection of SARS-CoV-2 antibody
- Secondary standard which allows assay to report data in IU/mL, retrospectively
- Calibrated to the WHO IS as part of the CS

	GM	95% CI	
Neut Ab	1300	981-1719	**IU/mL**
anti-RBD IgG	502	382-660	**BAU/mL**
anti-S1 IgG	588	398-870	**BAU/mL**
anti-Spike IgG	476	418-542	**BAU/mL**
anti-N IgG	747	214-2606	**BAU/mL**

Slides available, however this data are also included in the revised Datasheet available in our website; less than 130 vials left- cannot be used as run control

Intended use the standards

- WHO International Standard 20/136 is primary calibrant; distribution restricted to 5 ampoules per end user per year
- Availability of secondary reagents- 20/130 is almost depleted; few example of national standards;
- other secondary standard (?)
- Internal Standard/run control can be calibrated to the IS or to secondary reagents- no need for a CS
- How?

May Chu: We have been promoting the NIBSC Ab reference panel and would be happy to list this through our hub to the users in the network have using the COVID-19 Serology Control Panel (these are dried tube specimens) but sure that some of our users would be keen to have this for their testing regime.

When the standards will be available?

Our CSCP experience from the chat note above is that there are different neutralization assays developed for detecting SARS-CoV2 antibodies, especially the pseudoviral assays that are hard to compare, one test platform to another. What has been WHO/NIBSC solution or guidance?

Mark Page - NIBSC: The materials are available here https://www.nibsc.org/products/brm_product_catalogue/detail_page.aspx?catid=20/136 [HYPERLINK "https://www.nibsc.org/products/brm_product_catalogue/detail_page.aspx?catid=20/268"]
Related materials are listed here too https://www.nibsc.org/science_and_research/idd/cfar/covid-19_reagents.aspx

ZHOU, Tiequn: SARS-CoV-2 standards- related information are also available on WHO website: [HYPERLINK "https://www.who.int/news-room/feature-stories/detail/standardization-of-vaccines-for-coronavirus-disease-covid-19"].

Marc Salit: The Coronavirus Standards Working Group is conducting a study intended to make the International Unit widely and easily available by doing a secondary collaborative study that calibrates a panel of commercially available reference samples against the WHO IS. Our "Harmonization Study" is underway with 14 labs comparing a panel of 8 materials against the WHO IS. This puts all the materials on the same "ruler" — the IU — and will make propagation of the IU easy. Each commercial material will then come with a Certificate of Analysis that includes the value of that material in IU. This can be "leapfrogged" with metrological traceability. Think of it as the *kilogram* of SARS-CoV-2 virus content. Much much more on this work is here: [Coronavirus Standards Working Group — The Joint Initiative for Metrology in Biology](https://jimb.stanford.edu/covid-19-standards) All are welcome to join our open working group. Our results will be published in the open literature, and the manufacturers and distributors of the materials will be promoting the IU as features of their products. Here is a link to the précis for the Coronavirus Standards Working Group 'Harmonization Study': [20201111 CSWG Harmonization Study Description.pdf - Google Drive](https://drive.google.com/file/d/1XrjXsGqt81rilmyRuvMK-qeyn6kK08Re/view?usp=sharing)

How much can developers get IS at once? Is the quantity of IS limited?

Marc Salit: Our study is intended to make the supply of the IU inexhaustible by making it so you don't need the IU, but can buy a commercial material from your preferred vendor. There is a limited supply of the IS, so having commercial materials makes them available to everyone.

Mark Page - NIBSC: We have to limit each requestor to 5 ampoules per lab per year to preserve the standard for many years.

Are the neutralising antibody standards 250IU/ampoule polyclonal? (I see the panel is from pooled so will be polyclonal)

Ligia Pinto: We have a US serology standard available ([HYPERLINK "https://frederick.cancer.gov/seronet/serology-standard"])

Is the international standard tested in assays the include "all isotopes IgG, IgM, IgA" ?

Mark Page - NIBSC: The IS is a pool of convalescent plasma from 11 donors. The IS contains IgG, IgA and IgM

How was the neuralizing activity of the IS assessed?

Any SAF/BRA virus strain available?

We have used anti-SARS-CoV-2 Ab NIBSC code 20/130 standard during the clinical trail and calibrated an In-house standard. How different is the new standard from the already provied NIBSC standard i.e., 20/130?

If there is no regional or national standard, should the secondary standard use NIBSC's reference material(20/130)? Can I use the in-house standard instead of the sencondary standard?

Is the international standard tested with a real SARS-CoV-2 virus?

Giada Mattiuzzo-NIBSC: [HYPERLINK "https://www.who.int/publications/m/item/WHO-BS-2020.2403"] (report of collaborative study). The IS has been characterised in 23 neutralisation assay, 15 of those used live virus covering 9 isolates

Is it possible to use serum from horses immunized with RBD as secondary standards?

How much of a reduction in neutralisation would justify a new standard should a new variant arise with limited cross-neutralisation?

What would be acceptable uncertainty in calibration of secondary standard - if secondary standard was non-parallel uncertainty may be higher and dilution bias could result.

How can this IS approach be applied to "titer-based" neutralizing Ab assays? As in such assay, Ab levels are determined against a "cut-point" instead of a reference standard.

Do you think that the vaccine developers will be willing to make available the vaccine responses from clinical trials converted in IU?

Can we use the standard to standardise sera from experimental animals where we are looking at correlates of protection in animal models?

Is it possible to calibrate in-house pooled covalescent serum material against NIBSC's research reagent (20/130)?

Giada Mattiuzzo-NIBSC: Yes, 20/130 now is considered as a secondary standard and can be used to calibrated your in house pool of convalescent serum

Richard r.tedder@imperial.ac.uk: the use of human plasma/serum does have the confounding effect of IgM which may behave differently and non parallel

Our laboratory is developing a chemiluminescence immunoassay (qualitative). Could we use the IS to standardize the test?

Giada Mattiuzzo-NIBSC: The IS in qualitative assay can be used to express the limit of detection of the assay by serially dilution below endpoint. LOD for qualitative assays.

We also need to validate the test, to PCR (gold standard), Do you have a protocol that we can use?

Can you say more on your interpretation of the very different results seen in FFA with 501.v2 (L18F) ?

Do you have convalescent plasma from the latest wave and have you tested on the 501Y V2 variant?

The large plaque phenotype virus does not have any mutation in the multibasic cleavage site?

How are you evaluating reinfections with the new strain?

Have you tested sera from vaccinees against this variant?

Pfizer published a note claimed that their vaccine sera can neutralize the N501Y isogenic strain, do you think other mutations are important in this reduction in neutralizing the field isolates?

Do you have a comparison of all published IgG and NAb levels from several vaccines finished phase 3 trials?

To: 'Ralph Baric'[rbaric@email.unc.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Mark Suto'[suto@southernresearch.org]; 'Mark Denison'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'George Painter'[george.r.painter@emory.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]
Cc: 'Chandra Caldwell'[ccaldwel@email.unc.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Victoria Moore'[victoria_moore@unc.edu]; 'Hope Angel (angelh@ohsu.edu)'[angelh@ohsu.edu]; 'Evans, Carrie W.'[cevans@southernresearch.org]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Erica Bitten'[erica.bitten@emory.edu]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Stephanie Moore[smoore@peds.uab.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Thur 12/5/2019 10:55:01 AM (UTC-06:00)
Subject: Final Amendment 1 to AD3C Research Consortium Agreement
AD3C Agreement Fully Executed.pdf

Greetings:

On behalf of Mary Wyatt Bowers, please find attached a fully executed copy of Amendment Number 1 to the AD3C Research Consortium Agreement for your use.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

AMENDMENT NO. 1
TO
ANTIVIRAL DRUG DISCOVERY AND DEVELOPMENT CENTER (AD3C) RESEARCH CONSORTIUM AGREEMENT

This Amendment No. 1 to the Antiviral Drug Discovery and Development Center (AD3C) Research Consortium Agreement (the "First Amendment") is entered into as of this March 1, 2019 (the "First Amendment Effective Date") by and between the following institutions:

The Board of Trustees of the University of Alabama for the University of Alabama at Birmingham, a constitutionally created corporation of the State of Alabama and having its principal office at Birmingham, Alabama ("UAB");

The University of North Carolina at Chapel Hill, a nonprofit educational and research institution organized under the laws of North Carolina and having its principal office at Chapel Hill, North Carolina by and through the University of North Carolina School of Medicine ("UNC-CH"); and

The Washington University, a nonprofit educational and research institution, organized under the laws of Missouri and having its principal office at St. Louis, Missouri ("WU-STL");

Oregon Health and Science University, a nonprofit educational and research institution, organized under the laws of Oregon and having its principal office at Portland, Oregon ("OHSU");

Southern Research, a nonprofit research institution, organized under the laws of Alabama and having its principal office at Birmingham, Alabama ("SR");

Vanderbilt University Medical Center, a nonprofit educational and research institution organized under the laws of Tennessee and having its principal office at Nashville, Tennessee by and through the Vanderbilt University School of Medicine ("VANDERBILT");

The University of Texas Medical Branch at Galveston, a state institution of higher education organized under the laws of Texas and having its principal office at Galveston, Texas ("UTMB"); ("UTMB"); and

Emory University, with offices located at 1599 Clifton Road NE, 4th Floor, Mailstop 1599-001-1BA, Atlanta, GA 30322 ("EMORY").

The parties to this First Amendment listed above are singularly and collectively referred to herein as the "First Amendment Parties."

RECITALS

WHEREAS, UAB, UNC-CH, WU-STL, OHSU, SR, and VANDERBILT are parties to that certain Antiviral Drug Discovery and Development Center (AD3C) Research Consortium Agreement dated December 1, 2014, that may be amended from time to time (the "Agreement");

WHEREAS, UAB, UNC-CH, WU-STL, OHSU, SR, and VANDERBILT desire to amend

the Agreement in order to add UTMB and EMORY as parties thereto, and UTMB and EMORY desire to become parties to the Agreement; and

WHEREAS, the First Amendment Parties additionally desire to amend the Agreement to include additional grant funding obtained after the initial effective date of the Agreement, as well as to appropriately allocate the rights of the First Amendment Parties with respect to intellectual property developed prior to the First Amendment Effective Date.

NOW, THEREFORE, THE PARTIES AGREE AS FOLLOWS:

1. As of the First Amendment Effective Date, UTMB and EMORY shall join in the Agreement as parties thereto, and each reference to the "Original Parties," "Members of the Research Group," or "Members" in the Agreement shall refer to all First Amendment Parties, as defined above.

2. As of the First Amendment Effective Date, each reference to the "Prime NIAID Award" shall include both (i) Grant Number U19AI109680-01, awarded by the National Institute of Allergy and Infectious Diseases, National Institutes of Health, and (ii) Grant Number U19AI142759-01, awarded by the National Institute of Allergy and Infectious Diseases, National Institutes of Health.

3. Section 2.2. Compliance with the RFA. Section 2.2 shall be deleted in its entirety and replaced with the following language (revised language is italicized and underlined):

   "The Members of the Research Group each agree that the research program of the AD3C shall in all events be carried out in accordance with the requirements of the terms and conditions for the *Prime NIAID Award* set forth in the NIAID Request for Applications having a release date of November 23, 2012 *(as applicable to Grant Number U19AI109680-01) and the NIAID Request for Applications having a release date of November 30, 2017 (as applicable to Grant Number U19AI142759-01)* (collectively, the "RFA"), a copy of which is attached to this Agreement as **Schedule B** and incorporated herein by reference."

4. Section 4.1. The Principal Investigator. Section 4.1 shall be amended by deleting the phrase "(iv) together with appropriate other investigators of the CETR, attend a CETR Program Annual Meeting to be organized by NIAID staff at or near Bethesda, Maryland or at another NIAID-approved site;" and renumbering item (v) as item (iv).

5. Section 11.4. Acknowledgement of NIH and Collaborator Support. Section 11.4 shall be amended by deleting the first sentence in its entirety and replacing it with the following language:

   "The support of the NIH shall be acknowledged whenever publicizing the work under this Agreement in any media (including, but not limited to, publication of research results of AD3C Research Projects and/or Collaborative AD3C Research Projects in scientific journals) by including an acknowledgment substantially as follows: "This Project has been funded in whole or part with Federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, under Grant Number [U19AI109680-01

and/or U19AI142759-01, as applicable].""

6. Section 12.10. Licenses to Members and Affiliate Members. Section 12.10 shall be amended by deleting paragraph (b) in its entirety and replacing it with the following language (revised language is italicized and underlined):

   "(b) a non-exclusive, limited, non-sublicensable, royalty-free license of each Invention and Other Invention *that is made during the term of* ***such Member's or Affiliate Member's tenure as a*** *Member or Affiliate Member, as applicable,* and the associated patent rights arising therefrom, for its own non-commercial research, educational, *and* teaching purposes."

   For clarity, certain inventions and associated patent rights developed in connection with the performance of AD3C research under the Agreement prior to the First Amendment Effective Date are listed in attached Exhibit C, which is incorporated herein by reference, and UTMB and EMORY shall not be entitled to any license rights under Section 12.10(b) of the Agreement with respect to such inventions or patent rights.

7. Schedule A. Schedule A shall be amended by appending the document attached to this First Amendment as Exhibit A, the proposal submitted in connection with NIAID Grant Number U19AI142759-01.

8. Schedule B. Schedule B shall be amended by appending the document attached to this First Amendment as Exhibit B, the NIAID Request for Applications having a release date of November 30, 2017

9. Except as provided herein, the Agreement shall remain in full force and effect. If one or more provisions of this First Amendment are held to be unenforceable under applicable law, such provisions shall be excluded from this First Amendment and the balance of this First Amendment shall be interpreted as if such provisions were so excluded and shall be enforceable in accordance with its terms.

10. Capitalized terms used but not defined in this First Amendment have the meanings ascribed to them in the Agreement.

11. This First Amendment may be executed in separate counterparts, each of which shall be deemed an original and all of which together shall constitute one and the same instrument.

[Signature page follows]

IN WITNESS WHEREOF, the parties hereto have executed this First Amendment as of the date first above written.

SIGNATURE PAGES AND SCHEDULES FOLLOW

UAB

By: DocuSigned by: Melinda T. Cotten
A5F3F451BABE4A9...

Name: Melinda T. Cotten

Title: Associate Vice President, Research Business Operations

Date: 9/19/2019

Read and Acknowledged:

Principal Investigator: DocuSigned by: Dr. Richard Whitley
076042DF4BE4403...

Date: 9/19/2019

Institution

The University of North Carolina at Chapel Hill

By: _____

Name: Terry Magnuson

Title: Vice Chancellor for Research

Date: 7/9/19

Read and Acknowledged:

Principal Investigator: _____

Date: 06/28/19

WU STL

By: _____

Name: Megan M. White, JD
Director, Research Contracts

Title: _____

Date: 6/19/19

Read and Acknowledged:

Principal Investigator: _____

Date: 6/20/19

Institution Oregon Health & Science University

By: Lisa Fitzpatrick Digitally signed by Lisa Fitzpatrick DN: cn=Lisa Fitzpatrick, o=Oregon Health & Science University, ou=OPAM, email=fitzpat@ohsu.edu, c=US Date: 2019.07.24 11:01:43 -07'00'

Name: Lisa Fitzpatrick

Title: Manager Grants & Contracts, Office of Proposal & Award Management

Date: 7/24/19

Read and Acknowledged:

Principal Investigator: Daniel Streblow, PhD

Date: 15 Aug 2019

Southern Research

By: Tammy Whetter Digitally signed by Tammy Whetter Date: 2019.10.15 08:41:50 05'00'

Name: Tammy Whetter

Title: Manager, Contracts

Date: 10/15/2019

Read and Acknowledged:

Principal Investigator:

Date: 10/15/19

Vanderbilt University Medical Center

VB

By: _____

Name: Libby D. Salber

Director

Title: Office of Contracts

Date: 11/21/2019

Read and Acknowledged:

Principal Investigator: Mark R Denison

Date: Nov 21, 2019

UTMB

By: Ericia Huff

Name: Ericia J. Huff, CRA

Title: Director, Sponsored Programs

Date: 06/07/2019

Read and Acknowledged:

Principal Investigator: Pei-Yong Shi
Dr. Pei-Yong Shi

Date: June 6, 2019

Emory

By: _____

Name: Janette Hannam Hayes

Title: Associate Director

Date: 6/10/19

Read and Acknowledged:

By: _____

Principal Investigator: George Painter

Date: 6/10/2019

University of Colorado at Denver

By: _____

Name: Denise Queen
~~Contracts Manager~~
Office of Grants and Contracts

Title: _____

Date: 6/25/19

To: Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; jma[jma@sgul.ac.uk]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov];

Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; tcs38@psu.edu[tcs38@psu.edu]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; BUDA Mihaela[Mihaela.BUDA@edqm.eu]
Cc: Meera Chand[Meera.Chand@phe.gov.uk]; shane@lji.org[shane@lji.org]; thatziio@rockefeller.edu[thatziio@mail.rockefeller.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 1/26/2021 11:13:32 AM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday January 27 2:30PM CET (Geneva Time)

1. Meera Chand & Victoria Hall (PHE) – *The UK SIREN study first interim analysis: Do antibody positive healthcare workers have lower SARS-CoV-2 2 infection rates than antibody negative healthcare workers?*
2. Shane Crotty (LJI) - *Immunological memory to SARS-CoV-2 and COVID-19*
3. Theodora Hatziioannou (Rockefeller) - *Neutralizing antibody responses to SARS-CoV-2 following vaccination*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, January 24, 2021 2:01 PM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; ASiyer@mgh.harvard.edu; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Jilian.Sacks@finddx.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg; SALAMI, Kolawole; tcs38@psu.edu; angeliki.melidou@ecdc.europa.eu; BUDA Mihaela
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, January 27, 2021 5:30 AM-7:00 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Please note this meeting will be 1.5hrs instead of the usual one hour to allow for an additional presentation and discussion on the new variant.

Agenda to follow.

Join Zoom Meeting
https://who.zoom.us/j/3612568290

Meeting ID: 361 256 8290
One tap mobile
+41225910005,,3612568290# Switzerland
+41225910156,,3612568290# Switzerland

Dial by your location
- +41 22 591 00 05 Switzerland
- +41 22 591 01 56 Switzerland
- +41 31 528 09 88 Switzerland
- +41 43 210 70 42 Switzerland
- +41 43 210 71 08 Switzerland
- +1 253 215 8782 US (Tacoma)
- +1 720 928 9299 US (Denver)
- +1 971 247 1195 US (Portland)
- +1 213 338 8477 US (Los Angeles)
- +1 346 248 7799 US (Houston)
- +1 602 753 0140 US (Phoenix)
- +1 669 219 2599 US (San Jose)
- +1 669 900 9128 US (San Jose)
- +1 470 250 9358 US (Atlanta)
- +1 470 381 2552 US (Atlanta)
- +1 646 518 9805 US (New York)
- +1 646 558 8656 US (New York)
- +1 651 372 8299 US (Minnesota)
- +1 786 635 1003 US (Miami)
- +1 267 831 0333 US (Philadelphia)
- +1 301 715 8592 US (Washington D.C)
- +1 312 626 6799 US (Chicago)

Meeting ID: 361 256 8290
Find your local number: https://who.zoom.us/u/acLh9DwRd3

Join by SIP
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Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; adam.godzik@ucr.edu[adam.godzik@ucr.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; btk@lanl.gov[btk@lanl.gov]; lmwoga@fredhutch.org[lmwoga@fredhutch.org]; monte@duke.edu[monte@duke.edu]; spjwhelan@wustl.edu[spjwhelan@wustl.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Shi, Pei yong[peshi@UTMB.EDU]; McDermott, Adrian (NIH/VRC) [E][adrian.mcdermott@nih.gov]; Florian Krammer[florian.krammer@mssm.edu]; jbloom@fredhutch.org[jbloom@fredhutch.org]; Julie McElrath[jmcelrat@fredhutch.org]; kawaokay@svm.vetmed.wisc.edu[kawaokay@svm.vetmed.wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; noah.sather@seattlechildrens.org[noah.sather@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; mrolland@hivresearch.org[mrolland@hivresearch.org]; Baric, Ralph[rbaric@email.unc.edu]; Richard Webby[richard.webby@stjude.org]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; malik@hku.hk[malik@hku.hk]; Andrew B. Ward[andrew@scripps.edu]; Ali Ellebedy[ellebedy@wustl.edu]; mdiamond@wustl.edu[mdiamond@wustl.edu]; djs200@cam.ac.uk[djs200@cam.ac.uk]; jboon@wustl.edu[jboon@wustl.edu]; Aubree Gordon[gordonal@umich.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; harm.vanbakel@mssm.edu[harm.vanbakel@mssm.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Koup, Richard (NIH/VRC) [E][rkoup@mail.nih.gov]; Seder, Robert (NIH/VRC) [E][rseder@mail.nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Alessandro Sette[alex@lji.org]; Adam Godzik[Adam.Godzik@medsch.ucr.edu]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Schotsaert, Michael[michael.schotsaert@mssm.edu]
Cc: Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Fri 1/29/2021 1:33:15 PM (UTC-06:00)
Subject: SARS-CoV2 variant testing - next steps
Research Update Template.xlsx

Hi everyone,

Thanks for your participation in yesterday's initial meeting. We're looking forward to working with you all to characterize SARS-CoV2 variants and help inform decision making.

Scheduling regular meetings: Please go to the doodle poll here to select times that work for you by **COB Sunday January 31st.** We have people in multiple time zones so be as flexible as you can, and we will choose the best time for most.

Capabilities Template: Attached is a template for general updates on resources you may have. Please fill it out so that we can be aware of what your current capabilities are and send back to me and Leah Vincent (cc'd) by **COB Tuesday February 2nd.** We will use this when deciding who can do different experiments and assays as we move forward.

Group Structure: To maximize productivity, we're going to try a structure of breakout groups by topic so we can dive deeply into data by topic, address critical gaps, and decide next steps. Please look at the 3 breakout groups listed below and decide in advance of our next meeting which one you would like to be involved in.

Agenda:

- Epidemiology, Data and Resource Update (all)
- SARS-CoV2 Interagency Group Update (all)
- **Breakout groups: Early Detection and Analysis (genomics/structure), Assays and *In Vitro* analysis, and *In Vivo* analysis**
- Discuss current data, critical research gaps, priority experiments, and resources needed
- Group discussion of breakout progress
- Next steps – establish timeline for priority experiments, resource acquisition

Data Sharing: We will need to share data in near real-time as we get started. We are looking at options for sharing data directly with us at NIAID or with the larger group. If you have preferred ways to do this, please let me know.

Thank you, and we will speak next week!

Marciela DeGrace Ph.D.
Program Officer, Centers of Excellence for Influenza Research and Surveillance (CEIRS)

NIH/NIAID/DMID/RDB
Phone: 240-627-3460

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

To: Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; jma[jma@sgul.ac.uk]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov];

Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; tcs38@psu.edu[tcs38@psu.edu]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; BUDA Mihaela[Mihaela.BUDA@edqm.eu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 2/1/2021 2:27:16 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday February 3 2:30PM CET (Geneva Time)

1. Kurt Wibmer (NICD) - *SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma*
2. Aodhán Breathnach (St. George's NHS) - *A laboratory-based study of COVID-19 Immunity and Reinfections in South-West London*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, January 31, 2021 9:16 AM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in;

pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; ASiyer@mgh.harvard.edu; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Jilian.Sacks@finddx.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg; SALAMI, Kolawole; tcs38@psu.edu; angeliki.melidou@ecdc.europa.eu; BUDA Mihaela

Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, February 3, 2021 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

Join Zoom Meeting
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162.255.37.11 (US West)
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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; adam.godzik@ucr.edu[adam.godzik@ucr.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; btk@lanl.gov[btk@lanl.gov]; lmwoga@fredhutch.org[lmwoga@fredhutch.org]; monte@duke.edu[monte@duke.edu]; spjwhelan@wustl.edu[spjwhelan@wustl.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Shi, Pei yong[peshi@UTMB.EDU]; McDermott, Adrian (NIH/VRC) [E][adrian.mcdermott@nih.gov]; Florian Krammer[florian.krammer@mssm.edu]; jbloom@fredhutch.org[jbloom@fredhutch.org]; Julie McElrath[jmcelrat@fredhutch.org]; kawaokay@svm.vetmed.wisc.edu[kawaokay@svm.vetmed.wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; noah.sather@seattlechildrens.org[noah.sather@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; mrolland@hivresearch.org[mrolland@hivresearch.org]; Baric, Ralph[rbaric@email.unc.edu]; Richard Webby[richard.webby@stjude.org]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; malik@hku.hk[malik@hku.hk]; Andrew B. Ward[andrew@scripps.edu]; Ali Ellebedy[ellebedy@wustl.edu]; mdiamond@wustl.edu[mdiamond@wustl.edu]; djs200@cam.ac.uk[djs200@cam.ac.uk]; jboon@wustl.edu[jboon@wustl.edu]; Aubree Gordon[gordonal@umich.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; harm.vanbakel@mssm.edu[harm.vanbakel@mssm.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Koup, Richard (NIH/VRC) [E][rkoup@mail.nih.gov]; Seder, Robert (NIH/VRC) [E][rseder@mail.nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Alessandro Sette[alex@lji.org]; Adam Godzik[Adam.Godzik@medsch.ucr.edu]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; MacCannell, Duncan (CDC/DDID/NCEZID/OD)[fms2@CDC.GOV]; Weiss, Carol (FDA/CBER)[Carol.Weiss@fda.hhs.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Nelson Michael[nelson.l.michael2.civ@mail.mil]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; irina.maljkovicberry.ctr@mail.mil[irina.maljkovicberry.ctr@mail.mil]; jeffrey.r.currier.civ@mail.mil[jeffrey.r.currier.civ@mail.mil]; Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Mon 2/1/2021 1:51:28 PM (UTC-06:00)
Subject: SARS-CoV2 variant testing - next steps
Research Update Template.xlsx

Hi everyone,

I hope you all had a great weekend. A reminder to please fill out the doodle poll so we can confirm a regular time, and the capabilities template (attached), which will help with determining work in the future. We'll look to have our next meeting next week after we've been able to take into account everyone's schedules.

Thank you,

Marciela

From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 29, 2021 2:33 PM

Hi everyone,

Thanks for your participation in yesterday's initial meeting. We're looking forward to working with you all to characterize SARS-CoV2 variants and help inform decision making.

Scheduling regular meetings: Please go to the doodle poll here to select times that work for you by **COB Sunday January 31st.** We have people in multiple time zones so be as flexible as you can, and we will choose the best time for most.

Capabilities Template: Attached is a template for general updates on resources you may have. Please fill it out so that we can be aware of what your current capabilities are and send back to me and Leah Vincent (cc'd) by **COB Tuesday February 2nd.** We will use this when deciding who can do different experiments and assays as we move forward.

Group Structure: To maximize productivity, we're going to try a structure of breakout groups by topic so we can dive deeply into data by topic, address critical gaps, and decide next steps. Please look at the 3 breakout groups listed below and decide in advance of our next meeting which one you would like to be involved in.

Agenda:

- Epidemiology, Data and Resource Update (all)
- SARS-CoV2 Interagency Group Update (all)
- **Breakout groups: Early Detection and Analysis (genomics/structure), Assays and *In Vitro* analysis, and *In Vivo* analysis**

- Discuss current data, critical research gaps, priority experiments, and resources needed

- Group discussion of breakout progress
- Next steps – establish timeline for priority experiments, resource acquisition

Data Sharing: We will need to share data in near real-time as we get started. We are looking at options for sharing data directly with us at NIAID or with the larger group. If you have preferred ways to do this, please let me know.

Thank you, and we will speak next week!

Marciela DeGrace Ph.D.
Program Officer, Centers of Excellence for Influenza Research and Surveillance (CEIRS)
NIH/NIAID/DMID/RDB
Phone: 240-627-3460

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

From:	Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Location:	Call in at 1-888-806-5025 and use the passcode of 420976
Importance:	Normal
Subject:	Canceled: Monthly AD3C Teleconference for Project and Core Reporting
Start Time:	Thur 12/26/2019 3:30:00 PM (UTC-06:00)
End Time:	Thur 12/26/2019 5:00:00 PM (UTC-06:00)
Required Attendees:	'Alana Centilli'; 'Alec Hirsch'; 'Amy Sims'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Bob Bostwick'; 'Carrie Evans'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Sides, Kate'; 'Babu Tekwani'; 'fahmad@southernresearch.org'; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; Chad Petit; 'Clare O'Regan'
Optional Attendees:	'Morrison, Thomas'; 'Suto, Mark J.'; 'Evans, Carrie W.'; 'Bostwick, Bob'

Hi To Everyone:

The AD3C monthly call scheduled for Thursday, December 26 will be cancelled due to holiday schedules. I am sending a cancellation notice.

With kind regards,

Sara Davis
sadavis@peds.uab.edu

To: mark.denison@vumc.org[mark.denison@vumc.org]; rbaric@email.unc.edu[rbaric@email.unc.edu]; streblow@ohsu.edu[streblow@ohsu.edu]; mark_heisem@med.unc.edu[mark_heisem@med.unc.edu]; THOMAS.MORRISON@CUANSCHUTZ.EDU[THOMAS.MORRISON@CUANSCHUTZ.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; mdiamond@wustl.edu[mdiamond@wustl.edu]; Alec Hirsch[hirschal@ohsu.edu]; Tekwani, Babu[btekwani@southernresearch.org]; caugelli-szafran@southernresearch.org[caugelli-szafran@southernresearch.org]; suto@southernresearch.org[suto@southernresearch.org]; Bostwick, Bob[bbostwick@southernresearch.org]; Pathak, Ashish[apathak@southernresearch.org]; Painter, George R.[george.r.painter@emory.edu]; Gregory Bluemling, Gregory[gblueml@emory.edu]; Jay Nelson[nelsonj@ohsu.edu]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Fri 12/20/2019 5:07:10 PM (UTC-06:00)
Subject: AD3C Scientific Advisory Committee Report
191212_SACnotesAD3C_Final.pdf

Dear AD3C project and core site leaders,

I appreciate your assistance with the RPPR materials. I would like to share with you the scientific advisory committee's report from our annual meeting. They were quite impressed with all of the great work being done. There have been some items pointed out by the committee that will serve as a platform for our presentation at the reverse site visit February 11th, 2020. We will be in communication just after the new year to plan for that.

Additionally, please let me know who will be attending ICAR (March 30th - April 3rd Seattle, Washington) and a night during the conference that might be suitable for me to arrange an AD3C group dinner.

As always please let us know if you have any questions. Have a wonderful holiday!

Most sincerely,
Steph

Stephanie B. Moore, PhD | Instructor
Associate Director - Alabama Drug Discovery Alliance (ADDA)
Associate Administrative Director – Antiviral Drug Discovery and Development Center (AD3C)
Pediatrics, Division of Infectious Diseases
University of Alabama at Birmingham
Phone: 205-934-2973
Email: smoore@peds.uab.edu
Office address:
CHB 309D; 1600 6th Ave S.

AD3C External Scientific Advisory Committee
2019 Annual Report

The Annual AD3C investigators meeting was held on November 13-14, 2019 in Birmingham, AL. Four of the five SAC committee members participated either in person (Kara Carter) or via Turbo Meeting webinar/teleconference (Rick Keenan, Tom Shenk and Mike Bray). Following presentations by the four AD3C project investigators, a preliminary project review was completed by external SAC members. Stephanie Moore and Mary Wyatt Bowers were present to lead discussion and record notes.

Overall program review:
Strengths: As a whole, Kara Carter, who served on the external advisory board for the previous grant, noted that all projects had made good progress in this past year. Each seems to have a profile definition of the molecules which had not been achieved in past reviews. All agreed that integrating the cores' presentation into each project presentation was an effective means of highlighting the accomplishments of both. Cores are definitely highly functional and strong. The SAC was very impressed with the collaboration among all projects and cores as well as the caliber of the projects. It was noted that the academic/industry partnership that has been developed should serve as a model for other drug discovery programs.

Weaknesses: As noted in individual projects below, a standard thermal shift assay should be used in all projects to either identify or confirm the molecular target of compounds, but it doesn't appear that anyone is using it now. Also, all teams should include a structural biologist who can collaborate with a computational chemist in developing research plans.

Future Directions:

- Mike Diamond suggested the creation of a 'mega-table' with compound information (ADME) across projects regarding cross-reactivity across viruses with compounds and general screening. This idea was reiterated by the SAC.
- It was also suggested that those in academic groups might benefit from a tutorial on data analysis for assays related to drug development and discovery.

Individual Project Reviews:
Project 1 – Coronaviruses
Strengths: The project, in particular, now has a definition of profile for lead.
Assays are nice and the inclusion of human airway epithelial cells is an important system to keep using.

Weaknesses: The largest issue is the lack of chemical value. There does not appear to be a well-defined future direction for hits, and concerns were expressed about attempting to move compounds forward without relaxing the criteria too much. There was concern that there were few hits to investigate, other than possible remdesivir and β-d-N^4-hydroxycytidine (NHC)

analogs. The *in vivo* studies with NHC required a very high dose (500 mg/kg) to completely block SARS-CoV replication, which is likely not a reasonable path forward.

Future directions:

- As noted above, this project could benefit from analoging remdesivir or NHC – compounds known to have some efficacy against coronaviruses- and work from there.
- Specifically, since the NHC data was intriguing, it was highly recommended that MOA studies be started for RNA polymerase using thermal shift (CETSA). It was suggested that SR might have some resources that could benefit this area – such as their Chemistry Department's Structural Biology Laboratory with Mason Wu. Even if outsourcing is required, the SAC suggested that modeling studies could help to identify better chemical value. Another resource suggested was Project 3's group leader, Pei-Yong Shi; his expertise might be helpful here.
- Project 1 should continue the use of primary cells compared to transformed cell lines as these studies are very important factor for translational application.

Project 2 – Alphaviruses

Strengths: The SAC felt this project was the front runner and was the most advanced project of the four. Members were glad to know that compounds are being considered leads even without activity against VEEV; however, they did note that if there are compounds that have anti-VEEV activity, they should be made a priority. Chemistry is very advanced for this project. It was noted that this project is in very good shape, but should only focus on the most promising compounds with the best overall properties.

Weaknesses: The general concentration in the viral titer reduction assays was 10 micromolar and there is concern that apparent antiviral activity could indicate toxicity and therefore may be an artifact and not actual activity. Also, there was not a clear indication of what the next steps were going to be as the project moves forward (see suggestions below).

Future directions:

- Given its activity in a mouse model of CHIKV infection, compound 42718 deserves top priority. The compound 33001 was thought to be likely a host target and the group liked the suggestion of using biotinylated compounds to identify the host target as well as perhaps RNA-Seq studies. Also, it was suggested that to determine host interaction, the group could perform experiments in which the MOI is varied.
- This group needs to be thinking of what needs to happen for implementation of preclinical trials for lead compounds and do that. There have been no trials for CHIKV thus far, so Kara Carter suggested that it might be good to develop a consortia with other leaders to coordinate such trials. She suggested that George Painter at Emory might be a good resource for helping to define what the first clinical trial would look like. Project 2 leaders need to start attending and being aware of FDA advisory meetings for CHIKV, even if the topic is vaccine-related, because they can shed light on what needs to be defined as far as epi endpoints: acute disease and proof of mechanism with patient population, viremia, acute clinical arthralgia severity post 3 months (clinical

including stiffness scales and pain scales). For all of this to occur, they will need to have a well thought-out clinical trial that includes consideration of drug-drug interactions. Prioritize experiments that are in line with these future goals with the lead compound.

Project 3 – Flaviviruses

Strengths: The addition of Pei-Yong Shi with his structural focus and industry experience has greatly benefitted this project. Several participants noted that the structural analysis was beautiful and was well done. Mike Diamond also brings much to this project and has provided a good approach with mouse models.

Weaknesses: Identification and development of a pan-dengue compound would be useful, but members realize that it is very difficult, due to differences in serotype, structure and mutations that increase resistance. Previously, there has been a push for project leaders to explore commercial partners within these projects, however, for this project, several larger and mid sized pharmas are independently working on Dengue antivirals because there is market for such agents. This results in there being less potential for an industry collaboration for the disease.

Future directions: One member asked if dengue is serotyped when diagnosed. It was suggested that if serotyping is done routinely, this might be a viable approach to develop therapeutics that are serotype specific even if they do not show pan-dengue efficacy.

Project 4 – Influenza

Strengths: Given the challenges that this project has faced during the first 5-year grant period, Kara Carter commented that it had made substantial progress in the past year. The HTS Core, led by Bob Bostwick has done a fantastic job and the quality of screens is very high.

Weaknesses: Even with excellent screens, it is the quality of the compounds emerging from screening that determines progress. Libraries used were limited with few hits to pursue even with a number of approaches being used. Also, IP space wasn't discussed in the presentation.

Future directions:

- Since it is still relatively early days for this project, there was a question as to how the priority to IVB was currently being considered.
- The VX787 compound (used as a positive control in studies) should be looked into further. If it has a patent, the patent information could be very informative.
- *In vivo* models for this project need to be considered. SAC suggested ferret or cotton rat models, not just the mouse models that are being used or planned.
- Because of the focus of hitting RdRp, it would make sense to perform thermal shift assays right away in order to identify hits then utilize the cap-snatch inhibitor.
- One member commented that they would like to see more studies with the EIDD 2838 compound as well as potential combination studies with what is already "out there."

Core A – Administrative
Strengths: The benefit of frequent teleconferences, team meetings and interactions among all projects and cores is clear, and has resulted in good progress for all projects.

Weaknesses: Since this was the first annual meeting under this award, new SAC members noted that clearer direction to the members prior to the meeting would be helpful in future.

Future recommendations:

- The SAC said it would have been helpful to have slide decks provided ahead of time for note taking. For the next meeting, redacted versions of the slides with the final presentations will be requested.
- Although scheduling of the meeting earlier in the year may have benefited the SAC, it was concluded that the same November meeting dates for this year should be followed next year, since they do not overlap with most other major conferences.

Core B – HTS
As noted in individual project reviews, this Core is doing excellent work in providing promising compounds for all projects. (See specific comments in the project sections above.)

Core C – Med Chem
This core is also an obvious strength of the overall program and is doing very good work. (See specific comments in the project sections above.)

To: benjamin.tenoever@mssm.edu[benjamin.tenoever@mssm.edu]; casanova@rockefeller.edu[casanova@rockefeller.edu]; cristina.lanni@unipv.it[cristina.lanni@unipv.it]; seidahn@ircm.qc.ca[seidahn@ircm.qc.ca]; neville@sanjanalab.org[neville@sanjanalab.org]; wangjw28@163.com[wangjw28@163.com]; friedemann.weber@vetmed.uni-giessen.de[friedemann.weber@vetmed.uni-giessen.de]; MatamVijay.Kumar@UToledo.edu[MatamVijay.Kumar@UToledo.edu]; jerome.martin@univ-nantes.fr[jerome.martin@univ-nantes.fr]; jim.davie@umanitoba.ca[jim.davie@umanitoba.ca]; vardhans@mskcc.org[vardhans@mskcc.org]; akiko.iwasaki@yale.edu[akiko.iwasaki@yale.edu]; kksingh@uab.edu[kksingh@uab.edu]; diamond@wusm.wustl.edu[diamond@wusm.wustl.edu]; Huang, Cheng[chhuang@utmb.edu]; Schijns.virgil@gmail.com[Schijns.virgil@gmail.com]; mehul.s.suthar@emory.edu[mehul.s.suthar@emory.edu]; trana@ucsd.edu[trana@ucsd.edu]; kyyuen@hku.hk[kyyuen@hku.hk]; alain.thierry@inserm.fr[alain.thierry@inserm.fr]; Thirumala-Devi.Kanneganti@StJude.org[Thirumala-Devi.Kanneganti@StJude.org]; schanda@sbpdiscovery.org[schanda@sbpdiscovery.org]; kanta.subbarao@influenzacentre.org[kanta.subbarao@influenzacentre.org]; maria.capobianchi@inmi.it[maria.capobianchi@inmi.it]; nberdmann@uabmc.edu[nberdmann@uabmc.edu]; Salaha@lsuhsc.edu[Salaha@lsuhsc.edu]; agbowie@tcd.ie[agbowie@tcd.ie]; eric.solary@gustaveroussy.fr[eric.solary@gustaveroussy.fr]; chaz.langelier@ucsf.edu[chaz.langelier@ucsf.edu]; aemili@bu.edu[aemili@bu.edu]; Rudd Christopher E.[christopher.e.rudd@umontreal.ca]; mihai.netea@radboudumc.nl[mihai.netea@radboudumc.nl]; jain@steele.mgh.harvard.edu[jain@steele.mgh.harvard.edu]; David.Levy@nyulangone.org[David.Levy@nyulangone.org]; jean-claude.tardif[jean-claude.tardif@icm-mhi.org]; louis.flamand@crchudequebec.ulaval.ca[louis.flamand@crchudequebec.ulaval.ca]; eric.boilard@crchudequebec.ulaval.ca[eric.boilard@crchudequebec.ulaval.ca]; mossk@mcmaster.ca[mossk@mcmaster.ca]; marc.pouliot@crchudequebec.ulaval.ca[marc.pouliot@crchudequebec.ulaval.ca]; Grandvaux Nathalie[nathalie.grandvaux@umontreal.ca]; Bouvier Michel[michel.bouvier@umontreal.ca]; Shi, Pei yong[peshi@UTMB.EDU]; benjamin.terrier@aphp.fr[benjamin.terrier@aphp.fr]; prokuninal@mail.nih.gov[prokuninal@mail.nih.gov]; nancy.reich@stonybrook.edu[nancy.reich@stonybrook.edu]; obrient@mail.nih.gov[obrient@mail.nih.gov]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; rbaric@email.unc.edu[rbaric@email.unc.edu]; bpulend@stanford.edu[bpulend@stanford.edu]; wlhsu@dragon.nchu.edu.tw[wlhsu@dragon.nchu.edu.tw]; th.webster@neu.edu[th.webster@neu.edu]; bonam.srinivasa@inserm.fr[bonam.srinivasa@inserm.fr]; galter@mgh.harvard.edu[galter@mgh.harvard.edu]; nevan.krogan@ucsf.edu[nevan.krogan@ucsf.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; y.takahashi@gunma-u.ac.jp[y.takahashi@gunma-u.ac.jp]; luoping@berkeley.edu[luoping@berkeley.edu]
Cc: Christina Zhang[christina.zhang@mdpi.com]
From: Servant Marc[marc.servant@umontreal.ca]
Sent: Tue 2/16/2021 10:06:41 AM (UTC-06:00)
Subject: Invitation to a contribution on a special Issue in Cells (IF 4.37) “SARS-CoV-2, Viral Interference and the Antiviral Innate Immune Response: Challenges and Opportunities”

Dear colleagues,

The current pandemic involving SARS-CoV-2, a positive-sense single-stranded RNA virus that was recently showed to target components of the RIG-I like receptor (RLR) and the JAK/STAT pathways, has revealed a defect in the innate type I/III IFN antiviral responses in infected patients that are associated with robust virus replication and severe complications, i.e., inflammation and a “cytokine storm”, notably via the accumulation of monocytes, resulting in lung immunopathology, vascular leakage, and suboptimal T cell response. Thus, viral interference affecting the type I/III IFN antiviral response is likely a culprit here. However, this does not explain why older patients (and sometimes even young individuals) do not mount a proper and efficient innate type I/III IFN antiviral response as compared to others. Whereas autoantibodies against IFNa as well as IRF7 and TLR3 variants represent candidates to consider, other mechanisms are likely involved in the complex interplay that exists between the host, this coronavirus as well as the emerging SARS-CoV-2 variants.

With those considerations in mind, I was invited to act as a Guest Editor for the Special Issue “SARS-CoV-2, Viral Interference and the Antiviral Innate Immune Response: Challenges and Opportunities” in the journal Cells (IF 4.37) (http://www.mdpi.com/journal/cells). This Special Issue will cover the biology of SARS-CoV viruses and their intrinsic ability to antagonize type I/III IFN responses. It will also review our current understanding of the severe complications associated with SARS-CoV-2 infection and address how precision medicine approaches (i.e. high-definition medicine) and medicinal chemistry (direct-acting antiviral drugs, immunomodulators and others) could help in diagnosis, prevention, and treatment.

I would be very pleased if you would agree to contribute a research paper or comprehensive review (more than 5000 words in the main text and include at least two figures or tables) on any aspect related to this thematic. It is our belief that your contribution will significantly strengthen the scope of this special issue and choose to join us.

Looking forward to your positive reply.
Regards,

Prof. Marc Servant
Guest Editor

Below you will find some information that you may find useful when considering this invitation.

(1) For more details of this special issue, please see via the following link: https://www.mdpi.com/journal/cells/special_issues/SARS_immune

(2) The submission deadline is **31 October 2021**. Papers can be submitted anytime before the deadline and will be published online individually soon after they are accepted, as papers are published on an ongoing basis to ensure the fast publication for individual articles.

(3) Currently, the median time from submission to first decision in Cells is 16 days. The median time from submission to publication online is 35 days.

(4) An article processing charge (APC) of 2000 CHF (Swiss Francs) applies to papers accepted after peer review. However, Cells will offer discounts/waivers for scholars who have had a good publication record in the last 3 years. Just make a pre-submission request, providing your tentative title with abstract to Ms. Yvonne Feng of Cells yvonne.feng@mdpi.com for application. The final decision will be made after checking. It is our belief that your contribution will significantly strengthen the scope of this special issue and choose to join us. Look forward to your positive reply.

Manuscript Submission Information
Manuscripts should be submitted online at **www.mdpi.com** by **registering** and **logging in to this website**. Once you are registered, **click here to go to the submission form**. Manuscripts can be submitted until the deadline. All papers will be peer-reviewed. Accepted papers will be published continuously in the journal (as soon as accepted) and will be listed together on the special issue website. Research articles, review articles as well as short communications are invited. For planned papers, a title and short abstract (about 100 words) can be sent to the Editorial Office for announcement on this website.
Submitted manuscripts should not have been published previously, nor be under consideration for publication elsewhere (except conference proceedings papers). All manuscripts are thoroughly refereed through a single-blind peer-review process. A guide for authors and other relevant information for submission of manuscripts is available on the **Instructions for Authors** page. ***Cells*** is an international peer-reviewed open access monthly journal published by MDPI.
Please visit the **Instructions for Authors** page before submitting a manuscript. The **Article Processing Charge (APC)** for publication in this **open access** journal is 2000 CHF (Swiss Francs). Submitted papers should be well formatted and use good English. Authors may use MDPI's **English editing service** prior to publication or during author revisions.

Published Papers
This special issue is now open for submission.

To: 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Ralph Baric'[rbaric@email.unc.edu]; 'Mark Suto'[msuto@southernresearch.org]; 'kara.carter@evotec.com'[kara.carter@evotec.com]; 'Mike Bray'[mikebray10@gmail.com]; 'Fred Hayden'[fgh@virginia.edu]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Stephanie Moore[smoore@peds.uab.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'Alana Centilli'[acentilli@southernresearch.org]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Thur 1/9/2020 8:40:20 AM (UTC-06:00)
Subject: IMPORTANT: Logistics and Presentation Items for the AD3C Reverse Site Visit on February 11, 2020 in Rockville, MD
guest travel template.pdf
Blank AD3C Slide.pptx

Greetings and Happy New Year:

It is time to move forward with final plans for the AD3C Reverse Site Visit, scheduled for **Tuesday, February 11, 2020** at the NIAID Building, 5601 Fishers Lane. Rockville, MD. **In preparation for this visit, please read the following instructions carefully:**

- At this time, **please purchase a plane ticket using a domestic carrier and select a seat in economy class**, so your ticket can be reimbursed. For those who will be staying overnight, we suggest that you stay at the Hilton Washington DC/Rockville Hotel, 1750 Rockville Pike, Rockville, MD 20852, Phone is 301-468-1100 and the website link is https://www3.hilton.com/en/hotels/maryland/hilton-washington-dc-rockville-hotel-and-executive-meeting-ctr-IADMRHF/index.html. It is a short walk to the NIAID or a quick cab/Uber ride.

- Please use the attached form to keep track of your travel expenses and speed up reimbursement after the trip. It is important for you to sign the form before sending it to us with your receipts.

- If you will be arriving in the area on the evening of Monday, February 10 and would like to have dinner, **please let us know** so we will have a head count for making a group reservation at a nice local restaurant.

- In order to produce a presentation that contains uniform content for each project, please send the following items to Stephanie Moore at smoore@peds.uab.edu no later than **February 3, 2020** to be compiled into one presentation. There can be **10 slides** maximum per project that will take 20-25 minutes at most to cover. I have attached a blank AD3C slide if you would like to use it. Below are the areas that Maureen Beanan has requested that we cover:

    a. Status (1-2 slides - utilize timeline structure perhaps?)
    b. Accomplishments (2-3 slides)
    c. Proposed for upcoming year(s) (1-2 slides)
    d. Significant publications (1 slide)

Here are additional details on the meeting location, and the meeting agenda provided by NIH for your use, shown below:

Meeting Location:
NIAID
5601 Fishers Lane
Rockville MD 20852

Building Access: It is very important that you arrive at the building by **8:30 am Eastern Time** to allow sufficient time to get through security. Domestic travelers will need a government issued ID (i.e. driver's license) to enter the building. We plan to meet as a group in the lobby, but if you are early/late, please call Maureen Beanan at 301-339-4753 when you arrive at the lobby security station and she or one of her colleagues will come down to escort you.

Parking: Parking is available in the garage at 5635 Fishers Lane, Rockville, MD 20852 – the road to the garage is the first left after turning on to Fisher's Lane. The garage will be at the end of a road. Walk back out to Fisher's Lane, turn left and walk one block, cross the street to reach our building, about a 3 minute walk.

Meeting schedule: 9:00 to 11:00 am Part I: (~2.0 hours, including time for questions)
(Audience: This part of the meeting is open to all NIAID staff, including CETR Program Staff and all other interested NIAID staff)

9:00 am NIAID CETR staff welcome participants and Introductions (5 minutes)

9:05 am CETR presentations:

- Brief overview of the Center including the goals, administrative structure, projects, and cores – please include a slide summarizing the progress of depositing the genome sequences into NCBI in this part of the presentation;
- Report on Year 1 activities for each project (~15-20 minutes per project)
- Summarize the status of the project at the end of Year 1 (1 slide)
- Describe the progress on each project during year 1 and plans for remaining 4 years

11:00 am to 12:00 pm Part II: Discussion with CETR Program staff (~0.5 - 1 hour)
Possible topics:

- Senior NIAID staff questions
- Issues that have arisen during year and proposed options
- CETR Program updates
- Annual Progress Report questions

Thank you for agreeing to participate in the AD3C Reverse Site Visit. If you need any additional items or information, please contact any of our Administrative Core group members and we will be happy to assist you.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

Guest Travel **Date**_____ **Person's Name**_____

Points of Travel

Date	From	To	Mode

Transportation		Private Car, Rental Car, Plane, Train etc.
- Private Car mileage (Not rental cars)	_____ miles @ _____	
- Private Car mileage (Not rental cars)	_____ miles @ _____	
-Airfare/Train fare (Coach class only. Attach ticket stub.)		
-Rental Car (Attach original receipts. Give justification for why rental car was used instead of public transportation)		
-Taxi/Van (Including tips. Attach original receipts for fare where applicable.)		
-Parking (Attach receipt if applicable.)		
	Total Transportation	

Meals (Attach original receipts. Cannot include any alcoholic beverages.)

Date	Breakfast($)	Lunch($)	Dinner($)	Day Total ($)

Total Meals ($) _____

Hotel Room (Attach original receipts. Basic single occupancy room rate only.)

Date(s)	Rate($)	Number of Nights	Total ($)

Total Hotel ($) _____

Miscellaneous

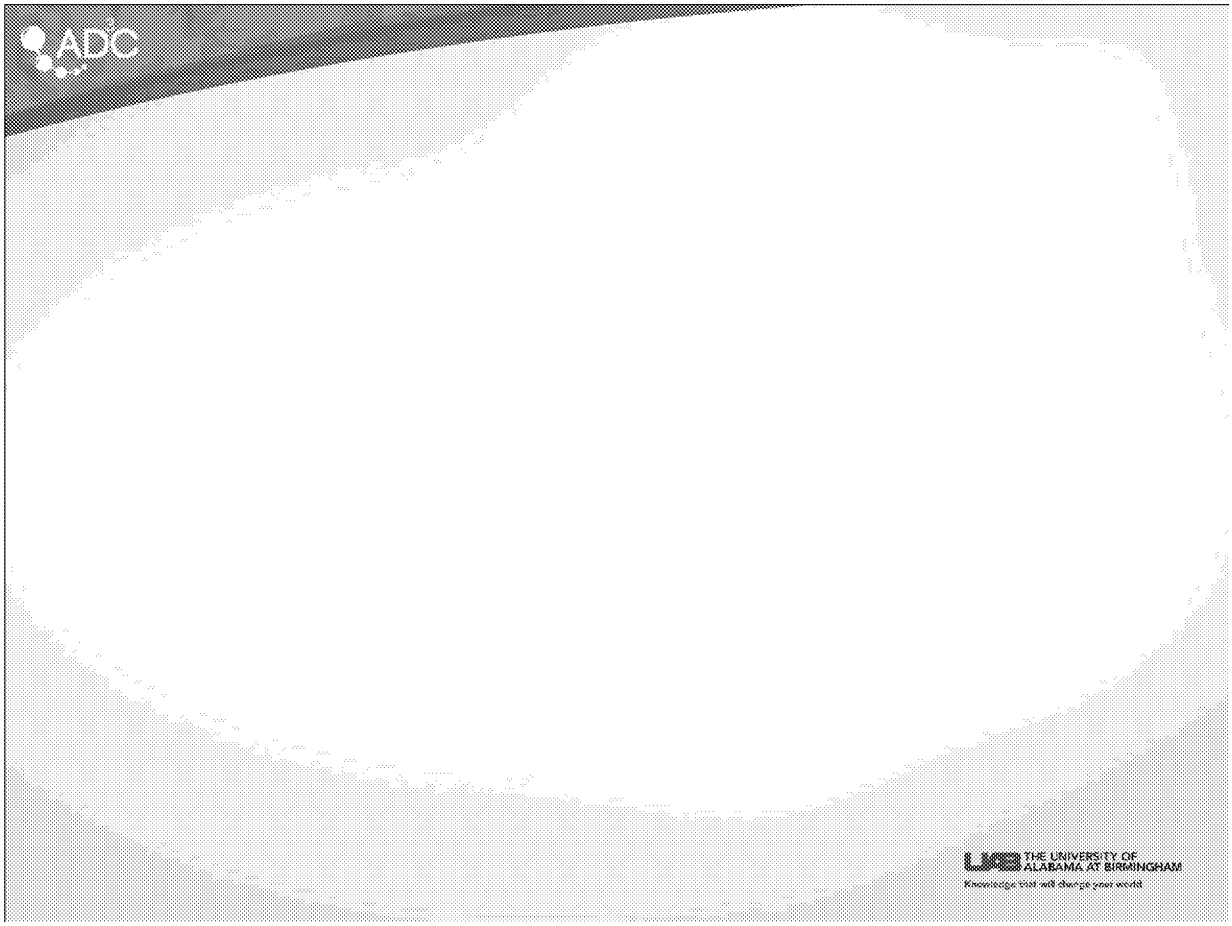
-Baggage Handling Tips (Receipts not required), etc.

Total Miscellaneous	

Total Reimbursement Requested _____

Certification: I hereby request reimbursement of the travel related expenses detailed above and do hereby certify that:
- the travel and expenses indicated hereon were incurred by me
- the expenses were incurred in the performance of official duties and pursuant to the travel authority granted to me by UAB
- I have not been and will not be reimbursed for any of these expenses by any other entity
- there are no alcoholic beverages included in these expenses
- I agree to the rate at which I am being reimbursed
- I have not previously billed UAB for any of these expenses
- this travel voucher has been completed in compliance with UAB policies

Signature _____ Date_____


ADC
THE UNIVERSITY OF ALABAMA AT BIRMINGHAM
Knowledge that will change your world

To: Alter, Galit[galter@partners.org]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Griffiths, Anthony[ahgriff@bu.edu]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; jma[jma@sgul.ac.uk]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov];

Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; SUBISSI, Lorenzo[subissil@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu)[luk_vandenberghe@meei.harvard.edu]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; SALAMI, Kolawole[salamik@who.int]; tcs38@psu.edu[tcs38@psu.edu]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; STRÖHER, Ute[stroheru@who.int]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 2/15/2021 11:45:40 AM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday February 17 2:30PM CET (Geneva Time)

1. Ellie Barnes and Susie Dunachie (Oxford) - *Vaccine-induced immunity provides more robust heterotypic immunity than natural infection to emerging SARS-CoV-2 variants of concern*
2. Alex Sigal (AHRI) - *Cross-neutralization by plasma antibodies elicited by 501Y.V2 and earlier variants of 501Y.V2 and B.1.1 using live virus*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, February 14, 2021 8:49 AM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in;

pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; ASiyer@mgh.harvard.edu; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Jilian.Sacks@finddx.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg; SALAMI, Kolawole; tcs38@psu.edu; angeliki.melidou@ecdc.europa.eu; BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, February 17, 2021 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
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64.211.144.160 (Brazil)
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207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; dbarouch[dbarouch@BIDMC.HARVARD.EDU]; Krogan, Nevan[Nevan.Krogan@ucsf.edu]; Paul Thomas[paul.thomas@stjude.org]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; stevens@anl.gov[stevens@anl.gov]; jjdavis@anl.gov[jjdavis@anl.gov]; Scheuermann, Richard[RScheuermann@jcvi.org]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; adam.godzik@ucr.edu[adam.godzik@ucr.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; btk@lanl.gov[btk@lanl.gov]; lmwoga@fredhutch.org[lmwoga@fredhutch.org]; monte@duke.edu[monte@duke.edu]; spjwhelan@wustl.edu[spjwhelan@wustl.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Shi, Pei yong[peshi@UTMB.EDU]; McDermott, Adrian (NIH/VRC) [E][adrian.mcdermott@nih.gov]; jbloom@fredhutch.org[jbloom@fredhutch.org]; Julie McElrath[jmcelrat@fredhutch.org]; kawaokay@svm.vetmed.wisc.edu[kawaokay@svm.vetmed.wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; noah.sather@seattlechildrens.org[noah.sather@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; mrolland@hivresearch.org[mrolland@hivresearch.org]; Baric, Ralph[rbaric@email.unc.edu]; Richard Webby[richard.webby@stjude.org]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; malik@hku.hk[malik@hku.hk]; Andrew B. Ward[andrew@scripps.edu]; Ali Ellebedy[ellebedy@wustl.edu]; mdiamond@wustl.edu[mdiamond@wustl.edu]; djs200@cam.ac.uk[djs200@cam.ac.uk]; jboon@wustl.edu[jboon@wustl.edu]; Aubree Gordon[gordonal@umich.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Koup, Richard (NIH/VRC) [E][rkoup@mail.nih.gov]; Seder, Robert (NIH/VRC) [E][rseder@mail.nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Alessandro Sette[alex@lji.org]; Adam Godzik[Adam.Godzik@medsch.ucr.edu]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; MacCannell, Duncan (CDC/DDID/NCEZID/OD)[fms2@CDC.GOV]; Weiss, Carol (FDA/CBER)[Carol.Weiss@fda.hhs.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Nelson Michael[nelson.l.michael2.civ@mail.mil]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; irina.maljkovicberry.ctr@mail.mil[irina.maljkovicberry.ctr@mail.mil]; jeffrey.r.currier.civ@mail.mil[jeffrey.r.currier.civ@mail.mil]; Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]
From: Krammer, Florian[florian.krammer@mssm.edu]
Sent: Fri 2/19/2021 8:25:06 AM (UTC-06:00)
Subject: Re: SARS-CoV-2 Variant Testing pipeline
Overview and recap and overview of last_FK 2_19_21.pptx

Dear all,

Please find the slides for the in vitro group attached.

Best,

Florian

From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Wednesday, February 3, 2021 12:20 PM
To: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Krammer, Florian; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; Van bakel, Harm; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]

Subject: SARS-CoV-2 Variant Testing pipeline
When: Friday, February 19, 2021 8:00 AM-9:30 AM.
Where: https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09

USE CAUTION: External Message.

Hello everyone,
Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.
If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.
Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.
Thank you, and looking forward to speaking on Friday February 12th.
Marciela
Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.
Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09
Meeting ID: 160 266 4950
Passcode: 073903
One tap mobile
+16692545252,,1602664950#,,,,*073903# US (San Jose)
+16468287666,,1602664950#,,,,*073903# US (New York)
Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
833 568 8864 US Toll-free
Meeting ID: 160 266 4950
Passcode: 073903
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u
Join by SIP
1602664950@sip.zoomgov.com
Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: 073903

Summary *In Vitro* Characterization group discussion

2/19/21

What data is needed

1. **Cross-neutralization data**
   - WT to variant
   - Variant to wt
   - Variant to variant
   - Should be a broad panel of pseudoneut (VSV as well as lenti) and neut assays, 2-3 labs per assay?
2. **Growth kinetics in representative cell lines**
   - Organoids/organ systems/air liquid interface cultures?
   - Primary cell lines?
   - Cells overexpressing ACE2/TMPRSS2
3. **Structural information**
   - What impact do NTD loop deletions have?
   - What impact do RBD mutations have?
   - Do heterotrimers present epitopes of wt+variants correctly (important for mRNA/vectored vaccines)
4. **Variant RBD affinity to ACE2**
   - This should include ACE2 binding to animal model ACE2
5. **Characterization of mutations in genes outside of S**
6. **Anticipate mutations (e.g. identified via libraries, escape mutagenesis, also based on variants) and characterize them ahead of time**
7. **Data sharing system?**

Reagents

- Sourcing virus
  - Several isolates from each variant
    - Faster sharing needed – both domestic and international
    - Avoid USDA permits, ship non-cultured clinical isolates or ship extracted RNA!
  - BEI should supply large volumes that are ready to use
  - Molecular clones are needed too
- Benchmarking
  - mAbs (Ellebedy, P. Wilson etc.)
  - Therapeutic mAbs (source??? REGN, Eli Lilly, VIR, AZ etc.)
  - Access to remdesivir or similar
  - Polyclonal serum panel post vaccination for Moderna, Pfizer, J&J, NVX, AZ
  - Polyclonal serum panel post infection (wt, B.1.1.7, B.1.351, P.1, E484K viruses etc.)
- Gene synthesis
  - For molecular clones (wt nt sequence)
  - For pseudotyped entry inhibition assays (codon optimized wt aa sequence)
  - For protein expression (codon optimized 2P/Hexapro ΔCS)

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com];

Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SCHWARTZ, Lauren[schwartzl@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Sun 2/21/2021 4:48:01 PM (UTC-06:00)
Subject: No call this week - WHO Working Group on COVID-19 Assays

Hi All,

The WHO Working Group on COVID-19 Assays will not be held this week due to a conflict with the 2021 Global Vaccine and Immunization Research Forum (https://gvirf.org/).

Many thanks,
Lauren - Bill, Simon and César

Lauren Schwartz, PhD
Consultant - COVID-19 Response
R&D Blueprint | Health Emergencies Programme
Mobile: +1 248 910 9571
Email: schwartzl@who.int

To: casanova@rockefeller.edu[casanova@rockefeller.edu]; cristina.lanni@unipv.it[cristina.lanni@unipv.it]; seidahn@ircm.qc.ca[seidahn@ircm.qc.ca]; neville@sanjanalab.org[neville@sanjanalab.org]; wangjw28@163.com[wangjw28@163.com]; friedemann.weber@vetmed.uni-giessen.de[friedemann.weber@vetmed.uni-giessen.de]; MatamVijay.Kumar@UToledo.edu[MatamVijay.Kumar@UToledo.edu]; jerome.martin@univ-nantes.fr[jerome.martin@univ-nantes.fr]; jim.davie@umanitoba.ca[jim.davie@umanitoba.ca]; vardhans@mskcc.org[vardhans@mskcc.org]; akiko.iwasaki@yale.edu[akiko.iwasaki@yale.edu]; kksingh@uab.edu[kksingh@uab.edu]; diamond@wusm.wustl.edu[diamond@wusm.wustl.edu]; Huang, Cheng[chhuang@utmb.edu]; Schijns.virgil@gmail.com[Schijns.virgil@gmail.com]; mehul.s.suthar@emory.edu[mehul.s.suthar@emory.edu]; trana@ucsd.edu[trana@ucsd.edu]; kyyuen@hku.hk[kyyuen@hku.hk]; alain.thierry@inserm.fr[alain.thierry@inserm.fr]; schanda@sbpdiscovery.org[schanda@sbpdiscovery.org]; kanta.subbarao@influenzacentre.org[kanta.subbarao@influenzacentre.org]; maria.capobianchi@inmi.it[maria.capobianchi@inmi.it]; nberdmann@uabmc.edu[nberdmann@uabmc.edu]; Salaha@lsuhsc.edu[Salaha@lsuhsc.edu]; agbowie@tcd.ie[agbowie@tcd.ie]; eric.solary@gustaveroussy.fr[eric.solary@gustaveroussy.fr]; chaz.langelier@ucsf.edu[chaz.langelier@ucsf.edu]; aemili@bu.edu[aemili@bu.edu]; Rudd Christopher E.[christopher.e.rudd@umontreal.ca]; mihai.netea@radboudumc.nl[mihai.netea@radboudumc.nl]; jain@steele.mgh.harvard.edu[jain@steele.mgh.harvard.edu]; David.Levy@nyulangone.org[David.Levy@nyulangone.org]; jean-claude.tardif[jean-claude.tardif@icm-mhi.org]; louis.flamand@crchudequebec.ulaval.ca[louis.flamand@crchudequebec.ulaval.ca]; eric.boilard@crchudequebec.ulaval.ca[eric.boilard@crchudequebec.ulaval.ca]; mossk@mcmaster.ca[mossk@mcmaster.ca]; marc.pouliot@crchudequebec.ulaval.ca[marc.pouliot@crchudequebec.ulaval.ca]; Bouvier Michel[michel.bouvier@umontreal.ca]; Shi, Pei yong[peshi@UTMB.EDU]; benjamin.terrier@aphp.fr[benjamin.terrier@aphp.fr]; prokuninal@mail.nih.gov[prokuninal@mail.nih.gov]; nancy.reich@stonybrook.edu[nancy.reich@stonybrook.edu]; obrient@mail.nih.gov[obrient@mail.nih.gov]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; rbaric@email.unc.edu[rbaric@email.unc.edu]; bpulend@stanford.edu[bpulend@stanford.edu]; wlhsu@dragon.nchu.edu.tw[wlhsu@dragon.nchu.edu.tw]; th.webster@neu.edu[th.webster@neu.edu]; bonam.srinivasa@inserm.fr[bonam.srinivasa@inserm.fr]; galter@mgh.harvard.edu[galter@mgh.harvard.edu]; nevan.krogan@ucsf.edu[nevan.krogan@ucsf.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; y.takahashi@gunma-u.ac.jp[y.takahashi@gunma-u.ac.jp]; luoping@berkeley.edu[luoping@berkeley.edu]
Cc: Christina Zhang[christina.zhang@mdpi.com]
From: Servant Marc[marc.servant@umontreal.ca]
Sent: Thur 2/18/2021 10:57:53 AM (UTC-06:00)
Subject: Invitation from Marc Servant- Guest Editor- special Issue-"SARS-CoV-2, Viral Interference and the Antiviral Innate Immune Response: Challenges and Opportunities"

Dear colleagues,

The current pandemic involving SARS-CoV-2, a positive-sense single-stranded RNA virus that was recently showed to target components of the RIG-I like receptor (RLR) and the JAK/STAT pathways, has revealed a defect in the innate type I/III IFN antiviral responses in infected patients that are associated with robust virus replication and severe complications, i.e., inflammation and a "cytokine storm", notably via the accumulation of monocytes, resulting in lung immunopathology, vascular leakage, and suboptimal T cell response. Thus, viral interference affecting the type I/III IFN antiviral response is likely a culprit here. However, this does not explain why older patients (and sometimes even young individuals) do not mount a proper and efficient innate type I/III IFN antiviral response as compared to others. Whereas autoantibodies against IFNa as well as IRF7 and TLR3 variants represent candidates to consider, other mechanisms are likely involved in the complex interplay that exists between the host, this coronavirus as well as the emerging SARS-CoV-2 variants.

With those considerations in mind, I was invited to act as a Guest Editor for the Special Issue "SARS-CoV-2, Viral Interference and the Antiviral Innate Immune Response: Challenges and Opportunities" in the journal Cells (IF 4.37) (http://www.mdpi.com/journal/cells). This Special Issue will cover the biology of SARS-CoV viruses and their intrinsic ability to antagonize type I/III IFN responses. It will also review our current understanding of the severe complications associated with SARS-CoV-2 infection and address how precision medicine approaches (i.e. high-definition medicine) and medicinal chemistry (direct-acting antiviral drugs, immunomodulators and others) could help in diagnosis, prevention, and treatment.

I would be very pleased if you would agree to contribute a research paper or comprehensive review (more than 5000 words in the main text and include at least two figures or tables) on any aspect related to this thematic. It is our belief that your contribution will significantly strengthen the scope of this special issue and choose to join us.

Looking forward to your positive reply.
Regards,

Prof. Marc Servant
Guest Editor

Below you will find some information that you may find useful when considering this invitation.

(1) For more details of this special issue, please see via the following link: https://www.mdpi.com/journal/cells/special_issues/SARS_immune

(2) The submission deadline is **31 October 2021**. Papers can be submitted anytime before the deadline and will be published online individually soon after they are accepted, as papers are published on an ongoing basis to ensure the fast publication for individual articles.

(3) Currently, the median time from submission to first decision in Cells is 16 days. The median time from submission to publication online is 35 days.

(4) An article processing charge (APC) of 2000 CHF (Swiss Francs) applies to papers accepted after peer review. However, Cells will offer discounts/waivers for scholars who have had a good publication record in the last 3 years. Just make a pre-submission request, providing your tentative title with abstract to Ms. Yvonne Feng of Cells yvonne.feng@mdpi.com for application. The final decision will be made after checking. It is our belief that your contribution will significantly strengthen the scope of this special issue and choose to join us. Look forward to your positive reply.

Manuscript Submission Information
Manuscripts should be submitted online at **www.mdpi.com** by **registering** and **logging in to this website**. Once you are registered, **click here to go to the submission form**. Manuscripts can be submitted until the deadline. All papers will be peer-reviewed. Accepted papers will be published continuously in the journal (as soon as accepted) and will be listed together on the special issue website. Research articles, review articles as well as short communications are invited. For planned papers, a title and short abstract (about 100 words) can be sent to the Editorial Office for announcement on this website.
Submitted manuscripts should not have been published previously, nor be under consideration for publication elsewhere (except conference proceedings papers). All manuscripts are thoroughly refereed through a single-blind peer-review process. A guide for authors and other relevant information for submission of manuscripts is available on the **Instructions for Authors** page. ***Cells*** is an international peer-reviewed open access monthly journal published by MDPI.
Please visit the **Instructions for Authors** page before submitting a manuscript. The **Article Processing Charge (APC)** for publication in this **open access** journal is 2000 CHF (Swiss Francs). Submitted papers should be well formatted and use good English. Authors may use MDPI's **English editing service** prior to publication or during author revisions.

Published Papers
This special issue is now open for submission.

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr)[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com];

Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SCHWARTZ, Lauren[schwartzl@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Sun 2/28/2021 11:39:01 AM (UTC-06:00)
Subject: No call this week - WHO Working Group on COVID-19 Assays

Hi All,

The WHO Working Group on COVID-19 Assays will not be held this week due to a conflict with the WHO Global consultation on COVID-19 therapeutics. Register with this link if you'd like to attend - https://who-e.zoom.us/webinar/register/WN_CNfywAEiTEWgqA_nEcjeow

Many thanks,
Lauren - Bill, Simon and César

Lauren Schwartz, PhD
Consultant - COVID-19 Response
R&D Blueprint | Health Emergencies Programme
Mobile: +1 248 910 9571
Email: schwartzl@who.int

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose

(Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]
Cc: alankhoo.imr[alankhoo.imr@gmail.com]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; viviana.simon@mssm.edu[viviana.simon@mssm.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 3/8/2021 12:00:43 PM (UTC-06:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday March 10 2:30PM CET (Geneva Time)

1. Alex Sette (LJI) - *Negligible impact of SARS-CoV-2 variants on CD4+ and CD8+ T cell reactivity in COVID-19 exposed donors and vaccinees*
2. Viviana Simon (MSSM) - *Analysis of immune responses to SARS-CoV-2 mRNA vaccination on a serological and monoclonal level*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, March 7, 2021 8:51 AM
To: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; 'HENAO RESTREPO, Ana Maria'; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya; zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, March 10, 2021 5:30 AM-6:30 AM (UTC-08:00) Pacific Time (US & Canada).
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Agenda to follow.

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To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak (daszak@ecohealthalliance.org)[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose

(Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; a.luttick[a.luttick@360biolabs.com]

Cc: Kemp, Troy (NIH/NCI) [C][kemptj@mail.nih.gov]; Pinto, Ligia (NIH/NCI) [C][pintol@mail.nih.gov]; Jacqueline Fryer[Jacqueline.Fryer@nibsc.org]

From: SCHWARTZ, Lauren[schwartzl@who.int]

Sent: Tue 3/16/2021 5:05:17 PM (UTC-05:00)

Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday March 17 2:30PM CET (Geneva Time)

1. Bill Dowling (CEPI) – Opening remarks
2. Ligia Pinto & Troy Kemp (NCI) - US SARS-CoV-2 Serology Standard: Background and How to use it
3. Jacqueline Fryer (NIBSC) - Proposed 1st WHO International Standard for SARS-CoV-2 Antigen

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, March 14, 2021 8:44 AM
To: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen Makar (Karen.Makar@gatesfoundation.org); David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; 'HENAO RESTREPO, Ana Maria'; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya; zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; Angela Luttick
Cc: Kemp, Troy (NIH/NCI) [C]; Pinto, Ligia (NIH/NCI) [C]
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, March 17, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

For those based in the US, please note the time of the meeting has shifted for two weeks given daylight savings.

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To: 'kara.carter@evotec.com'[kara.carter@evotec.com]; 'Fred Hayden'[fgh@virginia.edu]; 'Mark Suto'[msuto@southernresearch.org]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Stephanie Moore[smoore@peds.uab.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; 'Daniel Streblow'[streblow@ohsu.edu]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Tue 1/28/2020 9:30:19 AM (UTC-06:00)
Subject: AD3C Reverse Site Visit Dinner Reservation on February 10

Hello to Everyone:

Thank you again for your participation in the AD3C Reverse Site Visit on February 11, 2020. Dr. Whitley has made a reservation for dinner at Founding Farmers – Montgomery County at **7:00 pm** Eastern Time for Monday evening, February 10. The address of the restaurant is 12505 Park Potomac Avenue, Potomac, MD 20854 and the phone number is (301) 340-8783. The reservation is confirmed under Dr. Whitley's name.

If I can be of assistance, please let me know.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; florian.krammer (florian.krammer@mssm.edu)[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili

(changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; a.luttick[a.luttick@360biolabs.com]
Cc: Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Chiu, Charles[Charles.Chiu@ucsf.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 3/22/2021 7:05:07 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday March 24 2:30PM CET (Geneva Time)

1. Kevin Bewley (PHE) - *Neutralisation Assays for SARS-CoV-2; Wildtype and Pseudotyped virus*
2. Charles Chiu (UCSF) - *SARS-CoV-2: A Tale of 4 Variants*

-----Original Appointment-----

From: SCHWARTZ, Lauren
Sent: Sunday, March 21, 2021 9:05 AM
To: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; 'HENAO RESTREPO, Ana Maria'; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya; zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; Angela Luttick
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, March 24, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

For those based in the US, please note the time of the meeting has shifted for two weeks given daylight savings.

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207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; dbarouch[dbarouch@BIDMC.HARVARD.EDU]; Krogan, Nevan[Nevan.Krogan@ucsf.edu]; Paul Thomas[paul.thomas@stjude.org]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; stevens@anl.gov[stevens@anl.gov]; jjdavis@anl.gov[jjdavis@anl.gov]; Scheuermann, Richard[RScheuermann@jcvi.org]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; adam.godzik@ucr.edu[adam.godzik@ucr.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; btk@lanl.gov[btk@lanl.gov]; lmwoga@fredhutch.org[lmwoga@fredhutch.org]; monte@duke.edu[monte@duke.edu]; spjwhelan@wustl.edu[spjwhelan@wustl.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Shi, Pei yong[peshi@UTMB.EDU]; McDermott, Adrian (NIH/VRC) [E][adrian.mcdermott@nih.gov]; jbloom@fredhutch.org[jbloom@fredhutch.org]; Julie McElrath[jmcelrat@fredhutch.org]; kawaokay@svm.vetmed.wisc.edu[kawaokay@svm.vetmed.wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; noah.sather@seattlechildrens.org[noah.sather@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; mrolland@hivresearch.org[mrolland@hivresearch.org]; Baric, Ralph[rbaric@email.unc.edu]; Richard Webby[richard.webby@stjude.org]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; malik@hku.hk[malik@hku.hk]; Andrew B. Ward[andrew@scripps.edu]; Ali Ellebedy[ellebedy@wustl.edu]; mdiamond@wustl.edu[mdiamond@wustl.edu]; djs200@cam.ac.uk[djs200@cam.ac.uk]; jboon@wustl.edu[jboon@wustl.edu]; Aubree Gordon[gordonal@umich.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Koup, Richard (NIH/VRC) [E][rkoup@mail.nih.gov]; Seder, Robert (NIH/VRC) [E][rseder@mail.nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Alessandro Sette[alex@lji.org]; Adam Godzik[Adam.Godzik@medsch.ucr.edu]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; MacCannell, Duncan (CDC/DDID/NCEZID/OD)[fms2@CDC.GOV]; Weiss, Carol (FDA/CBER)[Carol.Weiss@fda.hhs.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Nelson Michael[nelson.l.michael2.civ@mail.mil]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; irina.maljkovicberry.ctr@mail.mil[irina.maljkovicberry.ctr@mail.mil]; jeffrey.r.currier.civ@mail.mil[jeffrey.r.currier.civ@mail.mil]; Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]; tbedford@fredhutch.org[tbedford@fredhutch.org]; Patrick C. Wilson[wilsonp@uchicago.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; Douek, Daniel (NIH/VRC) [E][ddouek@mail.nih.gov]
Cc: David Montefiori, Ph.D.[david.montefiori@duke.edu]; Michael, Nelson[nmichael@hivresearch.org]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; Peter Halfmann[peter.halfmann@wisc.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Gardner, Meredith Elizabeth Davis[meredith.davis.gardner@emory.edu]; Weaver, Scott[sweaver@UTMB.EDU]
From: Krammer, Florian[florian.krammer@mssm.edu]
Sent: Fri 4/2/2021 10:27:39 AM (UTC-05:00)
Subject: Re: SARS-CoV-2 Variant Testing pipeline

To follow up on our discussion from today. Here are first data about Sputnik V and the variants from the Benhur Lee lab.
https://www.medrxiv.org/content/10.1101/2021.03.31.21254660v1.full.pdf

Best,

Florian

From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Wednesday, February 3, 2021 12:20 PM
To: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>; dbarouch <dbarouch@BIDMC.HARVARD.EDU>; Krogan, Nevan <Nevan.Krogan@ucsf.edu>; Paul Thomas <paul.thomas@stjude.org>; Stacey Schultz-Cherry <stacey.schultz-cherry@stjude.org>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Lampley, Rebecca (NIH/NIAID) [C] <rebecca.lampley@nih.gov>; stevens@anl.gov <stevens@anl.gov>; jjdavis@anl.gov <jjdavis@anl.gov>; Scheuermann, Richard <RScheuermann@jcvi.org>; Eakin, Ann (NIH/NIAID) [E] <ann.eakin@nih.gov>; Brown, Liliana (NIH/NIAID) [E] <liliana.brown@nih.gov>; adam.godzik@ucr.edu <adam.godzik@ucr.edu>; Jason McLellan <jmclellan@austin.utexas.edu>; btk@lanl.gov <btk@lanl.gov>; lmwoga@fredhutch.org <lmwoga@fredhutch.org>; monte@duke.edu <monte@duke.edu>; spjwhelan@wustl.edu <spjwhelan@wustl.edu>; Suthar, Mehul <mehul.s.suthar@emory.edu>; Pei yong. Shi <peshi@UTMB.EDU>; McDermott, Adrian (NIH/VRC) [E] <adrian.mcdermott@nih.gov>; Krammer, Florian <florian.krammer@mssm.edu>; jbloom@fredhutch.org <jbloom@fredhutch.org>; Julie McElrath <jmcelrat@fredhutch.org>; kawaokay@svm.vetmed.wisc.edu <kawaokay@svm.vetmed.wisc.edu>; vimenach@utmb.edu <vimenach@utmb.edu>; noah.sather@seattlechildrens.org <noah.sather@seattlechildrens.org>; Matthew Frieman <mfrieman@som.umaryland.edu>; mrolland@hivresearch.org <mrolland@hivresearch.org>; Baric, Ralph <rbaric@email.unc.edu>; Richard Webby <richard.webby@stjude.org>; Garcia-Sastre,

Adolfo <Adolfo.Garcia-Sastre@mssm.edu>; malik@hku.hk <malik@hku.hk>; Andrew B. Ward <andrew@scripps.edu>; Ali Ellebedy <ellebedy@wustl.edu>; mdiamond@wustl.edu <mdiamond@wustl.edu>; djs200@cam.ac.uk <djs200@cam.ac.uk>; jboon@wustl.edu <jboon@wustl.edu>; Aubree Gordon <gordonal@umich.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; Van bakel, Harm <harm.vanbakel@mssm.edu>; Graham, Barney (NIH/VRC) [E] <bgraham@mail.nih.gov>; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Munster, Vincent (NIH/NIAID) [E] <vincent.munster@nih.gov>; Koup, Richard (NIH/VRC) [E] <rkoup@mail.nih.gov>; Seder, Robert (NIH/VRC) [E] <rseder@mail.nih.gov>; Ghedin, Elodie (NIH/NIAID) [E] <elodie.ghedin@nih.gov>; Alessandro Sette <alex@lji.org>; Adam Godzik <Adam.Godzik@medsch.ucr.edu>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Roberts, Chris (NIH/NIAID) [E] <paul.roberts@nih.gov>; Schotsaert, Michael <michael.schotsaert@mssm.edu>; MacCannell, Duncan (CDC/DDID/NCEZID/OD) <fms2@CDC.GOV>; Weiss, Carol (FDA/CBER) <Carol.Weiss@fda.hhs.gov>; Wentworth, David E. (CDC/DDID/NCIRD/ID) <gll9@cdc.gov>; Nelson Michael <nelson.l.michael2.civ@mail.mil>; gregory.d.gromowski.civ@mail.mil <gregory.d.gromowski.civ@mail.mil>; irina.maljkovicberry.ctr@mail.mil <irina.maljkovicberry.ctr@mail.mil>; jeffrey.r.currier.civ@mail.mil <jeffrey.r.currier.civ@mail.mil>; Vincent, Leah (NIH/NIAID) [E] <leah.vincent@nih.gov>; tbedford@fredhutch.org <tbedford@fredhutch.org>; Patrick C. Wilson <wilsonp@uchicago.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; Douek, Daniel (NIH/VRC) [E] <ddouek@mail.nih.gov>
Cc: David Montefiori, Ph.D. <david.montefiori@duke.edu>; Michael, Nelson <nmichael@hivresearch.org>; Zhou, Bin (CDC/DDID/NCIRD/ID) <nmb7@cdc.gov>; Peter Halfmann <peter.halfmann@wisc.edu>; Holbrook, Michael (NIH/NIAID) [C] <michael.holbrook@nih.gov>; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; Gardner, Meredith Elizabeth Davis <meredith.davis.gardner@emory.edu>; Weaver, Scott <sweaver@UTMB.EDU>
Subject: SARS-CoV-2 Variant Testing pipeline
When: Friday, April 2, 2021 8:30 AM-9:30 AM.
Where: https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09

Hello everyone,
Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.
If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.
Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.
Thank you, and looking forward to speaking on Friday February 12th.
Marciela
Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.
Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09
Meeting ID: 160 266 4950
Passcode: 073903
One tap mobile
+16692545252,,1602664950#,,,,*073903# US (San Jose)
+16468287666,,1602664950#,,,,*073903# US (New York)
Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
833 568 8864 US Toll-free
Meeting ID: 160 266 4950
Passcode: 073903
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u
Join by SIP
1602664950@sip.zoomgov.com
Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: 073903

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili

(changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; a.luttick[a.luttick@360biolabs.com]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; arjun.rustagi[arjun.rustagi@stanford.edu]; sastanley[sastanley@berkeley.edu]; Pillai, Satish[Satish.Pillai@ucsf.edu]; joe[joe@czbiohub.org]; raul.andino[raul.andino@ucsf.edu]; charles.chiu[charles.chiu@ucsf.edu]; GSimmons[GSimmons@vitalant.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; amy.kistler[amy.kistler@czbiohub.org]; cblish[cblish@stanford.edu]; bertozzi[bertozzi@stanford.edu]; tdcarroll[tdcarroll@ucdavis.edu]; douglas_fox[douglas_fox@berkeley.edu]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; t.desilva[t.desilva@sheffield.ac.uk]; Lance.Turtle[Lance.Turtle@liverpool.ac.uk]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; William James[william.james@path.ox.ac.uk]; Meera.Chand[Meera.Chand@phe.gov.uk]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; KurtW[KurtW@nicd.ac.za]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; viviana.simon[viviana.simon@mssm.edu]; pintol[pintol@mail.nih.gov]; kemptj[kemptj@mail.nih.gov]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Camille Escadafal[Camille.Escadafal@finddx.org]; Cassels, Fred[fcassels@path.org]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 3/29/2021 6:54:55 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday March 31 2:30PM CET (Geneva Time)

1. Thushan de Silva (U. Sheffield) & Lance Turtle (U. Liverpool)- *T-cell and antibody responses to first BNT162b2 vaccine dose in previously SARS-CoV-2-infected and infection-naive UK healthcare workers: a multicentre, prospective, observational cohort study.*
2. Simon Funnell (PHE) - *An update on the CEPI funded Agility project*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, March 28, 2021 1:30 PM
To: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; 'HENAO RESTREPO, Ana Maria'; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya;

zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; Jacqueline.Fryer@nibsc.org; Kevin Bewley (Kevin.bewley@phe.gov.uk)
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, March 31, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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3612568290@zoomcrc.com

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162.255.37.11 (US West)
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115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)

213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Alana Centilli[acentilli@southernresearch.org]; Alec Hirsch[hirschal@ohsu.edu]; Amelia George[Amelia.s.george@vumc.org]; Anish Avadukoot[avadukoot@southernresearch.org]; Ardina Pruijssers[ardina.pruijssers@vumc.org]; Ashish Pathak[apathak@southernresearch.org]; Babu Tekwani[btekwani@southernresearch.org]; Bob Bostwick[bostwick@southernresearch.org]; Carrie Evans[evans@southernresearch.org]; Chad Petit[cpetit@uab.edu]; Chelsea Tompkins[ctompkins@peds.uab.edu]; Clare O'Regan[coregan@wustl.edu]; Corinne Augelli-Szafran[caugelli-szafran@southernresearch.org]; Daniel Streblow[streblow@ohsu.edu]; Erica Bitten[erica.bitten@emory.edu]; Fahim Ahmad[fahmad@southernresearch.org]; George Painter[george.r.painter@emory.edu]; Greg Bluemling[gblueml@emory.edu]; Jay Nelson[nelsonj@ohsu.edu]; Jessica Smith[smijessi@ohsu.edu]; Kathy Keith[kak@uab.edu]; Lynn Rasmussen[rasmussen@southernresearch.org]; Maria Agostini[Maria.l.agostini@vanderbilt.edu]; Mark Denison[mark.denison@vumc.org]; Mark Heise[mark_heisem@med.unc.edu]; Mark Suto[suto@southernresearch.org]; Mason Wu[mwu@southernresearch.org]; Michael Diamond[diamond@borcim.wustl.edu]; Miranda Nebane[nebane@southernresearch.org]; Narayan Chaurasiya[nchaurasiya@southernresearch.org]; Nicole Haese[haese@ohsu.edu]; Omar Moukha-Chafiq[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; Rachel Graham[rlgraham@email.unc.edu]; Ralph Baric[rbaric@email.unc.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Ron Swanstrom[risunc@med.unc.edu]; Sarah M. Dowdy[smdowdy@peds.uab.edu]; Shalisa Sanders[ssanders@southernresearch.org]; Shilpa Dutta[sdutta@southernresearch.org]; Shuntai Zhou[shuntaiz@email.unc.edu]; Sixue Zhang[szhang66@uab.edu]; Stephanie Moore[smoore@peds.uab.edu]; Thomas Morrison[thomas.morrison@ucdenver.edu]; Tia Hughes[tia.m.hughes@vumc.org]; Tim Sheahan[sheahan@email.unc.edu]; Toni Baric[antoinette_baric@med.unc.edu]; Victor DeFilippis[defilipp@ohsu.edu]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Stephanie Moore[smoore@peds.uab.edu]; Sara Davis[sadavis@peds.uab.edu]
From: Sarah M. Dowdy[smdowdy@peds.uab.edu]
Sent: Fri 4/2/2021 2:01:51 PM (UTC-05:00)
Subject: AD3C Year 3 NOA: Subawards

Dear AD3C Project Leaders,

We are pleased to inform you that UAB has received the NOA for Year 3!

Antiviral Drug Discovery and Development Center (AD3C)
5U19AI142759-03
Year 3: 3/1/2021 – 2/28/2022

NIH has fully funded our Year 3 request, so you can expect your subawards to match the budgets you submitted with the last RPPR. We are now drafting the subaward requests for our OSP.

- IACUC approval: If you have an updated Animal Research IACUC approval, please provide this document to us.
- FINAL INVOICES: You have 60 days to invoice after the end of the period – deadline end of this month. To date, only 1 site has sent me a Final Invoice. Please remind your financial support to submit these.

Thank you for all your hard work!

Sarah M. Dowdy, MPH | Clinical Research Administrator III
UAB | The University of Alabama at Birmingham

Department of Pediatrics, Infectious Diseases
CHB 303D | 1600 7th Ave South | Birmingham, AL 35233
P: 205.638.2606

Department of Pediatrics, Neurology
CIRC 235A | 1719 6th Ave South | Birmingham, AL 35294
P: 205.996.7633 | F: 205.996.7333

smdowdy@peds.uab.edu

(Telecommuting intermittently as of 16Mar2020. If you are not able to reach me at above phone, please call my cell 205.441.0862)

To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili

(changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; a.luttick[a.luttick@360biolabs.com]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; arjun.rustagi[arjun.rustagi@stanford.edu]; sastanley[sastanley@berkeley.edu]; Pillai, Satish[Satish.Pillai@ucsf.edu]; joe[joe@czbiohub.org]; raul.andino[raul.andino@ucsf.edu]; charles.chiu[charles.chiu@ucsf.edu]; GSimmons[GSimmons@vitalant.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; amy.kistler[amy.kistler@czbiohub.org]; cblish[cblish@stanford.edu]; bertozzi[bertozzi@stanford.edu]; tdcarroll[tdcarroll@ucdavis.edu]; douglas_fox[douglas_fox@berkeley.edu]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; t.desilva[t.desilva@sheffield.ac.uk]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; William James[william.james@path.ox.ac.uk]; Meera.Chand[Meera.Chand@phe.gov.uk]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; KurtW[KurtW@nicd.ac.za]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; viviana.simon[viviana.simon@mssm.edu]; pintol[pintol@mail.nih.gov]; kemptj[kemptj@mail.nih.gov]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Camille Escadafal[Camille.Escadafal@finddx.org]; Cassels, Fred[fcassels@path.org]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 4/13/2021 10:43:31 AM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday April 14 2:30PM CET (Geneva Time)

1. Prabuddha Kundu (Premas Biotech) - *SARS CoV2 Antigens and Multiplexed ELISA Platform for Sero surveillance*
2. Julian Hiscox (U. Liverpool) - *Sequence analysis of SARS-CoV-2 in nasopharyngeal samples from patients with COVID-19 illustrates population variation and diverse phenotypes, placing the in vitro growth properties of B.1.1.7 and B.1.351 lineage viruses in context*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, April 11, 2021 7:47 AM
To: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Krause, Philip; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; Crozier, Ian (NIH) [C]; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya;

zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema; Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; cjmiller@UCDAVIS.EDU; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; Jacqueline.Fryer@nibsc.org; Kevin.Bewley@phe.gov.uk; Camille.Escadafal@finddx.org; fcassels@path.org; Carol.Sabourin@hhs.gov; Yusibov, Vidadi (OS/ASPR/BARDA)
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, April 14, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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To: alex.sigal@ahri.org[alex.sigal@ahri.org]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Griffiths, Anthony[ahgriff@bu.edu]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov]; sot1@cdc.gov[sot1@cdc.gov]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; malik (malik@hku.hk)[malik@hku.hk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; sujan@lji.org[sujan@lji.org]; daniela@lji.org[daniela@lji.org]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; changguili

(changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; tcs38@psu.edu[tcs38@psu.edu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; jma[jma@sgul.ac.uk]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Kelvin, Alyson[alyson.kelvin@usask.ca]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; ramadany[ramadany@sfda.gov.sa]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; KAZI, Fatema[kazif@who.int]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; a.luttick[a.luttick@360biolabs.com]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; arjun.rustagi[arjun.rustagi@stanford.edu]; sastanley[sastanley@berkeley.edu]; Pillai, Satish[Satish.Pillai@ucsf.edu]; joe[joe@czbiohub.org]; raul.andino[raul.andino@ucsf.edu]; charles.chiu[charles.chiu@ucsf.edu]; GSimmons[GSimmons@vitalant.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; amy.kistler[amy.kistler@czbiohub.org]; cblish[cblish@stanford.edu]; bertozzi[bertozzi@stanford.edu]; tdcarroll[tdcarroll@ucdavis.edu]; douglas_fox[douglas_fox@berkeley.edu]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; t.desilva[t.desilva@sheffield.ac.uk]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; William James[william.james@path.ox.ac.uk]; Meera.Chand[Meera.Chand@phe.gov.uk]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; KurtW[KurtW@nicd.ac.za]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; viviana.simon[viviana.simon@mssm.edu]; pintol[pintol@mail.nih.gov]; kemptj[kemptj@mail.nih.gov]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Camille Escadafal[Camille.Escadafal@finddx.org]; Cassels, Fred[fcassels@path.org]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]

Cc: Iturriza-Gomara, Miren[miturrizagomara@path.org]; engeong.ooi@duke-nus.edu.sg[engeong.ooi@duke-nus.edu.sg]; Darin Edwards[darin.edwards@modernatx.com]

From: SCHWARTZ, Lauren[schwartzl@who.int]

Sent: Mon 4/19/2021 4:27:27 PM (UTC-05:00)

Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday April 21 2:30PM CET (Geneva Time)

1. Darin Edwards (Moderna) - *Updated mRNA vaccines to address SARS-CoV-2 variants that drive reduction in neutralization*
2. Eng Eong Ooi (Duke NUS) - *T cells as correlates of protection from Covid-19*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, April 18, 2021 1:31 PM
To: SCHWARTZ, Lauren; alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; munoz-fontela@bnitm.de; ahgriff@bu.edu; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; Vasan.Vasan@csiro.au; eric.vangieson@darpa.mil; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; david.montefiori@duke.edu; sarah.mudrak@duke.edu; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Krause, Philip; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; cheryl@gisaid.org; christian.brechot@pasteur.fr; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; mksong@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; sujan@lji.org; daniela@lji.org; Liz.Miller@lshtm.ac.uk; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Barbara.Schnierle@pei.de; tcs38@psu.edu; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; rafael.delgado@salud.madrid.org; y.m.vasiliev@spbniivs.ru; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; d.goldblatt@ucl.ac.uk; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; rbaric@email.unc.edu; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; 'KNEZEVIC, Ivana'; SCHWARTZ, Lauren; SWAMINATHAN, Soumya; zlshi@wh.iov.cn; Youngmee Jee; ramadany@sfda.gov.sa; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; KAZI, Fatema;

Jiae Kim; Ruben.Donis@hhs.gov; alankhoo.imr@gmail.com; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; cjmiller@UCDAVIS.EDU; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; Jacqueline.Fryer@nibsc.org; Kevin.Bewley@phe.gov.uk; Camille.Escadafal@finddx.org; fcassels@path.org; Carol.Sabourin@hhs.gov; Vidadi.Yusibov@hhs.gov
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, April 21, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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Join by SIP
3612568290@zoomcrc.com

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162.255.37.11 (US West)
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Meeting ID: 361 256 8290

To: Macoubray, Aaron[amacoubray@rti.org]; Macoubray, Aaron[amacoubray@rti.org]; Garry, Robert F[rfgarry@tulane.edu]; Cross, Robert W.[rwcross@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; MacDonald, Pia[pmacdonald@rti.org]; Pardis Sabeti[pardis@broadinstitute.org]; Kristian Andersen[andersen@scripps.edu]; Bronwyn MacInnis[bronwyn@broadinstitute.org]; mmgraw[mmgraw@scripps.edu]; Kevin Olival[olival@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; Linde, Amber (NIH/NIAID) [E][amber.linde@nih.gov]; julie.dyall@nih.gov[julie.dyall@nih.gov]; Weldon, Caroline[caweldon@UTMB.EDU]; Hongying Li[li@ecohealthalliance.org]; Cadhla Firth[firth@ecohealthalliance.org]; linfa.wang[linfa.wang@duke-nus.edu.sg]; Eric Laing[eric.laing@usuhs.edu]; rbaric@email.unc.edu[rbaric@email.unc.edu]; christopher.broder@usuhs.edu[christopher.broder@usuhs.edu]; Aleksei Chmura[chmura@ecohealthalliance.org]; Emily Hagan[hagan@ecohealthalliance.org]; Shi, Pei yong[peshi@UTMB.EDU]; McLellan, Susan[sumclell@UTMB.EDU]; Paessler, Slobodan[SLPAESSL@utmb.edu]; Megan Averill[megan.averill@duke.edu]; Vasilakis, Nikolaos[nivasila@utmb.edu]; kga1978@gmail.com[kga1978@gmail.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]; Florese, Ruth (NIH/NIAID) [E][ruth.florese@nih.gov]
From: Quiner, Claire[cquiner@rti.org]
Sent: Fri 4/23/2021 4:38:07 PM (UTC-05:00)
Subject: EBOV discussion follow up
CREID_EBOV Discussion_Minutes.docx

Thank you everyone for the robust discussion and knowledge sharing today. See the attached minutes and the items for follow up below:

EBOV Discussion Follow up:

1. Slobodan Paessler (UTMB) will explore his connections from CDC HIV labs which routinely get samples out
    a. One located in Jaws and the other is in Abuja
    b. Will forward contact to Sara W.
2. Jean will follow up with Division of AIDS (DAIDS) colleagues to see if there is any additional local support for this
3. Moody and company will provide general ideas on the cold chain problems, share barcode methods, vendors and SOPs. Will share over email

Have a wonderful weekend.

Best,
Claire

Claire A. Quiner, MPH, MCP
she/her/hers

RTI International
Research Public Health Analyst
Global Public Health Impact Center
3040 Cornwallis Road
Research Triangle Park, NC 27709
Email: cquiner@rti.org

CREID EBOV Discussion Notes

Participants: Bob Garry, Bob Cross, Scott Weaver, Pia MacDonald, Tony Moody, Slobodan Paessler, Jean Patterson, Sara Woodson, Susan McLellan, Candice Beaubien, Ruth Florese, Julie Dyall, Amber Linde, Chris Broder, Claire Quiner, Megan Averill, Hongying Li, Aaron Macoubray

Agenda:

1. Relevance of and most pressing research questions of purported 5 yr recrudescence of EBOV Options/recommendations for enhancing infrastructure including biorepository and inventory system – specifically cold chain power supply.
2. Also, recommendations for inventory software and SOPs

MINUTES

- EBOV Update - DRC
  - 11 confirmed cases, 6 deaths. Mostly in the eastern part of the country
  - Likely recrudescence and sexual transmission
- EBOV Update – Guinea
  - Likely also recrudescence
  - Not quite settled. 23 cases (16 confirmed, 12 deaths)
  - Sequence data suggests this is a case of recrudescence
  - 5000+ people vaccinated
  - 4 new cases reported in April

Discussion –

- Another update re: Sierra Leone
  - Active effort to solidify the borders and limit traffic between countries.
- International help ongoing
  - Molecular reagents and RDTs
  - Brought PPEs
- Suspected cases in Sierra Leone could likely be Lassa
- J&J has donated a large number of vaccines to Sierra Leone
- Bob Cross scheduled to engage field activities (mosquito trapping, bat trapping, etc.) in support of other partners
- Were any of the confirmed cases previously vaccinated?
  - Not sure, but probably not
  - Vaccine rollout has not been particularly robust
- Pia: How has the CREID focused research changed with this outbreak? Did you pivot to do this?
  - Bob: Goal was to look into trapping efforts on the border with Guinea
  - Large deforestation going on. Could be driving bat populations away from Sierra Leone
- Fewer cases of COVID-19 in Sierra Leone. Even before these outbreaks, were planning some of these trips
- Does Sierra Leone have access to enough testing to really understand the COVID situation?
  - They have been doing some sequencing. Maybe not ideal, but don't think there is rampant COVID-19 there
  - There is a network of testing centers around the country including Kenema

- Could be some resistance to beta-coronaviruses in West Africa
    - Need to look into this
- What is currently known about persistence of EBOV in humans?
    - Ebola is an endemic disease that allows it to get into many hosts
    - In monkeys, it can be found in the eyes and the reproductive system, but usually connected to the vasculature.
    - Once the virus gets into the tissues, they are harder to clear with monoclonal antibodies
    - Might be interesting to connect a COVID-19 case to these EBOV cases. May depress the immune system enough to cause some shedding
    - Evidence of the same organs having been affected in humans as shown in monkeys
    - Longitudinal studies will be really important. Need to set up more long-term programs
- Sierra Leone has the most survivors
    - Many are involved in survivor trials
- Sociological questions re: stigma, antisocial behaviors towards survivors
    - Need to get the messaging right about dealing with survivors
    - Real possibility that we could prevent or suppress reemergence of the virus by giving these people vaccinations
- After the last major outbreak was there evidence of spillback into wildlife?
    - It is a possibility, but less likely than it being hosted in humans
    - Not even sure what Ebola does in its natural reservoir
        i. Likely bats have it and are shedding
    - Important to do ecological analysis
- Can you use the molecular clock to determine whether this was recrudescence?
    - Clock was slowed down. Only about 5 mutations of the period of time, compared to 18-20. Unlikely to happen in a reservoir
- Opens the door to Lassa which resides in the rodent population and is persistent
    - Persistence in humans not well understood
    - Hope to be able to treat late cases of Lassa to figure out whether recrudescence is possible
- Need to look at survivors to help understand what is going on in terms of reemergence

What is the sampling availability for these samples?

- Cold chain is an issue.
- Power is an issue
- Would take a couple million dollars to stabilize things
- Logistics of getting samples was not previously an issue. Effective despite power issues. After the Ebola outbreak and other NGOs came in, there were issues around moving samples without approvals, everything was tightened significantly, so it is much more difficult now.
    - High stress to work up samples in country
    - Kenema working towards building up the solar system.
    - Could use assistance to best set this up
    - Battery life is different in that part of the world compared to the US
- Slobodan: In Jos, there is a large HIV center funded by NIH with a robust energy network. Very well set up. They collect Lassa patient samples.
    - Could be useful to connect with who is in charge of that
- Sara: Would the SL government allow samples to be temporarily stored in Nigeria?

    - Bob: Discussed moving samples to another lab with working freezers in Sierra Leone, but shot down
        i. Want their own power systems repaired
        ii. If actively working towards that, could use other temporary solutions
    - Slobodan: Through CDC Nigeria, they can get anything out. Very willing to share
- May want to consider Freetown. They have more stable power
    - Discussed this too, but the focus is getting the power set up in Kenema and self sufficient
- How necessary is a -80 freezer if you have liquid nitrogen?
    - Could be an option to put another nitrogen machine there that's good
    - Might actually be more efficient to run a nitrogen machine vs. consistent power
- Solar could potentially power the hospital with a large enough solar farm
- Key to getting samples out of Nigeria is all through NCDC now. Helped to get everything to NCDC and have them ship samples.
- Can you reconstruct EBOV in the lab?
    - Have reverse genetics in the lab and have been working with CDC. This is in the architecture of the grant as a backup plan

Inventory system

- Old school, paper based.
    - Samples catalogued or aliquoted
    - Not catalogued
- Need something easy, lower tech
    - Not yet moved to a barcoding system
- Tony: Lots of experience barcoding and inventory management systems
    - Inventory systems: everything will be a lift
    - Need to develop a list of all the vendors
        - Are there import export restrictions on any of these?
- Tony and the biorepository can work to pull all of these things together as it will be a value to everyone
    - Can come up with recommendations and options
    - Would recommend barcoding and an electronic system

EBOV Discussion Follow up:

1. Slobodan "Boba" Paessler will explore his connections from CDC HIV labs which routinely get samples out
    a. One located in Jos and the other is in Abuja
    b. Will forward contact to Sara W.
2. Jean will follow up with DAIDS (Division of AIDS) colleagues to see if there is any additional local support for this
3. Moody and company will provide general ideas on the cold chain problems, share barcode methods, vendors and SOPs. Will share over email

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Mon 4/26/2021 7:25:29 PM (UTC-05:00)
Subject: RE: Congratulations!

Hi Pei-Yong, Thanks, I look forward to lifting a beer together when we get past the pandemic. Hope you are well. Ralph

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From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Monday, April 26, 2021 6:18 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Congratulations!

Dear Ralph,

Congratulations for being elected to the National Academy of Sciences! It is a well-deserved recognition.

All my best wishes from Galveston!

Pei-Yong

To: Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; a.luttick[a.luttick@360biolabs.com]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Kelvin, Alyson[alyson.kelvin@usask.ca]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; malik (malik@hku.hk)[malik@hku.hk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; ramadany[ramadany@sfda.gov.sa]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; alex.sigal@ahri.org[alex.sigal@ahri.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; KAZI, Fatema[kazif@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; jma[jma@sgul.ac.uk]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; t.desilva[t.desilva@sheffield.ac.uk]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; William James[william.james@path.ox.ac.uk]; Meera.Chand[Meera.Chand@phe.gov.uk]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; KurtW[KurtW@nicd.ac.za]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Griffiths, Anthony[ahgriff@bu.edu]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov];

sot1@cdc.gov[sot1@cdc.gov]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; daniela@lji.org[daniela@lji.org]; Krammer, Florian[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; tcs38@psu.edu[tcs38@psu.edu]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; Theodora Hatziioannou[thatziio@rockefeller.edu]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; arjun.rustagi[arjun.rustagi@stanford.edu]; sastanley[sastanley@berkeley.edu]; Pillai, Satish[Satish.Pillai@ucsf.edu]; joe[joe@czbiohub.org]; raul.andino[raul.andino@ucsf.edu]; charles.chiu[charles.chiu@ucsf.edu]; GSimmons[GSimmons@vitalant.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; amy.kistler[amy.kistler@czbiohub.org]; cblish[cblish@stanford.edu]; bertozzi[bertozzi@stanford.edu]; tdcarroll[tdcarroll@ucdavis.edu]; douglas_fox[douglas_fox@berkeley.edu]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; viviana.simon[viviana.simon@mssm.edu]; pintol[pintol@mail.nih.gov]; kemptj[kemptj@mail.nih.gov]; Cassels, Fred[fcassels@path.org]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; sujan@lji.org[sujan@lji.org]; Camille Escadafal[Camille.Escadafal@finddx.org]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 4/26/2021 6:47:35 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

For this week's meeting, we are deviating from the usual presentation format and will have a panel discussion instead. The

discussion will focus on immune assays for SARS-CoV-2 variants and the use of the WHO International Standard.

Best,
Lauren - Bill, Simon and César

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, April 25, 2021 9:53 AM
To: Vasan.Vasan@csiro.au; a.luttick@360biolabs.com; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; liyl@cde.org.cn; liub@cde.org.cn; tlying@fudan.edu.cn; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; baihe@nmpa.gov.cn; zlshi@wh.iov.cn; mafranco@javeriana.edu.co; rawcraig@yahoo.com; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; emmanuelle.charton@edqm.eu; BUDA Mihaela; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; munoz-fontela@bnitm.de; christian.drosten@charite.de; Barbara.Schnierle@pei.de; rafael.delgado@salud.madrid.org; cheryl@gisaid.org; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; christian.brechot@pasteur.fr; jokim@ivi.int; mksong@ivi.int; dboyle@path.org; tdelossantos@path.org; bleader@path.org; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'KNEZEVIC, Ivana'; SWAMINATHAN, Soumya; malik@hku.hk; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; dancohen@tauex.tau.ac.il; Youngmee Jee; alankhoo.imr@gmail.com; celine.gurry@cepi.net; y.m.vasiliev@spbniivs.ru; ramadany@sfda.gov.sa; linfa.wang@duke-nus.edu.sg; engeong.ooi@duke-nus.edu.sg; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon@korea.kr; limhy0919@korea.kr; angeliki.melidou@ecdc.europa.eu; Eeva Broberg; qiang.pan-hammarstrom@ki.se; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; supaporn.p@dmsc.mail.go.th; pilailuk.o@dmsc.mail.go.th; pawinee.k@redcross.or.th; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; fjc37@cam.ac.uk; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; r.tedder@imperial.ac.uk; katie.doores@kcl.ac.uk; Liz.Miller@lshtm.ac.uk; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; jma@sgul.ac.uk; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; teresa.lambe@ndm.ox.ac.uk; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; Jacqueline.Fryer@nibsc.org; Kevin.Bewley@phe.gov.uk; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; ahgriff@bu.edu; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; sarah.mudrak@duke.edu; Mayra.Garcia@fda.hhs.gov; Krause, Philip; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; jmcelrat@fredhutch.org; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; vyusibov@indianabiosciences.org; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; daniela@lji.org; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; william.lee@health.ny.gov; tcs38@psu.edu; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; msalit@stanford.edu; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; rbaric@email.unc.edu; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; SCHWARTZ, Lauren; thatziio@rockefeller.edu; Jiae Kim; Ruben.Donis@hhs.gov; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu;

charles.chiu@ucsf.edu; GSimmons@vitalant.org; cjmiller@UCDAVIS.EDU; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; fcassels@path.org; Carol.Sabourin@hhs.gov; Vidadi.Yusibov@hhs.gov; miturrizagomara@path.org; david.montefiori@duke.edu; sujan@lji.org; Camille.Escadafal@finddx.org
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, April 28, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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To: Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; a.luttick[a.luttick@360biolabs.com]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Kelvin, Alyson[alyson.kelvin@usask.ca]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; liub (liub@cde.org.cn)[liub@cde.org.cn]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; johan.holst@cepi.net[johan.holst@cepi.net]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Peter Daszak[daszak@ecohealthalliance.org]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Boyle, David[dboyle@path.org]; de los Santos, Tala[tdelossantos@path.org]; Leader, Troy[bleader@path.org]; COSTA, Alejandro Javier[costaa@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; MORGAN, Oliver[omorgan@who.int]; PERKINS, Mark[perkinsm@who.int]; RIVEROS BALTA, Ximena[lauriex@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; YOO, Si Hyung[yoos@who.int]; SUBISSI, Lorenzo[subissil@who.int]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; ZHOU, Tiequn[ZhouT@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SWAMINATHAN, Soumya[swaminathans@who.int]; malik (malik@hku.hk)[malik@hku.hk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Celine Gurry (Celine.gurry@cepi.net)[Celine.gurry@cepi.net]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; ramadany[ramadany@sfda.gov.sa]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; alex.sigal@ahri.org[alex.sigal@ahri.org]; pennym@nicd.ac.za[pennym@nicd.ac.za]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; STRÖHER, Ute[stroheru@who.int]; SANDS, Anita[sandsa@who.int]; BRANGEL, Polina[brangelp@who.int]; KAZI, Fatema[kazif@who.int]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; jma[jma@sgul.ac.uk]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; t.desilva[t.desilva@sheffield.ac.uk]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; William James[william.james@path.ox.ac.uk]; Meera Chand[Meera.Chand@phe.gov.uk]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; KurtW[KurtW@nicd.ac.za]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Griffiths, Anthony[ahgriff@bu.edu]; SGalloway@cdc.gov[SGalloway@cdc.gov]; lny1@cdc.gov[lny1@cdc.gov]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; mbo2@cdc.gov[mbo2@cdc.gov];

sot1@cdc.gov[sot1@cdc.gov]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; Krause, Philip[philip.krause@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; Peden, Keith[keith.peden@fda.hhs.gov]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; shane@lji.org[shane@lji.org]; erica (erica@lji.org)[erica@lji.org]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; alex@lji.org[alex@lji.org]; daniela@lji.org[daniela@lji.org]; Krammer, Florian[florian.krammer@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; tcs38@psu.edu[tcs38@psu.edu]; Alter, Galit[galter@partners.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; gweiss@uci.edu[gweiss@uci.edu]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ydm9@cdc.gov[ydm9@cdc.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Shi, Pei yong[peshi@UTMB.EDU]; Lisa@amicitiam.com[Lisa@amicitiam.com]; PNorris@vitalant.org[PNorris@vitalant.org]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; Theodora Hatziioannou[thatziio@rockefeller.edu]; jakim[jakim@hivresearch.org]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; arjun.rustagi[arjun.rustagi@stanford.edu]; sastanley[sastanley@berkeley.edu]; Pillai, Satish[Satish.Pillai@ucsf.edu]; joe[joe@czbiohub.org]; raul.andino[raul.andino@ucsf.edu]; charles.chiu[charles.chiu@ucsf.edu]; GSimmons[GSimmons@vitalant.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; amy.kistler[amy.kistler@czbiohub.org]; cblish[cblish@stanford.edu]; bertozzi[bertozzi@stanford.edu]; tdcarroll[tdcarroll@ucdavis.edu]; douglas_fox[douglas_fox@berkeley.edu]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; viviana.simon[viviana.simon@mssm.edu]; pintol[pintol@mail.nih.gov]; kemptj[kemptj@mail.nih.gov]; Cassels, Fred[fcassels@path.org]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; sujan@lji.org[sujan@lji.org]; Camille Escadafal[Camille.Escadafal@finddx.org]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; w.a.paxton@liverpool.ac.uk[w.a.paxton@liverpool.ac.uk]; rahmed[rahmed@emory.edu]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]

Cc: Clayton, Marilyn[mclayto@emory.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 5/10/2021 4:33:16 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday May 12 2:30PM CET (Geneva Time)

1. Rafi Ahmed (Emory) - *Immune Memory to COVID-19*
2. Alex Sigal (AHRI) - TBD

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 9, 2021 8:44 AM
To: Vasan.Vasan@csiro.au; a.luttick@360biolabs.com; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; scott.napper@usask.ca; tracey.thue@usask.ca; liyl@cde.org.cn; liub@cde.org.cn; tlying@fudan.edu.cn; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; baihe@nmpa.gov.cn; zlshi@wh.iov.cn; mafranco@javeriana.edu.co; rawcraig@yahoo.com; Marco.Cavaleri@ema.europa.eu; Ragini.Shivji@ema.europa.eu; emmanuelle.charton@edqm.eu; BUDA Mihaela; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; munoz-fontela@bnitm.de; christian.drosten@charite.de; Barbara.Schnierle@pei.de; rafael.delgado@salud.madrid.org; cheryl@gisaid.org; valentina.bernasconi@cepi.net; carolyn.clark@cepi.net; william.dowling@cepi.net; elwyn.griffiths@cepi.net; johan.holst@cepi.net; arun.kumar@cepi.net; amy.c.shurtleff@cepi.net; solomon.yimer@cepi.net; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; christian.brechot@pasteur.fr; jokim@ivi.int; mksong@ivi.int; dboyle@path.org; tdelossantos@path.org; bleader@path.org; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; dj56wood@gmail.com; ZHOU, Tiequn; 'KNEZEVIC, Ivana'; SWAMINATHAN, Soumya; malik@hku.hk; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; dancohen@tauex.tau.ac.il; Youngmee Jee; alankhoo.imr@gmail.com; celine.gurry@cepi.net; y.m.vasiliev@spbniivs.ru; ramadany@sfda.gov.sa; linfa.wang@duke-nus.edu.sg; engeong.ooi@duke-nus.edu.sg; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon@korea.kr; limhy0919@korea.kr; angeliki.melidou@ecdc.europa.eu; Eeva Broberg; qiang.pan-hammarstrom@ki.se; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; supaporn.p@dmsc.mail.go.th; pilailuk.o@dmsc.mail.go.th; pawinee.k@redcross.or.th; b.haagmans@erasmusmc.nl; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; fjc37@cam.ac.uk; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@dstl.gov.uk; JLPRIOR@dstl.gov.uk; r.tedder@imperial.ac.uk; katie.doores@kcl.ac.uk; Liz.Miller@lshtm.ac.uk; Giada.Mattiuzzo@nibsc.org; philip.minor2@gmail.com; Clare.Morris@nibsc.org; Mark.Page@nibsc.org; Nicola.Rose@nibsc.org; Christine.bruce@phe.gov.uk; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Julia.Tree@phe.gov.uk; Mary.Matheson@phe.gov.uk; jma@sgul.ac.uk; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; teresa.lambe@ndm.ox.ac.uk; t.desilva@sheffield.ac.uk; Lance.Turtle@liverpool.ac.uk; susie.dunachie@ndm.ox.ac.uk; paul.klenerman@medawar.ox.ac.uk; ellie.barnes@ndm.ox.ac.uk; william.james@path.ox.ac.uk; Meera.Chand@phe.gov.uk; Victoria.Hall@phe.gov.uk; KurtW@nicd.ac.za; Aodhan.Breathnach@stgeorges.nhs.uk; alain.townsend@imm.ox.ac.uk; Jacqueline.Fryer@nibsc.org; Kevin.Bewley@phe.gov.uk; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; Gerald.Kovacs@hhs.gov; James.Little@hhs.gov; Ashley.Smith1@hhs.gov; ahgriff@bu.edu; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; nax3@cdc.gov; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; john.c.trefry.civ@mail.mil; georgia.tomaras@duke.edu; sarah.mudrak@duke.edu; Mayra.Garcia@fda.hhs.gov; Philip.Krause@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; jmcelrat@fredhutch.org; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; dbarouch@bidmc.harvard.edu; luk_vandenberghe@meei.harvard.edu; ASiyer@mgh.harvard.edu; vyusibov@indianabiosciences.org; shane@lji.org; erica@lji.org; schendel@lji.org; alex@lji.org; daniela@lji.org; florian.krammer@mssm.edu; golinger@MRIGLOBAL.ORG; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; clint.florence@nih.gov; janet.lathey@nih.gov; erik.stemmy@nih.gov; larry.wolfraim@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; johnsonreed@niaid.nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; vincent.munster@nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; barney.graham@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; william.lee@health.ny.gov; tcs38@psu.edu; galter@partners.org; tomwhite42450@gmail.com;

pbieniasz@mail.rockefeller.edu; msalit@stanford.edu; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; stanley-perlman@uiowa.edu; MFrieman@som.umaryland.edu; mit666666@pitt.edu; jwm1@pitt.edu; rbaric@email.unc.edu; ydm9@cdc.gov; aysegul.nalca.civ@mail.mil; gustavo.f.palacios.civ@mail.mil; margaret.l.pitt.civ@mail.mil; peshi@UTMB.EDU; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; kmodjarrad@eidresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; SCHWARTZ, Lauren; thatziio@rockefeller.edu; Jiae Kim; Ruben.Donis@hhs.gov; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; satish.pillai@ucsf.edu; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; cjmiller@UCDAVIS.EDU; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; viviana.simon@mssm.edu; pintol@mail.nih.gov; kemptj@mail.nih.gov; fcassels@path.org; Carol.Sabourin@hhs.gov; Vidadi.Yusibov@hhs.gov; miturrizagomara@path.org; david.montefiori@duke.edu; sujan@lji.org; Camille.Escadafal@finddx.org; g.pollakis@liverpool.ac.uk; w.a.paxton@liverpool.ac.uk; rahmed@emory.edu; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, May 12, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: rbaric@email.unc.edu[rbaric@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Rahm Gummuluru[rgummulu@bu.edu]; Cheng, Genhong[GCheng@mednet.ucla.edu]; Chen, Benjamin[benjamin.chen@mssm.edu]; Mothes, Walther[walther.mothes@yale.edu]; Iwasaki, Akiko[akiko.iwasaki@yale.edu]; Freed, Eric (NIH/NCI) [E][efreed@mail.nih.gov]; paul.spearman@cchmc.org[paul.spearman@cchmc.org]; 'Weiss, Susan'[weisssr@pennmedicine.upenn.edu]; tgallag@luc.edu[tgallag@luc.edu]; sbaker1@luc.edu[sbaker1@luc.edu]; peter.palese@mssm.edu[peter.palese@mssm.edu]; spg1@columbia.edu[spg1@columbia.edu]; hsmalik@fredhutch.org[hsmalik@fredhutch.org]; memerman@fredhutch.org[memerman@fredhutch.org]; Su, Lishan[lishan_su@med.unc.edu]
From: Liu, Shan-Lu[liu.6244@osu.edu]
Sent: Fri 5/21/2021 10:25:14 AM (UTC-05:00)
Subject: Faculty Position in Emerging and Re-emerging Viruses at The Ohio State University
Virology Faculty Positions at OSU.pdf

Dear colleagues:

Greetings! I hope you all are doing well.

We have several virology positions opening – see below and attached, and I would very much appreciate it if you could help forward the email to some potentially interested individuals.

Thank you so much!

Shan-Lu

Multiple Faculty Positions in Emerging and Re-emerging Viruses

The Ohio State University College of Veterinary Medicine invites applications for multiple research-intensive tenure-track faculty positions at the Assistant or Associate Professor level in emerging and re-emerging viruses that expand and build upon our programmatic strengths, expertise, assets and impact. Areas of interest include, but are not limited to virus-host interactions, animal models, ecology, immunology, genetics and evolution, structural biology, and zoonotic transmission. Successful candidates will join a highly interactive virology and infectious disease research community on campus that is an integral part of the university's Infectious Disease Institute, including the Center for Retrovirus Research, Center of Microbiome Science, and a newly NIH-funded center, STOP-COVID. These positions are part of the university's new initiatives on research for academic excellence. The College of Veterinary Medicine has a long and outstanding history of research excellence in Signature Programs, including research focus areas in infectious diseases, comparative oncology, neuromusculoskeletal sciences, molecular virology, epidemiology, and vaccine development.

Applicants should have a doctoral degree (PhD, DVM, MD or equivalent) with advanced training in virology, viral immunology or related fields. Academic rank and salary are commensurate with experience. Candidates at the rank of Associate Professor should have demonstrated research productivity and evidence of an independently funded and sustainable research program, as well as experience working with interdisciplinary research teams. Candidates at the rank of Assistant Professor should have training, experience, excellent scholarship, and demonstrated evidence of the likelihood of obtaining and maintaining an independently funded and sustainable research program. All candidates should have interest in programmatic synergy with existing members of the Ohio State faculty.

Columbus, Ohio's capital and largest city and the 14th largest city in the US, offers a wide range of affordable housing, many cultural and recreational opportunities, excellent schools, easy commute and a strong economy with growing industries in biomedical science, finance, insurance, healthcare, retail and e-commerce and information technology. Columbus has consistently been rated as one of the top U.S. cities for quality of life and one of the best places for business and careers in part due to a strong multicultural population and efforts to foster and embrace diversity, equity and inclusion. Residents enjoy the many amenities of the city including professional sports teams, museums, Columbus Zoo and Aquarium, outstanding restaurants, performing arts, metro parks, and more.

Applications should be submitted via email as a single PDF including (1) a cover letter; (2) curriculum vitae; (3) a summary of past research accomplishments; (4) a statement that addresses (i) your future research directions, (ii) your teaching and mentoring philosophy, and (iii) how you foresee integrating diversity and inclusion into your research, teaching and professional service; and (5) the names and contact information of four professional references.

Application materials should be submitted to Casey Hofmann (hofmann.75@osu.edu), or via website: https://www.nature.com/naturecareers/job/open-faculty-search-the-ohio-state-university-osu-739648. Review of applications will begin June 1, 2021 and continue until positions are filled. Inquiries may be directed to the chair of the search committee, Dr. Shan-Lu Liu (liu.6244@osu.edu).

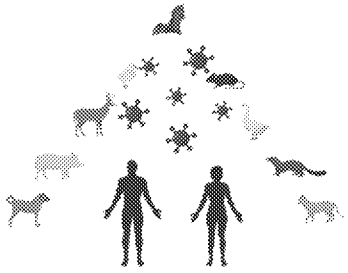
The Ohio State University is committed to establishing a culturally and intellectually diverse environment, encouraging all members of our learning community to reach their full potential. We are responsive to dual-career families and strongly promote work-life balance to support our community members through a suite of institutional policies. To build a diverse workforce, qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, or protected veteran status. EEO/AA employer.

Multiple Faculty Positions in Emerging and Re-emerging Viruses

THE OHIO STATE UNIVERSITY

The Ohio State University College of Veterinary Medicine invites applications for multiple research-intensive tenure-track faculty positions at the Assistant or Associate Professor level in emerging and re-emerging viruses that expand and build upon our programmatic strengths, expertise, assets and impact. Areas of interest include, but are not limited to virus-host interactions, animal models, ecology, immunology, genetics and evolution, structural biology, and zoonotic transmission. Successful candidates will join a highly interactive virology and infectious disease research community on campus that is an integral part of the university's Infectious Disease Institute, including the Center for Retrovirus Research, Center of Microbiome Science, and a newly NIH-funded center, STOP-COVID. These positions are part of the university's new initiatives on research for academic excellence. The College of Veterinary Medicine has a long and outstanding history of research excellence in Signature Programs, including research focus areas in infectious diseases, comparative oncology, neuromusculoskeletal sciences, molecular virology, epidemiology, and vaccine development.

Applicants should have a doctoral degree (PhD, DVM, MD or equivalent) with advanced training in virology, viral immunology or related fields. Academic rank and salary are commensurate with experience. Candidates at the rank of Associate Professor should have demonstrated research productivity and evidence of an independently funded and sustainable research program, as well as experience working with interdisciplinary research teams. Candidates at the rank of Assistant Professor should have training, experience, excellent scholarship, and demonstrated evidence of the likelihood of obtaining and maintaining an independently funded and sustainable research program. All candidates should have interest in programmatic synergy with existing members of the Ohio State faculty.



Columbus, Ohio's capital and largest city and the 14th largest city in the US, offers a wide range of affordable housing, many cultural and recreational opportunities, excellent schools, easy commute and a strong economy with growing industries in biomedical science, finance, insurance, healthcare, retail and e-commerce and information technology. Columbus has consistently been rated as one of the top U.S. cities for quality of life and one of the best places for business and careers in part due to a strong multicultural population and efforts to foster and embrace diversity, equity and inclusion. Residents enjoy the many amenities of the city including professional sports teams, museums, Columbus Zoo and Aquarium, outstanding restaurants, performing arts, metro parks, and more.

Applications should be submitted via email as a single PDF including (1) a cover letter; (2) curriculum vitae; (3) a summary of past research accomplishments; (4) a statement that addresses (i) your future research directions, (ii) your teaching and mentoring philosophy, and (iii) how you foresee integrating diversity and inclusion into your research, teaching and professional service; and (5) the names and contact information of four professional references.

Application materials should be submitted to Casey Hofmann (hofmann.75@osu.edu) or via website: https://www.nature.com/naturecareers/job/open-faculty-search-the-ohio-state-university-osu-739648. Review of applications will begin June 1, 2021 and continue until positions are filled. Inquiries may be directed to the chair of the search committee, Dr. Shan-Lu Liu (liu.6244@osu.edu).

The Ohio State University is committed to establishing a culturally and intellectually diverse environment, encouraging all members of our learning community to reach their full potential. We are responsive to dual-career families and strongly promote work-life balance to support our community members through a suite of institutional policies. To build a diverse workforce, qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, or protected veteran status. EEO/AA employer.

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song

(mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Byrareddy, Siddappa

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Agenda to follow.

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To: rahmed[rahmed@emory.edu]; Alter, Galit[galter@partners.org]; raul.andino[raul.andino@ucsf.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; bertozzi[bertozzi@stanford.edu]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish[cblish@stanford.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; tdcarroll[tdcarroll@ucdavis.edu]; Cassels, Fred[fcassels@path.org]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Meera Chand[Meera.Chand@phe.gov.uk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; charles.chiu[charles.chiu@ucsf.edu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; t.desilva[t.desilva@sheffield.ac.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; joe[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Camille Escadafal[Camille.Escadafal@finddx.org]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; douglas_fox[douglas_fox@berkeley.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Karen Gooch[karen.gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Griffiths, Anthony[ahgriff@bu.edu]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; William James[william.james@path.ox.ac.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj[kemptj@mail.nih.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; jakim[jakim@hivresearch.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler[amy.kistler@czbiohub.org]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Krammer, Florian[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; a.luttick[a.luttick@360biolabs.com]; jma[jma@sgul.ac.uk]; MacGill,

Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; w.a.paxton@liverpool.ac.uk[w.a.paxton@liverpool.ac.uk]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol[pintol@mail.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; arjun.rustagi[arjun.rustagi@stanford.edu]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; SANDS, Anita[sandsa@who.int]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons[GSimmons@vitalant.org]; viviana.simon[viviana.simon@mssm.edu]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; sastanley[sastanley@berkeley.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; SUBISSI, Lorenzo[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; sid.byrareddy[sid.byrareddy@unmc.edu]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 5/17/2021 6:58:31 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call. **Please note, you will have to download the most recent version of Zoom to attend the call.**

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday May 17 2:30PM CET (Geneva Time)

1. Galit Alter (Harvard) – *Early cross-coronavirus reactive signatures of protective humoral immunity against COVID-19*
2. Discussion of international standard and variants

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 16, 2021 8:11 AM
To: rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; a.luttick@360biolabs.com; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; ramadany@sfda.gov.sa; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; angeliki.melidou@ecdc.europa.eu; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; cjmiller@UCDAVIS.EDU; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris@cdph.ca.gov; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan;

Carol.Sabourin@hhs.gov; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; Byrareddy, Siddappa
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, May 19, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: rahmed[rahmed@emory.edu]; Alter, Galit[galter@partners.org]; raul.andino[raul.andino@ucsf.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; bertozzi[bertozzi@stanford.edu]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish[cblish@stanford.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; tdcarroll[tdcarroll@ucdavis.edu]; Cassels, Fred[fcassels@path.org]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Meera Chand[Meera.Chand@phe.gov.uk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; charles.chiu[charles.chiu@ucsf.edu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; t.desilva[t.desilva@sheffield.ac.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; joe[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Camille Escadafal[Camille.Escadafal@finddx.org]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; douglas_fox[douglas_fox@berkeley.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Karen Gooch[karen.gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Griffiths, Anthony[ahgriff@bu.edu]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; William James[william.james@path.ox.ac.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj[kemptj@mail.nih.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; jakim[jakim@hivresearch.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler[amy.kistler@czbiohub.org]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Krammer, Florian[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; a.luttick[a.luttick@360biolabs.com]; jma[jma@sgul.ac.uk]; MacGill,

Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; w.a.paxton@liverpool.ac.uk[w.a.paxton@liverpool.ac.uk]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol[pintol@mail.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; arjun.rustagi[arjun.rustagi@stanford.edu]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; SANDS, Anita[sandsa@who.int]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; SCHWARTZ, Lauren[schwartzl@who.int]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons[GSimmons@vitalant.org]; viviana.simon[viviana.simon@mssm.edu]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; sastanley[sastanley@berkeley.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; SUBISSI, Lorenzo[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; sid.byrareddy[sid.byrareddy@unmc.edu]; awchung@unimelb.edu.au[awchung@unimelb.edu.au]; Breeze.Cavell[Breeze.Cavell@phe.gov.uk]; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP)[gbu3@cdc.gov]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Sun 5/23/2021 2:35:47 PM (UTC-05:00)
Subject: No WHO Working Group on COVID-19 Assays this week

Dear All,

There will be no COVID-19 assays call this week because of a conflict with the WHO meeting on correlates of protection (**registration** - https://who-e.zoom.us/webinar/register/WN_V7h9i_1mQbaT7vVAW7RS9A). We will resume next week Wednesday June 2, 2021.

Best,
Lauren - Bill, Simon and César

Lauren Schwartz, PhD
Consultant - COVID-19 Response
R&D Blueprint | Health Emergencies Programme
Mobile: +1 248 910 9571
Email: schwartzl@who.int

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Suthar, Mehul; rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song

(mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP)

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To: Suthar, Mehul[mehul.s.suthar@emory.edu]; rahmed[rahmed@emory.edu]; Alter, Galit[galter@partners.org]; raul.andino[raul.andino@ucsf.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; bertozzi[bertozzi@stanford.edu]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish[cblish@stanford.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; tdcarroll[tdcarroll@ucdavis.edu]; Cassels, Fred[fcassels@path.org]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Meera Chand[Meera.Chand@phe.gov.uk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; charles.chiu[charles.chiu@ucsf.edu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; t.desilva[t.desilva@sheffield.ac.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; joe[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Camille Escadafal[Camille.Escadafal@finddx.org]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; douglas_fox[douglas_fox@berkeley.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Karen Gooch[karen.gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Griffiths, Anthony[ahgriff@bu.edu]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; William James[william.james@path.ox.ac.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj[kemptj@mail.nih.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; jakim[jakim@hivresearch.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler[amy.kistler@czbiohub.org]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Krammer, Florian[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; a.luttick[a.luttick@360biolabs.com]; jma[jma@sgul.ac.uk]; MacGill,

Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; MORGAN, Oliver[omorgan@who.int]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; w.a.paxton@liverpool.ac.uk[w.a.paxton@liverpool.ac.uk]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol[pintol@mail.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; arjun.rustagi[arjun.rustagi@stanford.edu]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; SANDS, Anita[sandsa@who.int]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons[GSimmons@vitalant.org]; viviana.simon[viviana.simon@mssm.edu]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; sastanley[sastanley@berkeley.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; SUBISSI, Lorenzo[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; sid.byrareddy[sid.byrareddy@unmc.edu]; awchung@unimelb.edu.au[awchung@unimelb.edu.au]; Breeze.Cavell[Breeze.Cavell@phe.gov.uk]; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP)[gbu3@cdc.gov]

From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 5/31/2021 4:51:30 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 2 2:30PM CET (Geneva Time)

1. Mehul Suthar (Emory) - *The durability of infection- and vaccine-induced antibody responses against SARS-CoV-2 and emerging variants*
2. Simon Funnell (PHE) - Update from the viral propagation subgroup

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 30, 2021 8:18 AM
To: Suthar, Mehul; rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; a.luttick@360biolabs.com; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; ramadany@sfda.gov.sa; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; angeliki.melidou@ecdc.europa.eu; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; cjmiller@UCDAVIS.EDU; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris@cdph.ca.gov; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk;

arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan@phe.gov.uk; Carol.Sabourin@hhs.gov; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; sid.byrareddy@unmc.edu; awchung@unimelb.edu.au; Breeze.Cavell@phe.gov.uk; gbu3@cdc.gov
Subject: WHO Working Group on COVID-19 Assays
When: Wednesday, June 2, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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To: Denison, Mark[mark.denison@vumc.org]; Daniel Streblow[streblow@ohsu.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Ralph Baric[rbaric@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]
Cc: Richard Whitley, M.D.[RWhitley@peds.uab.edu]
From: Stephanie Moore[smoore@peds.uab.edu]
Sent: Sun 2/9/2020 1:55:38 PM (UTC-06:00)
Subject: Reverse Site Final Presentation

Hello all,

Looking forward to seeing everyone tomorrow. The final presentation may be found on the AD3C Sharefile. Please let me know if you can't find it and do share it with your teams.

This link should take you to login and then to the file:
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Thank you and safe travels!

Stephanie

To: rahmed@emory.edu[rahmed@emory.edu]; galter@partners.org[galter@partners.org]; raul.andino@ucsf.edu[raul.andino@ucsf.edu]; maria.baca-estrada@canada.ca[maria.baca-estrada@canada.ca]; baihe@nmpa.gov.cn[baihe@nmpa.gov.cn]; rbaric@email.unc.edu[rbaric@email.unc.edu]; ellie.barnes@ndm.ox.ac.uk[ellie.barnes@ndm.ox.ac.uk]; dbarouch@bidmc.harvard.edu[dbarouch@bidmc.harvard.edu]; cheryl@gisaid.org[cheryl@gisaid.org]; Valentina Bernasconi[valentina.bernasconi@cepi.net]; bertozzi@stanford.edu[bertozzi@stanford.edu]; Kevin.Bewley@phe.gov.uk[Kevin.Bewley@phe.gov.uk]; shinjini.bhatnagar@thsti.res.in[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish@stanford.edu[cblish@stanford.edu]; Bok, Karin (NIH/VRC) [E][karin.bok@nih.gov]; dboyle@path.org[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; brangelp@who.int[brangelp@who.int]; Aodhan.Breathnach@stgeorges.nhs.uk[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot[christian.brechot@pasteur.fr]; Eeva Broberg[Eeva.Broberg@ecdc.europa.eu]; Christine.bruce@phe.gov.uk[Christine.bruce@phe.gov.uk]; BUDA Mihaela[Mihaela.BUDA@edqm.eu]; Miles.Carroll[Miles.Carroll@phe.gov.uk]; zuz4@cdc.gov[zuz4@cdc.gov]; tdcarroll@ucdavis.edu[tdcarroll@ucdavis.edu]; fcassels@path.org[fcassels@path.org]; fjc37@cam.ac.uk[fjc37@cam.ac.uk]; Marco.Cavaleri@ema.europa.eu[Marco.Cavaleri@ema.europa.eu]; Meera.Chand@phe.gov.uk[Meera.Chand@phe.gov.uk]; MONALISA.CHATTERJI@gatesfoundation.org[MONALISA.CHATTERJI@gatesfoundation.org]; emmanuelle.charton@edqm.eu[emmanuelle.charton@edqm.eu]; charles.chiu@ucsf.edu[charles.chiu@ucsf.edu]; MAY.CHU@CUANSCHUTZ.EDU[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark[carolyn.clark@cepi.net]; dancohen@tauex.tau.ac.il[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; mafranco@javeriana.edu.co[mafranco@javeriana.edu.co]; costaa@who.int[costaa@who.int]; htq4@cdc.gov[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; ian.crozier@nih.gov[ian.crozier@nih.gov]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; tdelossantos@path.org[tdelossantos@path.org]; t.desilva@sheffield.ac.uk[t.desilva@sheffield.ac.uk]; emmie.dewit@nih.gov[emmie.dewit@nih.gov]; marciela.degrace@nih.gov[marciela.degrace@nih.gov]; rafael.delgado@salud.madrid.org[rafael.delgado@salud.madrid.org]; joe@czbiohub.org[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666@pitt.edu[mit666666@pitt.edu]; Ruben.Donis@hhs.gov[Ruben.Donis@hhs.gov]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; William Dowling[william.dowling@cepi.net]; christian.drosten@charite.de[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie@ndm.ox.ac.uk[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; Camille.Escadafal@finddx.org[Camille.Escadafal@finddx.org]; darryl.falzarano@usask.ca[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; clint.florence@nih.gov[clint.florence@nih.gov]; douglas_fox@berkeley.edu[douglas_fox@berkeley.edu]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Jacqueline.Fryer@nibsc.org[Jacqueline.Fryer@nibsc.org]; Simon.Funnell@phe.gov.uk[Simon.Funnell@phe.gov.uk]; Luc Gagnon[luc.gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia@fda.hhs.gov[Mayra.Garcia@fda.hhs.gov]; bhx1@cdc.gov[bhx1@cdc.gov]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; Nick.Gilbert@ed.ac.uk[Nick.Gilbert@ed.ac.uk]; d.goldblatt@ucl.ac.uk[d.goldblatt@ucl.ac.uk]; Karen Gooch[Karen.Gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; barney.graham@nih.gov[barney.graham@nih.gov]; Elwyn Griffiths[elwyn.griffiths@cepi.net]; ahgriff@bu.edu[ahgriff@bu.edu]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; ilj2@cdc.gov[ilj2@cdc.gov]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Victoria.Hall@phe.gov.uk[Victoria.Hall@phe.gov.uk]; Carl.Hanson@cdph.ca.gov[Carl.Hanson@cdph.ca.gov]; thatziio@rockefeller.edu[thatziio@rockefeller.edu]; rzh7@cdc.gov[rzh7@cdc.gov]; henaorestrepoa@who.int[henaorestrepoa@who.int]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; paul.hodgson@usask.ca[paul.hodgson@usask.ca]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; Johan Holst[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; tkh4@cdc.gov[tkh4@cdc.gov]; irahetar@who.int[irahetar@who.int]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; miturrizagomara@path.org[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; william.james@path.ox.ac.uk[william.james@path.ox.ac.uk]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee[jeey62@gmail.com]; djernigan@cdc.gov[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj@mail.nih.gov[kemptj@mail.nih.gov]; alankhoo.imr@gmail.com[alankhoo.imr@gmail.com]; Jiae Kim[jakim@hivresearch.org]; Jacqueline.Kirchner[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler@czbiohub.org[amy.kistler@czbiohub.org]; paul.klenerman@medawar.ox.ac.uk[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; m.koopmans@erasmusmc.nl[m.koopmans@erasmusmc.nl]; Gerald.Kovacs@hhs.gov[Gerald.Kovacs@hhs.gov]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; Phil Krause[philip.krause@fda.hhs.gov]; skrebs@hivresearch.org[skrebs@hivresearch.org]; Greg Kulnis[greg.kulnis@nexelis.com]; Arun Kumar[arun.kumar@cepi.net]; renuka.kumar@gladstone.ucsf.edu[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; bleader@path.org[bleader@path.org]; leejooyeon@korea.kr[leejooyeon@korea.kr]; william.lee@health.ny.gov[william.lee@health.ny.gov]; MSLEVER@dstl.gov.uk[MSLEVER@dstl.gov.uk]; liyl@cde.org.cn[liyl@cde.org.cn]; changguili@aliyun.com[changguili@aliyun.com]; lyhchengdu@163.com[lyhchengdu@163.com]; limhy0919@korea.kr[limhy0919@korea.kr]; James.Little@hhs.gov[James.Little@hhs.gov]; liub@cde.org.cn[liub@cde.org.cn]; a.luttick@360biolabs.com[a.luttick@360biolabs.com]; jma@sgul.ac.uk[jma@sgul.ac.uk]; Tracy.MacGill@fda.hhs.gov[Tracy.MacGill@fda.hhs.gov]; ramadany@sfda.gov.sa[ramadany@sfda.gov.sa]; Karen Makar[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; adrian.mcdermott@nih.gov[adrian.mcdermott@nih.gov]; jmcelrat@fredhutch.org[jmcelrat@fredhutch.org]; Guruprasad[gmedigeshi@thsti.res.in]; angeliki.melidou@ecdc.europa.eu[angeliki.melidou@ecdc.europa.eu];

jwm1@pitt.edu[jwm1@pitt.edu]; Liz.Miller@lshtm.ac.uk[Liz.Miller@lshtm.ac.uk]; cjmiller@UCDAVIS.EDU[cjmiller@UCDAVIS.EDU]; philip.minor2@gmail.com[philip.minor2@gmail.com]; kmodjarrad@eidresearch.org[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris@cdph.ca.gov[MaryKate.Morris@cdph.ca.gov]; sarah.mudrak@duke.edu[sarah.mudrak@duke.edu]; munoz-fontela@bnitm.de[munoz-fontela@bnitm.de]; vincent.munster@nih.gov[vincent.munster@nih.gov]; Todd.Myers@fda.hhs.gov[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ@mail.mil[aysegul.nalca.civ@mail.mil]; scott.napper@usask.ca[scott.napper@usask.ca]; MNELSON@dstl.gov.uk[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o@dmsc.mail.go.th[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; golinger@MRIGLOBAL.ORG[golinger@MRIGLOBAL.ORG]; engeong.ooi@duke-nus.edu.sg[engeong.ooi@duke-nus.edu.sg]; melanie.ott@gladstone.ucsf.edu[melanie.ott@gladstone.ucsf.edu]; jokim@ivi.int[jokim@ivi.int]; mark.page@nibsc.org[mark.page@nibsc.org]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; map1@cdc.gov[map1@cdc.gov]; xdv3@cdc.gov[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; w.a.paxton@liverpool.ac.uk[w.a.paxton@liverpool.ac.uk]; Keith.Peden@fda.hhs.gov[Keith.Peden@fda.hhs.gov]; sheila.a.peel2.civ@mail.mil[sheila.a.peel2.civ@mail.mil]; malik@hku.hk[malik@hku.hk]; perkinsm@who.int[perkinsm@who.int]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; supaporn.p@dmsc.mail.go.th[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol@mail.nih.gov[pintol@mail.nih.gov]; margaret.l.pitt.civ@mail.mil[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; g.pollakis@liverpool.ac.uk[g.pollakis@liverpool.ac.uk]; JLPRIOR@dstl.gov.uk[JLPRIOR@dstl.gov.uk]; arimoin@g.ucla.edu[arimoin@g.ucla.edu]; lauriex@who.int[lauriex@who.int]; Nicola.Rose@nibsc.org[Nicola.Rose@nibsc.org]; arjun.rustagi@stanford.edu[arjun.rustagi@stanford.edu]; Kathryn Ryan[kathryn.ryan@phe.gov.uk]; Carol.Sabourin@hhs.gov[Carol.Sabourin@hhs.gov]; Jilian.Sacks@finddx.org[Jilian.Sacks@finddx.org]; salamik@who.int[salamik@who.int]; msalit@stanford.edu[msalit@stanford.edu]; sandsa@who.int[sandsa@who.int]; erica@lji.org[erica@lji.org]; moorthyv@who.int[moorthyv@who.int]; schendel@lji.org[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; schwartzl@who.int[schwartzl@who.int]; PScott@eidresearch.org[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; yoos@who.int[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons@vitalant.org[GSimmons@vitalant.org]; viviana.simon@mssm.edu[viviana.simon@mssm.edu]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; mksong@ivi.int[mksong@ivi.int]; sastanley@berkeley.edu[sastanley@berkeley.edu]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; subissil@who.int[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; swaminathans@who.int[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; nax3@cdc.gov[nax3@cdc.gov]; tracey.thue@usask.ca[tracey.thue@usask.ca]; georgia.tomaras@duke.edu[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend@imm.ox.ac.uk[alain.townsend@imm.ox.ac.uk]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; john.c.trefry.civ@mail.mil[john.c.trefry.civ@mail.mil]; Lance.Turtle@liverpool.ac.uk[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[Luk_Vandenberghe@MEEI.HARVARD.EDU]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan.Vasan@csiro.au[Vasan.Vasan@csiro.au]; y.m.vasiliev@spbniivs.ru[y.m.vasiliev@spbniivs.ru]; David Vaughn[David.Vaughn@gatesfoundation.org]; Debra.Wadford@cdph.ca.gov[Debra.Wadford@cdph.ca.gov]; wangjz@nifdc.org.cn[wangjz@nifdc.org.cn]; wangyc@nifdc.org.cn[wangyc@nifdc.org.cn]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Jerry.Weir@fda.hhs.gov[Jerry.Weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; gll9@cdc.gov[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW@nicd.ac.za[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; dj56wood@gmail.com[dj56wood@gmail.com]; xumiaobj@126.com[xumiaobj@126.com]; Solomon Abebe Yimer[solomon.yimer@cepi.net]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; Vidadi.Yusibov@hhs.gov[Vidadi.Yusibov@hhs.gov]; vyusibov@indianabiosciences.org[vyusibov@indianabiosciences.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; zhout@who.int[zhout@who.int]; sid.byrareddy@unmc.edu[sid.byrareddy@unmc.edu]; awchung@unimelb.edu.au[awchung@unimelb.edu.au]; Breeze.Cavell@phe.gov.uk[Breeze.Cavell@phe.gov.uk]; gbu3@cdc.gov[gbu3@cdc.gov]; mehul.s.suthar@emory.edu[mehul.s.suthar@emory.edu]; LDumont@vitalant.org[LDumont@vitalant.org]

From: William Dowling[william.dowling@cepi.net]
Sent: Wed 6/9/2021 8:34:01 AM (UTC-05:00)
Subject: FW: Global consultation on SARS-CoV-2 variants of concern and their impact on public health interventions, 10 June 2021

Concept note_Global consultation on SARS-CoV-2 variants_10June2021.pdf
Agenda_Global consultation on SARS-CoV-2 variants_10June2021.pdf

Dear all
I am sending this to all on the WHO COVID-19 assays working group in case you have not already received it.
Best regards
Bill Dowling

From: rdblueprint <rdblueprint@who.int>
Sent: Wednesday, June 9, 2021 4:57 AM
Subject: Global consultation on SARS-CoV-2 variants of concern and their impact on public health interventions, 10 June 2021

Dear all,
WHO will host a virtual global consultation on SARS-CoV-2 Variants of Concern and their Impact on Public Health Interventions scheduled to take place on **Thursday, 10 June 2021** from **13:00-16:30 Geneva time**.

This consultation will be an opportunity for WHO and partners to review and summarize the current evidence of the impact of SARS-CoV-2 variants of concern on public health interventions and outline information needs and decision-making processes. Attached is the concept note and agenda for the webinar.

Please register below to receive your personal connection link.

Join from a PC, Mac, iPad, iPhone or Android device
Click here to register or copy the link below in your browser.
https://who.zoom.us/webinar/register/WN_x8NoyjRaQX6qHmjmzad0Nw
Description : Global consultation on SARS-CoV-2 Variants of Concern and their Impact on Public Health Interventions.

Please share this with your networks. Should you encounter any problem to register, please contact Ms Josine Umugwaneza at (jumugwaneza@who.int).

Kind regards
Neddy MAFUNGA
on behalf of the WHO R&D Blueprint Secretariat

Sensitivity: CEPI Internal

World Health Organization

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Global Consultation on SARS-CoV-2 Variants of Concern and their Impact on Public Health Interventions

10 June, 13:00-16:30 CEST

Zoom (Please register in advance here)

Concept Note

Background

On 29 March 2021, WHO convened the Global Consultation on a Decision Framework for Assessing the Impact of SARS-CoV-2 Variants of Concern (VOCs) on Public Health Interventions. This was the first global forum for WHO and stakeholders to outline a global risk monitoring and assessment framework, including critical steps for the detection, monitoring, and assessment of SARS-CoV-2 variants, and to provide an overview of the available evidence on current VOCs and their impact on public health interventions. WHO and partners reviewed potential decision-making processes with respect to analyzing the impact of VOCs, evaluating and modifying vaccines, and issuing policy recommendations. At the time of the consultation, no changes to public health interventions due to the VOCs were recommended.

However, noting the upsurge in COVID-19 cases in parts of the world and the emergence of the B.1.617 VOC, there is an urgent need for the global community to come together again to review and synthesize the available evidence of the impact of VOCs on public health interventions. This will ensure continued coordination and harmonization for interpreting results, issuing recommendations, and communicating to the public.

WHO will convene this second consultation, which is scheduled for 10 June 2021 from 13:00-16:30 CEST, with all stakeholders to continue implementing the global risk monitoring and assessment framework. The consultation will also be an opportunity for WHO to outline decision-making processes for COVID-19 vaccine composition, if needed.[1]

The consultation will be guided by the following key questions:

- How are data on VOCs and evidence of their impact on public health interventions being generated?
- Based on the current VOC data and evidence, what decisions, if any, need to be made by policymakers with respect to COVID-19 prevention and control?
- How can global decision-making processes be further clarified and strengthened?

Objectives:

1. Review and summarize the existing evidence of the impact of VOCs on public health interventions
2. Engage global stakeholders to outline the information needs and decision-making processes for assessing the impact of VOCs on public health interventions
3. Outline decision-making processes for COVID-19 vaccine composition, if needed

Outcomes:

1. Synthesis of the current evidence, challenges, and solutions for VOCs and their impact on public health interventions, including current COVID-19 vaccines
2. Common understanding of the current triggers, roles and responsibilities, and information needs and standards to guide policy recommendations for VOCs

If you have any questions regarding this consultation, please contact Christopher Chadwick, Marie-Ange Wambo, and Josine Umugwaneza.

[1] Please note that the consultation will not be the forum for making evidence-based recommendations on COVID-19 vaccine composition but will address how such a recommendation, if needed, will be made in the future.

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Global consultation on SARS-CoV-2 variants of concern and their impact on public health interventions

10 June 2021, 13:00 - 16:30 CEST

Zoom (**Please register in advance here**)

Tentative agenda

TIME	TOPIC	SPEAKERS
13:00-13:05	Opening remarks	Mike Ryan, WHO
13:05-13:10	Updates on the WHO global risk monitoring and assessment framework for SARS-CoV-2 variants	Sylvie Briand, WHO
SESSION 1: FOCUS ON SARS-COV-2 VARIANTS		
13:10-14:10	Update on VOI/VOC designation process and naming system	Lorenzo Subissi, WHO
	Global epidemiological situation with SARS-CoV-2 variants	Brett Archer, WHO
	Risk assessing SARS-CoV-2 variants	Wendy Barclay, Imperial College London
	Moderator: Maria Van Kerkhove, WHO	
SESSION 2: EVIDENCE FRAMEWORK FOR VARIANTS & COVID-19 VACCINES		
14:10-15:20	Topics:	
	• Decision-making process and methods to decide if a modified vaccine or a new vaccine is needed (10 mins)	Philip Krause, Chairperson, WHO research expert group on COVID-19 vaccines
	• Review and critical appraisal of randomized evidence on vaccines and variants (10 mins)	Isabelle Boutron Université de Paris
	• Review and critical appraisal of non-randomized evidence on vaccines and variants (10 mins)	Julian Higgins University of Bristol
	• Developers' corner – current data and plans for evaluation of the effect of variants on vaccine efficacy/effectiveness (20 mins)	Randall N Hyer, Moderna Philip Dormitzer, Pfizer Rabun Mallory, Novavax

		Steven Gong, Clover Biopharmaceuticals Allen Lien, Medigen Vaccine Biologics Corp Raches Ella, Bharat Biotech Robert Coleman, Codagenix Punee Pitisuttithum, Mahidol University Trina Racine, Vaccine and Infectious Disease Org. (VIDO) Luigi Aurisicchio, Takis/Rottapharm Biotech Christine Roberts GeneOne Life Science, Inc
	• Preliminary considerations of other epidemiological data to inform decisions (20 mins)	<u>Panel discussion</u> Helen Rees, Wits RHI, University of Witwatersrand Mary Ramsay, Immunization, Hepatitis, and Blood Safety department, Public Health England | HPA John Peter Figueroa, University of the West Indies, Jamaica
	Moderator: Kanta Subbarao	David Wentworth, Virology surveillance and diagnosis branch, Influenza Division, NCIRD, US CDC

SESSION 3: IMPACT ON PUBLIC HEALTH DECISION-MAKING

15:20-15:50	Perspectives of regulators and developers for variants and COVID-19 vaccines *Moderator: Marco Cavaleri, EMA*	Chang-Joon Bae, MFDS Marco Cavaleri, EMA Adam Hacker, CEPI Philip Krause, FDA
15:50-16:20	Impact of variants on public health decision-making: • Global perspective • Country level perspectives *Moderator: Nyka Alexander, WHO*	Hanna Nohynek, SAGE Christine Carrington, Trinidad & Tobago Nazeem Muhajarine, CoVaRR-Net
16:20-16:30	Concluding remarks	Jaouad Mahjour, WHO

To: Maaike Everts, Ph.D.[meverts@peds.uab.edu]; Mark Prichard, PhD.[MPrichard@peds.uab.edu]; Mary Wyatt Bowers[MWBowers@peds.uab.edu]; Richard Whitley, M.D.[RWhitley@peds.uab.edu]; Tameca Winston[twinston@peds.uab.edu]; 'Alana Centilli'[acentilli@southernresearch.org]; 'Alec Hirsch'[hirschal@ohsu.edu]; 'Amy Sims'[sims0018@ad.unc.edu]; 'Ardina Pruijssers'[ardina.pruijssers@vumc.org]; 'Ashish Pathak'[apathak@southernresearch.org]; 'Bob Bostwick'[bostwick@southernresearch.org]; 'Carrie Evans'[evans@southernresearch.org]; 'Corinne Augelli-Szafran'[caugelli-szafran@southernresearch.org]; 'Daniel Streblow'[streblow@ohsu.edu]; 'Debra Warren'[dewarren@DOM.wustl.edu]; 'Erica Bitten'[erica.bitten@emory.edu]; 'George Painter'[george.r.painter@emory.edu]; Avery, Gloria J.[gjavery@UTMB.EDU]; 'Greg Bluemling'[gblueml@emory.edu]; 'Hope Angel'[angelh@ohsu.edu]; 'Javier Gomez'[Jcampos-gomez@southernresearch.org]; 'Jay Nelson'[nelsonj@ohsu.edu]; 'Jessica Smith'[smijessi@ohsu.edu]; 'Jim Chappell'[jim.chappell@Vanderbilt.edu]; 'Lynn Rasmussen'[rasmussen@southernresearch.org]; 'Maria Agostini'[Maria.I.agostini@vanderbilt.edu]; 'Mark Denison'[mark.denison@vanderbilt.edu]; 'Mark Heise'[mark_heisem@med.unc.edu]; 'Mark Suto'[suto@southernresearch.org]; 'Mason Wu'[mwu@southernresearch.org]; 'Michael Diamond'[diamond@borcim.wustl.edu]; 'Michelle Almajano'[Michelle.Almajano@gilead.com]; 'Miranda Nebane'[nebane@southernresearch.org]; 'Nichole Tower'[tower@southernresearch.org]; 'Omar Moukha-Chafiq'[omoukha-chafiq@southernresearch.org]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rachel Graham'[rlgraham@email.unc.edu]; 'Ralph Baric'[rbaric@email.unc.edu]; 'Thomas Morrison'[thomas.morrison@ucdenver.edu]; 'Tim Sheahan'[sheahan@email.unc.edu]; 'Tomas Cihlar'[Tomas.Cihlar@gilead.com]; 'Toni Baric'[antoinette_baric@med.unc.edu]; 'Victor DeFilippis'[defilipp@ohsu.edu]
From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]
Sent: Tue 1/22/2019 11:13:41 AM (UTC-06:00)
Subject: RE: Monthly AD3C Teleconference for Project and Core Reporting
January 22 2019 AD3C Agenda.pdf

Hello To Everyone:

Please be reminded of the AD3C monthly call scheduled for this **Thursday, January 24 at 3:30 pm Central Time.** Attached please find the meeting agenda. If you would like to share any slides with the group, please send them to me by 12:00 pm on the day of the call and I will send them via e-mail to the conference call participants.

With best regards and many thanks,

Sara Davis | Program Coordinator II
Direct Line: 205.996.7804 | sadavis@peds.uab.edu

-----Original Appointment-----
From: Antiviral Drug Discovery and Development Center-AD3C
Sent: Monday, January 14, 2019 9:27 AM
To: Antiviral Drug Discovery and Development Center-AD3C; Maaike Everts, Ph.D.; Mark Prichard, PhD.; Mary Wyatt Bowers; Richard Whitley, M.D.; Tameca Winston; 'Alana Centilli'; 'Alec Hirsch'; 'Amy Sims'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Bob Bostwick'; 'Carrie Evans'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Debra Warren'; 'Erica Bitten'; 'George Painter'; 'Gloria Avery'; 'Greg Bluemling'; 'Hope Angel'; 'Javier Gomez'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; 'Mason Wu'; 'Michael Diamond'; 'Michelle Almajano'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; 'Pei-Yong Shi'; 'Rachel Graham'; 'Ralph Baric'; 'Thomas Morrison'; 'Tim Sheahan'; 'Tomas Cihlar'; 'Toni Baric'; 'Victor DeFilippis'
Cc: 'Rasmussen, Lynn'; 'Bostwick, Bob'; 'Diamond, Michael'
Subject: Monthly AD3C Teleconference for Project and Core Reporting
When: Thursday, January 24, 2019 3:30 PM-5:00 PM (UTC-06:00) Central Time (US & Canada).
Where: Call in at 1-888-806-5025 and use the passcode of **552.136**

Here is the 2019 notice for the monthly conference call for the AD3C grant. Please contact me if you need anything or have questions.

Sara Davis
sadavis@peds.uab.edu

AD3C Teleconference Agenda
January 22, 2019, 3:30 p.m. CST

Meeting Number: (888) 806-5025 **Participant code: 420976**

1. Admin Core

   - Re-competition info: JIT documents uploaded/received by NIAID
   - Budget status update
   - Final report due June 28, including CETR Final Report Additional Materials
   - Consortium agreement amendment in process
   - Consider abstract ICAR Baltimore (May 12-15 2019, deadline Jan 31; list of speakers https://www.isar-icar.com/page-1075346)

2. Project progress updates

   - Project 1 – Flavi (JNelson, AHirsch, MDiamond; Core B BBostwick; Core C APathak)

   - Project 2 – Corona (MDenison, RBaric; Core B BBostwick; Core C APathak)

   - Project 3 – Alpha (DStreblow, MHeise, TMorrison; Core B BBostwick; Core C APathak)

   - Project 4 – Influenza (RWhitley, MPrichard, JCampos-Gomez; Core B BBostwick; Core C OMoukha-Chafiq)

To: Krammer, Florian[florian.krammer@mssm.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; dbarouch[dbarouch@BIDMC.HARVARD.EDU]; Krogan, Nevan[Nevan.Krogan@ucsf.edu]; Paul Thomas[paul.thomas@stjude.org]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; stevens@anl.gov[stevens@anl.gov]; jjdavis@anl.gov[jjdavis@anl.gov]; Scheuermann, Richard[RScheuermann@jcvi.org]; Eakin, Ann (NIH/NIAID) [E][ann.eakin@nih.gov]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; adam.godzik@ucr.edu[adam.godzik@ucr.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; btk@lanl.gov[btk@lanl.gov]; lmwoga@fredhutch.org[lmwoga@fredhutch.org]; monte@duke.edu[monte@duke.edu]; spjwhelan@wustl.edu[spjwhelan@wustl.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; McDermott, Adrian (NIH/VRC) [E][adrian.mcdermott@nih.gov]; jbloom@fredhutch.org[jbloom@fredhutch.org]; Julie McElrath[jmcelrat@fredhutch.org]; kawaokay@svm.vetmed.wisc.edu[kawaokay@svm.vetmed.wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; noah.sather@seattlechildrens.org[noah.sather@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; mrolland@hivresearch.org[mrolland@hivresearch.org]; Baric, Ralph[rbaric@email.unc.edu]; Richard Webby[richard.webby@stjude.org]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; malik@hku.hk[malik@hku.hk]; Andrew B. Ward[andrew@scripps.edu]; Ali Ellebedy[ellebedy@wustl.edu]; mdiamond@wustl.edu[mdiamond@wustl.edu]; djs200@cam.ac.uk[djs200@cam.ac.uk]; jboon@wustl.edu[jboon@wustl.edu]; Aubree Gordon[gordonal@umich.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Koup, Richard (NIH/VRC) [E][rkoup@mail.nih.gov]; Seder, Robert (NIH/VRC) [E][rseder@mail.nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Alessandro Sette[alex@lji.org]; Adam Godzik[Adam.Godzik@medsch.ucr.edu]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; MacCannell, Duncan (CDC/DDID/NCEZID/OD)[fms2@CDC.GOV]; Weiss, Carol (FDA/CBER)[Carol.Weiss@fda.hhs.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Nelson Michael[nelson.l.michael2.civ@mail.mil]; gregory.d.gromowski.civ@mail.mil[gregory.d.gromowski.civ@mail.mil]; irina.maljkovicberry.ctr@mail.mil[irina.maljkovicberry.ctr@mail.mil]; jeffrey.r.currier.civ@mail.mil[jeffrey.r.currier.civ@mail.mil]; Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]
From: Shi, Pei yong[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=8906C46397AE48488FCC55537DC5D6D3-SHI, PEI YO]
Sent: Fri 2/19/2021 10:00:08 AM (UTC-06:00)
Subject: RE: SARS-CoV-2 Variant Testing pipeline
Overview and recap and overview Feb 19 2021.pptx

Dear all,
I have added the summary for in vivo group to Florian's slide deck.
Best,
Pei-Yong

From: Krammer, Florian <florian.krammer@mssm.edu>
Sent: Friday, February 19, 2021 8:25 AM
To: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>; dbarouch <dbarouch@BIDMC.HARVARD.EDU>; Krogan, Nevan <Nevan.Krogan@ucsf.edu>; Paul Thomas <paul.thomas@stjude.org>; stacey schultz-cherry <stacey.schultz-cherry@stjude.org>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Lampley, Rebecca (NIH/NIAID) [C] <rebecca.lampley@nih.gov>; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard <RScheuermann@jcvi.org>; Eakin, Ann (NIH/NIAID) [E] <ann.eakin@nih.gov>; Brown, Liliana (NIH/NIAID) [E] <liliana.brown@nih.gov>; adam.godzik@ucr.edu; Jason McLellan <jmclellan@austin.utexas.edu>; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul <mehul.s.suthar@emory.edu>; Shi, Pei yong <peshi@UTMB.EDU>; McDermott, Adrian (NIH/VRC) [E] <adrian.mcdermott@nih.gov>; jbloom@fredhutch.org; Julie McElrath <jmcelrat@fredhutch.org>; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet <vimenach@UTMB.EDU>; noah.sather@seattlechildrens.org; Matthew Frieman <mfrieman@som.umaryland.edu>; mrolland@hivresearch.org; Baric, Ralph <rbaric@email.unc.edu>; Richard Webby <richard.webby@stjude.org>; Garcia-Sastre, Adolfo <adolfo.garcia-sastre@mssm.edu>; malik@hku.hk; Andrew B. Ward <andrew@scripps.edu>; Ali Ellebedy <ellebedy@wustl.edu>; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon <gordonal@umich.edu>; stanley-perlman@uiowa.edu; Van bakel, Harm <harm.vanbakel@mssm.edu>; Graham, Barney (NIH/VRC) [E] <bgraham@mail.nih.gov>; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Munster, Vincent (NIH/NIAID) [E] <vincent.munster@nih.gov>; Koup, Richard (NIH/VRC) [E] <rkoup@mail.nih.gov>; Seder, Robert (NIH/VRC) [E] <rseder@mail.nih.gov>; Ghedin, Elodie (NIH/NIAID) [E] <elodie.ghedin@nih.gov>; Alessandro Sette <alex@lji.org>; Adam Godzik <Adam.Godzik@medsch.ucr.edu>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Roberts, Chris (NIH/NIAID) [E] <paul.roberts@nih.gov>; Schotsaert, Michael <michael.schotsaert@mssm.edu>; MacCannell, Duncan (CDC/DDID/NCEZID/OD) <fms2@CDC.GOV>; Weiss, Carol (FDA/CBER) <Carol.Weiss@fda.hhs.gov>; Wentworth, David E. (CDC/DDID/NCIRD/ID) <gll9@cdc.gov>; Nelson Michael <nelson.l.michael2.civ@mail.mil>; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E] <leah.vincent@nih.gov>
Subject: Re: SARS-CoV-2 Variant Testing pipeline

Dear all,

Please find the slides for the in vitro group attached.

Best,

Florian

From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Wednesday, February 3, 2021 12:20 PM
To: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Krammer, Florian; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; Van bakel, Harm; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]
Subject: SARS-CoV-2 Variant Testing pipeline
When: Friday, February 19, 2021 8:00 AM-9:30 AM.
Where: https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting

https://www.zoomgov.com/j/1602664950?pwd=MmhuQUE2SUZ6SnZYSG9LU0RPZm5sQT09

Meeting ID: 160 266 4950

Passcode: 073903

One tap mobile

+16692545252,,1602664950#,,,,*073903# US (San Jose)

+16468287666,,1602664950#,,,,*073903# US (New York)

Dial by your location

+1 669 254 5252 US (San Jose)

+1 646 828 7666 US (New York)

+1 551 285 1373 US

+1 669 216 1590 US (San Jose)

833 568 8864 US Toll-free

Meeting ID: 160 266 4950

Passcode: 073903

Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP

1602664950@sip.zoomgov.com

Join by H.323

161.199.138.10 (US West)

161.199.136.10 (US East)

Meeting ID: 160 266 4950

Passcode: 073903

Summary *In Vitro* Characterization group discussion

2/19/21

What data is needed

1. **Cross-neutralization data**
   - WT to variant
   - Variant to wt
   - Variant to variant
   - Should be a broad panel of pseudoneut (VSV as well as lenti) and neut assays, 2-3 labs per assay?
2. **Growth kinetics in representative cell lines**
   - Organoids/organ systems/air liquid interface cultures?
   - Primary cell lines?
   - Cells overexpressing ACE2/TMPRSS2
3. **Structural information**
   - What impact do NTD loop deletions have?
   - What impact do RBD mutations have?
   - Do heterotrimers present epitopes of wt+variants correctly (important for mRNA/vectored vaccines)
4. **Variant RBD affinity to ACE2**
   - This should include ACE2 binding to animal model ACE2
5. **Characterization of mutations in genes outside of S**
6. **Anticipate mutations (e.g. identified via libraries, escape mutagenesis, also based on variants) and characterize them ahead of time**
7. **Data sharing system?**

Reagents

- Sourcing virus
  - Several isolates from each variant
    - Faster sharing needed – both domestic and international
    - Avoid USDA permits, ship non-cultured clinical isolates or ship extracted RNA!
  - BEI should supply large volumes that are ready to use
  - Molecular clones are needed too
- Benchmarking
  - mAbs (Ellebedy, P. Wilson etc.)
  - Therapeutic mAbs (source??? REGN, Eli Lilly, VIR, AZ etc.)
  - Access to remdesivir or similar
  - Polyclonal serum panel post vaccination for Moderna, Pfizer, J&J, NVX, AZ
  - Polyclonal serum panel post infection (wt, B.1.1.7, B.1.351, P.1, E484K viruses etc.)
- Gene synthesis
  - For molecular clones (wt nt sequence)
  - For pseudotyped entry inhibition assays (codon optimized wt aa sequence)
  - For protein expression (codon optimized 2P/Hexapro ΔCS)

In Vivo group discussion

2/19/21

What to do

1. Characterize variants in three animal models
   - Mouse model
     - K18-hACE2 mice
     - Wild-type immune-competent mice
   - Hamster mode
   - NHP model (limited for prioritized experiments)
   - Share results from the three models and decide which models will be prioritized for variant analysis
2. In vivo variant testing
   - Infect and challenge with homologous and heterologous variant viruses
   - Immunize with vaccines and then challenge with original and variant viruses
   - Test dose range for immunization
   - Shelf infected- or vaccine-immunized animals for later challenge with variant viruses

Notes:

1. Prioritize variants for in vivo testing based on (i) clinical and epidemiological information and (ii) in vitro assay results (e.g., neutralization titers, replication kinetics in human airway culture)

2. Share results from different teams and task groups in real time.

From: sadavis@peds.uab.edu[sadavis@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; Amelia George; Anish Avadukoot; Ardina Pruijssers; Ashish Pathak; Babu Tekwani; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; Chelsea Tompkins; Clare O'Regan; Corinne Augelli-Szafran; 'Daniel Streblow'; 'Erica Bitten'; Fahim Ahmad; George Painter; Greg Bluemling; 'Jay Nelson'; Jessica Smith; Jim Chappell; Kathy Keith; Lynn Rasmussen; 'Maria Agostini'; Mark Denison ; Mark Heise; 'Mark Suto'; Mason Wu; 'Michael Diamond'; 'Miranda Nebane'; Narayan Chaurasiya; Nichole Tower; Nicole Haese; Omar Moukha-Chafiq; Shi, Pei yong; Rachel Graham; 'Ralph Baric'; Richard Whitley, M.D.; Ron Swanstrom; Sarah M. Dowdy; Shalisa Sanders; Shilpa Dutta; Shuntai Zhou; Sixue Zhang; Tameca Winston; Thomas Morrison; Tia Hughes; Tim Sheahan; 'Toni Baric'; Victor DeFilippis

Location: https://uab.zoom.us/j/96769424930?pwd=S05hZzdsZz09 **552.136**

Importance: Normal

Subject: FW: AD3C Monthly Meeting

Start Time: Thur 1/28/2021 3:30:00 PM (UTC-06:00)

End Time: Thur 1/28/2021 5:00:00 PM (UTC-06:00)

Required Attendees: 'Alana Centilli'; 'Alec Hirsch'; Amelia George; Anish Avadukoot; Ardina Pruijssers; Ashish Pathak; Babu Tekwani; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; Chelsea Tompkins; Clare O'Regan; Corinne Augelli-Szafran; 'Daniel Streblow'; 'Erica Bitten'; Fahim Ahmad; George Painter; Greg Bluemling; 'Jay Nelson'; Jessica Smith; Jim Chappell; Kathy Keith; Lynn Rasmussen; 'Maria Agostini'; Mark Denison ; Mark Heise; 'Mark Suto'; Mason Wu; 'Michael Diamond'; 'Miranda Nebane'; Narayan Chaurasiya; Nichole Tower; Nicole Haese; Omar Moukha-Chafiq; Shi, Pei yong; Rachel Graham; 'Ralph Baric'; Richard Whitley, M.D.; Ron Swanstrom; Sarah M. Dowdy; Shalisa Sanders; Shilpa Dutta; Shuntai Zhou; Sixue Zhang; Tameca Winston; Thomas Morrison; Tia Hughes; Tim Sheahan; 'Toni Baric'; Victor DeFilippis

-----Original Appointment-----
From: Stephanie Moore
Sent: Wednesday, January 6, 2021 12:21 PM
To: Stephanie Moore; Antiviral Drug Discovery and Development Center-AD3C; Sara Davis
Subject: AD3C Monthly Meeting
When: Occurs the fourth Thursday of every 1 month(s) effective 1/28/2021 until 10/28/2021 from 3:30 PM to 5:00 PM (UTC-06:00) Central Time (US & Canada).
Where:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fuab.zoom.us%2Fj%2F96769424930%3Fpwd%3DMm9Wd3EwOC8rZXFKaHR6S05hZzdsZz09&data=04%7C01%7Cpeshi%40utmb.edu%7C4724f355f369472934ec08d8b27273b5%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637455551923655613%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=wMYNPG5w2QwN0i1XdTCbZF7BcQvvo0HxFXp2xD2UtXk%3D&reserved=0

When: Thursday, January 28, 2021 3:30 PM-5:00 PM. (UTC-06:00) Central Time (US & Canada)

Where:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fuab.zoom.us%2Fj%2F96769424930%3Fpwd%3DMm9Wd3EwOC8rZXFKaHR6S05hZzdsZz09&data=04%7C01%7Cpeshi%40utmb.edu%7C4724f355f369472934ec08d8b27273b5%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637455551923655613%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=wMYNPG5w2QwN0i1XdTCbZF7BcQvvo0HxFXp2xD2UtXk%3D&reserved=0

+~+~+~+~+~+~+~+~+~+
Hello all,

Here is the invite for our monthly AD3C meeting, scheduled for the fourth Thursday of each month from 3:30 to 5:00 pm Central Time.

Thank you!

AD3C administrative team

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick

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Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

For those based in the US, please note the time of the meeting has shifted for two weeks given daylight savings.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Vasan, Vasan (H&B, Geelong ACDP); a.luttick; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); tlying (tlying@fudan.edu.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); baihe (baihe@nmpa.gov.cn); zlshi (zlshi@wh.iov.cn); Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); rawcraig@yahoo.com; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); christian.drosten (christian.drosten@charite.de); Barbara.Schnierle (Barbara.Schnierle@pei.de); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; epstein@ecohealthalliance.org; Peter Daszak; christian.brechot (christian.brechot@pasteur.fr); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); Boyle, David; de los Santos, Tala; Leader, Troy; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; malik (malik@hku.hk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); Daniel Cohen (dancohen@tauex.tau.ac.il); Youngmee Jee (jeey62@gmail.com); alankhoo.imr; Celine Gurry (Celine.gurry@cepi.net); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); ramadany; linfa.wang (linfa.wang@duke-nus.edu.sg); engeong.ooi; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); qiang.pan-hammarstrom@ki.se; Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); pilailuk.o (pilailuk.o@dmsc.mail.go.th); pawinee.k@redcross.or.th; B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Javier Castillo-Olivares Pallardo; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); r.tedder@imperial.ac.uk; katie.doores (katie.doores@kcl.ac.uk); Liz Miller (Liz.Miller@lshtm.ac.uk); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; jma; GILBERT Nick; Goldblatt, David; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Griffiths, Anthony; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Chu, May; eric.vangieson@darpa.mil; john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); Sarah Mudrak, Ph.D.; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; McElrath MD PhD, Julie; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Vidadi Yusibov (vyusibov@indianabiosciences.org); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; daniela@lji.org; Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Lee, William T (HEALTH); tcs38@psu.edu; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Marc L Salit (msalit@stanford.edu); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu);

wilsonp@uchicago.edu; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); rbaric (rbaric@email.unc.edu); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); Theodora Hatziioannou; jakim; Donis, Ruben (OS/ASPR/BARDA); renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; viviana.simon; pintol; kemptj; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA); Iturriza-Gomara, Miren; david.montefiori@duke.edu; sujan@lji.org; Camille Escadafal; Pollakis, Georgios; w.a.paxton@liverpool.ac.uk; rahmed; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song

(mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont

Sent: Sun 6/6/2021 10:19:56 AM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and zoom information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 9 2:30PM CET (Geneva Time)

1. Theodora Hatziioannou (Rockefeller) - *Evolution of neutralizing antibody responses to SARS-CoV-2*
2. Larry Dumont (Vitalant Research)- *SARS-CoV-2 Antibody persistence in COVID-19 convalescent plasma donors: Dependency on assay format and applicability to serosurveillance*

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER,

Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont

Sent: Sun 6/13/2021 2:38:34 PM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and zoom information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 16 2:30PM CET (Geneva Time)

1. Amy Chung (U. Melbourne) - *Simultaneous evaluation of antibodies that inhibit SARS-CoV-2 RBD variants with a novel competitive multiplex assay*
2. David Goldblatt (UCL) - *Comparing immune responses between SARS-CoV-2 vaccines, correlates of protection and variant immunity*

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+1 669 900 9128 US (San Jose)
+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 646 518 9805 US (New York)

+1 646 558 8656 US (New York)
+1 651 372 8299 US (Minnesota)
+1 786 635 1003 US (Miami)
+1 267 831 0333 US (Philadelphia)
+1 301 715 8592 US (Washington D.C)
+1 312 626 6799 US (Chicago)
Meeting ID: 361 256 8290
Find your local number: https://who.zoom.us/u/acLh9DwRd3

Join by SIP
3612568290@zoomcrc.com

Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: Antiviral Drug Discovery and Development Center-AD3C[ad3c@peds.uab.edu]

Attendees: 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Jessica Eagar; Tameca Winston; 'Nicole Haese'

Importance: Normal

Subject: Canceled: Monthly AD3C Project/Core Teleconference Call

Start Time: Thur 1/23/2020 3:30:00 PM (UTC-06:00)

End Time: Thur 1/23/2020 5:00:00 PM (UTC-06:00)

Required Attendees: Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Tameca Winston; 'Nicole Haese'

Optional Attendees: 'Suto, Mark J.'; 'Rasmussen, Lynn'; 'Swanstrom, Ronald I'; 'Morrison, Thomas'; 'Sides, Kate'

Hello To Everyone:

Just to be safe, I am sending a second message to confirm the cancellation of the monthly AD3C Project/Core Zoom Meeting call at this time. I may have cancelled the Zoom meeting, but not removed this entry from your calendars. This message should accomplish the latter, and remove it from your Outlook calendar. At this time, because many of our institutions are not operating at full capacity, there isn't a lot of monthly progress to report at this time. When we are back to normal operations, we will send a new meeting notice.

However, if anyone would like to discuss anything during this time, please reach out to our Admin Core group and we can arrange a call as needed.

Thank you!

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
Cell Phone: 205.725.0543 | sadavis@peds.uab.edu

Importance:	Normal
Subject:	Canceled: Monthly AD3C Project/Core Teleconference Call
Start Time:	Thur 3/26/2020 8:30:00 PM (UTC)
End Time:	Thur 3/26/2020 10:00:00 PM (UTC)
Required Attendees:	Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; Stephanie Moore; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Jessica Eagar; Tameca Winston; 'Nicole Haese'
Optional Attendees:	'Suto, Mark J.'; 'Rasmussen, Lynn'; 'Swanstrom, Ronald I'; 'Morrison, Thomas'; 'Sides, Kate'

Hello To Everyone:

This is the notice for the monthly AD3C Teleconference. We will be trying to use Zoom, instead of our previous carrier, AT&T. The connection information is shown below. The meeting can be accessed by computer using the link below, if they have a microphone in the computer. You may also connect by phone, using the dial in numbers provided, and then the meeting ID, followed by the pound sign (#).

Join from PC, Mac, Linux, iOS or Android: https://uasystem.zoom.us/j/ **552.136**

Or iPhone one-tap :
US: +16465588656,, **552.136** or +16699006833,, **552.136**

Or Telephone: Dial US: +1 646 558 8656 or +1 669 900 6833
Meeting ID: **552.136**

As always, if you want to share any slides or materials, please send them to me by 1:00 pm the day of the call, and I will distribute them to everyone.

If I can be of assistance, please let me know.

With kind regards,

Sara Davis | Program Coordinator II
UAB Research and Pediatric Virology/Pediatrics/Infectious Diseases
UAB | The University of Alabama at Birmingham
CHB Room 303| 1600 7th Avenue S | Birmingham, AL 35233-1711
P: 205.996.7804 | sadavis@peds.uab.edu

Celebrate our 50th anniversary with us!

From: Stephanie Moore[smoore@peds.uab.edu]

Attendees: Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Jessica Eagar; Tameca Winston; 'Nicole Haese'

Location: https://uasystem.zoom.us/ **552.136**

Importance: Normal

Subject: AD3C Meeting

Start Time: Mon 4/6/2020 4:00:00 PM (UTC-05:00)

End Time: Mon 4/6/2020 5:00:00 PM (UTC-05:00)

Required Attendees: Stephanie Moore; Antiviral Drug Discovery and Development Center-AD3C; 'Alana Centilli'; 'Alec Hirsch'; 'Ardina Pruijssers'; 'Ashish Pathak'; 'Babu Tekwani'; 'Bob Bostwick'; 'Carrie Evans'; Chad Petit; 'Clare O'Regan'; 'Corinne Augelli-Szafran'; 'Daniel Streblow'; 'Erica Bitten'; 'Fahim Ahmad'; 'George Painter'; 'Greg Bluemling'; 'Hope Angel'; 'Jay Nelson'; 'Jessica Smith'; 'Jim Chappell'; 'Lynn Rasmussen'; 'Maria Agostini'; 'Mark Denison'; 'Mark Heise'; 'Mark Suto'; Mary Wyatt Bowers; 'Mason Wu'; 'Michael Diamond'; 'Miranda Nebane'; 'Nichole Tower'; 'Omar Moukha-Chafiq'; Shi, Pei yong; 'Rachel Graham'; 'Ralph Baric'; Richard Whitley, M.D.; 'Ron Swanstrom'; 'Shuntai Zhou'; 'Thomas Morrison'; 'Tim Sheahan'; 'Toni Baric'; 'Victor DeFilippis'; 'Amelia.s.george@vumc.org'; 'Hughes, Tia M'; 'kak@uab.edu'; Jessica Eagar; Tameca Winston; 'Nicole Haese'

When: Monday, April 06, 2020 4:00 PM-5:00 PM. (UTC-06:00) Central Time (US & Canada)
Where: https://uasystem.zoom.us/j/ **552.136**

~~*~*~*~*~*~*~*~*

Hello all,
Thank you for everyone who was able to respond. Based on those we did have, we will hold a meeting today at 4pm (Central).
-Stephanie

From: Stephanie Moore <smoore@peds.uab.edu>
Date: Saturday, April 4, 2020 at 12:39 PM
To: Antiviral Drug Discovery and Development <ad3c@peds.uab.edu>, 'Alana Centilli' <acentilli@southernresearch.org>, 'Alec Hirsch' <hirschal@ohsu.edu>, 'Ardina Pruijssers' <ardina.pruijssers@vumc.org>, 'Ashish Pathak' <apathak@southernresearch.org>, 'Babu Tekwani' <btekwani@southernresearch.org>, 'Bob Bostwick' <bostwick@southernresearch.org>, 'Carrie Evans' <evans@southernresearch.org>, Chad Petit <cpetit@uab.edu>, 'Clare O'Regan' <coregan@wustl.edu>, 'Corinne Augelli-Szafran' <caugelli-szafran@southernresearch.org>, 'Daniel Streblow' <streblow@ohsu.edu>, 'Erica Bitten' <erica.bitten@emory.edu>, 'Fahim Ahmad' <fahmad@southernresearch.org>, 'George Painter' <george.r.painter@emory.edu>, 'Greg Bluemling' <gblueml@emory.edu>, 'Hope Angel' <angelh@ohsu.edu>, 'Jay Nelson' <nelsonj@ohsu.edu>, 'Jessica Smith' <smijessi@ohsu.edu>, 'Jim Chappell' <jim.chappell@Vanderbilt.edu>, 'Lynn Rasmussen' <rasmussen@southernresearch.org>, 'Maria Agostini' <Maria.l.agostini@vanderbilt.edu>, 'Mark Denison' <mark.denison@vanderbilt.edu>, 'Mark Heise' <mark_heisem@med.unc.edu>, 'Mark Suto' <suto@southernresearch.org>, Mary Wyatt Bowers <MWBowers@peds.uab.edu>, 'Mason Wu' <mwu@southernresearch.org>, 'Michael Diamond' <diamond@borcim.wustl.edu>, 'Miranda Nebane' <nebane@southernresearch.org>, 'Nichole Tower' <tower@southernresearch.org>, 'Omar Moukha-Chafiq' <omoukha-chafiq@southernresearch.org>, Pei-Yong Shi <peshi@utmb.edu>, 'Rachel Graham' <rlgraham@email.unc.edu>, 'Ralph Baric' <rbaric@email.unc.edu>, "Richard Whitley, M.D." <RWhitley@peds.uab.edu>, 'Ron Swanstrom' <risunc@med.unc.edu>, 'Shuntai Zhou' <shuntaiz@email.unc.edu>,

'Thomas Morrison' <thomas.morrison@ucdenver.edu>, 'Tim Sheahan' <sheahan@email.unc.edu>, 'Toni Baric' <antoinette_baric@med.unc.edu>, 'Victor DeFilippis' <defilipp@ohsu.edu>, "'Amelia.s.george@vumc.org'" <Amelia.s.george@vumc.org>, "'Hughes, Tia M'" <tia.m.hughes@vumc.org>, "'kak@uab.edu'" <kak@uab.edu>, Jessica Eagar <JEagar@uab.edu>, Tameca Winston <twinston@peds.uab.edu>, 'Nicole Haese' <haese@ohsu.edu>
Subject: AD3C Project/Core Teleconference Call

Hello all AD3C members,

Hoping this email finds you safe and well. Although we did cancel last week's call, we would like to follow up with everyone and have a check-in. Further, we would like to update and obtain feedback from everyone on some of the COVID-19 work. Attached please find the virtual screens that we received from SR's Med Chem group:
1. Virtual screen of 102K library against exonuclease site of SARS nsP14 crystal structure.
2. Virtual screen of 122K library against conserved binding site of SARS/COVID-19 main protease crystal structures
3. Repurposing of drugs/compounds from literature according to cheminformatics analysis (not included in current HTS library).

A presentation is attached for further details. In total, 52 compounds were sorted and initially 38 compounds will be accessed for SARS/COVID-19 SAR assays (See excel file for details). Some of these will be purchased from commercial sources in coming days.

A doodle poll may be found here in order to schedule in such a tight turn around:
https://doodle.com/poll/emrk69gb327hqa9a
Please do this at your earliest convenience. Hope you all have a nice weekend and stay safe and well.

Thank you all,

Stephanie
Cell: 205-563-8565

Steph Moore is inviting you to a scheduled Zoom meeting.

Join from PC, Mac, Linux, iOS or Android: https://uasystem.zoom.us/j/ **552.136**

Or iPhone one-tap :
US: +13126266799,, **552.136** or +16465588656,, **552.136**
Or Telephone:
Dial(for higher quality, dial a number based on your current location):
US: +1 312 626 6799 or +1 646 558 8656 or +1 253 215 8782 or +1 301 715 8592 or +1 346 248 7799 or +1 669 900 6833
Meeting ID: **552.136**
International numbers available: https://uasystem.zoom.us/u/ad51e2Cisc

Or an H.323/SIP room system:
H.323:
162.255.37.11 (US West)
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115.114.115.7 (India Hyderabad)
213.19.144.110 (EMEA)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)

207.226.132.110 (Japan)
Meeting ID: 552.136

SIP: 552.136@zoomcrc.com

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina; gweiss@uci.edu; ZHOU, Tiequn; YOO, Si Hyung; Sutter Roland

Sent: Mon 11/9/2020 2:50:14 AM (UTC-06:00)

Subject: [COVID-19] 37th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwho.zoom.us%2Fj%2F96515071032&data=04%7C01%7Cpeshi%40utmb.edu%7C84376630c17940796b0708d8848c76c8%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637405086121769810%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=KEZmB%2FA4uNMZQEcB3acYHb2q3lw02m5HEbDTcUaoBbk%3D&reserved=0

Meeting ID: 965 1507 1032
Passcode: ?p47?Spa

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From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina

Location: https://who.zoom.us/j/94806447981

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

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Sent: Sun 3/21/2021 11:04:50 AM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

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Agenda to follow.

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From: Macoubray, Aaron[amacoubray@rti.org]

Attendees: Bronwyn MacInnis; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan

Location: https://rtiorg.zoom.us/j/98355183025?pwd= 552.136

Importance: Normal

Subject: CREID EBOV Discussion

Start Time: Fri 4/23/2021 2:00:00 PM (UTC-05:00)

End Time: Fri 4/23/2021 3:00:00 PM (UTC-05:00)

Required Attendees: Macoubray, Aaron; rfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov

Optional Attendees: kga1978@gmail.com

Hi all,

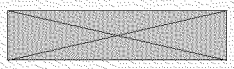
I've added others from your Research Centers to this invite. Please feel free to forward this invitation to the most appropriate representative on the topic from your RC, and to other CREID Network members as you see fit.

Thank you very much,

Aaron

Required Attendees: Macoubray, Aaron; rfgarry@tulane.edu; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; pardis@broadinstitute.org; Kristian Andersen; bronwyn@broadinstitute.org; mmgraw; olival@ecohealthalliance.org; daszak@ecohealthalliance.org; Quiner, Claire; jean.patterson@nih.gov; sara.woodson@nih.gov; Beaubien, Candice (NIH/NIAID) [E; Linde, Amber (NIH/NIAID) [E; julie.dyall@nih.gov

Optional Attendees: kga1978@gmail.com



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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; 'HENAO RESTREPO, Ana Maria'; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; philip.krause@fda.hhs.gov; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts (johan.neyts@kuleuven.be); slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org;

luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; 'WOOD, David John'; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov; Griffiths, Anthony; Andrew Jones; Reed, Douglas S; David Vaughn; Thomas Friedrich; Long, James (OS/ASPR/BARDA) (CTR); Eddins, Ryan (OS/ASPR/BARDA); Sinha, Tanima (OS/ASPR/BARDA); Revelli, David; Knight, Brittany; Lohman, Kent

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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; Crozier, Ian (NIH) [C]; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; Krause, Philip; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts@kuleuven.be; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org;

luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov; ibz1@cdc.gov; kyle.rosenke@nih.gov; caroline.foo@kuleuven.be; t.sulpice; gabriella.worwa@nih.gov; Vidadi.Yusibov@hhs.gov; François Briand; Griffiths, Anthony; S. Herfst; Reed, Douglas S; Thomas Friedrich; Carolyn Clark; Malkevich, Nina (OS/ASPR/BARDA) (CTR); Wright, Katina (OS/ASPR/BARDA); Revelli, David; Unrath, Marya (ASPR/BARDA/NCD) (CTR); Lee-Parritz, David; Olinger, Gene; Lohman, Kent

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; Krause, Philip; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts@kuleuven.be; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org;

luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov; ibz1@cdc.gov; kyle.rosenke@nih.gov; caroline.foo@kuleuven.be; t.sulpice@physiogenex.com; gabriella.worwa@nih.gov; Vidadi.Yusibov@hhs.gov; François Briand; Griffiths, Anthony; S. Herfst; David Vaughn; Reed, Douglas S; Kortekaas, Jeroen; Dr. Hanne Andersen; Sinha, Tanima (OS/ASPR/BARDA); Brys, April (OS/ASPR/BARDA); Thomas Friedrich; Unrath, Marya (ASPR/BARDA/NCD) (CTR); Revelli, David; Taha, Mohamad (HC/SC); sanjuanola@gmail.com

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Agenda to follow.

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Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion (rcarrion@TxBiomed.org); res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN,

Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; Byrareddy, Siddappa; Robert JEFF Hogan; Kortekaas, Jeroen; S. Herfst; Thomas Friedrich; Reed, Douglas S; Griffiths, Anthony; Revelli, David; Andrew Jones; Wright, Katina (OS/ASPR/BARDA); Stylianos Bournazos; Unrath, Marya (ASPR/BARDA/NCD) (CTR)

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; Luis.Lugo.mil@afrims.org; Matthew.Reed.mil@afrims.org; franck.TOURET@univ-amu.fr; sandrine.lesellier@anses.fr; romain.volmer@envt.fr; Pearl.Bamford@health.gov.au; Jin.Zhu@health.gov.au; Ruben.Donis@hhs.gov; Karl.Erlandson@hhs.gov; Lakshmi.Jayashankar@hhs.gov; James.Little@hhs.gov; Andrew.Phipps@hhs.gov; Carol.Sabourin@hhs.gov; John.Treanor@hhs.gov; Vidadi.Yusibov@hhs.gov; sivkog@battelle.org; Russell.Ray@bcm.edu; verschoor@bprc.nl; verstrepen@bprc.nl; langermans@bprc.nl; mlewis@bioqual.com; MONALISA.CHATTERJI@gatesfoundation.org; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; Karen.Makar@gatesfoundation.org; David.Vaughn@gatesfoundation.org; munoz-fontela@bnitm.de; estefania.rodriguez@bnitm.de; ahgriff@bu.edu; Honko, Anna; dustin.johnson@canada.ca; sean.li@canada.ca; dean.smith@canada.ca; nax3@cdc.gov; ibz1@cdc.gov; roger.le-grand@cea.fr; pauline.maisonnasse@cea.fr; sekim@krict.re.kr; kandeil_a@hotmail.com; carolyn.clark@cepi.net; william.dowling@cepi.net; amy.c.shurtleff@cepi.net; shanchao@wh.iov.cn; rkiatchula@gmail.com; seos@cnu.ac.kr; lisambrosseau@gmail.com; mto@umn.edu; mito@ciea.or.jp; tyamamoto@ciea.or.jp; mesteban@cnb.csic.es; jfgarcia@cnb.csic.es; l.enjuanes@cnb.csic.es; mopargal@rams.colostate.edu; Tony.Schountz@colostate.edu; angierasmussen@gmail.com; scordo@qb.fcen.uba.ar; sinabavari@comcast.net; dgdiel@cornell.edu; res2025@med.cornell.edu; Vasan.Vasan@csiro.au; pduprex@pitt.edu; joanne@pitt.edu; agw13@pitt.edu; AKelvin@dal.ca; john.c.trefry.civ@mail.mil; jennifer.m.kishimori.mil@mail.mil; kanta.subbarao@influenzacentre.org; REIRELAND@mail.dstl.gov.uk; MSLEVER@dstl.gov.uk; MNELSON@mail.dstl.gov.uk; JLPRIOR@dstl.gov.uk; amelia.karlsson@duke.edu; danielle.anderson@duke-nus.edu.sg; Marco.Cavaleri@ema.europa.eu; Lowen, Anice; mariette.ducatez@envt.fr; S. Herfst; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; Hana.Golding@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; tony.wang@fda.hhs.gov; Krause, Philip; robin.levis@fda.hhs.gov; Martin.Beer@fli.de; ThomasC.Mettenleiter@fli.de; ldenisy@yahoo.com; rhakami@gmu.edu; Asisa.Volz@tiho-hannover.de; dbarouch@bidmc.harvard.edu; esulkowska@rics.bwh.harvard.edu; luk_vandenberghe@meei.harvard.edu; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; daniel.martinez-arguelles@canada.ca; lawton.stubbert@canada.ca; jfwchan@hku.hk; hlchen@hku.hk; CarlosAlberto.Guzman@helmholtz-hzi.de; florian.krammer@mssm.edu; lisa.chakrabarti@pasteur.fr; christiane.gerke@pasteur.fr; nadia.khelef@pasteur.fr; seungtaek.kim@ip-korea.org; mksong@ivi.int; joaquim.segales@irta.cat; julia.vergara@irta.cat; tomeri@iibr.gov.il; nirp@iibr.gov.il; nnagata@niid.go.jp; tksuzuki@nih.go.jp; terry.k.besch.ctr@mail.mil; jricht@vet.k-state.edu; Ali.Mirazimi@folkhalsomyndigheten.se; horer@ku.edu.tr; snumouse@snu.ac.kr; kai.dallmeier@kuleuven.be; johan.neyts@kuleuven.be; caroline.foo@kuleuven.be; erica@lji.org; muhammad.munir@lancaster.ac.uk; drevelli@lovelacebiomedical.org; cdang@lcr.org; sutter@micro.vetmed.uni-muenchen.de; kupke@staff.uni-marburg.de; randy.albrecht@mssm.edu; Adolfo.Garcia-Sastre@mssm.edu; peter.palese@mssm.edu; michael.schotsaert@mssm.edu; tenoever@gmail.com; golinger@mriglobal.org; marlene.espinozamoraga@mssm.edu; Giada.Mattiuzzo@nibsc.org; Mark.Page@nibsc.org; clint.florence@nih.gov; mary.lane@nih.gov; pickettte@niaid.nih.gov; erik.stemmy@nih.gov; ian.crozier@nih.gov; lisa.hensley@nih.gov; Michael.holbrook@nih.gov; connie.schmaljohn@nih.gov; emmie.dewit@nih.gov; feldmannh@niaid.nih.gov; vincent.munster@nih.gov; barney.graham@nih.gov; jorgen.de.jonge@rivm.nl; suchinda.m@chula.ac.th; Anthony Holmes - NC3Rs; Elliot Lilley - NC3Rs; Mark Prescott - NC3Rs; kristine.macartney@health.nsw.gov.au; patrick.reid@unmc.edu; yu.cong@nih.gov; Marzi, Andrea (NIH/NIAID) [E; bosioc@niaid.nih.gov; gabriella.worwa@nih.gov; Neil.Berry@nibsc.org; philip.minor2@gmail.com; Nicola.Rose@nibsc.org; que.dang@nih.gov; sheri.hild@nih.gov; neeltje.vandoremalen@nih.gov; kyle.rosenke@nih.gov; fcassels@path.org; Bernhard.Kerscher@pei.de; Barbara.Schnierle@pei.de; qinchuan@pumc.edu.cn; SPERGEL@email.chop.edu; darwyn.kobasa@canada.ca; bradley.pickering@canada.ca; t.sulpice@physiogenex.com; f.briand@physiogenex.com; tcs38@psu.edu; Miles.Carroll@phe.gov.uk; Simon.Funnell@phe.gov.uk; Yper.Hall@phe.gov.uk; Ann.Rawkins@phe.gov.uk; Javier.Salguero@phe.gov.uk; Sally.Sharpe@phe.gov.uk; Julia.Tree@phe.gov.uk; caroline.melo@rivm.nl; ajones@mail.rockefeller.edu; ravetch@mail.rockefeller.edu; russori@njms.rutgers.edu; salgampa@njms.rutgers.edu; Delgado Vazquez.Rafael; Rana A. Al Madany; fkoide@southernresearch.org; s.a.arakelov@spbniivs.ru; i.v.krasilnikov@spbniivs.ru; y.m.vasiliev@spbniivs.ru; hwan.kim@stonybrook.edu; WaickmaA@upstate.edu; alankhoo.imr@gmail.com; rcarrion@txbiomed.org; LMartinez@txbiomed.org; JTorrelles@txbiomed.org; tverakit@gmail.com; bobomok@hku.hk; anna@thsti.res.in; david.lee-parritz@tufts.edu; croy (croy@tulane.edu); Jason.Kindrachuk@umanitoba.ca; cjmiller@ucdavis.edu; Das, Soumita; rbaric@email.unc.edu; lgralins@email.unc.edu; Sheahan, Timothy Patrick; gustavo.palacios@gmail.com; dmissiak@bsd.uchicago.edu; fgrey@exseed.ed.ac.uk; dsreed@cvr.pitt.edu; Gary.Kobinger@crchudequebec.ulaval.ca; Paul.Lambert@unige.ch; y.jacob.hou@unc.edu; scartner@uab.edu; edohm@uab.edu; kevinharrod@uabmc.edu; jjkobie@uabmc.edu; troyrandall@uabmc.edu; jhogan@uga.edu; paul-mccray@uiowa.edu; stanley-perlman@uiowa.edu; J.P.Stewart@liverpool.ac.uk; xavier.de-lamballerie@univ-amu.fr; CDillen@som.umaryland.edu; MFrieman@som.umaryland.edu; SBradfute@salud.unm.edu; baczenas@wisc.edu; slfeinberg@wisc.edu; thomasf@primate.wisc.edu; dhoconno@wisc.edu; anja.kipar@uzh.ch; christian.c.hofer.mil@mail.mil; jay.w.hooper.civ@mail.mil; grace.m.lidl.mil@mail.mil; aysegul.nalca.civ@mail.mil;

margaret.l.pitt.civ@mail.mil; mitchell.palmer@usda.gov; trbrasel@UTMB.EDU; abukreye@utmb.edu; mmeitzen@utmb.edu; peshi@UTMB.EDU; sktseng@UTMB.EDU; darryl.falzarano@usask.ca; Volker.gerdts@usask.ca; paul.hodgson@usask.ca; stittelaar@viroclinics.com; wim.vanderpoel@wur.nl; nora.gerhards@wur.nl; jeroen.kortekaas@wur.nl; nadia.oreshkova@wur.nl; Martha.Alexander-Miller@wakehealth.edu; kmodjarrad@eidresearch.org; mdiamond@wustl.edu; BRANGEL, Polina; HENAO RESTREPO, Ana Maria; KAZI, Fatema; 'KNEZEVIC, Ivana'; SATHIYAMOORTHY, Vaseeharan; PREZIOSI, Marie-pierre; RIVEROS BALTA, Ximena; 'SALAMI, Kolawole'; SCHWARTZ, Lauren; YOO, Si Hyung; SWAMINATHAN, Soumya; WOOD, David John; ZHOU, Tiequn; dbolton@hivresearch.org; sharon.daye2.mil@mail.mil; Damron, Fredrick; Martinez, Ivan; lisette.cornelissen@wur.nl; ivan.marazzi@mssm.edu; wenchun0617@gate.sinica.edu.tw; Victoria.Wahl@ST.DHS.GOV; michael.hevey@ST.DHS.GOV; Paul.Dabisch@ST.DHS.GOV; Stylianos Bournazos; Robert JEFF Hogan; Thomas Friedrich; Griffiths, Anthony; David Vaughn; Reed, Douglas S; Revelli, David; Dr. Hanne Andersen; Eddins, Ryan (OS/ASPR/BARDA); Brys, April (OS/ASPR/BARDA); Sinha, Tanima (OS/ASPR/BARDA)

Sent: Sun 4/25/2021 11:56:58 AM (UTC-05:00)

Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: Young, Jennifer (AE)[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=939434b3dc894caab01c10e93943d292-Young, Jenn]

Attendees: "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu> : "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, "McGlaughon, Ben" <benmcg@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>,; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.

Location: https://zoom.us/j/9095677699?pwd= **552.136**

Importance: Normal

Subject: A38 Ad Hoc Meeting: Mouse-adapted Models for SARS-CoV-2

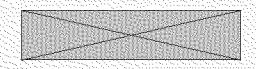
Start Time: Tue 9/1/2020 1:00:00 PM (UTC-05:00)

End Time: Tue 9/1/2020 2:00:00 PM (UTC-05:00)

Required Attendees: Young, Jennifer (AE); Toni Baric; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.

Please see the below teleconference information for tomorrow's meeting at 1pm – 2pm (CDT)/ 2pm – 3pm (EDT).

Required Attendees: Young, Jennifer (AE); Toni Baric; Baric, Ralph S; McGlaughon, Ben; Graham, Rachel; Beasley, David W.; Tseng, Chien-Te K.; Menachery, Vineet; Massey, Christopher; Viner, Rebekah L.



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From: Karen Makar[Karen.Makar@gatesfoundation.org]

Attendees: tom@vaxxinity.com; David Vaughn; michael.schotsaert@mssm.edu; daraporn.p@bionet-asia.com; aetyang@kemri-wellcome.org; juan.moliva@nih.gov; yuri.vasiliev@hotmail.com; janet.lathey@nih.gov; elizabethleakey@gmail.com; may@vakzine-manager.de; daniel.martinez-arguelles@canada.ca; jinalb@nicd.ac.za; dr.annie.degroot@gmail.com; Fyezah Jehan; igor.smolenov@cloverbiopharma.com; k.j.von.eije@umcg.nl; amandacabralsilva@yahoo.com.br; tamala.mallettmoore@sanofi.com; imran@phcglobal.org; SGalloway@cdc.gov; Jeeninga@viroclinics.com; leid@who.int; tong.wu@canada.ca; jose.luis.di.fabio@cepi.net; D.Shah@wellcome.org; elizabeth.daglish@astrazeneca.com; Ockenhouse, Chris; Keith Klugman; vryab@mail.ru; William Dowling; sian.jones@pfizer.com; cuchip@who.int; THOMAS.JAENISCH@CUANSCHUTZ.EDU; jennifer@immunoprecise.com; marcelo.koike@gmail.com; grantr@who.int; lecoest@gmail.com; Mihaela.Nosca@Seqirus.com; sabinoec@gmail.com; harin.l@bionet-asia.com; chenhongyin@walvax.com; david.montefiori@duke.edu; Tom Mooney; Philip.Minor2@gmail.com; lindy.durrant@nottingham.ac.uk; jailal.ablack@entospharma.com; alcantaraluiz42@gmail.com; kelly.taylor@cihr-irsc.gc.ca; Lethanhtuyet@vabiotech.com.vn; michael.wiseman@health.gov.au; robert.j.oconnell.mil@mail.mil; federica.mori@reithera.com; lode.schuerman@gsk.com; andrew.pollard@paediatrics.ox.ac.uk; ji-hong.kim@sk.com; cookee@who.int; REIRELAND@mail.dstl.gov.uk; jane.s@bionet-asia.com; munoz-fontela@bnitm.de; Tseng, Chien-Te K.; preziosim@who.int; SUyoga@kemri-wellcome.org; Stephen.Savarino@sanofi.com; kishore.turaga@biologicale.com; sarah.frise@astrazeneca.com; paola.stefanelli@iss.it; vfa3@cdc.gov; tim.spector@kcl.ac.uk; claudioc@gsespa.cl; sanchezg@une.net.co; Corinne.Jouquelet-Royer@sanofi.com; lidia.oostvogels@curevac.com; dorits@imbm.org; leejooyeon@korea.kr; marc.veldhoen@medicina.ulisboa.pt; huruoyu@walvax.com; joaquim.segales@irta.cat; kandeil_a@hotmail.com; Deborah King; mff7@cdc.gov; inho.cheong@sk.com; sutter@micro.vetmed.uni-muenchen.de; annapurnavyakarnam@gmail.com; marion.vermeulen@sanbs.org.za; moncef.m.slaoui59@gmail.com; narcisa.x.mesaros@gsk.com; Elliot.Lilley@nc3rs.org.uk; teodora.aktas@folkhalsomyndigheten.se; Jin.gao@fda.hhs.gov; linfa.wang@duke-nus.edu.sg; liya.wassie@ahri.gov.et; thomazella16@gmail.com; achidi.eric@gmail.com; kovac@axon-neuroscience.eu; tom.monath@crozetbiopharma.com; nadirkocak@yahoo.com; rajeev.dhere@seruminstitute.com; kathleen.victoir@pasteur.fr; farah.qamar@aku.edu; sastanley@berkeley.edu; brosen@novavax.com; wilsonp@uchicago.edu; iman.satti@ndm.ox.ac.uk; raburn.mallory@astrazeneca.com; kathytai@medigenvac.com; twosned@googlemail.com; EShumba@aslm.org; HRees@wrhi.ac.za; stephanie.longet@phe.gov.uk; martin.bexon@bexonclinical.com; kate.broderick@inovio.com; Mark_Ic_Chen@ncid.sg; mlewis@bioqual.com; pereyaslovd@who.in; leli@who.int; liupengfei@zhifeishengwu.com; carole.verhoeven@seqirus.com; tianyuan1@sinopharm.com; vgarg@altimmune.com; bo_zhong@sinocelltech.com; guy.vernet@pasteur.fr; nhuskins@completegenomics.com; shuping_xu@sinocelltech.com; Stanley Plotkin; Padmini Srikantiah; llena@globalhealthstrategies.com; BBrande1@its.jnj.com; jean.patterson@nih.gov; adams_andrew_charles@lilly.com; Alena.Khromava@sanofi.com; iowusu@noguchi.ug.edu.gh; wenchun0617@gate.sinica.edu.tw; dapengzhoulab@tongji.edu.cn; xuefeng.yu@cansinotech.com; Norio.tamura@shionogi.co.jp; anita.suresh@finddx.org; joanne.langley@dal.ca; vrezelj@its.jnj.com; pieter.neels@vaccine-advice.be; renuka.kumar@gladstone.ucsf.edu; giorgio.fedele@iss.it; natalie.anosova@sanofi.com; fms2@cdc.gov; hana.golding@fda.hhs.gov; SofoniasT@africa-union.org; sudhirbabji@cmcvellore.ac.in; fderrar@pasteur.dz; kjambo@mlw.mw; s.saikrishna@indimmune.com; Kaitlyn.dambach@nih.gov; Jwilbur@mesoscale.com; Jason.Kindrachuk@umanitoba.ca; mimidarko66; rama.akondy@ashoka.edu.in; bottazzi@bcm.edu; slfeinberg@wisc.edu; seguina@medicago.com; gustavo.f.palacios.civ@mail.mil; saranya.sridhar@sanofi.com; n.okba@erasmusmc.nl; jeanie.jacquet@cepi.net; drbdmore@gmail.com; Brown ScD, Elizabeth R; Nick Andrews; Curcio, Daniel; supaporn.p@dmsc.mail.go.th; romain.volmer@envt.fr; magnus.ysander@astrazeneca.com; yabdiche@immunoprecise.com; dancohen@tauex.tau.ac.i; wangyc@nifdc.org.cn; dsantororosa@gmail.com; ofrinr@who.int; pieter.pannus@sciensano.be; coleman@codagenix.com; xavier.de-lamballerie@univ-amu.fr; alex@lji.org; rfaden@jhu.edu; MRabeh@dha.gov.ae; najwa.khuri@gmail.com; Chan_Cheng_Leng@hsa.gov.sg; krystian.jazdzewski@warsawgenomics.pl; Agnes_Chan@hsa.gov.sg; y.m.vasiliev@spbniivs.ru; AFO@ssi.dk; anja.kipar@uzh.ch; Madhavi.Yadavalli@astrazeneca.com; stephen.p.lockhart@pfizer.com; Susan.Mather@pfizer.com; Gerald Voss; sylvie.van-der-werf@pasteur.fr; dnkhong@sk.com; rjanssen@dynavax.com; emmerich@bnitm.de; alena.dabrazhynetskaya@fda.hhs.gov; creanywo@hku.hk; Stephan.Harbarth@hcuge.ch; kizzmekia.corbett@nih.gov; magdalena.spolnicka@policja.gov.pl; maria.salomao@butantan.gov.br; intl@ibto.ir; Pearl.Bamford@health.gov.au; galter@partners.org; rhonda.kuolee@nrc-cnrc.gc.ca; ADriscoll@som.umaryland.edu; John.Forde@phe.gov.uk; MWFREEMAN@mgh.harvard.edu; mayra.moura@butantan.gov.br; rscharf@path.org; JAYANTHI.WOLF@MERCK.COM; Christine.bruce@phe.gov.uk; chien@vabiotech.com.vn; ztq9@cdc.gov; Georgia Tomaras, Ph.D.; charu.sabharwal@pfizer.com; dpark@broadinstitute.org; ydm9@cdc.gov; fdubovsky@novavax.com; bernadettemrg5@gmail.com; mike.fisher@oncimmune.com; salgampa@njms.rutgers.edu; jean-luc.gala@uclouvain.be; jccastellanos@husi.org.co; ulrike.jaegle@curevac.com; amhashem@kau.edu.sa; rolf.fendel@uni-tuebingen.de; kpancer@pzh.gov.pl; chad.irwin@canada.ca; joser.arribas@salud.madrid.org; elizabeth.gabitzsch@immunitybio.com; cgomez@javeriana.edu.co; fangxing@zhifeishengwu.com;

irenenor@usp.br; beatriz.lucchesi@butantan.gov.br; vivek.rao@igib.res.in; horer@ku.edu.tr; AP.AlmeidaAranha@cepi.net; maksyutov_ra@vector.nsc.ru; ross.upshur@gmail.com; p.kellam@imperial.ac.uk; Lewis, Kristen; marciela.degrace@nih.gov; Helen.mao@cansinotech.com; whausdorff@path.org; iad7@cdc.gov; Ajoke Sobanjo-ter Meulen; m.addo@uke.de; leila.luheshi@nanoporetech.com; lwelch@iavi.org; farshad@vaxxinity.com; Steve Hadley; gingras@lunenfeld.ca; amenezes@globalhealthstrategies.com; kmohan@bharatbiotech.com; karin.vandenberg@sanbs.org.za; bob.small@cepi.net; Shitong Huan; s.borregaard@ctc-north.com; maina.lazou.jackson@cepi.net; gcanuel@osivax.com; sethc@africa-union.org; angeliki.melidou@ecdc.europa.eu; shahid.jameel@ashoka.edu.in; barbara.schnierle@pei.de; Giada.mattiuzzo@nibsc.org; annev@nicd.ac.za; Audrey Hutter; adam.hacker@cepi.net; araki-yasuhiro@pmda.go.jp; sjp97@medschl.cam.ac.uk; anzj@chinacdc.cn; enakouney@gmail.com; Kaslow, David; pebodyr@who.int; oliver.schoenborn-kellenberger@curevac.com; antonella.folgori@reithera.com; cyrus.yang@sbc-biotech.com; trbrasel@utmb.edu; demooij@viroclinics.com; tksuzuki@niid.go.jp; Maria.Syrochkina@pfizer.com; Diana_Koh@hsa.gov.sg; nicole.gilberger@bnitm.de; cooldrdax@gmail.com; AAgweyu@kemri-wellcome.org; ckrubiner@CGDEV.ORG; Guang Li; giulianaxm@gmail.com; PScott@eidresearch.org; mesteban@cnb.csic.es; lili53@sinopharm.com; david.stewart@csl.com.au; philippa.matthews@ndm.ox.ac.uk; xhatzi@med.uth.gr; mario.christodoulou@cepi.net; ruoyuhu@walvax.com; POndoa@aslm.org; ullas@tifr.res.in; MAHIPALAP@who.int; xdv3@cdc.gov; Susan.Hopkins@phe.gov.uk; grode@vakzine-manager.de; pauline.maisonnasse@cea.fr; petra.budde@oncimmune.com; kaijie.pan@pfizer.com; Gary.Kobinger@crchudequebec.ulaval.ca; helen.thompson@bristol.ac.uk; manisha.tirvassen@cepi.net; nataliapasternak@gmail.com; prasadsd@bharatbiotech.com; Jyoti.logani@nic.in; norah.fu@walvax.com; wangxiludev@126.com; michelle.hoffmann@axon-neuroscience.eu; apinya.k@bionet-asia.com; joanna-trees.merckx@mcgill.ca; affrade@yahoo.com.br; helga.junker@curevac.com; slamola@path.org; Yyue315@vip.126.com; Kayla Laserson; ycwu@cde.org.tw; sungskim63@gmail.com; renald.gilbert@cnrc-nrc.gc.ca; christian.taucher@valneva.com; jwolf@heatbio.com; sebastian.ols@ki.se; ladda.s@bionet-asia.com; doug.holtzman@icosavax.com; lfries@novavax.com; ephcicm@nus.edu.sg; gll9@cdc.gov; atila@usp.br; roy.duncan@dal.ca; m.pryor@360biolabs.com; drkim@ivi.int; andrew.gorringe@phe.gov.uk; belll@who.int; aysegul.nalca.civ@mail.mil; catherine.whittaker@phe.gov.uk; marykate.morris@cdph.ca.gov; vfumado@hsjdbcn.org; akbulut@medicine.ankara.edu.tr; jen.gommerman@utoronto.ca; Luis.Lugo.mil@afrims.org; KKoram@noguchi.ug.edu.gh; yang_wang@sinocelltech.com; chhsu296@cde.org.tw; sunL@antibodychina.com; ping_zhan@sinocelltech.com; ttbiozyc@aliyun.com; Farid.Khan2@Pfizer.com; justins@microsoft.com; xinqq@sinovac.com; imaginapolo@gmail.com; frank.rockhold@duke.edu; huong72us@yahoo.com; xiedeying@sinopharm.com; therese.solstad@legemiddelverket.no; pardis@broadinstitute.org; Eduard.Salakhov@gmail.com; michael.malison@gmail.com; julia.vergara@irta.cat; ploemen@viroclinics.com; wangjz@nifdc.org.cn; epstein@ecohealthalliance.org; MStanford@imv-inc.com; alef.costa@saude.gov.br; CVHerst@flowpharma.com; Romain.Martischang@hcuge.ch; Cheryl@iliadbio.com; rajatonirinas@who.int; molho@viroclinics.com; liguifan@biominhai.com; Clare.Morris@nibsc.org; walter_straus@merck.com; CKeech@Novavax.com; PNorris@vitalant.org; vrunda.parikh@pfizer.com; cleide.garcez@fiocruz.br; sekim@krict.re.kr; FRIEDE, Martin Howell; 13718415635@163.com; lanqinying@walvax.com; limhy0919@korea.kr; raul.andino@ucsf.edu; hsaeb@phcc.gov.qa; sergey.kozhin@rdif.ru; avillarreal@indicasat.org.pa; heather.rubino@pfizer.com; albert.jan.van.hoek@rivm.nl; t.brehm@uke.de; christoph.rademacher@mpikg.mpg.de; jessica.lee@gmail.com; langermans@bprc.nl; srashid@atcc.org; annied@epivax.com; ekagucia@kemri-wellcome.org; nicolew@nicd.ac.za; Raj Ghosh; vera.gattas@butantan.giv.br; aleksandra.wesolowska@wum.edu.pl; patricia.braga@butantan.gov.br; FStruyf@ITS.JNJ.com; nymyung@sk.com; peter.palese@mssm.edu; costaa@who.int; elana_jaffe@med.unc.edu; dean.follmann@nih.gov; caroline.melo@rivm.nl; thatziio@rockefeller.edu; sayamrym@niid.go.jp; George Siber; wassana.w@bionet-asia.com; bwilliams@who.int; vittoria.offeddu@ird.global; tapia@mpi-magdeburg.mpg.de; Christina.Bareja@health.gov.au; jzejda@sum.edu.pl; ustjugov@biocad.ru; mlipsitc@hsph.harvard.edu; chaber@modernatx.com; fernando.p.polack@vanderbilt.edu; Tong-ming.Fu@sanofi.com; Susie.dunachie@ndm.ox.ac.uk; chuxiafei@zhifeishengwu.com; Stefania.Capone@reithera.com; Barbara Mahon; jqt8@cdc.gov; shabir.madhi@wits.ac.za; suchinda.m@chula.ac.th; ThomasC.Mettenleiter@fli.de; jim.buttery@monash.edu; david.rhew@microsoft.com; Kwasi.amfo@cepi.net; hstaines@sgul.ac.uk; nicholas.kitchin@pfizer.com; vrasolof@pasteur.mg; dingfan@zhifeishengwu.com; freidlg@who.int; vekemansj@who.int; hombachj@who.int; zengming@biominhai.com; ghkim33@korea.kr; John.Treanor@hhs.gov; tlying@fudan.edu.cn; dbarouch@bidmc.harvard.edu; brian.greenwood@lshtm.ac.uk; jeff_sachs@merck.com; hartka@bluewin.ch; Brooke Peetz (AgileOne); jprice@greffex.com; peshi@UTMB.EDU; lingyi.zheng@sanofi.com; msalit@stanford.edu; gaofu@chinacdc.cn; mlegars@its.jnj.com; katarina.prosenc@nlzoh.si; Vernon_LEE@moh.gov.sg; Emilio Emini; liu.michael222@gmail.com; daniela@lji.org; alan.kimura@curevac.com; taolifeng@zhifeishengwu.com; balaji.more@zyduscadila.com; carlos.diazgranados@sanofi.com; sgupta@iavi.org; judy.wen@icosavax.com; daniel.larremore@colorado.edu; lmoise@epivax.com; shinjini.bhatnagar@thsti.res.in; william.lee@health.ny.gov; sharris@altimmune.com; yjs199307@163.com; greanggrai.h@bionet-asia.com; annagiulia.stigliano@reithera.com; fchowdhury@icddrb.org; ajones@rockefeller.edu; dthea@bu.edu; saowanee.s@bionet-asia.com; valentina.bernasconi@cepi.net; jilian.sacks@finddx.org;

glynnsa@nhlbi.nih.gov; Gopa.Raychaudhuri@fda.hhs.gov; veronica.suarez@seqirus.com; samanthapaston@gmail.com; jill_gilmour@hotmail.co.uk; francesco.x.berlandascorza@gsk.com; dboyle@path.org; c.dahlke@uke.de; Anushri Singhvi; alexander.precioso@butantan.gov.br; nfaria@ic.ac.uk; paul.kristiansen; roland.tschismarov@themisbio.com; devan_mehrotra@merck.com; linsen.du@bravovax.com; miock.kim@sk.com; amelia.karlsson@duke.edu; yoshiyama1962@yahoo.co.jp; SPortillo@som.umaryland.edu; lhampton@gavi.org; connie.cai@gatesfoundation.org; TranBaQuang.Truong@sanofi.com; almonther@hotmail.com; soninov@rosminzdrav.ru; tonya.villafana@astrazeneca.com; min.dong@cloverbiopharma.com; pisano@vakzine-manager.de; wei.tu@fda.hhs.gov; gnorheim@vaccibody.com; nhj1114@mogam.re.kr; darwyn.kobasa@canada.ca; syeum10@korea.kr; Phil.yang@immunitybio.com; cassandra.overking@fda.hhs.gov; gmeller@iavi.org; faiz.ahmadkhan@mcgill.ca; christian.cao@ucalgary.ca; lucas.ribeiro@saude.gov.br; MBxVend-1@yahoo.co.uk; Julia.Tree@phe.gov.uk; bo_long@sinocelltech.com; sujan@lji.org; xuzhu@ucas.ac.cn; nigel.crawford@mcri.edu.au; mayara_bastos@yahoo.com.br; darryl.falzarano@usask.ca; ercument.karasulu@ege.edu.tr; david.vallo@astrazeneca.com; karineamicis@gmail.com; wangling@niaid.nih.gov; cecile.artaud@pasteur.fr; liz.miller@lshtm.ac.uk; Ajoke Sobanjo-ter Meulen; monica.conde@butantan.gov.br; juliana.viscondi@butantan.gov.br; CHOONG_May_Ling@hsa.gov.sg; amol.chaudhari@cepi.net; IVMARTINEZ@hsc.wvu.edu; zobstfeld@wesleyan.edu; jimin@walvax.com; mawiddowson@itg.be; Darin.Edwards@modernatx.com; brian.zabel@lakepharma.com; Elena.Matveeva@rdif.ru; Rolando.pajon@modernatx.com; Email:jplested@novavax.com; helen.thomas@cepi.net; zhout@who.int; Kai Dallmeier; lny1@cdc.gov; sheahan@email.unc.edu; helena.wilcox@ndm.ox.ac.uk; michael.wall@canada.ca; wangkai1@genomics.cn; Matthew.Reed.mil@afrims.org; d.watterson@uq.edu.au; mihaelacarla.nosca@seqirus.com; Mallory.Shriver@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; wrastawicki@pzh.gov.pl; lixin_yan@sinocelltech.com; guy.gorochov@sorbonne-universite.fr; Padeshpa@gmail.com; stroheru@who.int; Tom Kariuki; lydie.marcelon@sanofi.com; nirp@iibr.gov.il; mubangizid; tom@covaxx.com; douglas_fox@berkeley.edu; Ted.Tsai@Takeda.com; kwright@iavi.org; christine.colvis@nih.gov; ajones@mail.rockefeller.edu; maggie.luo@cloverbiopharma.com; Jer-Ming Chia; pawinee.k@redcross.or.th; hromadka@axon-neuroscience.eu; a.pan@asst-cremona.it; alariqil@who.int; peter.smith@lshtm.ac.uk; SlackCa@ukzn.ac.za; tom.tipton@phe.gov.uk; vankerkhovem@who.int; jwilbur@meso-scale.com; dr.rakesh3105@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; xing.li@fda.hhs.gov; winnie.x.janssens@gsk.com; cristina.tato@czbiohub.org; daclark@sgul.ac.uk; miriam.onishi@anvisa.gov.br; quliang@sinopharm.com; philipp.mann@curevac.com; Peter Patriarca; adriane.oliveira@anvisa.gov.br; sebastianms@gisaid.org; In-Kyu Yoon; mbo2@cdc.gov; mpernice@dynavax.com; dotuandat@vabiotech.com.vn; jacob@cmcsph.org; Lakshmi.Jayashankar@hhs.gov; nicole.roth@curevac.com; pickettte@niaid.nih.gov; Carol.Sabourin@hhs.gov; croy@tulane.edu; samiah.kanwar@aku.edu; Harish Iyer; richard.webby@stjude.org; dyu@dynavax.com; haylee@sk.com; Jean Lang; anahita.fathi.us@gmail.com; jessica.lee@inovio.com; jerry.weir@fda.hhs.gov; may.chu@cuanschutz.edu; anthony.macaluso@tonixpharma.com; macalvo@uach.cl; PFast@iavi.org; deoliveira@ukzn.ac.za; gdt@duke.edu; mmsiq@ioc.fiocruz.br; p.smith@lshtm.ac.uk; r.heyderman@ucl.ac.uk; zhangw@who.int; tasker@codagenix.com; azimt@who.int; christopher.da.costa@cepi.net; mksong@ivi.int; carniel@pasteur-yaounde.org; woodd@who.int; melanie.saville@cepi.net; vmoeder@illumina.com; sameer.parekh@seruminstitute.com; alex.sigal@ahri.org; mark.page@nibsc.org; melanie.ott@gladstone.ucsf.edu; karen.goldenthal@gmail.com; nadia.ansari@aku.edu; mt2f@virginia.edu; Kirsty Le Doare; amit.k.srivastava@pfizer.com; Supriya Kumar; res2025@med.cornell.edu; breeze.cavell@phe.gov.uk; horikoshiy@who.int; christian.drosten@charite.de; lydaespitia@unisinu.edu.co; smihwang@sk.com; liub@cde.org.cn; dave.boyle@lakepharma.com; 195046403@qq.com; william.windsor@cuanschutz.edu; anja.schiel@noma.no; giovanetti.marta@gmail.com; madhis@rmpru.co.za; Arnaud.Marchant@ulb.be; scordo@qb.fcen.uba.ar; desteo.ch@gmail.com; Youyi Fong; cwchou476@cde.org.tw; descherm@bni-hamburg.de; Jessica.liu@tigermedgrp.com; Mpasetti@som.umaryland.edu; leanne.robinson@burnet.edu.au; mazhari@wehi.edu.au; christina.henderson@uq.edu.au; noel.tordo@pasteur.fr; ploeman@viroclinics.com; RChikwamba@csir.co.za; zhangyuting@zhifeishengwu.com; monika.lindemann@uk-essen.de; martinbexon@yahoo.co.uk; karen.martins@hhs.gov; Asisa.Volz@tiho-hannover.de; dmissiak@bsd.uchicago.edu; gmackenzie@mrc.gm; marciabarbosavs@gmail.com; zhaozhimei89@163.com; a.a.khazaeli@gmail.com; reveizl@paho.org; mary.marovich@nih.gov; librada.f@bionet-asia.com; cdigermanio@vitalant.org; anh.wartel@ivi.int; allenlien@medigenvac.com; larry.wolfraim@nih.gov; robert.chen@cepi.net; zryn@walvax.com; Ashley.Smith1@hhs.gov; zhaoyuping@medleader.com.cn; tomwhite42450@gmail.com; brosen@novavax.net; agoodridge@indicasat.org.pa; mceuppe1@its.jnj.com; sunil.shewale@seruminstitute.com; dayejung@eubiologics.com; maghsoodlu@yahoo.com; rkoup@mail.nih.gov; freedmanne@mail.nih.gov; julie.joseph@canada.ca; vanessa.infante@butantan.gov.br; Liz.Miller@phe.gov.uk; LMeyers@epivax.com; John N. Nkengasong; GSimmons@vitalant.org; carolina.pingret@anvisa.gov.br; mehmet.ozturk@ibg.edu.tr; ruben.rizzi@biontech.de; lawton.stubbert@canada.ca; mcjm.sturkenboom@gmail.com; roberto.camerini@reithera.com; shanchao@wh.iov.cn; r.kobbe@uke.edu; xywang@shmu.edu.cn; lori.newman@nih.gov; patricia.garcia@upch.pe; mariella.zaroni@anvisa.gov.br; Matthew.Bonaparte@sanofi.com; Ragini.Shivji@ema.europa.eu; MNELSON@dstl.gov.uk; jcsedrik@path.org; imwei1@163.com; lea.sewell@pfizer.com; esulkowska@rics.bwh.harvard.edu; david.spiro@nih.gov; Karl.Erlandson@hhs.gov;

evan.sturtevant@hhs.gov; john.c.trefry.civ@mail.mil; sarina@instem.res.in; Abbie.Bown@phe.gov.uk; tj.chen@chanzuckerberg.com; avandebo@its.jnj.com; wangpw@ivdc.chinacdc.cn; OumaE@africa-union.org; dkim22@its.jnj.com; allergypk@gmail.com; dipyaman.iicb@gmail.com; pujingster@163.com; ebolakim@sk.com; shashikanth4257@bharatbiotech.com; eric.vangieson@darpa.mil; YenewK@africa-union.org; ygrad@hsph.harvard.edu; seongeun@sk.com; FOO_Yang_Tong@hsa.gov.sg; mit666666@pitt.edu; yangfeng@chazenbio.com; livia.vinhal@saude.gov.br; Ann.Rawkins@phe.gov.uk; cdang@lcr.org; mafarodriguez@unisalle.edu.co; zhangj@xmu.edu.cn; colwill@lunenfeld.ca; alan.liss@cepi.net; verstrepen@bprc.nl; 308041407@qq.com; christian.brechot@pasteur.fr; liyl@cde.org.cn; sonja.henne@cepi.net; mona.mohsen@saiba-biotech.com; jmcelrat@fredhutch.org; brian.ward@mcgill.ca; dong.shen@rnaimmune.com; hyl01@tsinghua.org.cn; r.kobbe@uke.de; Phanhonghoa@vabiotech.com.vn; Adam.Finn@bristol.ac.uk; igor.balashov@vaxine.net; hopr@uaem.mx; robert.wawrzinek@mpikg.mpg.de; mengx@sinovac.com; wdj@adaptvac.com; Cblish@stanford.edu; tyzhang1003@163.com; linjinzhong@fudan.edu.cn; gregory.d.gromowski.civ@mail.mil; sheetal.gandotra@igib.res.in; lei.shi@walvax.com; dustin.johnson@canada.ca; Tony.Schountz@colostate.edu; s.a.arakelov@spbniivs.ru; jason.fernandes@canada.ca; wildersmitha@who.int; pdeshpande@indimmune.com; verschoor@bprc.nl; Mike Whelan; James.Milligan@seqirus.com; ben.miller.13@ucl.ac.uk; pgilbert@fredhutch.org; aleksander.masny@policja.gov.pl; roice.fulton@cepi.net; silviacosta@usp.br; baihe@nmpa.gov.cn; Nicole Frahm; pilailuk.o@dmsc.mail.go.th; katom@who.int; Poonepalli_ANURADHA@hsa.gov.sg; tanakat@who.int; sheetal.gandotra@igib.in; zhiping.ye@fda.hhs.gov; savino@ioc.fiocruz.br; CCassetti@niaid.nih.gov; Wenfeng Gong; s.mccormack@ucl.ac.uk; rtchen1135@gmail.com; xumingjue0922@126.com; fred@imophoron.com; tdcarroll@ucdavis.edu; TSmith@inovio.com; lja2002@qatar-med.cornell.edu; drevelli@lovelacebiomedical.org; zhangyan@ivdc.chinacdc.cn; Abena.Amoah@lshtm.ac.uk; Vanessa.Fontana@curevac.com; arimoin@ucla.edu; rafael.delgado@salud.madrid.org; ricardo.palacios@butantan.gov.br; satyajit@iiserpune.ac.in; Rong.Xu@sabin.org; mary@mwuconsulting.com; susanne.rauch@curevac.com; lisa@amicitiam.com; cgast@path.org; Dong, Haiyan; Pillets@medicago.com; katharina.hartmann@cepi.net; kraehliv@staff.uni-marburg.de; Carlos.GuzmanQuilo@sanofi.com; Lynda Stuart; simon.funnell@phe.gov.uk; bernhard.kerscher@pei.de; Toher, Margaret; mgursel@metu.edu.tr; pennym@nicd.ac.za; bernadette.murgue@inserm.fr; olaf-oliver.wolz@curevac.com; mariann.bringsvaerd@cepi.net; Kriti Arora; dparmar@zydustherapeutics.com; M.Whittaker@wellcome.ac.uk; alejandra.gurtman@pfizer.com; jing_jiang201906@sina.com; jennifer.bath99@yahoo.com; RZahn@its.jnj.com; somchaiya@gpo.or.th; lawrence.reiter@providencetherapeutics.com; rbaric@email.unc.edu; Jacqueline.Miller@modernatx.com; dnovack@dynavax.com; david.lee-parritz@tufts.edu; Kathryn Rutkowski; bernadette.hendrickx@cepi.net; ytakahas@niid.go.jp; Rebecca.Harris@sanofi.com; Elizabeth Butler; angel@wedo-projects.com; wardmi@who.int; brooke.bozick@nih.gov; Jin.Zhu@health.gov.au; derrick.crook@ndcls.ox.ac.uk; mvinge@vaccibody.com; r.shattock@imperial.ac.uk; ramadany@sfda.gov.sa; Farah_MOHAMED_HANIFF@ncid.sg; enwereg@who.int; maria.cassia@hc.fm.usp.br; kum.ungchusak@gmail.com; Jeff.Yang@cloverbiopharma.com; ldunkle@novavax.com; mdohmd@snu.ac.kr; jeff.sachs@merck.com; msavoia@usp.br; fguirakhoo@geovax.com; sh@stemcro.com; k.chappell@uq.edu.au; fkoide@southernresearch.org; jlh66@cam.ac.uk; jmarien@itg.be; marmorato.mariana@gmail.com; drsahoo@indimmune.com; melanie.l.delannoy@gsk.com; paul.licciardi@mcri.edu.au; heather.gidding@sydney.edu.au; ravetch@mail.rockefeller.edu; Tom.Pilcher@dhsc.gov.uk; kwonseoyeon@sk.com; landryn@medicago.com; tomeri@iibr.gov.il; makwenyao@gmail.com; michael.holbrook@nih.gov; Zepp@mail.uni-mainz.de; richard.siggers@canada.ca; lbmulenga@yahoo.com; xin.fang@cloverbiopharma.com; Klaus.Cichutek@pei.de; pe_shu_ai@hsa.gov.sg; Anya Asuncion (Opus); lisa.hensley@nih.gov; raafat.fahim@cepi.net; liweihua8@sinopharm.com; jricht@vet.k-state.edu; shoubai.chao@cansinotech.com; nelias@nimr-mmrc.org; luc.gagnon@nexelis.com; Giovanni Della Cioppa; tijsma@viroclinics.com; sophiev@hku.hk; Arun Kumar; anna.may@joinzoe.com; nussen; esthel.vanbrackel@kuleuven.be; gustavo.santos@anvisa.gov.br; Susanne.EDER-LINGELBACH@valneva.com; HKaranja@kemri-wellcome.org; trvrb; mfkung@cde.org.tw; guido.grandi@unitn.it; alan@sanbi.ac.za; florian.krammer@mssm.edu; Sarah Mudrak, Ph.D.; jpattyn@gavi.org; marco.krieger@fiocruz.br; marilia.santini@ini.fiocruz.br; amishahbrown@inovio.com; chantal.veira@cepi.net; inbanathanf@who.int; geert.lerouxroels@ugent.be; olga.rovira@cepi.net; cori@chanzuckerberg.com; kcyau@hku.hk; huangenqi@zhifeishengwu.com; tracey.thue@usask.ca; lcho@novavax.com; marzia@niaid.nih.gov; d.dunn@ucl.ac.uk; robbert.x.van-der-most@gsk.com; mariangela.cavarelli@cea.fr; wuzy@263.net; john.talian@curevac.com; djernigan@cdc.gov; Andrew.Phipps@hhs.gov; jing.sun@cansinotech.com; carolina.blades@anvisa.gov.br; bertozzi@stanford.edu; hwan.kim@stonybrook.edu; natalie.marchevsky@paediatrics.ox.ac.uk; qasimattock@gmail.com; afrozaakter@icddrb.org; cassia.cearley@icosavax.com; dhoconno@wisc.edu; rgonzalez@uaem.mx; eunlyeong.park@ivi.int; imam.tauheed@icddrb.org; omar.sued@huesped.org.ar; nsalisch@its.jnj.com; kwonseoyeon@skdiscovery.com; teresa.lambe@ndm.ox.ac.uk; pramod.pujari@seruminstitute.com; giselle.castillo@pfizer.com; tesfaye.gelanew@ahri.gov.et; fqadri@icddrb.org; robertcoffman121@outlook.com; farshad@covaxx.com; lmercer@path.org; clemens.ralf@outlook.com; Tony.Wang@fda.hhs.gov; yoonyeong@sk.com; gtapiaca@its.jnj.com; kazif@who.int; Chelsea Bond (Opus); kmodjarrad@eidresearch.org; anissa.cheung@fda.hhs.gov; Gustavo.palacios@gmail.com; natalia@providencetherapeutics.com; ranga.cs@cdsco.nic.in; bologa.monica@gmail.com; jricht@ksu.edu; stanley-perlman@uiowa.edu; Celeste.Marsh@health.gov.au; chantal.reusken@rivm.nl;

paul.fine@lshtm.ac.uk; binuphilip@zyduscadila.com; fywu658@cde.org.tw; lapujadeo@who.int; karin.bok@nih.gov; clint.florence; gsellp@who.int; Shailesh.DEWASTHALY@valneva.com; Hongquan.wan@fda.hhs.gov; tasnuva.ahmed@icddrb.org; maria.baca-estrada@canada.ca; matthias.klose@curevac.com; amy.fix@scendea.com; mhasanul.kaisar@icddrb.org; kim.mulholland@lshtm.ac.uk; zengbing@sinopharm.com; indrajeet@bionet-asia.com; pcahn@huesped.org.ar; christian.bottomley@lshtm.ac.uk; taufiqur@icddrb.org; elizabeth.patino@butantan.gov.br; Surender.Khurana@fda.hhs.gov; franck.touret@univ-amu.fr; revans@who.int; ndiayesire@hotmail.fr; phil.yang@nantworks.com; juleen.gayed@pfizer.com; hychen@cde.org.tw; maaroufi@pasteur.ma; tingting.yan@mail.utoronto.ca; sabinoec@usp.br; malik@hku.hk; stephen.lockhart@pfizer.com; ruoyu.hu@walvax.com; bcowling@hku.hk; tkh4@cdc.gov; zhongkaishi28@gmail.com; aottosen@unicef.org; barnorj@who.int; nadia.oreshkova@wur.nl; adebola.olayinka@ncdc.gov.ng; joan@joinzoe.com; nadia.tornieporth@cepi.net; gftsai@cde.org.tw; 1531287517@qq.com; vongs@who.int; bond.court@gmail.com; rkiatchula@gmail.com; ywsohn09@gmail.com; JLPRIOR@dstl.gov.uk; snumouse@snu.ac.kr; kingpfph@sina.com; yjlee@eubiologics.com; robert.bailer@q2labsolutions.com; bronwyn@broadinstitute.org; khirullin@mail.ru; moorthyv; anice.lowen@emory.edu; dguyongellin@osivax.com; liliana.brown@nih.gov; fanxin7@sinopharm.com; katrin.ramsauer@themisbio.com; dean.smith@canada.ca; kate81@korea.kr; judith.absalon@pfizer.com; Christophe.Gregoire@sanofi.com; yangyunkai@sinopharm.com; 57667504@innovax.cn; juzdias@gmail.com; Todd.Suscovich@seromyx.com; gromova@biopharma-excellence.com; fguirakhoo@unitedneuroscience.com; anand.drk@gmail.com; eric.osoro@wsu.edu; zengxizi@kangtai.com; stephane.bancel@modernatx.com; zhongzaixin@zhifeishengwu.com; dsz@imbcams.com.cn; a.luttick@360biolabs.com; Gerald.Kovacs@hhs.gov; Zhanghua_Lan@sinocelltech.com; hutiny@Who.int; solomon.yimer@cepi.net; paul-mccray@uiowa.edu; nuno.faria@zoo.ox.ac.uk; J.P.Stewart@liverpool.ac.uk; sbrowne@altimmune.com; jins.park@sk.com; matthew.snape@paediatrics.ox.ac.uk; jkonyndyk@usaid.gov; maria-angeles.x.ceregido@gsk.com; lmartinez@txbiomed.org; robin.levis@fda.hhs.gov; stig.tollefsen@cepi.net; thyde@cdc.gov; matthew.hohenboken@seqirus.com; bergerii@who.int; sameeullah@bs.qau.edu.pk; rehman.zaira@yahoo.com; james.huleatt@sanofi.com; Molly.Lamb@cuanschutz.edu; jldeen@up.edu.ph; sandsa@who.int; vincent.munster@nih.gov; Holger Kanzler; jinbo.gou@cansinotech.com; acope@iavi.org; rosemaryaudu@yahoo.com; rodrigo.correa@fiocruz.br; irahetar@who.int; arandhaw@fredhutch.org; shaumik.islam@icddrb.org; Sophie Mathewson; paul@medigenvac.com; pgarg@thsti.res.in; pamela.proud@phe.gov.uk; carolina.argondizo@usp.br; loy@who.int; asmronger@gmail.com; wbrooks3@jhu.edu; schwartz@pasteur.fr; Jakob Cramer; hanwx@sinovac.com; paul.hodgson@usask.ca; Hang.Xie@fda.hhs.gov; jorge.osorio@wisc.edu; Hendrik Jan Thibaut; adamou.rafiou@gmail.com; tdelossantos@path.org; brett.barnett@cepi.net; danielbrasseur@gmail.com; ASiyer@mgh.harvard.edu; robert.paris@modernatx.com; raquel.guiomar@insa.min-saude.pt; Ali.Mirazimi@folkhalsomyndigheten.se; diane.descamps@aphp.fr; jschindler@imv-inc.com; Johan Neyts; brangelp@who.int; javadi11@hzdr.de; MCELROYA@pitt.edu; eric@providencetherapeutics.com; ggj2@cdc.gov; wangyilin@medleader.com.cn; swaminathans@who.int; chr.vin@web.de; erich.tauber@themisbio.com; jeroen.kortekaas@wur.nl; joshua.liang@cloverbiopharma.com; kristy.tomas@health.gov.au; hjanes@fredhutch.org; agw13@pitt.edu; ihsangursel@bilkent.edu.tr; Anthony.Scott@lshtm.ac.uk; kevinkumarkansagra@zyduscadila.com; Anna.JefferySmith@phe.gov.uk; Harry Kleanthous; freire@bio.fiocruz.br; jkalil@pq.cnpq.br; jlehrman@iavi.org; mcortese@vaxart.com; tranminhn@who.int; troyrandall@uabmc.edu; m.koopmans@erasmusmc.nl; anu.raghunathan@ncl.res.in; Eeva.Broberg@ecdc.europa.eu; yoos@who.int; senta.walton@usz.ch; Nieuwburg@viroclinics.com; julianna.pieknik@fda.hhs.gov; mdjjh@nmc.or.kr; andrew.p.hollands.civ@mail.mil; cwonodi1@jhu.edu; Mia.Crampin@lshtm.ac.uk; Charlie Weller; wuting@xmu.edu.cn; wangruyue@zhifeishengwu.com; svein.rune.andersen@legemiddelverket.no; bhagwat.gunale@seruminstitute.com; pingping.zhang@pfizer.com; Bev.Menner@csl.com.au; rodriguezhernandezc@who.int; daniel.brasseur@cepi.net; WaickmaA@upstate.edu; clsilva@fmrp.usp.br; Isis Kanevsky; joanna.zmurko@q2labsolutions.com; Lloyd.Mulenga@moh.gov.zm; Julie.Lobjeois@sanofi.com; xumiaobj@126.com; agartlan@fredhutch.org; Khadija.Jarik@international.gc.ca; ann.eakin@nih.gov; jeff@stabilitech.com; annap@auth.gr; liuying@medleader.com.cn; tedross@uga.edu; varma.bhupathiraju@biologicale.com; paul.lambert@unige.ch; marc.eloit@pasteur.fr; wdj@expres2ionbio.com; SMalhotra@iavi.org; dj56wood@gmail.com; yuho74@hotmail.com; barney.graham@nih.gov; nadege.ripley@modernatx.com; charles.chiu@ucsf.edu; sumitbhushan@panaceabiotec.com; tom@covaxx.xom; gasparr@who.int; bgraham@mail.nih.gov; nb@rdif.ru; rodewaldl@chinacdc.cn; lorna.mcinroy@phe.gov.uk; beatrice.n.laupeze@gsk.com; muldersm@who.int; rkiat@chula.ac.th; Jorge Kalil; kim.brolin@ecdc.europa.eu; cherylc@nicd.ac.za; STorhaug@vaccibody.com; Lienanhha.do@mcri.edu.au; katrin.leitmeyer@ecdc.europa.eu; rahul.arora@balliol.ox.ac.uk; marion.gruber@fda.hhs.gov; donna.ambrosino1@gmail.com; David Blazes; Imran Nisar; dlggpp@gmail.com; shimian.zou@nih.gov; marisol.simoes@bio.fiocruz.br; carl.hanson@cdph.ca.gov; shinj@who.int; MAFRANCO@JAVERIANA.EDU.CO; rebecca.klein1@merck.com; a.agrawal@igib.in; miyazakikrauser@who.int; eliana.barros@butantan.gov.br; stephanie.longet@well.ox.ac.uk; sihindawi@yahoo.com; luk_vandenberghe@meei.harvard.edu; rmallory@novavax.com; CHOO_Qiuyi@hsa.gov.sg; dginete@sciphil.org; reinel120305@gmail.com; mayor@ncbs.res.in; medeiros@bio.fiocruz.br; brian.greewood@lshtm.ac.uk; pbieniasz@mail.rockefeller.edu; marta.diaz@salud.madrid.org; Suellen.Nicholson@vidrl.org.au; rodrigueza@paho.org; Gilbert, Peter B;

mireilledosso@yahoo.fr; okeibunorj@who.int; cindy.x.gutzeit@gsk.com; rawleigh.howe@ahri.gov.et; Jacqueline.Shea@inovio.com; eyangoh@pasteur-yaounde.org; boulayi@medicago.com; jokim@ivi.int; carla.brichesi@anvisa.gov.br; songqiaoqiao@ystwt.com; nbhat@path.org; ravindra.gupta@ucl.ac.uk; lizhigang@biominhai.com; russori@njms.rutgers.edu; mirajw@who.int; dsreed@cvr.pitt.edu; Heather.Whitaker@phe.gov.uk; nbaylor@biologicsconsulting.com; wim.vanderpoel@wur.nl; Tracy.MacGill@fda.hhs.gov; James.Little@hhs.gov; alka.dbt@nic.in; Bogdana.Coudsy@sanofi.com; elliot@stabilitech.com; cbstauft@gmail.com; Tamala.MallettMoore@sanofipasteur.com; alyson.kelvin@usask.ca; perkinsm@who.int; thall@sgul.ac.uk; niklas.bobrovitz@mail.utoronto.ca; sroberts@altimmune.com; Bethany_Gauthier@hms.harvard.edu; GWeiding@its.jnj.com; deven.parmar@zydusdiscovery.ae; dr.petrov_jordan@yahoo.com; Antonia.Ho@glasgow.ac.uk; zoeteweij@viroclinics.com; dlaufer@iavi.org; alessandro.torelli@vismederi.com; stoback@novavax.com; francois.p.roman@gsk.com; roberta.piorelli@butantan.gov.br; dailp@biols.ac.cn; gweiss@uci.edu; Keith.Peden@fda.hhs.gov; rachna.gupta@sanofi.com; priti.shah@astrazeneca.com; Joe Rininger; nax3@cdc.gov; kristine.rose@cepi.net; martin.plante@nrc-cnrc.gc.ca; Nupur.Sengupta@biologicale.com; Frieman, Matthew; alemseged.abdissa@ahri.gov.et; srinivas.murthy; joe@czbiohub.org; csv@ssi.dk; hironorinakagami@gmail.com; ckchew@crc.gov.my; Piyush.patel@providencetherapeutics.com; sapan4252@bharatbiotech.com; Buitendijk@viroclinics.com; fmarks@ivi.int; wanxilu@zhifeishengwu.com; Bassam.Hallis@phe.gov.uk; changguili@aliyun.com; sot1@cdc.gov; jenifer.healy@abbott.com; tuliodna@gmail.com; qinjian_zhao@xmu.edu.cn; merryn.voysey@paediatrics.ox.ac.uk; payden@who.int; matthew.cheng@mcgill.ca; liujiankai@biominhai.com; keiko.simon@inovio.com; geldmacher@lrz.uni-muenchen.de; m.noursadeghi@ucl.ac.uk; brenda.valente@anvisa.gov.br; nnagata@niid.go.jp; tksuzuki@nih.go.jp; patrick.reid@unmc.edu; pogueg1@RJRT.com; Robin Mogg; lvrizzo@einstein.br; ls.shashidhara@ashoka.edu.in; Marco.Cavaleri@ema.europa.eu; mto@umn.edu; sue.costa@unisi.it; Pasi.Penttinen@ecdc.europa.eu; crowcroftn@who.int; joseph.chiu@nih.gov; mueller@wehi.edu.au; jguthmiller@uchicago.edu; Kristen Earle; tzyyyuin.chong@cloverbiopharma.com; gayle.pulle@canada.ca; Hisham.Fyyaz@sanofi.com; rachel.park@eubiologics.com; tinaoneko@gmail.com; c.weller@wellcome.org; tenoever@gmail.com; kalisvar_marimuthu@ttsh.com.sg; yumei_huang@sinocelltech.com; ellar@bharatbiotech.com; koningsf@who.int; carolyn.clark@cepi.net; Jordan Tappero; oliver.schoenborn-kellenberger@cogitars.com; h.skirrow@imperial.ac.uk; Scott Dowell; Georgina Murphy; Judy Hubbard

Sent: Tue 4/13/2021 1:02:27 AM (UTC-05:00)

Subject: UPDATED: Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

COVAX ES Workshop April 16th draft Agenda v1.pdf

Dear All,

Final agenda COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants attached.

Friendly reminder if you have not yet registered please use highlighted link by Wednesday, April 14th EOD.

Thank you.
Judy

Dear all,

We are emailing to invite you to a webinar workshop led by the COVAX Enabling Sciences SWAT Team on April 16, 2021, from 6:00-9:00 PT / 14:00-17:00 CET.

The topic of the workshop is "**Global and local approaches to detect and interpret SARS-CoV-2 variants**". The goal of the workshop is to discuss how to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. This requires connecting local pathogen genomic sequencing and epidemiology with high quality virology and immunology. There will also be a discussion of how immunological knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making.

This workshop is organized by the COVAX Enabling SWAT team co-led by CEPI and the Bill & Melinda Gates Foundation.

To attend the workshop, please register here by Wednesday, April 14th EOD. This workshop will be held on Zoom and you will find the Zoom link within the registration portal a couple of days before the event. Once you have registered, there will be an option to add this event to your calendar. In addition to the Zoom link being in your registration portal, our systems will also email you the Zoom link information on three occasions (the day before the event, one hour before the event, and once we go-live). *Please ensure our emails are not going into the junk folder.*

As email lists are imperfect, please forward this email invite to the appropriate contact(s) in your organization and contact Judy Hubbard at the Gates Foundation (Judy.Hubbard@gatesfoundation.com) to indicate who from your group should be invited. Please note that anyone who was forwarded the original calendar save the date may not have necessarily received this email, but may register using the same link provided above.

We look forward to your participation at the workshop.

Thank you.
Judy Hubbard, sent on behalf of

Karen Makar, PhD (BMGF)
William Dowling, PhD (CEPI)
COVAX Enabling Sciences SWAT Team Co-Leads

COVAX

CEPI Gavi unicef World Health Organization

Workshop Agenda

Global and local approaches to detect and interpret SARS-CoV2 variants

DATE	TI ME	LOCATION
Friday, April 16th, 2021	06:00 – 9:00 PT/ 15:00 – 18:00 CET	Zoom Webinar

We all share a common goal to develop safe and effective vaccines. The Enabling Sciences SWAT team aims to provide cross-cutting product-agnostic support to COVID-19 vaccine developers in the area of diagnostics, standards and animal models.

Rapid assessment of the biological impacts of new variants of SARS-CoV-2 requires the collaboration of epidemiologists, virologists and immunologists at the local and global level. However, these efforts are often disconnected from one another, resulting in delays and an incomplete picture of the implications for vaccines and diagnostics.

The objective of this workshop is to share information on how to efficiently connect local pathogen genomic sequencing, epidemiology, virology and immunology to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. There will be a discussion of how knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making. We will discuss ideas for best practices for assessing virus neutralization activity, and approaches to standardizing assays and protocols to improve interpretation of results generated in different labs and geographies

This workshop is convened by the COVAX Enabling Sciences SWAT team, which is co-led by CEPI and the WHO and includes members from the Bill & Melinda Gates Foundation, NIAID and industry. COVAX is the vaccines pillar of the Access to COVID-19 Tools (ACT) Accelerator, co-led by Gavi, the Coalition for Epidemic Preparedness Innovations (CEPI) and WHO. COVAX aims to accelerate the development and manufacture of COVID-19 vaccines, and to guarantee fair and equitable access to appropriate, safe and efficacious vaccines for all countries.

Time (CET)	Presentation Title *(TBD)*	Speaker(s)
15:00-15:05	Welcome and meeting objectives	*TBC, ES SWAT*
15:05-15:20	South Africa Pathogen Genomics Sequencing & AfCDC PGI program	**Tulio DeOliveira,** KRISP
15:20-15:30	Assessing immunological implications of VoCs in South Africa	**Penny Moore,** NICD

15:30-15:40	Immune escape and evidence for re-infection with P.1 in Brazil	**Ester Sabino**, U. Sao Paulo
15:40-15:50	Impact of B.1.1.7 on vaccine induced immune responses	**Ravi Gupta,** Cambridge
15:50-16:00	India Consortium for COVID-19 genomics	**Anurag Agrawal**, CSIR/IGIB
16:00-16:25	**Panel Discussion**	Moderated by **Karen Makar**, BMGF
16:25-16:30	*BREAK*	
16:30-16:40	WHO framework for response to new COVID vaccines	**Sylvie Briand,** WHO
16:40-16:50	Pulling it all together in the COG-UK	**Sharon Peacock,** COG-UK
16:50-17:00	CEPI's Agility program: a centralised approach to evaluate VoCs	**Simon Funnell**, PHE
17:00-17:10	Virus stock and sequencing QC- best practices & available resources	**Sujatha Rashid**, BEI
17:10-17:20	SARS-CoV-2 Interagency Group (SIG) Variant Assessment/Characterization	*TBC, NIAID*
17:20-17:30	ACTIV/TRACE OpenData portal	**Christine Colvis,** NIH/NCATS
17:30-17:55	**Panel Discussion**	Moderated by**: Bill Dowling,** CEPI
17:55-18:00	Wrap up & Next Steps	*TBC, ES SWAT*

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Lane, Chelsea (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Taylor, Ebony (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Taylor, Ebony (NIH/NIAID) [E]

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 4/24/2020 2:30:00 PM (UTC)
End Time:	Fri 4/24/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance: Normal

Start Time: Fri 5/22/2020 2:30:00 PM (UTC)

End Time: Fri 5/22/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance:	Normal
Start Time:	Fri 9/25/2020 2:30:00 PM (UTC)
End Time:	Fri 9/25/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/9/2020 2:30:00 PM (UTC)
End Time:	Fri 10/9/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/23/2020 2:30:00 PM (UTC)
End Time:	Fri 10/23/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/6/2020 3:30:00 PM (UTC)
End Time:	Fri 11/6/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/20/2020 3:30:00 PM (UTC)
End Time:	Fri 11/20/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Hi all,
Just to let you all know in advance, we are expecting NIAID leadership to be joining this call on Friday. Please be prepared to present all the work you have completed thus far for model development and any MCM studies (if applicable). Please also be prepared to mention your capacity for MCM studies starting in January 2021.

11/20/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (UNC, UTMB, USU, CSU)
- Rotating check-in with individual sites (11/20: UNC; 12/4: UTMB; 12/18: USU; 1/15: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/4/2020 3:30:00 PM (UTC)
End Time:	Fri 12/4/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]

Hi all,

On December 4th, we will go more in depth into the hamster models at USU and CSU. Please see the updated agenda below.

12/4/2020 Agenda:

- **General Updates (Erik)**
- **In depth A38 Site Updates for USU and CSU (hamster models)**
- **If there is time – we will go through brief updates for UNC and UTMB**
- **Rotating check-in with individual sites (~~11/20: UNC~~; 12/4: UTMB; 12/18: USU; 1/15: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 12/18/2020 3:30:00 PM (UTC)
End Time:	Fri 12/18/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

12/18/2020 Agenda:

- General Updates (Erik)
- Brief updates for all A38 contractor sites
- Rotating check-in with individual sites (~~11/20: UNC~~;~~12/4: UTMB~~; 12/18: USU; 1/15: CSU)

Note: this will be our last bi-weekly meeting of 2020.

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal

Subject: Canceled: A38 Task Order Bi-weekly Call

Start Time: Fri 1/15/2021 3:30:00 PM (UTC)

End Time: Fri 1/15/2021 5:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 1/29/2021 3:30:00 PM (UTC)
End Time:	Fri 1/29/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

Note: for this Friday, January 29th, please include within your site's presentations whether your site is able to perform aerosol delivery of Tx compounds (and if so, what methods you use). A slide or two max should be sufficient.

1/29/2021 Agenda:

- **General Updates (Erik)**
- **Brief updates for all A38 contractor sites**
- **Rotating check-in with individual sites (*1/29: UNC*; 2/12: UTMB; 2/26: USU; 3/12: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 2/12/2021 3:30:00 PM (UTC)
End Time:	Fri 2/12/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

***Note*:** for this Friday, February 12th, please be prepared for a discussion on testing of dexamethasone (that your site has already conducted, or that is in your queue). Please refer to the email that I sent on Thursday, 2/4/2020.

2/12/2021 Agenda:

- **General Updates (Erik)**
- **First 15minutes – discussion regarding testing of dexamethasone**
- ***Brief* 10-15 minute updates for all A38 contractor sites**
- **Rotating check-in with individual sites (~~1/29: UNC~~; *2/12: UTMB*; 2/26: USU; 3/12: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 2/26/2021 3:30:00 PM (UTC)
End Time:	Fri 2/26/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Palin, Amy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

2/26/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~; *2/26: USU*; 3/12: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 3/12/2021 3:30:00 PM (UTC)
End Time:	Fri 3/12/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Eakin, Ann (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/12/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites. *Note*: please include about a 5 minute high level summary on your thoughts/experiences on positive controls (for Tx studies) for the model(s) that you are developing. If you have any data you can summarize, that would be great. It is okay if you don't have extensive experience with this.**
- **Rotating check-in with individual sites (~~1/29: UNC~~;~~2/12: UTMB~~;~~2/26: USU~~; *3/12: CSU*)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 3/26/2021 2:30:00 PM (UTC)
End Time:	Fri 3/26/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

3/26/2021 Agenda:

- **General Updates (Chelsea)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC*; 4/9: UTMB; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 4/9/2021 2:30:00 PM (UTC)
End Time:	Fri 4/9/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/9/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (~~3/26: UNC~~; *4/9: UTMB*; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 4/23/2021 2:30:00 PM (UTC)
End Time:	Fri 4/23/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Morrey, John; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

4/23/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC; 4/9: UTMB*; 4/23: USU; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 5/7/2021 2:30:00 PM (UTC)
End Time:	Fri 5/7/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/7/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (*3/26: UNC; 4/9: UTMB*; *4/23: USU*; 5/7: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

Importance:	Normal
Start Time:	Fri 5/21/2021 2:30:00 PM (UTC)
End Time:	Fri 5/21/2021 4:00:00 PM (UTC)
Required Attendees:	Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Menachery, Vineet; LeGros, Erika; Schilling, Beth A.; McNees, Andrew G.; Massey, ChristopherLane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, ChristopherDevin Hansen
Optional Attendees:	Vily, Aytaj (NIH/NIAID) [E]Young, Jennifer (AE)Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

5/21/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (5/21: UNC; 6/4: UTMB; 6/18: USU; 7/2: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 6/4/2021 2:30:00 PM (UTC)
End Time:	Fri 6/4/2021 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]Devin Hansen
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/4/2021 Agenda:

- **General Updates (Erik)**
- **Updates for all A38 contractor sites.**
- **Rotating check-in with individual sites (~~5/21: UNC~~; 6/4: UTMB; 6/18: USU; 7/2: CSU)**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Subject:	Canceled: A38 Task Order Bi-weekly Call
Start Time:	Fri 7/2/2021 2:30:00 PM (UTC)
End Time:	Fri 7/2/2021 4:00:00 PM (UTC)
Required Attendees:	Massey, Christopher; McNees, Andrew G.; Schilling, Beth A.; LeGros, Erika; Menachery, Vineet; Beasley, David W.; Viner, Rebekah L.; Taylor Bray, Christy J.; Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]
Optional Attendees:	Young, Jennifer (AE)Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

***Canceling our meeting on July 2nd due to the holiday weekend.**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal

Start Time: Fri 6/18/2021 2:30:00 PM (UTC)

End Time: Fri 6/18/2021 4:00:00 PM (UTC)

Required Attendees: Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Menachery, Vineet; LeGros, Erika; Schilling, Beth A.; McNees, Andrew G.; Massey, ChristopherLane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]Devin Hansen

Optional Attendees: Young, Jennifer (AE)Taylor, Ebony (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan

6/18/2021 Agenda:

- General Updates (Erik)
- Updates for all A38 contractor sites.
- Rotating check-in with individual sites (~~5/21: UNC~~; ~~6/4: UTMB~~; 6/18: USU; 7/30: CSU)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 7/16/2021 3:00:00 PM (UTC)
End Time:	Fri 7/16/2021 4:30:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Christy Taylor Bray; Rebekah Viner; Beasley, David; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Gordon, Jennifer (NIH/NIAID) [E]; Taylor, Kimberly (NIH/NIAID) [E]Devin Hansen
Optional Attendees:	Taylor, Ebony (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Maciel, Milton (NIH/NIAID) [E]; Boggiano, Cesar (NIH/NIAID) [E]

****Please note shift in time by 30 minutes to 11am EST.**

7/16/2021 Agenda:

- General Updates (Erik)
- Brief slide deck (~6-10 slides) on models developed at each A38 site. Please include:
  - Model kinetics & pathology phenotypes (as noted in your 1-pager/info sheets);
  - Whether your model is suitable for testing of vaccines, antivirals, anti-inflammatory agents, mAbs, etc., and what controls can be utilized in your model (and the optimal timing and routes for dosing, etc.);
  - What assays/reagents are available for testing of immune responses in your model (and please include any relevant cytokine data if available);
- Another 2-3 slides with your Site's final data for testing of dexamethasone. Please ensure that histopathology analyses (and any additional analyses, e.g. cytokine if appropriate) can be completed by this date.

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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Richard Bowen

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]

Optional Attendees: Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Meeting ID: 161 887 1310
Password: **552.136**

Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Monthly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 4/24/2020 2:30:00 PM (UTC)
End Time:	Fri 4/24/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]
Optional Attendees:	Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

To: Stein, David Adam[Dave.Stein@oregonstate.edu]; E.J.Snijder@lumc.nl[E.J.Snijder@lumc.nl]; rbaric@email.unc.edu[rbaric@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; raul.andino@ucsf.edu[raul.andino@ucsf.edu]; randy.albrecht@mssm.edu[randy.albrecht@mssm.edu]; Paessler, Slobodan[SLPAESSL@utmb.edu]; bneuman@tamu[bneuman@tamu]
Cc: Moulton, Hong[Hong.Moulton@oregonstate.edu]
From: Diamond, Michael[mdiamond@wustl.edu]
Sent: Thur 3/12/2020 10:19:54 AM (UTC-05:00)
Subject: Re: covid ppmo testing

We are already at capacity and cannot take on any new countermeasure strategies
Mike

From: Stein, David Adam <Dave.Stein@oregonstate.edu>
Sent: Thursday, March 12, 2020 10:09 AM
To: E.J.Snijder@lumc.nl <E.J.Snijder@lumc.nl>; rbaric@email.unc.edu <rbaric@email.unc.edu>; peshi@utmb.edu <peshi@utmb.edu>; Diamond, Michael <mdiamond@wustl.edu>; raul.andino@ucsf.edu <raul.andino@ucsf.edu>; randy.albrecht@mssm.edu <randy.albrecht@mssm.edu>; slpaessl@utmb.edu <slpaessl@utmb.edu>; bneuman@tamu <bneuman@tamu>
Cc: Moulton, Hong <Hong.Moulton@oregonstate.edu>
Subject: covid ppmo testing

Hi Guys,
Just wondering if any of you have any suggestions for us regarding a research lab, preferably based in US, that may be interested to pursue testing of PPMO targeted against SARS2_CoV RNA. Of course, it would be necessary that the lab have BSL 3+ facilities.

From the attached paper you can see that PPMO worked well vs SARS1 in cell cultures (never got to try it in vivo). We make PPMO in our lab at OSU. PPMO are not available commercially.

We already have some testing of PPMO vs SARS2 in the works, but are interested to find a reserach lab that may wish to join in and possibly write a grant with us to pursue various project/possibilities. If you would like to discuss please let me know and perhaps we can have a quick phone call.

With Regards,
Dave

David Stein

Moulton Lab

Dept. of Biomedical Sciences

College of Veterinary Medicine

Oregon State University

Corvallis, OR 97331

541-231-1332 (dave cell)

dave.stein@oregonstate.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]; Baric, Ralph S[rbaric@email.unc.edu]
Cc: tcbaric@med.unc.edu[tcbaric@med.unc.edu]
From: Paessler, Slobodan[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=8de919c12fef4f0880e1b1f73a462e30-Paessler, S]
Sent: Thur 4/9/2020 3:57:07 PM (UTC-05:00)
Subject: Re: Remdesivir resistant mutants

Thanks, Vineet for email and thank you Ralph for consideration!

Best,
Bobo

Slobodan Paessler, D.V.M., Ph.D.
Professor, Department of Pathology
John S. Dunn Distinguished Chair in Biodefense
Director, Galveston National Laboratory Preclinical Studies Core
Director, Animal Biosafety Level 3, Institute for Human Infections and Immunity
Member, WHO Collaborating Center for Tropical Diseases
University of Texas Medical Branch
5.200D Galveston National Laboratory
Galveston, Texas 77555-0609
Tel: Office 409-266-6913; lab 409-747-2489
FAX: 409-747-0762
email: slpaessl@utmb.edu
http://www.utmb.edu/scvd/faculty/paessler.asp

From: "Menachery, Vineet" <vimenach@UTMB.EDU>
Date: Thursday, April 9, 2020 at 3:55 PM
To: "Baric, Ralph S" <rbaric@email.unc.edu>
Cc: Slobodan Paessler <SLPAESSL@utmb.edu>, "tcbaric@med.unc.edu" <tcbaric@med.unc.edu>
Subject: Remdesivir resistant mutants

Hey Ralph,

Bobo Paessler and his group at UTMB are working on COVID-19 work and are interested in the remedesivir mutants from the Science Translation Medicine paper. I do not have these mutants in my lab and don't have capacity to make them at the moment.

Is it possible for you to provide the MERS-CoV or MHV-CoV remdesivir mutants (virus) to him?

Alternatively, would you be willing to share the SARS/MERS recombinant plasmid system with him so that they can generate the mutants themselves. Bobo is willing to go through the formal paperwork process and will request them directly from you. I will provide the plasmids if you agree.

Thanks

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: JUDY.HUBBARD@gatesfoundation.org[JUDY.HUBBARD@gatesfoundation.org]

Attendees: Harry Kleanthous; Holger Kanzler; Max Silverman; David Vaughn; Anastazia Older Aguilar; Colleen Woods; Kriti Arora; Susan Barnett; Ajoke Sobanjo-ter Meulen; Anna DU; Emilio Emini; Judy Hubbard; David Robinson; Nina Russell; Anushri Singhvi; Chris Karp; Peter Dull; Scott Dowell; Vivian Hsu; Kristen Earle; Julia Kuhn; Steve Hadley; Janet White; Heather Ann Brauer; Jacqueline Kirchner; Max Silverman; Kavita Malling (Camber Collective); Natalie Revelle; Chris Chen; Vidya Vasu-Devan; Ros Hollingsworth; Laura Powell; Email Recovery Approval; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; Monalisa Chatterji; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; Kai Dallmeier; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; Dillen, Carly; edohm@uab.edu; Ruben.Donis@hhs.gov; William Dowling; mariette.ducatez@envt.fr; pduprex@pitt.edu; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence; joanne@pitt.edu; thomasf@primate.wisc.edu; Frieman, Matthew; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Garcia-Sastre, Adolfo; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; henaorestrepoa@who.int; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; kazif@who.int; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline Kirchner; knezevici; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; philip.krause@fda.hhs.gov; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; Roger Le Grand; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot

Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; moorthyv; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; Johan Neyts; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; lauriex@who.int; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; salamik@who.int; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; Erica Ollmann Saphire; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; schwartzl@who.int; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; Shi, Pei yong; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; yoos@who.int; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; swaminathans@who.int; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Tseng, Chien-Te K.; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David Vaughn; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; woodd@who.int; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; zhout@who.int; Jin.Zhu@health.gov.au; alex.sigal@ahri.org; rawcraig@yahoo.com; Gerald.Kovacs@hhs.gov; Ashley.Smith1@hhs.gov; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; valentina.bernasconi@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net;

johan.holst@cepi.net; Arun Kumar; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; MNELSON@dstl.gov.uk; Georgia Tomaras, Ph.D.; david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Ragini.Shivji@ema.europa.eu; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; cheryl@gisaid.org; christian.brechot@pasteur.fr; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; Sharon Schendel; alex@lji.org; sujan@lji.org; daniela@lji.org; liz.miller@lshtm.ac.uk; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; janet.lathey@nih.gov; larry.wolfraim@nih.gov; johnsonreed@niaid.nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Christine.bruce@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; Goldblatt, David; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; gustavo.f.palacios.civ@mail.mil; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; costaa@who.int; omorgan@who.int; perkinsm@who.int; subissil@who.int; dj56wood@gmail.com; STRÖHER, Ute; sandsa@who.int; irahetar@who.int; zlshi@wh.iov.cn; Youngmee Jee; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; Jiae Kim; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; Pillai, Satish; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; fernando.p.polack@vanderbilt.edu; Celeste.Marsh@health.gov.au; kim.Mulholland@lshtm.ac.uk; achidi.eric@gmail.com; macalvo@uach.cl; rodewaldl@chinacdc.cn; AFO@ssi.dk; hutiny@Who.int; sylvain.baize@pasteur.fr; mariangela.cavarelli@cea.fr; alariqil@who.int; may@bnitm.de; Jakob Cramer; Harish Iyer; Gagandeep Kang; Kayla Laserson; alemseged.abdissa@ahri.gov.et; azimt@who.int; cawthornea@who.int; adane.mihret@ahri.gov.et; ephcicm@nus.edu.sg; Vernon_LEE@moh.gov.sg; cherylc@nicd.ac.za;

madhis@rmpru.co.za; mdohmd@snu.ac.kr; joser.arribas@salud.madrid.org; marta.diaz@salud.madrid.org; Katrin.Leitmeyer@ecdc.europa.eu; bergerii@who.int; feikind@who.int; grantr@who.int; Stephan.Harbarth@hcuge.ch; vankerkhovem@who.int; kum.ungchusak@gmail.com; albert.jan.van.hoek@rivm.nl; chantal.reusken@rivm.nl; mawiddowson@itg.be; Gayatri.Amirthalingam@phe.gov.uk; Nick Andrews; Andrew.Gorringe@phe.gov.uk; Bassam.Hallis@phe.gov.uk; Liz.Miller@phe.gov.uk; ccassetti@niaid.nih.gov; glynnsa@nhlbi.nih.gov; Graham, Barney (NIH/VRC) [E]; kdk6@cdc.gov; Barbara Mahon; MCELROYA@pitt.edu; ztq9@cdc.gov; Padmini Srikantiah; Jordan Tappero; jqt8@cdc.gov; rgonzalez@uaem.mx; hopr@uaem.mx; m.addo@uke.de; Mark_Ic_Chen@ncid.sg; Romain.Martischang@hcuge.ch; shimian.zou@nih.gov; Christina.Bareja@health.gov.au; John.Forde@phe.gov.uk; JinalB@nicd.ac.za; vekemansj@who.int; paola.stefanelli@iss.it; liya.wassie@ahri.gov.et; vongs@who.int; starkullaj@who.int; mahamuda@who.int; reveizl@paho.org; rodrigueza@paho.org; leitejul@paho.org; vicarian@paho.org; pebodyr@who.int; rawleigh.howe@ahri.gov.et; THOMAS.JAENISCH@CUANSCHUTZ.EDU; ayola-akim.adegnika@medizin.uni-tuebingen.de; t.brehm@uke.de; adamou.rafiou@gmail.com; bernadettemrg5@gmail.com; bernadette.murgue@inserm.fr; gmackenzie@mrc.gm; Anthony.Scott@lshtm.ac.uk; SUyoga@kemri-wellcome.org; atanuri1@gmail.com; ggj2@cdc.gov; wbrooks3@jhu.edu; kkotloff@som.umaryland.edu; ADriscoll@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; SHakre@eidresearch.org; derrick.crook@ndcls.ox.ac.uk; csv@ssi.dk; schwartz@pasteur.fr; marc.eloit@pasteur.fr; srinivas.murthy; matthew.cheng@mcgill.ca; nymadawa@gyals.mn; wuzy@263.net; gaofu@chinacdc.cn; Mpasetti@som.umaryland.edu; aleksandra.wesolowska@wum.edu.pl; cuchip@who.int; per.ashorn@tuni.fi; kwatrag@rmpru.co.za; jmarien@itg.be; KArien@itg.be; adebola.olayinka@ncdc.gov.ng; bcowling@hku.hk; Suellen.Nicholson@vidrl.org.au; paul.licciardi@mcri.edu.au; lienanhha.do@mcri.edu.au; marc-alexandre.lafrance.1@ulaval.ca; paul.fine@lshtm.ac.uk; krystian.jazdzewski@warsawgenomics.pl; jzejda@sum.edu.pl; freidlg@who.int; taufiqur@icddrb.org; fqadri@icddrb.org; r.heyderman@ucl.ac.uk; mff7@cdc.gov; Heather.Whitaker@phe.gov.uk; tonoletej@who.int; annev@nicd.ac.za; shinj@who.int; johnvparry@ntlworld.com; leli@who.int; krishnanv@who.int; revans@who.int; belll@who.int; juneja@tifr.res.in; violetafonsecaocampos@gmail.com; twosned@googlemail.com; alain.townsend@imm.ox.ac.uk; sanchezg@une.net.co; muldersm@who.int; pereyaslovd@who.in; mueller@wehi.edu.au; leanne.robinson@burnet.edu.au; claudioc@gsespa.cl; drmlaman@yahoo.com; ffntoumi@hotmail.com; rajatonirinas@who.int; Kirsty Le Doare; Joe.Fitchett@mologic.co.uk; hstaines@sgul.ac.uk; thall@sgul.ac.uk; okeibunorj@who.int; barnorj@who.int; heather.gidding@sydney.edu.au; mayara_bastos@yahoo.com.br; faiz.ahmadkhan@mcgill.ca; louis.patrick.haraoui@usherbrooke.ca; yuemei.fan@tuni.fi; almonther@hotmail.com; philippa.matthews@ndm.ox.ac.uk; Abbie.Bown@phe.gov.uk; hsaeb@phcc.gov.qa; intl@ibto.ir; dorits@imbm.org; dthea@bu.edu; yoshiyama1962@yahoo.co.jp; ullas@tifr.res.in; jsshastri@gmail.com; Audrey Hutter; cooldrdax@gmail.com; inbanathanf@who.int; muhammadqasim.qasim@otago.ac.nz; ofrinr@who.int; payden@who.int; vokatya@who.int; tranminhn@who.int; cgomez@javeriana.edu.co; jccastellanos@husi.org.co; katom@who.int; snsmarlowe@doctors.org.uk; arashirot@who.int; lOwusu@noguchi.ug.edu.gh;

eric.osoro@wsu.edu; HarbiNa2@NGHA.MED.SA; amhashem@kau.edu.sa; bwilliams@who.int; radegbola@hotmail.com; jean-luc.gala@uclouvain.be; rosemaryaudu@yahoo.com; sandeepdogra@gmail.com; allergypk@gmail.com; maghsoodlu@yahoo.com; peshghi64@gmail.com; a.a.khazaeli@gmail.com; Bethany_Gauthier@hms.harvard.edu; vittoria.offeddu@ird.global; MAHIPALAP@who.int; ian.marr@menzies.edu.au; Abena.Amoah@lshtm.ac.uk; Mia.Crampin@lshtm.ac.uk; Antonia.Ho@glasgow.ac.uk; javadi11@hzdr.de; asmronger@gmail.com; Kaitlyn.Vette@health.nsw.gov.au; magdalena.spolnicka@policja.gov.pl; aleksander.masny@policja.gov.pl; marc.veldhoen@medicina.ulisboa.pt; MRabeh@dha.gov.ae; susie.dunachie@ndm.ox.ac.uk; necla.tulek@atilim.edu.tr; sophiev@hku.hk; koningsf@who.int; Lloyd.Mulenga@moh.gov.zm; lbmulenga@yahoo.com; mastershakil@hotmail.com; rahul.arora@balliol.ox.ac.uk; christian.cao@ucalgary.ca; liu.michael222@gmail.com; niklas.bobrovitz@mail.utoronto.ca; tingting.yan@mail.utoronto.ca; a.pan@asst-cremona.it; s.testa@asst-cremona.it; alessia.zoncada@tin.it; nicolew@nicd.ac.za; GWarimwe@kemri-wellcome.org; HKaranja@kemri-wellcome.org; dancohen@tauex.tau.ac.i; sabinoec@usp.br; patricia.garcia@upch.pe; zobstfeld@wesleyan.edu; amyjanel@gmail.com; liliana.brown@nih.gov; lori.newman@nih.gov; descherm@bni-hamburg.de; emmerich@bnitm.de; charlotte.thalin@sll.se; voneijek@who.int; avillarreal@indicasat.org.pa; agoodridge@indicasat.org.pa; r.a.mckendry@ucl.ac.uk; jint@ustc.edu.cn; Email; monika.lindemann@uk-essen.de; ygrad@hsph.harvard.edu; KHerbst@ahri.org; daniel.larremore@colorado.edu; william.windsor@cuanschutz.edu; Molly.Lamb@cuanschutz.edu; rolf.fendel@uni-tuebingen.de; jguthmiller@uchicago.edu; mzrein@infynity-biomarkers.com; mike.fisher@oncimmune.com; kjambo@mlw.mw; petra.budde@oncimmune.com; oon_tek_ng@ncid.sg; kalisvar_marimuthu@ttsh.com.sg; Farah_MOHAMED_HANIFF@ncid.sg; a.t.decruz.20@ucl.ac.uk; ben.miller.13@ucl.ac.uk; mafarodriguez@unisalle.edu.co; Anna.JefferySmith@phe.gov.uk; keti.glonti@gmail.com; imaginapolo@gmail.com; Maria.Zambon@phe.gov.uk; Jennifer.Yates@health.ny.gov; gingras@lunenfeld.ca; jen.gommerman@utoronto.ca; lewish@who.int; daclark@sgul.ac.uk; omar.nyabi@uclouvain.be; giorgio.fedele@iss.it; Rachel.Halkerston@phe.gov.uk; pamela.proud@phe.gov.uk; kpancer@pzh.gov.pl; wegene.borena@i-med.ac.at; wrastawicki@pzh.gov.pl; sungskim63@gmail.com; vfa3@cdc.gov; teodora.aktas@folkhalsomyndigheten.se; Email: jplested@novavax.com; bkhatri@lunenfeld.ca; tesfaye.gelanew@ahri.gov.et; juan.moliva@nih.gov; anne.werner@nih.gov; gabriela.alvarado@nih.gov; Breeze Cavell; wangling@niaid.nih.gov; eunsung.yang@nih.gov; yi.zhang3@nih.gov; nicole.doriarose@nih.go; lorna.mcinroy@phe.gov.uk; mazhari@wehi.edu.au; zhuna@ivdc.chinacdc.cn; maony@ivdc.chinacdc.cn; zhuzhen@ivdc.chinacdc.cn; zhangyan@ivdc.chinacdc.cn; wangpw@ivdc.chinacdc.cn; sanghwan.seo@ivi.int; vfumado@hsjdbcn.org; xhatzi@med.uth.gr; tatjana.vilibic-cavlek@hzjz.hr; annap@auth.gr; andargachew.mulu@ahri.gov.et; viki.indenbaum@sheba.health.gov.il; colwill@lunenfeld.ca; ytakahas@niid.go.jp; sayamrym@niid.go.jp; tksuzuki@niid.go.jp; raquel.guiomar@insa.min-saude.pt; merit.melin@thl.fi; katarina.prosenc@nlzoh.si; jwilbur@meso-scale.com; Celine.Parsy-Kowalska@oncimmune.com; Imran Nisar; Fyezah Jehan; lcorey@fredhutch.org; m.noursadeghi@ucl.ac.uk; fabienne.brilot@sydney.edu.au; lja2002@qatar-med.cornell.edu; mdjjh@nmc.or.kr; AAgweyu@kemri-wellcome.org; katherine.gallagher@lshtm.ac.uk; AEtyang@kemri-wellcome.org;

	ekagucia@kemri-wellcome.org; Christian.Bottomley@LSHTM.ac.uk; SPortillo@som.umaryland.edu; nicole.gilberger@bnitm.de; sudhirbabji@cmcvellore.ac.in; Mallory.Shriver@som.umaryland.edu; freedmanne@mail.nih.gov; galter@mgh.harvard.edu; kristian@andersen-lab.com; trvrb; pbieniasz@rockefeller.edu; Bjorkman, Pamela J.; jbloom@fredhutch.org; burton@scripps.edu; mmdavis@stanford.edu; deoliveira@ukzn.ac.za; gd312@cam.ac.uk; embrya@niaid.nih.gov; katie.ewer@ndm.ox.ac.uk; agartlan@fredhutch.org; r.fouchier@erasmusmc.nl; ggaiha@mgh.harvard.edu; dh2994@cumc.columbia.edu; Nick Jackson; yoshihiro.kawaoka@wisc.edu; akiko.iwasaki@yale.edu; paul.kellam@kymab.com; neil@ipd.uw.edu; btk@lanl.gov; karin.lore@ki.se; J. Christopher Love; darrenpatrickmartin@gmail.com; monte@duke.edu; felipe.naveca@fiocruz.br; nussen@mail.rockefeller.edu; Erica Ollmann Saphire; sjp97@medschl.cam.ac.uk; mpepper@uw.edu; bpulend@stanford.edu; rino.r.rappuoli@gsk.com; sabinoec@gmail.com; senjutisaha@gmail.com; schief@scripps.edu; gideon.schreiber@weizmann.ac.il; gavin.screaton@medsci.ox.ac.uk; djs200@cam.ac.uk; varadar; dveesler@uw.edu; bwalker@mgh.harvard.edu; andrew@scripps.edu; wilson@scripps.edu; wyatt@scripps.edu
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Subject:	Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

From: JUDY.HUBBARD@gatesfoundation.org[JUDY.HUBBARD@gatesfoundation.org]

Attendees: tom@vaxxinity.com; David Vaughn; michael.schotsaert@mssm.edu; daraporn.p@bionet-asia.com; aetyang@kemri-wellcome.org; juan.moliva@nih.gov; yuri.vasiliev@hotmail.com; janet.lathey@nih.gov; elizabethleakey@gmail.com; may@vakzine-manager.de; daniel.martinez-arguelles@canada.ca; jinalb@nicd.ac.za; dr.annie.degroot@gmail.com; Fyezah Jehan; igor.smolenov@cloverbiopharma.com; k.j.von.eije@umcg.nl; amandacabralsilva@yahoo.com.br; tamala.mallettmoore@sanofi.com; imran@phcglobal.org; SGalloway@cdc.gov; Jeeninga@viroclinics.com; leid@who.int; tong.wu@canada.ca; jose.luis.di.fabio@cepi.net; D.Shah@wellcome.org; elizabeth.daglish@astrazeneca.com; Ockenhouse, Chris; Keith Klugman; vryab@mail.ru; William Dowling; sian.jones@pfizer.com; cuchip@who.int; THOMAS.JAENISCH@CUANSCHUTZ.EDU; jennifer@immunoprecise.com; marcelo.koike@gmail.com; grantr@who.int; lecoest@gmail.com; Mihaela.Nosca@Seqirus.com; sabinoec@gmail.com; harin.l@bionet-asia.com; chenhongyin@walvax.com; david.montefiori@duke.edu; Tom Mooney; Philip.Minor2@gmail.com; lindy.durrant@nottingham.ac.uk; jailal.ablack@entospharma.com; alcantaraluiz42@gmail.com; kelly.taylor@cihr-irsc.gc.ca; Lethanhtuyet@vabiotech.com.vn; michael.wiseman@health.gov.au; robert.j.oconnell.mil@mail.mil; federica.mori@reithera.com; lode.schuerman@gsk.com; andrew.pollard@paediatrics.ox.ac.uk; ji-hong.kim@sk.com; cookee@who.int; REIRELAND@mail.dstl.gov.uk; jane.s@bionet-asia.com; munoz-fontela@bnitm.de; sktseng@UTMB.EDU; preziosim@who.int; SUyoga@kemri-wellcome.org; Stephen.Savarino@sanofi.com; kishore.turaga@biologicale.com; sarah.frise@astrazeneca.com; paola.stefanelli@iss.it; vfa3@cdc.gov; tim.spector@kcl.ac.uk; claudioc@gsespa.cl; sanchezg@une.net.co; Corinne.Jouquelet-Royer@sanofi.com; lidia.oostvogels@curevac.com; dorits@imbm.org; leejooyeon@korea.kr; marc.veldhoen@medicina.ulisboa.pt; huruoyu@walvax.com; joaquim.segales@irta.cat; kandeil_a@hotmail.com; Deborah King; mff7@cdc.gov; inho.cheong@sk.com; sutter@micro.vetmed.uni-muenchen.de; annapurnavyakarnam@gmail.com; marion.vermeulen@sanbs.org.za; moncef.m.slaoui59@gmail.com; narcisa.x.mesaros@gsk.com; Elliot.Lilley@nc3rs.org.uk; teodora.aktas@folkhalsomyndigheten.se; Jin.gao@fda.hhs.gov; linfa.wang@duke-nus.edu.sg; liya.wassie@ahri.gov.et; thomazella16@gmail.com; achidi.eric@gmail.com; kovac@axon-neuroscience.eu; tom.monath@crozetbiopharma.com; nadirkocak@yahoo.com; rajeev.dhere@seruminstitute.com; kathleen.victoir@pasteur.fr; farah.qamar@aku.edu; sastanley@berkeley.edu; brosen@novavax.com; wilsonp@uchicago.edu; iman.satti@ndm.ox.ac.uk; raburn.mallory@astrazeneca.com; kathytai@medigenvac.com; twosned@googlemail.com; EShumba@aslm.org; HRees@wrhi.ac.za; stephanie.longet@phe.gov.uk; martin.bexon@bexonclinical.com; kate.broderick@inovio.com; Mark_Ic_Chen@ncid.sg; mlewis@bioqual.com; pereyaslovd@who.in; leli@who.int; liupengfei@zhifeishengwu.com; carole.verhoeven@seqirus.com; tianyuan1@sinopharm.com; vgarg@altimmune.com; bo_zhong@sinocelltech.com; guy.vernet@pasteur.fr; nhuskins@completegenomics.com; shuping_xu@sinocelltech.com; Stanley Plotkin; Padmini Srikantiah; Ilena@globalhealthstrategies.com; BBrande1@its.jnj.com; jean.patterson@nih.gov; adams_andrew_charles@lilly.com; Alena.Khromava@sanofi.com; iowusu@noguchi.ug.edu.gh; wenchun0617@gate.sinica.edu.tw; dapengzhoulab@tongji.edu.cn; xuefeng.yu@cansinotech.com;

Norio.tamura@shionogi.co.jp; anita.suresh@finddx.org; joanne.langley@dal.ca; vrezelj@its.jnj.com; pieter.neels@vaccine-advice.be; renuka.kumar@gladstone.ucsf.edu; giorgio.fedele@iss.it; natalie.anosova@sanofi.com; fms2@cdc.gov; hana.golding@fda.hhs.gov; SofoniasT@africa-union.org; sudhirbabji@cmcvellore.ac.in; fderrar@pasteur.dz; kjambo@mlw.mw; s.saikrishna@indimmune.com; Kaitlyn.dambach@nih.gov; Jwilbur@mesoscale.com; Jason.Kindrachuk@umanitoba.ca; mimidarko66; rama.akondy@ashoka.edu.in; bottazzi@bcm.edu; slfeinberg@wisc.edu; seguina@medicago.com; gustavo.f.palacios.civ@mail.mil; saranya.sridhar@sanofi.com; n.okba@erasmusmc.nl; jeanie.jacquet@cepi.net; drbdmore@gmail.com; Brown ScD, Elizabeth R; Nick Andrews; Curcio, Daniel; supaporn.p@dmsc.mail.go.th; romain.volmer@envt.fr; magnus.ysander@astrazeneca.com; yabdiche@immunoprecise.com; dancohen@tauex.tau.ac.i; wangyc@nifdc.org.cn; dsantororosa@gmail.com; ofrinr@who.int; pieter.pannus@sciensano.be; coleman@codagenix.com; xavier.de-lamballerie@univ-amu.fr; alex@lji.org; rfaden@jhu.edu; MRabeh@dha.gov.ae; najwa.khuri@gmail.com; Chan_Cheng_Leng@hsa.gov.sg; krystian.jazdzewski@warsawgenomics.pl; Agnes_Chan@hsa.gov.sg; y.m.vasiliev@spbniivs.ru; AFO@ssi.dk; anja.kipar@uzh.ch; Madhavi.Yadavalli@astrazeneca.com; stephen.p.lockhart@pfizer.com; Susan.Mather@pfizer.com; Gerald Voss; sylvie.van-der-werf@pasteur.fr; dnkhong@sk.com; rjanssen@dynavax.com; emmerich@bnitm.de; alena.dabrazhynetskaya@fda.hhs.gov; creanywo@hku.hk; Stephan.Harbarth@hcuge.ch; kizzmekia.corbett@nih.gov; magdalena.spolnicka@policja.gov.pl; maria.salomao@butantan.gov.br; intl@ibto.ir; Pearl.Bamford@health.gov.au; galter@partners.org; rhonda.kuolee@nrc-cnrc.gc.ca; ADriscoll@som.umaryland.edu; John.Forde@phe.gov.uk; MWFREEMAN@mgh.harvard.edu; mayra.moura@butantan.gov.br; rscharf@path.org; JAYANTHI.WOLF@MERCK.COM; Christine.bruce@phe.gov.uk; chien@vabiotech.com.vn; ztq9@cdc.gov; Georgia Tomaras, Ph.D.; charu.sabharwal@pfizer.com; dpark@broadinstitute.org; ydm9@cdc.gov; fdubovsky@novavax.com; bernadettemrg5@gmail.com; mike.fisher@oncimmune.com; salgampa@njms.rutgers.edu; jean-luc.gala@uclouvain.be; jccastellanos@husi.org.co; ulrike.jaegle@curevac.com; amhashem@kau.edu.sa; rolf.fendel@uni-tuebingen.de; kpancer@pzh.gov.pl; chad.irwin@canada.ca; joser.arribas@salud.madrid.org; elizabeth.gabitzsch@immunitybio.com; cgomez@javeriana.edu.co; fangxing@zhifeishengwu.com; irenenor@usp.br; beatriz.lucchesi@butantan.gov.br; vivek.rao@igib.res.in; horer@ku.edu.tr; AP.AlmeidaAranha@cepi.net; maksyutov_ra@vector.nsc.ru; ross.upshur@gmail.com; p.kellam@imperial.ac.uk; Lewis, Kristen; marciela.degrace@nih.gov; Helen.mao@cansinotech.com; whausdorff@path.org; iad7@cdc.gov; Ajoke Sobanjo-ter Meulen; m.addo@uke.de; leila.luheshi@nanoporetech.com; lwelch@iavi.org; farshad@vaxxinity.com; Steve Hadley; gingras@lunenfeld.ca; amenezes@globalhealthstrategies.com; kmohan@bharatbiotech.com; karin.vandenberg@sanbs.org.za; bob.small@cepi.net; Shitong Huan; s.borregaard@ctc-north.com; maina.lazou.jackson@cepi.net; gcanuel@osivax.com; sethc@africa-union.org; angeliki.melidou@ecdc.europa.eu; shahid.jameel@ashoka.edu.in; barbara.schnierle@pei.de; Giada.mattiuzzo@nibsc.org; annev@nicd.ac.za; Audrey Hutter; adam.hacker@cepi.net; araki-yasuhiro@pmda.go.jp; sjp97@medschl.cam.ac.uk; anzj@chinacdc.cn; enakouney@gmail.com; Kaslow, David; pebodyr@who.int; oliver.schoenborn-kellenberger@curevac.com; antonella.folgori@reithera.com; cyrus.yang@sbc-biotech.com; Brasel, Trevor;

demooij@viroclinics.com; tksuzuki@niid.go.jp; Maria.Syrochkina@pfizer.com; Diana_Koh@hsa.gov.sg; nicole.gilberger@bnitm.de; cooldrdax@gmail.com; AAgweyu@kemri-wellcome.org; ckrubiner@CGDEV.ORG; Guang Li; giulianaxm@gmail.com; PScott@eidresearch.org; mesteban@cnb.csic.es; lili53@sinopharm.com; david.stewart@csl.com.au; philippa.matthews@ndm.ox.ac.uk; xhatzi@med.uth.gr; mario.christodoulou@cepi.net; ruoyuhu@walvax.com; POndoa@aslm.org; ullas@tifr.res.in; MAHIPALAP@who.int; xdv3@cdc.gov; Susan.Hopkins@phe.gov.uk; grode@vakzine-manager.de; pauline.maisonnasse@cea.fr; petra.budde@oncimmune.com; kaijie.pan@pfizer.com; Gary.Kobinger@crchudequebec.ulaval.ca; helen.thompson@bristol.ac.uk; manisha.tirvassen@cepi.net; nataliapasternak@gmail.com; prasadsd@bharatbiotech.com; Jyoti.logani@nic.in; norah.fu@walvax.com; wangxiludev@126.com; michelle.hoffmann@axon-neuroscience.eu; apinya.k@bionet-asia.com; joanna-trees.merckx@mcgill.ca; affrade@yahoo.com.br; helga.junker@curevac.com; slamola@path.org; Yyue315@vip.126.com; Kayla Laserson; ycwu@cde.org.tw; sungskim63@gmail.com; renald.gilbert@cnrc-nrc.gc.ca; christian.taucher@valneva.com; jwolf@heatbio.com; sebastian.ols@ki.se; ladda.s@bionet-asia.com; doug.holtzman@icosavax.com; lfries@novavax.com; ephcicm@nus.edu.sg; gll9@cdc.gov; atila@usp.br; roy.duncan@dal.ca; m.pryor@360biolabs.com; drkim@ivi.int; andrew.gorringe@phe.gov.uk; belll@who.int; aysegul.nalca.civ@mail.mil; catherine.whittaker@phe.gov.uk; marykate.morris@cdph.ca.gov; vfumado@hsjdbcn.org; akbulut@medicine.ankara.edu.tr; jen.gommerman@utoronto.ca; Luis.Lugo.mil@afrims.org; KKoram@noguchi.ug.edu.gh; yang_wang@sinocelltech.com; chhsu296@cde.org.tw; sunL@antibodychina.com; ping_zhan@sinocelltech.com; ttbiozyc@aliyun.com; Farid.Khan2@Pfizer.com; justins@microsoft.com; xinqq@sinovac.com; imaginapolo@gmail.com; frank.rockhold@duke.edu; huong72us@yahoo.com; xiedeying@sinopharm.com; therese.solstad@legemiddelverket.no; pardis@broadinstitute.org; Eduard.Salakhov@gmail.com; michael.malison@gmail.com; julia.vergara@irta.cat; ploemen@viroclinics.com; wangjz@nifdc.org.cn; epstein@ecohealthalliance.org; MStanford@imv-inc.com; alef.costa@saude.gov.br; CVHerst@flowpharma.com; Romain.Martischang@hcuge.ch; Cheryl@iliadbio.com; rajatonirinas@who.int; molho@viroclinics.com; liguifan@biominhai.com; Clare.Morris@nibsc.org; walter_straus@merck.com; CKeech@Novavax.com; PNorris@vitalant.org; vrunda.parikh@pfizer.com; cleide.garcez@fiocruz.br; sekim@krict.re.kr; FRIEDE, Martin Howell; 13718415635@163.com; lanqinying@walvax.com; limhy0919@korea.kr; raul.andino@ucsf.edu; hsaeb@phcc.gov.qa; sergey.kozhin@rdif.ru; avillarreal@indicasat.org.pa; heather.rubino@pfizer.com; albert.jan.van.hoek@rivm.nl; t.brehm@uke.de; christoph.rademacher@mpikg.mpg.de; jessica.lee@gmail.com; langermans@bprc.nl; srashid@atcc.org; annied@epivax.com; ekagucia@kemri-wellcome.org; nicolew@nicd.ac.za; Raj Ghosh; vera.gattas@butantan.giv.br; aleksandra.wesolowska@wum.edu.pl; patricia.braga@butantan.gov.br; FStruyf@ITS.JNJ.com; nymyung@sk.com; peter.palese@mssm.edu; costaa@who.int; elana_jaffe@med.unc.edu; dean.follmann@nih.gov; caroline.melo@rivm.nl; thatziio@rockefeller.edu; sayamrym@niid.go.jp; George Siber; wassana.w@bionet-asia.com; bwilliams@who.int; vittoria.offeddu@ird.global; tapia@mpi-magdeburg.mpg.de; Christina.Bareja@health.gov.au; jzejda@sum.edu.pl; ustjugov@biocad.ru; mlipsitc@hsph.harvard.edu; chaber@modernatx.com; fernando.p.polack@vanderbilt.edu; Tong-ming.Fu@sanofi.com; Susie.dunachie@ndm.ox.ac.uk; chuxiafei@zhifeishengwu.com;

Stefania.Capone@reithera.com; Barbara Mahon; jqt8@cdc.gov; shabir.madhi@wits.ac.za; suchinda.m@chula.ac.th; ThomasC.Mettenleiter@fli.de; jim.buttery@monash.edu; david.rhew@microsoft.com; Kwasi.amfo@cepi.net; hstaines@sgul.ac.uk; nicholas.kitchin@pfizer.com; vrasolof@pasteur.mg; dingfan@zhifeishengwu.com; freidlg@who.int; vekemansj@who.int; hombachj@who.int; zengming@biominhai.com; ghkim33@korea.kr; John.Treanor@hhs.gov; tlying@fudan.edu.cn; dbarouch@bidmc.harvard.edu; brian.greenwood@lshtm.ac.uk; jeff_sachs@merck.com; hartka@bluewin.ch; Brooke Peetz (AgileOne); jprice@greffex.com; peshi@UTMB.EDU; lingyi.zheng@sanofi.com; msalit@stanford.edu; gaofu@chinacdc.cn; mlegars@its.jnj.com; katarina.prosenc@nlzoh.si; Vernon_LEE@moh.gov.sg; Emilio Emini; liu.michael222@gmail.com; daniela@lji.org; alan.kimura@curevac.com; taolifeng@zhifeishengwu.com; balaji.more@zyduscadila.com; carlos.diazgranados@sanofi.com; sgupta@iavi.org; judy.wen@icosavax.com; daniel.larremore@colorado.edu; lmoise@epivax.com; shinjini.bhatnagar@thsti.res.in; william.lee@health.ny.gov; sharris@altimmune.com; yjs199307@163.com; greanggrai.h@bionet-asia.com; annagiulia.stigliano@reithera.com; fchowdhury@icddrb.org; ajones@rockefeller.edu; dthea@bu.edu; saowanee.s@bionet-asia.com; valentina.bernasconi@cepi.net; jilian.sacks@finddx.org; glynnsa@nhlbi.nih.gov; Gopa.Raychaudhuri@fda.hhs.gov; veronica.suarez@seqirus.com; samanthapaston@gmail.com; jill_gilmour@hotmail.co.uk; francesco.x.berlandascorza@gsk.com; dboyle@path.org; c.dahlke@uke.de; Anushri Singhvi; alexander.precioso@butantan.gov.br; nfaria@ic.ac.uk; paul.kristiansen; roland.tschismarov@themisbio.com; devan_mehrotra@merck.com; linsen.du@bravovax.com; miock.kim@sk.com; amelia.karlsson@duke.edu; yoshiyama1962@yahoo.co.jp; SPortillo@som.umaryland.edu; lhampton@gavi.org; connie.cai@gatesfoundation.org; TranBaQuang.Truong@sanofi.com; almonther@hotmail.com; soninov@rosminzdrav.ru; tonya.villafana@astrazeneca.com; min.dong@cloverbiopharma.com; pisano@vakzine-manager.de; wei.tu@fda.hhs.gov; gnorheim@vaccibody.com; nhj1114@mogam.re.kr; darwyn.kobasa@canada.ca; syeum10@korea.kr; Phil.yang@immunitybio.com; cassandra.overking@fda.hhs.gov; gmeller@iavi.org; faiz.ahmadkhan@mcgill.ca; christian.cao@ucalgary.ca; lucas.ribeiro@saude.gov.br; MBxVend-1@yahoo.co.uk; Julia.Tree@phe.gov.uk; bo_long@sinocelltech.com; sujan@lji.org; xuzhu@ucas.ac.cn; nigel.crawford@mcri.edu.au; mayara_bastos@yahoo.com.br; darryl.falzarano@usask.ca; ercument.karasulu@ege.edu.tr; david.vallo@astrazeneca.com; karineamicis@gmail.com; wangling@niaid.nih.gov; cecile.artaud@pasteur.fr; liz.miller@lshtm.ac.uk; Ajoke Sobanjo-ter Meulen; monica.conde@butantan.gov.br; juliana.viscondi@butantan.gov.br; CHOONG_May_Ling@hsa.gov.sg; amol.chaudhari@cepi.net; IVMARTINEZ@hsc.wvu.edu; zobstfeld@wesleyan.edu; jimin@walvax.com; mawiddowson@itg.be; Darin.Edwards@modernatx.com; brian.zabel@lakepharma.com; Elena.Matveeva@rdif.ru; Rolando.pajon@modernatx.com; Email:jplested@novavax.com; helen.thomas@cepi.net; zhout@who.int; Kai Dallmeier; lny1@cdc.gov; sheahan@email.unc.edu; helena.wilcox@ndm.ox.ac.uk; michael.wall@canada.ca; wangkai1@genomics.cn; Matthew.Reed.mil@afrims.org; d.watterson@uq.edu.au; mihaelacarla.nosca@seqirus.com; Mallory.Shriver@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; wrastawicki@pzh.gov.pl; lixin_yan@sinocelltech.com; guy.gorochov@sorbonne-universite.fr; Padeshpa@gmail.com; stroheru@who.int; Tom Kariuki;

lydie.marcelon@sanofi.com; nirp@iibr.gov.il; mubangizid; tom@covaxx.com; douglas_fox@berkeley.edu; Ted.Tsai@Takeda.com; kwright@iavi.org; christine.colvis@nih.gov; ajones@mail.rockefeller.edu; maggie.luo@cloverbiopharma.com; Jer-Ming Chia; pawinee.k@redcross.or.th; hromadka@axon-neuroscience.eu; a.pan@asst-cremona.it; alariqil@who.int; peter.smith@lshtm.ac.uk; SlackCa@ukzn.ac.za; tom.tipton@phe.gov.uk; vankerkhovem@who.int; jwilbur@meso-scale.com; dr.rakesh3105@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; xing.li@fda.hhs.gov; winnie.x.janssens@gsk.com; cristina.tato@czbiohub.org; daclark@sgul.ac.uk; miriam.onishi@anvisa.gov.br; quliang@sinopharm.com; philipp.mann@curevac.com; Peter Patriarca; adriane.oliveira@anvisa.gov.br; sebastianms@gisaid.org; In-Kyu Yoon; mbo2@cdc.gov; mpernice@dynavax.com; dotuandat@vabiotech.com.vn; jacob@cmcsph.org; Lakshmi.Jayashankar@hhs.gov; nicole.roth@curevac.com; pickettte@niaid.nih.gov; Carol.Sabourin@hhs.gov; croy@tulane.edu; samiah.kanwar@aku.edu; Harish Iyer; richard.webby@stjude.org; dyu@dynavax.com; haylee@sk.com; Jean Lang; anahita.fathi.us@gmail.com; jessica.lee@inovio.com; jerry.weir@fda.hhs.gov; may.chu@cuanschutz.edu; anthony.macaluso@tonixpharma.com; macalvo@uach.cl; PFast@iavi.org; deoliveira@ukzn.ac.za; gdt@duke.edu; mmsiq@ioc.fiocruz.br; p.smith@lshtm.ac.uk; r.heyderman@ucl.ac.uk; zhangw@who.int; tasker@codagenix.com; azimt@who.int; christopher.da.costa@cepi.net; mksong@ivi.int; carniel@pasteur-yaounde.org; woodd@who.int; melanie.saville@cepi.net; vmoeder@illumina.com; sameer.parekh@seruminstitute.com; alex.sigal@ahri.org; mark.page@nibsc.org; melanie.ott@gladstone.ucsf.edu; karen.goldenthal@gmail.com; nadia.ansari@aku.edu; mt2f@virginia.edu; Kirsty Le Doare; amit.k.srivastava@pfizer.com; Supriya Kumar; res2025@med.cornell.edu; breeze.cavell@phe.gov.uk; horikoshiy@who.int; christian.drosten@charite.de; lydaespitia@unisinu.edu.co; smihwang@sk.com; liub@cde.org.cn; dave.boyle@lakepharma.com; 195046403@qq.com; william.windsor@cuanschutz.edu; anja.schiel@noma.no; giovanetti.marta@gmail.com; madhis@rmpru.co.za; Arnaud.Marchant@ulb.be; scordo@qb.fcen.uba.ar; desteo.ch@gmail.com; Youyi Fong; cwchou476@cde.org.tw; descherm@bni-hamburg.de; Jessica.liu@tigermedgrp.com; Mpasetti@som.umaryland.edu; leanne.robinson@burnet.edu.au; mazhari@wehi.edu.au; christina.henderson@uq.edu.au; noel.tordo@pasteur.fr; ploeman@viroclinics.com; RChikwamba@csir.co.za; zhangyuting@zhifeishengwu.com; monika.lindemann@uk-essen.de; martinbexon@yahoo.co.uk; karen.martins@hhs.gov; Asisa.Volz@tiho-hannover.de; dmissiak@bsd.uchicago.edu; gmackenzie@mrc.gm; marciabarbosavs@gmail.com; zhaozhimei89@163.com; a.a.khazaeli@gmail.com; reveizl@paho.org; mary.marovich@nih.gov; librada.f@bionet-asia.com; cdigermanio@vitalant.org; anh.wartel@ivi.int; allenlien@medigenvac.com; larry.wolfraim@nih.gov; robert.chen@cepi.net; zryn@walvax.com; Ashley.Smith1@hhs.gov; zhaoyuping@medleader.com.cn; tomwhite42450@gmail.com; brosen@novavax.net; agoodridge@indicasat.org.pa; mceuppe1@its.jnj.com; sunil.shewale@seruminstitute.com; dayejung@eubiologics.com; maghsoodlu@yahoo.com; rkoup@mail.nih.gov; freedmanne@mail.nih.gov; julie.joseph@canada.ca; vanessa.infante@butantan.gov.br; Liz.Miller@phe.gov.uk; LMeyers@epivax.com; John N. Nkengasong; GSimmons@vitalant.org; carolina.pingret@anvisa.gov.br; mehmet.ozturk@ibg.edu.tr; ruben.rizzi@biontech.de; lawton.stubbert@canada.ca; mcjm.sturkenboom@gmail.com;

roberto.camerini@reithera.com; shanchao@wh.iov.cn; r.kobbe@uke.edu; xywang@shmu.edu.cn; lori.newman@nih.gov; patricia.garcia@upch.pe; mariella.zaroni@anvisa.gov.br; Matthew.Bonaparte@sanofi.com; Ragini.Shivji@ema.europa.eu; MNELSON@dstl.gov.uk; jcsedrik@path.org; imwei1@163.com; lea.sewell@pfizer.com; esulkowska@rics.bwh.harvard.edu; david.spiro@nih.gov; Karl.Erlandson@hhs.gov; evan.sturtevant@hhs.gov; john.c.trefry.civ@mail.mil; sarina@instem.res.in; Abbie.Bown@phe.gov.uk; tj.chen@chanzuckerberg.com; avandebo@its.jnj.com; wangpw@ivdc.chinacdc.cn; OumaE@africa-union.org; dkim22@its.jnj.com; allergypk@gmail.com; dipyaman.iicb@gmail.com; pujingster@163.com; ebolakim@sk.com; shashikanth4257@bharatbiotech.com; eric.vangieson@darpa.mil; YenewK@africa-union.org; ygrad@hsph.harvard.edu; seongeun@sk.com; FOO_Yang_Tong@hsa.gov.sg; mit666666@pitt.edu; yangfeng@chazenbio.com; livia.vinhal@saude.gov.br; Ann.Rawkins@phe.gov.uk; cdang@lcr.org; mafarodriguez@unisalle.edu.co; zhangj@xmu.edu.cn; colwill@lunenfeld.ca; alan.liss@cepi.net; verstrepen@bprc.nl; 308041407@qq.com; christian.brechot@pasteur.fr; liyl@cde.org.cn; sonja.henne@cepi.net; mona.mohsen@saiba-biotech.com; jmcelrat@fredhutch.org; brian.ward@mcgill.ca; dong.shen@rnaimmune.com; hyl01@tsinghua.org.cn; r.kobbe@uke.de; Phanhonghoa@vabiotech.com.vn; Adam.Finn@bristol.ac.uk; igor.balashov@vaxine.net; hopr@uaem.mx; robert.wawrzinek@mpikg.mpg.de; mengx@sinovac.com; wdj@adaptvac.com; Cblish@stanford.edu; tyzhang1003@163.com; linjinzhong@fudan.edu.cn; gregory.d.gromowski.civ@mail.mil; sheetal.gandotra@igib.res.in; lei.shi@walvax.com; dustin.johnson@canada.ca; Tony.Schountz@colostate.edu; s.a.arakelov@spbniivs.ru; jason.fernandes@canada.ca; wildersmitha@who.int; pdeshpande@indimmune.com; verschoor@bprc.nl; Mike Whelan; James.Milligan@seqirus.com; ben.miller.13@ucl.ac.uk; pgilbert@fredhutch.org; aleksander.masny@policja.gov.pl; roice.fulton@cepi.net; silviacosta@usp.br; baihe@nmpa.gov.cn; Nicole Frahm; pilailuk.o@dmsc.mail.go.th; katom@who.int; Poonepalli_ANURADHA@hsa.gov.sg; tanakat@who.int; sheetal.gandotra@igib.in; zhiping.ye@fda.hhs.gov; savino@ioc.fiocruz.br; CCassetti@niaid.nih.gov; Wenfeng Gong; s.mccormack@ucl.ac.uk; rtchen1135@gmail.com; xumingjue0922@126.com; fred@imophoron.com; tdcarroll@ucdavis.edu; TSmith@inovio.com; lja2002@qatar-med.cornell.edu; drevelli@lovelacebiomedical.org; zhangyan@ivdc.chinacdc.cn; Abena.Amoah@lshtm.ac.uk; Vanessa.Fontana@curevac.com; arimoin@ucla.edu; rafael.delgado@salud.madrid.org; ricardo.palacios@butantan.gov.br; satyajit@iiserpune.ac.in; Rong.Xu@sabin.org; mary@mwuconsulting.com; susanne.rauch@curevac.com; lisa@amicitiam.com; cgast@path.org; Dong, Haiyan; Pillets@medicago.com; katharina.hartmann@cepi.net; kraehliv@staff.uni-marburg.de; Carlos.GuzmanQuilo@sanofi.com; Lynda Stuart; simon.funnell@phe.gov.uk; bernhard.kerscher@pei.de; Toher, Margaret; mgursel@metu.edu.tr; pennym@nicd.ac.za; bernadette.murgue@inserm.fr; olaf-oliver.wolz@curevac.com; mariann.bringsvaerd@cepi.net; Kriti Arora; dparmar@zydustherapeutics.com; M.Whittaker@wellcome.ac.uk; alejandra.gurtman@pfizer.com; jing_jiang201906@sina.com; jennifer.bath99@yahoo.com; RZahn@its.jnj.com; somchaiya@gpo.or.th; lawrence.reiter@providencetherapeutics.com; rbaric@email.unc.edu; Jacqueline.Miller@modernatx.com; dnovack@dynavax.com; david.lee-parritz@tufts.edu; Kathryn Rutkowski; bernadette.hendrickx@cepi.net; ytakahas@niid.go.jp; Rebecca.Harris@sanofi.com; Elizabeth Butler; angel@wedo-projects.com; wardmi@who.int; brooke.bozick@nih.gov; Jin.Zhu@health.gov.au; derrick.crook@ndcls.ox.ac.uk;

mvinge@vaccibody.com; r.shattock@imperial.ac.uk; ramadany@sfda.gov.sa; Farah_MOHAMED_HANIFF@ncid.sg; enwereg@who.int; maria.cassia@hc.fm.usp.br; kum.ungchusak@gmail.com; Jeff.Yang@cloverbiopharma.com; ldunkle@novavax.com; mdohmd@snu.ac.kr; jeff.sachs@merck.com; msavoia@usp.br; fguirakhoo@geovax.com; sh@stemcro.com; k.chappell@uq.edu.au; fkoide@southernresearch.org; jlh66@cam.ac.uk; jmarien@itg.be; marmorato.mariana@gmail.com; drsahoo@indimmune.com; melanie.l.delannoy@gsk.com; paul.licciardi@mcri.edu.au; heather.gidding@sydney.edu.au; ravetch@mail.rockefeller.edu; Tom.Pilcher@dhsc.gov.uk; kwonseoyeon@sk.com; landryn@medicago.com; tomeri@iibr.gov.il; makwenyao@gmail.com; michael.holbrook@nih.gov; Zepp@mail.uni-mainz.de; richard.siggers@canada.ca; lbmulenga@yahoo.com; xin.fang@cloverbiopharma.com; Klaus.Cichutek@pei.de; pe_shu_ai@hsa.gov.sg; Anya Asuncion (Opus); lisa.hensley@nih.gov; raafat.fahim@cepi.net; liweihua8@sinopharm.com; jricht@vet.k-state.edu; shoubai.chao@cansinotech.com; nelias@nimr-mmrc.org; luc.gagnon@nexelis.com; Giovanni Della Cioppa; tijsma@viroclinics.com; sophiev@hku.hk; Arun Kumar; anna.may@joinzoe.com; nussen; esthel.vanbrackel@kuleuven.be; gustavo.santos@anvisa.gov.br; Susanne.EDER-LINGELBACH@valneva.com; HKaranja@kemri-wellcome.org; trvrb; mfkung@cde.org.tw; guido.grandi@unitn.it; alan@sanbi.ac.za; florian.krammer@mssm.edu; Sarah Mudrak, Ph.D.; jpattyn@gavi.org; marco.krieger@fiocruz.br; marilia.santini@ini.fiocruz.br; amishahbrown@inovio.com; chantal.veira@cepi.net; inbanathanf@who.int; geert.lerouxroels@ugent.be; olga.rovira@cepi.net; cori@chanzuckerberg.com; kcyau@hku.hk; huangenqi@zhifeishengwu.com; tracey.thue@usask.ca; lcho@novavax.com; marzia@niaid.nih.gov; d.dunn@ucl.ac.uk; robbert.x.van-der-most@gsk.com; mariangela.cavarelli@cea.fr; wuzy@263.net; john.talian@curevac.com; djernigan@cdc.gov; Andrew.Phipps@hhs.gov; jing.sun@cansinotech.com; carolina.blades@anvisa.gov.br; bertozzi@stanford.edu; hwan.kim@stonybrook.edu; natalie.marchevsky@paediatrics.ox.ac.uk; qasimattock@gmail.com; afrozaakter@icddrb.org; cassia.cearley@icosavax.com; dhoconno@wisc.edu; rgonzalez@uaem.mx; eunlyeong.park@ivi.int; imam.tauheed@icddrb.org; omar.sued@huesped.org.ar; nsalisch@its.jnj.com; kwonseoyeon@skdiscovery.com; teresa.lambe@ndm.ox.ac.uk; pramod.pujari@seruminstitute.com; giselle.castillo@pfizer.com; tesfaye.gelanew@ahri.gov.et; fqadri@icddrb.org; robertcoffman121@outlook.com; farshad@covaxx.com; lmercer@path.org; clemens.ralf@outlook.com; Tony.Wang@fda.hhs.gov; yoonyeong@sk.com; gtapiaca@its.jnj.com; kazif@who.int; Chelsea Bond (Opus); kmodjarrad@eidresearch.org; anissa.cheung@fda.hhs.gov; Gustavo.palacios@gmail.com; natalia@providencetherapeutics.com; ranga.cs@cdsco.nic.in; bologa.monica@gmail.com; jricht@ksu.edu; stanley-perlman@uiowa.edu; Celeste.Marsh@health.gov.au; chantal.reusken@rivm.nl; paul.fine@lshtm.ac.uk; binuphilip@zyduscadila.com; fywu658@cde.org.tw; lapujadeo@who.int; karin.bok@nih.gov; clint.florence; gsellp@who.int; Shailesh.DEWASTHALY@valneva.com; Hongquan.wan@fda.hhs.gov; tasnuva.ahmed@icddrb.org; maria.baca-estrada@canada.ca; matthias.klose@curevac.com; amy.fix@scendea.com; mhasanul.kaisar@icddrb.org; kim.mulholland@lshtm.ac.uk; zengbing@sinopharm.com; indrajeet@bionet-asia.com; pcahn@huesped.org.ar; christian.bottomley@lshtm.ac.uk; taufiqur@icddrb.org; elizabeth.patino@butantan.gov.br; Surender.Khurana@fda.hhs.gov; franck.touret@univ-amu.fr; revans@who.int; ndiayesire@hotmail.fr;

phil.yang@nantworks.com; juleen.gayed@pfizer.com; hychen@cde.org.tw; maaroufi@pasteur.ma; tingting.yan@mail.utoronto.ca; sabinoec@usp.br; malik@hku.hk; stephen.lockhart@pfizer.com; ruoyu.hu@walvax.com; bcowling@hku.hk; tkh4@cdc.gov; zhongkaishi28@gmail.com; aottosen@unicef.org; barnorj@who.int; nadia.oreshkova@wur.nl; adebola.olayinka@ncdc.gov.ng; joan@joinzoe.com; nadia.tornieporth@cepi.net; gftsai@cde.org.tw; 1531287517@qq.com; vongs@who.int; bond.court@gmail.com; rkiatchula@gmail.com; ywsohn09@gmail.com; JLPRIOR@dstl.gov.uk; snumouse@snu.ac.kr; kingpfph@sina.com; yjlee@eubiologics.com; robert.bailer@q2labsolutions.com; bronwyn@broadinstitute.org; khirullin@mail.ru; moorthyv; anice.lowen@emory.edu; dguyongellin@osivax.com; liliana.brown@nih.gov; fanxin7@sinopharm.com; katrin.ramsauer@themisbio.com; dean.smith@canada.ca; kate81@korea.kr; judith.absalon@pfizer.com; Christophe.Gregoire@sanofi.com; yangyunkai@sinopharm.com; 57667504@innovax.cn; juzdias@gmail.com; Todd.Suscovich@seromyx.com; gromova@biopharma-excellence.com; fguirakhoo@unitedneuroscience.com; anand.drk@gmail.com; eric.osoro@wsu.edu; zengxizi@kangtai.com; stephane.bancel@modernatx.com; zhongzaixin@zhifeishengwu.com; dsz@imbcams.com.cn; a.luttick@360biolabs.com; Gerald.Kovacs@hhs.gov; Zhanghua_Lan@sinocelltech.com; hutiny@Who.int; solomon.yimer@cepi.net; paul-mccray@uiowa.edu; nuno.faria@zoo.ox.ac.uk; J.P.Stewart@liverpool.ac.uk; sbrowne@altimmune.com; jins.park@sk.com; matthew.snape@paediatrics.ox.ac.uk; jkonyndyk@usaid.gov; maria-angeles.x.ceregido@gsk.com; lmartinez@txbiomed.org; robin.levis@fda.hhs.gov; stig.tollefsen@cepi.net; thyde@cdc.gov; matthew.hohenboken@seqirus.com; bergerii@who.int; sameeullah@bs.qau.edu.pk; rehman.zaira@yahoo.com; james.huleatt@sanofi.com; Molly.Lamb@cuanschutz.edu; jldeen@up.edu.ph; sandsa@who.int; vincent.munster@nih.gov; Holger Kanzler; jinbo.gou@cansinotech.com; acope@iavi.org; rosemaryaudu@yahoo.com; rodrigo.correa@fiocruz.br; irahetar@who.int; arandhaw@fredhutch.org; shaumik.islam@icddrb.org; Sophie Mathewson; paul@medigenvac.com; pgarg@thsti.res.in; pamela.proud@phe.gov.uk; carolina.argondizo@usp.br; loy@who.int; asmronger@gmail.com; wbrooks3@jhu.edu; schwartz@pasteur.fr; Jakob Cramer; hanwx@sinovac.com; paul.hodgson@usask.ca; Hang.Xie@fda.hhs.gov; jorge.osorio@wisc.edu; Hendrik Jan Thibaut; adamou.rafiou@gmail.com; tdelossantos@path.org; brett.barnett@cepi.net; danielbrasseur@gmail.com; ASiyer@mgh.harvard.edu; robert.paris@modernatx.com; raquel.guiomar@insa.min-saude.pt; Ali.Mirazimi@folkhalsomyndigheten.se; diane.descamps@aphp.fr; jschindler@imv-inc.com; Johan Neyts; brangelp@who.int; javadi11@hzdr.de; MCELROYA@pitt.edu; eric@providencetherapeutics.com; ggj2@cdc.gov; wangyilin@medleader.com.cn; swaminathans@who.int; chr.vin@web.de; erich.tauber@themisbio.com; jeroen.kortekaas@wur.nl; joshua.liang@cloverbiopharma.com; kristy.tomas@health.gov.au; hjanes@fredhutch.org; agw13@pitt.edu; ihsangursel@bilkent.edu.tr; Anthony.Scott@lshtm.ac.uk; kevinkumarkansagra@zyduscadila.com; Anna.JefferySmith@phe.gov.uk; Harry Kleanthous; freire@bio.fiocruz.br; jkalil@pq.cnpq.br; jlehrman@iavi.org; mcortese@vaxart.com; tranminhn@who.int; troyrandall@uabmc.edu; m.koopmans@erasmusmc.nl; anu.raghunathan@ncl.res.in; Eeva.Broberg@ecdc.europa.eu; yoos@who.int; senta.walton@usz.ch; Nieuwburg@viroclinics.com; julianna.pieknik@fda.hhs.gov; mdjjh@nmc.or.kr; andrew.p.hollands.civ@mail.mil; cwonodi1@jhu.edu; Mia.Crampin@lshtm.ac.uk; Charlie Weller; wuting@xmu.edu.cn;

wangruyue@zhifeishengwu.com; svein.rune.andersen@legemiddelverket.no; bhagwat.gunale@seruminstitute.com; pingping.zhang@pfizer.com; Bev.Menner@csl.com.au; rodriguezhernandezc@who.int; daniel.brasseur@cepi.net; WaickmaA@upstate.edu; clsilva@fmrp.usp.br; Isis Kanevsky; joanna.zmurko@q2labsolutions.com; Lloyd.Mulenga@moh.gov.zm; Julie.Lobjeois@sanofi.com; xumiaobj@126.com; agartlan@fredhutch.org; Khadija.Jarik@international.gc.ca; ann.eakin@nih.gov; jeff@stabilitech.com; annap@auth.gr; liuying@medleader.com.cn; tedross@uga.edu; varma.bhupathiraju@biologicale.com; paul.lambert@unige.ch; marc.eloit@pasteur.fr; wdj@expres2ionbio.com; SMalhotra@iavi.org; dj56wood@gmail.com; yuho74@hotmail.com; barney.graham@nih.gov; nadege.ripley@modernatx.com; charles.chiu@ucsf.edu; sumitbhushan@panaceabiotec.com; tom@covaxx.xom; gasparr@who.int; bgraham@mail.nih.gov; nb@rdif.ru; rodewaldl@chinacdc.cn; lorna.mcinroy@phe.gov.uk; beatrice.n.laupeze@gsk.com; muldersm@who.int; rkiat@chula.ac.th; Jorge Kalil; kim.brolin@ecdc.europa.eu; cherylc@nicd.ac.za; STorhaug@vaccibody.com; Lienanhha.do@mcri.edu.au; katrin.leitmeyer@ecdc.europa.eu; rahul.arora@balliol.ox.ac.uk; marion.gruber@fda.hhs.gov; donna.ambrosino1@gmail.com; David Blazes; Imran Nisar; dlggpp@gmail.com; shimian.zou@nih.gov; marisol.simoes@bio.fiocruz.br; carl.hanson@cdph.ca.gov; shinj@who.int; MAFRANCO@JAVERIANA.EDU.CO; rebecca.klein1@merck.com; a.agrawal@igib.in; miyazakikrauser@who.int; eliana.barros@butantan.gov.br; stephanie.longet@well.ox.ac.uk; sihindawi@yahoo.com; luk_vandenberghe@meei.harvard.edu; rmallory@novavax.com; CHOO_Qiuyi@hsa.gov.sg; dginete@sciphil.org; reinel120305@gmail.com; mayor@ncbs.res.in; medeiros@bio.fiocruz.br; brian.greewood@lshtm.ac.uk; pbieniasz@mail.rockefeller.edu; marta.diaz@salud.madrid.org; Suellen.Nicholson@vidrl.org.au; rodrigueza@paho.org; Gilbert, Peter B; mireilledosso@yahoo.fr; okeibunorj@who.int; cindy.x.gutzeit@gsk.com; rawleigh.howe@ahri.gov.et; Jacqueline.Shea@inovio.com; eyangoh@pasteur-yaounde.org; boulayi@medicago.com; jokim@ivi.int; carla.brichesi@anvisa.gov.br; songqiaoqiao@ystwt.com; nbhat@path.org; ravindra.gupta@ucl.ac.uk; lizhigang@biominhai.com; russori@njms.rutgers.edu; mirajw@who.int; dsreed@cvr.pitt.edu; Heather.Whitaker@phe.gov.uk; nbaylor@biologicsconsulting.com; wim.vanderpoel@wur.nl; Tracy.MacGill@fda.hhs.gov; James.Little@hhs.gov; alka.dbt@nic.in; Bogdana.Coudsy@sanofi.com; elliot@stabilitech.com; cbstauft@gmail.com; Tamala.MallettMoore@sanofipasteur.com; alyson.kelvin@usask.ca; perkinsm@who.int; thall@sgul.ac.uk; niklas.bobrovitz@mail.utoronto.ca; sroberts@altimmune.com; Bethany_Gauthier@hms.harvard.edu; GWeiding@its.jnj.com; deven.parmar@zydusdiscovery.ae; dr.petrov_jordan@yahoo.com; Antonia.Ho@glasgow.ac.uk; zoeteweij@viroclinics.com; dlaufer@iavi.org; alessandro.torelli@vismederi.com; stoback@novavax.com; francois.p.roman@gsk.com; roberta.piorelli@butantan.gov.br; dailp@biols.ac.cn; gweiss@uci.edu; Keith.Peden@fda.hhs.gov; rachna.gupta@sanofi.com; priti.shah@astrazeneca.com; Joe Rininger; nax3@cdc.gov; kristine.rose@cepi.net; martin.plante@nrc-cnrc.gc.ca; Nupur.Sengupta@biologicale.com; Frieman, Matthew; alemseged.abdissa@ahri.gov.et; srinivas.murthy; joe@czbiohub.org; csv@ssi.dk; hironorinakagami@gmail.com; ckchew@crc.gov.my; Piyush.patel@providencetherapeutics.com; sapan4252@bharatbiotech.com; Buitendijk@viroclinics.com; fmarks@ivi.int; wanxilu@zhifeishengwu.com; Bassam.Hallis@phe.gov.uk; changguili@aliyun.com; sot1@cdc.gov; jenifer.healy@abbott.com; tuliodna@gmail.com; qinjian_zhao@xmu.edu.cn;

	merryn.voysey@paediatrics.ox.ac.uk; payden@who.int; matthew.cheng@mcgill.ca; liujiankai@biominhai.com; keiko.simon@inovio.com; geldmacher@lrz.uni-muenchen.de; m.noursadeghi@ucl.ac.uk; brenda.valente@anvisa.gov.br; nnagata@niid.go.jp; tksuzuki@nih.go.jp; patrick.reid@unmc.edu; pogueg1@RJRT.com; Robin Mogg; lvrizzo@einstein.br; ls.shashidhara@ashoka.edu.in; Marco.Cavaleri@ema.europa.eu; mto@umn.edu; sue.costa@unisi.it; Pasi.Penttinen@ecdc.europa.eu; crowcroftn@who.int; joseph.chiu@nih.gov; mueller@wehi.edu.au; jguthmiller@uchicago.edu; Kristen Earle; tzyyyuin.chong@cloverbiopharma.com; gayle.pulle@canada.ca; Hisham.Fyyaz@sanofi.com; rachel.park@eubiologics.com; tinaoneko@gmail.com; c.weller@wellcome.org; tenoever@gmail.com; kalisvar_marimuthu@ttsh.com.sg; yumei_huang@sinocelltech.com; ellar@bharatbiotech.com; koningsf@who.int; carolyn.clark@cepi.net; Jordan Tappero; oliver.schoenborn-kellenberger@cogitars.com; h.skirrow@imperial.ac.uk; Scott Dowell; Georgina Murphy; Judy Hubbard
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Subject:	UPDATED: Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Luis.Lugo.mil@afrims.org; Matthew.Reed.mil@afrims.org; franck.TOURET@univ-amu.fr; LESELLIER Sandrine (sandrine.lesellier@anses.fr); Romain Volmer (romain.volmer@envt.fr); BAMFORD, Pearl; ZHU, Jin; Donis, Ruben (OS/ASPR/BARDA); Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Little, James (OS/ASPR/BARDA); Andrew.Phipps; Sabourin, Carol (OS/ASPR/BARDA); Treanor, John (OS/ASPR/BARDA) (CTR); Yusibov, Vidadi (OS/ASPR/BARDA); Sivko, Gloria S; Russell.Ray@bcm.edu; verschoor (verschoor@bprc.nl); verstrepen@bprc.nl; langermans (langermans@bprc.nl); mlewis (mlewis@bioqual.com); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); estefania.rodriguez (estefania.rodriguez@bnitm.de); Griffiths, Anthony; Honko, Anna; dustin.johnson (dustin.johnson@canada.ca); sean.li (sean.li@canada.ca); dean.smith (dean.smith@canada.ca); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); Roger Le Grand (roger.le-grand@cea.fr); Pauline Maisonnasse (pauline.maisonnasse@cea.fr); sekim (sekim@krict.re.kr); kandeil_a (kandeil_a@hotmail.com); Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); shanchao (shanchao@wh.iov.cn); rkiatchula (rkiatchula@gmail.com); seos@cnu.ac.kr; lisambrosseau@gmail.com; mto@umn.edu; mito@ciea.or.jp; tyamamoto@ciea.or.jp; mesteban (mesteban@cnb.csic.es); Juan García Arriaza (jfgarcia@cnb.csic.es); l.enjuanes@cnb.csic.es; mopargal (mopargal@rams.colostate.edu); Tony.Schountz@colostate.edu; angierasmussen@gmail.com; scordo (scordo@qb.fcen.uba.ar); sinabavari@comcast.net; dgdiel@cornell.edu; res2025; Vasan, Vasan (H&B, Geelong ACDP); Duprex, Paul; Flynn, Joanne L; White, Alexander G; Alyson Kelvin; john.c.trefry.civ (john.c.trefry.civ@mail.mil); jennifer.m.kishimori.mil@mail.mil; kanta.subbarao (kanta.subbarao@influenzacentre.org); REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON@mail.dstl.gov.uk; JLPRIOR (JLPRIOR@dstl.gov.uk); Amelia Karlsson (amelia.karlsson@duke.edu); danielle.anderson (danielle.anderson@duke-nus.edu.sg); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); anice.lowen; mariette.ducatez@envt.fr; S. Herfst; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); Golding, Hana; MacGill, Tracy; Tony.Wang (Tony.Wang@fda.hhs.gov); Krause, Philip; Levis, Robin; Martin.Beer (Martin.Beer@fli.de); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); Idenisy (Idenisy@yahoo.com); rhakami@gmu.edu; Asisa.Volz (Asisa.Volz@tiho-hannover.de); dbarouch (dbarouch@bidmc.harvard.edu); esulkowska@rics.bwh.harvard.edu; Vandenberghe, Luk; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; daniel.martinez-arguelles; lawton.stubbert@canada.ca; jfwchan (jfwchan@hku.hk); hlchen (hlchen@hku.hk); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); Krammer, Florian; lisa.chakrabarti@pasteur.fr; Christiane Gerke (christiane.gerke@pasteur.fr); Nadia KHELEF (nadia.khelef@pasteur.fr); Seungtaek Kim (seungtaek.kim@ip-korea.org); Manki Song (mksong@ivi.int); Segales, Joaquim; Vergara, Julia; tomeri (tomeri@iibr.gov.il); nirp (nirp@iibr.gov.il); nnagata@niid.go.jp; Tadaki (tksuzuki@nih.go.jp);

terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Juergen Richt (jricht@vet.k-state.edu); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); horer@ku.edu.tr; snumouse (snumouse@snu.ac.kr); kai.dallmeier (kai.dallmeier@kuleuven.be); johan.neyts (johan.neyts@kuleuven.be); caroline.foo; erica (erica@lji.org); Munir, Muhammad; David Revelli (drevelli@lovelacebiomedical.org); Chi Van Dang (cdang@lcr.org); sutter (sutter@micro.vetmed.uni-muenchen.de); kupke (kupke@staff.uni-marburg.de); Albrecht, Randy; Garcia-Sastre, Adolfo; peter.palese@mssm.edu; Schotsaert, Michael; tenoever@gmail.com; Olinger, Gene; marlene.espinozamoraga; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Mark Page (Mark.Page@nibsc.org); Florence, Clint (NIH/NIAID) [E]; mary.lane@nih.gov; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; feldmannh@niaid.nih.gov; Munster, Vincent (NIH/NIAID) [E]; Graham, Barney (NIH/VRC) [E]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Elliot Lilley - NC3Rs; Mark Prescott - NC3Rs; Kristine Macartney (kristine.macartney@health.nsw.gov.au); patrick.reid@unmc.edu; yu.cong@nih.gov; marzia; bosioc@niaid.nih.gov; gabriella.worwa; Neil Berry (Neil.Berry@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Nicola Rose (Nicola.Rose@nibsc.org); que.dang@nih.gov; Hild, Sheri (NIH/OD) [E]; neeltje.vandoremalen@nih.gov; kyle.rosenke; Cassels, Fred; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); Barbara.Schnierle (Barbara.Schnierle@pei.de); qinchuan (qinchuan@pumc.edu.cn); SPERGEL@email.chop.edu; darwyn.kobasa@canada.ca; bradley.pickering (bradley.pickering@canada.ca); t.sulpice; f.briand; tcs38@psu.edu; Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Yper.Hall (Yper.Hall@phe.gov.uk); Ann Rawkins (Ann.Rawkins@phe.gov.uk); Javier Salguero (Javier.Salguero@phe.gov.uk); Sally Sharpe (Sally.Sharpe@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); caroline.melo@rivm.nl; ajones; ravetch; Riccardo Russo; salgampa (salgampa@njms.rutgers.edu); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); ramadany; fkoide (fkoide@southernresearch.org); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); Hwan K Kim (hwan.kim@stonybrook.edu); WaickmaA@upstate.edu; alankhoo.imr; rcarrion (rcarrion@TxBiomed.org); LMartinez@txbiomed.org; JTorrelles@txbiomed.org; Techakitiroj Chatkul (tverakit@gmail.com); bobomok@hku.hk; anna (anna@thsti.res.in); Lee-Parritz, David; croy (croy@tulane.edu); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); Chris Miller (cjmiller@ucdavis.edu); sodas; rbaric (rbaric@email.unc.edu); lgralins@email.unc.edu; sheahan; gustavo.palacios (gustavo.palacios@gmail.com); dmissiak (dmissiak@bsd.uchicago.edu); GREY Finn (fgrey@exseed.ed.ac.uk); dsreed@cvr.pitt.edu; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); Paul.Lambert (Paul.Lambert@unige.ch); y.jacob.hou@unc.edu; Cartner, Samuel Corbin; Dohm, Erik Daniel; kevinharrod (kevinharrod@uabmc.edu); Kobie, James J; troyrandall (troyrandall@uabmc.edu); jhogan@uga.edu; paul-mccray (paul-mccray@uiowa.edu); Perlman, Stanley; Stewart, James; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); CDillen@som.umaryland.edu; Frieman, Matthew; SBradfute@salud.unm.edu; JOHN JAMES BACZENAS; SHELBY L O'CONNOR; thomasf@primate.wisc.edu; DAVID H O'CONNOR (dhoconno@wisc.edu); anja.kipar@uzh.ch; christian.c.hofer.mil@mail.mil; jay.w.hooper.civ

(jay.w.hooper.civ@mail.mil); grace.m.lidl.mil@mail.mil; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mitchell.palmer@usda.gov; Brasel, Trevor; Bukreyev, Alexander; Eitzen, Melissa M.; Shi, Pei yong; Tseng, Chien-Te K.; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; stittelaar (stittelaar@viroclinics.com); wim.vanderpoel@wur.nl; Gerhards, Nora; jeroen.kortekaas (jeroen.kortekaas@wur.nl); Oreshkova, Nadia; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Kayvon Modjarrad (kmodjarrad@eidresearch.org); mdiamond (mdiamond@wustl.edu); BRANGEL, Polina; HENAO RESTREPO, Ana Maria; KAZI, Fatema; KNEZEVIC, Ivana; SATHIYAMOORTHY, Vaseeharan; PREZIOSI, Marie-pierre; RIVEROS BALTA, Ximena; SALAMI, Kolawole; YOO, Si Hyung; SWAMINATHAN, Soumya; WOOD, David John; ZHOU, Tiequn; dbolton@hivresearch.org; sharon.daye2.mil@mail.mil; Damron, Fredrick; IVMARTINEZ; lisette.cornelissen; ivan.marazzi; wenchun0617; Victoria.Wahl; Hevey, Michael (CTR); Paul.Dabisch; Stylianos Bournazos

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Cc: William Dowling[william.dowling@cepi.net]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Pierre Gsell[gsellp@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]
To: sandra cordo[scordo@qb.fcen.uba.ar]; Pearl.Bamford@health.gov.au[Pearl.Bamford@health.gov.au]; kristine.macartney@health.nsw.gov.au[kristine.macartney@health.nsw.gov.au]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Vasan Vasan[Vasan.Vasan@csiro.au]; Jin.Zhu@health.gov.au[Jin.Zhu@health.gov.au]; Kai Dallmeier[kai.dallmeier@kuleuven.be]; Johan Neyts[johan.neyts@kuleuven.be]; Alyson Kelvin[AKelvin@dal.ca]; Darryl Falzarano[darryl.falzarano@usask.ca]; Volker.gerdts@usask.ca[Volker.gerdts@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; dustin.johnson@canada.ca[dustin.johnson@canada.ca]; Jason Kindrachuk[Jason.Kindrachuk@umanitoba.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; Gary Kobinger[Gary.Kobinger@crchudequebec.ulaval.ca]; Li, Sean (HC/SC)[sean.li@canada.ca]; dean.smith@canada.ca[dean.smith@canada.ca]; 秦川[qinchuan@pumc.edu.cn]; shanchao@wh.iov.cn[shanchao@wh.iov.cn]; kandeil_a@hotmail.com[kandeil_a@hotmail.com]; Cavaleri Marco[Marco.Cavaleri@ema.europa.eu]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; christiane.gerke@pasteur.fr[christiane.gerke@pasteur.fr]; nadia.khelef@pasteur.fr[nadia.khelef@pasteur.fr]; Roger Le[roger.le-grand@cea.fr]; LESELLIER Sandrine[sandrine.lesellier@anses.fr]; Pauline Maisonnasse[pauline.maisonnasse@cea.fr]; romain.volmer@envt.fr[romain.volmer@envt.fr]; Martin Beer[Martin.Beer@fli.de]; CarlosAlberto.Guzman@helmholtz-hzi.de[CarlosAlberto.Guzman@helmholtz-hzi.de]; Kerscher, Bernhard[Bernhard.Kerscher@pei.de]; kupke@staff.uni-marburg.de[kupke@staff.uni-marburg.de]; Mettenleiter, Thomas C.[ThomasC.Mettenleiter@fli.de]; Cesar Munoz-Fontela[munoz-fontela@bnitm.de]; Estefania Bni[estefania.rodriguez@bnitm.de]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; sutter@micro.vetmed.uni-muenchen.de[sutter@micro.vetmed.uni-muenchen.de]; Asisa.Volz@tiho-hannover.de[Asisa.Volz@tiho-hannover.de]; Carolyn Clark[carolyn.clark@cepi.net]; William Dowling[william.dowling@cepi.net]; Pierre Gsell[gsellp@who.int]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; PREZIOSI, Marie-pierre[preziosim@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; swaminathans@who.int[swaminathans@who.int]; Chi Van Dang[cdang@lcr.org]; woodd@who.int[woodd@who.int]; jfwchan[jfwchan@hku.hk]; hlchen@hku.hk[hlchen@hku.hk]; anna@thsti.res.in[anna@thsti.res.in]; tomeri@iibr.gov.il[tomeri@iibr.gov.il]; Nir Paran[nirp@iibr.gov.il]; mito@ciea.or.jp[mito@ciea.or.jp]; nnagata@niid.go.jp[nnagata@niid.go.jp]; tksuzuki@nih.go.jp[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; s.a.arakelov@spbniivs.ru[s.a.arakelov@spbniivs.ru]; i.v.krasilnikov@spbniivs.ru[i.v.krasilnikov@spbniivs.ru]; ldenisy@yahoo.com[ldenisy@yahoo.com]; y.m.vasiliev@spbniivs.ru[y.m.vasiliev@spbniivs.ru]; danielle.anderson@duke-nus.edu.sg[danielle.anderson@duke-nus.edu.sg]; sekim@krict.re.kr[sekim@krict.re.kr]; seungtaek.kim@ip-korea.org[seungtaek.kim@ip-korea.org]; mksong@ivi.int[mksong@ivi.int]; Enjuanes_Luis[l.enjuanes@cnb.csic.es]; Mariano Esteban Rodriguez[mesteban@cnb.csic.es]; JUAN FRANCISCO GARCIA ARRIAZA[jfgarcia@cnb.csic.es]; Quim Segales[joaquim.segales@irta.cat]; Vergara, Julia[julia.vergara@irta.cat]; Ali.Mirazimi@folkhalsomyndigheten.se[Ali.Mirazimi@folkhalsomyndigheten.se]; Paul.Lambert@unige.ch[Paul.Lambert@unige.ch]; suchinda.m@chula.ac.th[suchinda.m@chula.ac.th]; rkiatchula@gmail.com[rkiatchula@gmail.com]; tverakit@gmail.com[tverakit@gmail.com]; jorgen.de.jonge@rivm.nl[jorgen.de.jonge@rivm.nl]; Gerhards, Nora[nora.gerhards@wur.nl]; B. Haagmans[b.haagmans@erasmusmc.nl]; Kortekaas, Jeroen[jeroen.kortekaas@wur.nl]; langermans@bprc.nl[langermans@bprc.nl]; Nadia Oreshkova[nadia.oreshkova@wur.nl]; B. Rockx[b.rockx@erasmusmc.nl]; Koert Stittelaar[stittelaar@viroclinics.com]; Poel, Wim van der[wim.vanderpoel@wur.nl]; Neil Berry[Neil.Berry@nibsc.org]; Miles Carroll[Miles.Carroll@phe.gov.uk]; Simon Funnell[Simon.Funnell@phe.gov.uk]; fgrey@exseed.ed.ac.uk[fgrey@exseed.ed.ac.uk]; Yper Hall[Yper.Hall@phe.gov.uk]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; MSLEVER@dstl.gov.uk[MSLEVER@dstl.gov.uk]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; philip.minor2@gmail.com[philip.minor2@gmail.com]; muhammad.munir@lancaster.ac.uk[muhammad.munir@lancaster.ac.uk]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; Mark Page[Mark.Page@nibsc.org]; JLPRIOR@dstl.gov.uk[JLPRIOR@dstl.gov.uk]; Ann.Rawkins@phe.gov.uk[Ann.Rawkins@phe.gov.uk]; Nicola.Rose@nibsc.org[Nicola.Rose@nibsc.org]; Javier Salguero[Javier.Salguero@phe.gov.uk]; Sally.Sharpe@phe.gov.uk[Sally.Sharpe@phe.gov.uk]; J.P.Stewart@liverpool.ac.uk[J.P.Stewart@liverpool.ac.uk]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; Randy Albrecht[randy.albrecht@mssm.edu]; Martha.Alexander-Miller@wakehealth.edu[Martha.Alexander-Miller@wakehealth.edu]; Ralph Baric[rbaric@email.unc.edu]; Dan Barouch[dbarouch@bidmc.harvard.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; terry.k.besch.ctr@mail.mil[terry.k.besch.ctr@mail.mil]; dbolton@hivresearch.org[dbolton@hivresearch.org]; Angela Bosco-Lauth[mopargal@rams.colostate.edu]; Brasel, Trevor[trbrasel@UTMB.EDU]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; Ricardo Carrion, Jr.[rcarrion@txbiomed.org]; Cartner, Samuel Corbin[scartner@uab.edu]; fcassels@path.org[fcassels@path.org]; Monalisa Chatterji[MONALISA.CHATTERJI@gatesfoundation.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; que.dang@nih.gov[que.dang@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Diamond, Michael[mdiamond@wustl.edu]; Erik Dohm[edohm@uab.edu]; Ruben.Donis@hhs.gov[Ruben.Donis@hhs.gov]; Duprex, Paul[pduprex@pitt.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; Feldmann, Heinrich (NIH/NIAID) [E][feldmannh@niaid.nih.gov]; clint.florence@nih.gov[clint.florence@nih.gov]; Flynn, Joanne L[joanne@pitt.edu]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; Matthew Frieman[MFrieman@som.umaryland.edu]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; golinger@mriglobal.org[golinger@mriglobal.org]; Hana.Golding@fda.hhs.gov[Hana.Golding@fda.hhs.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Lisa E Gralinski[lgralins@email.unc.edu]; Griffiths, Anthony[ahgriff@bu.edu]; kevinharrod@uabmc.edu[kevinharrod@uabmc.edu]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; sheri.hild@nih.gov[sheri.hild@nih.gov]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; jay.w.hooper.civ@mail.mil[jay.w.hooper.civ@mail.mil]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; Amelia Karlsson[amelia.karlsson@duke.edu]; hwan.kim@stonybrook.edu[hwan.kim@stonybrook.edu]; Jacqueline Kirchner[Jacqueline.Kirchner@gatesfoundation.org]; Harry.Kleanthous@gatesfoundation.org[Harry.Kleanthous@gatesfoundation.org]; fkoide@southernresearch.org[fkoide@southernresearch.org]; Krammer, Florian[florian.krammer@mssm.edu];

philip.krause@fda.hhs.gov[philip.krause@fda.hhs.gov]; mary.lane@nih.gov[mary.lane@nih.gov]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; Levis, Robin[robin.levis@fda.hhs.gov]; Dr. Mark Lewis[mlewis@bioqual.com]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Karen.Makar@gatesfoundation.org[Karen.Makar@gatesfoundation.org]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; cjmiller@ucdavis.edu[cjmiller@ucdavis.edu]; woodd@who.int, jfwchan <jfwchan@hku.hk> , hlchen@hku.hk, anna@thsti.res.in, nnagata@niid.go.jp, tksuzuki@nih.go.jp, ldenisy@yahoo.com, y.m.vasiliev@spbniivs.ru, s.a.arakelov@spbniivs.ru, i.v.krasilnikov@spbniivs.ru, danielle.anderson@duke-nus.edu.sg, sekim@krict.re.kr, seungtaek.kim@ip-korea.org, mksong@ivi.int, Mariano Esteban Rodriguez <mesteban@cnb.csic.es>, JUAN FRANCISCO GARCIA ARRIAZA <jfgarcia@cnb.csic.es>, Luis Enjuanes <l.enjuanes@cnb.csic.es>, Quim Segales <joaquim.segales@irta.cat>, Vergara Julia[dmissiak@bsd.uchicago.edu]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; aysegul.nalca.civ@mail.mil[aysegul.nalca.civ@mail.mil]; DAVID H O'CONNOR[dhoconno@wisc.edu]; mto@umn.edu[mto@umn.edu]; gustavo.palacios@gmail.com[gustavo.palacios@gmail.com]; Peter Palese[peter.palese@mssm.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]; pickettte@niaid.nih.gov[pickettte@niaid.nih.gov]; margaret.l.pitt.civ@mail.mil[margaret.l.pitt.civ@mail.mil]; troyrandall@uabmc.edu[troyrandall@uabmc.edu]; Angela Rasmussen[alr2105@cumc.columbia.edu]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; drevelli@lovelacebiomedical.org[drevelli@lovelacebiomedical.org]; Juergen Richt[jricht@vet.k-state.edu]; Chad Roy[croy@tulane.edu]; Carol.Sabourin@hhs.gov[Carol.Sabourin@hhs.gov]; Padmini Salgame[salgampa@njms.rutgers.edu]; erica@lji.org[erica@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Michael Schotsaert[michael.schotsaert@mssm.edu]; sivkog@battelle.org[sivkog@battelle.org]; Spergel, Jonathan[SPERGEL@email.chop.edu]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; Elizabeth Sulkowski[elizabethsulkowski44@gmail.com]; nax3@cdc.gov[nax3@cdc.gov]; John.Treanor@hhs.gov[John.Treanor@hhs.gov]; john.c.trefry.civ@mail.mil[john.c.trefry.civ@mail.mil]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; luk_vandenberghe@meei.harvard.edu[luk_vandenberghe@meei.harvard.edu]; David.Vaughn@gatesfoundation.org[David.Vaughn@gatesfoundation.org]; Wang, Tony[tony.wang@fda.hhs.gov]; renee.wegrzyn@darpa.mil[renee.wegrzyn@darpa.mil]; White, Alexander G[agw13@pitt.edu]; seos@cnu.ac.kr[seos@cnu.ac.kr]; k.chappell@uq.edu.au[k.chappell@uq.edu.au]; Stephen Kent[skent@unimelb.edu.au]; Adam Wheatley[a.wheatley@unimelb.edu.au]; Hyon Xhi Tan[hyon.tan@unimelb.edu.au]; Shi, Pei yong[peshi@UTMB.EDU]; guilfoyle@viroclinics.com[guilfoyle@viroclinics.com]
From: Cesar Munoz-Fontela[munoz-fontela@bnitm.de]
Sent: Wed 9/16/2020 10:38:44 AM (UTC-05:00)
Subject: WHO COVID-19 Animal Models Group Call-Agenda
Mail Attachment.ics
Webex_Meeting.ics

Dear all,

This Thursday we will have a call focused on COVID-19 enhanced disease. We will have three short presentations on that topic followed by a panel call. The panel call format will be as follows

(1) Question to be discussed: What can we learn about VAERD/ADE from animal models and how can we improve this knowledge in the future?

(**2) Background**: With more than 200 COVID-19 vaccine candidates in the pipeline and near 20 in clinical trials there is an increasing concern that some of these vaccines may cause VAERD or ADE. Most if not all of the vaccines in trials are not specifically addressing VAERD/ADE through immunological assays (e. g. Th1 vs Th2 bias, total Ab titers vs Neut Ab ratio etc)

* How can research in animal models help to address these concerns?
* How predictive are animal model studies for human VAERD?
* What should be the minimum information required from vaccine developers in preclinical and clinical investigations?

(3) Format: Each panelist would address the aforementioned questions (or other relevant points) in a 2-3 min verbal high-level single summary. This would be followed by Q/A discussion with the whole group.

Please find below the agenda and webex invite for this call. We are looking forward to your participation and input on this important discussion

Very best regards to all

César, Simon and Bill.

Agenda: WHO COVID-19 Animal Models Group Call- Thursday 17-SEP-2020 3PM CET

Presentations

1- Nadia Oreshkova (Wageningen)

2- Kate Guilfoyle (Viroclinics)

3- Clint Florence (NIH)

Panel Discussion

Panelists: Miles Carroll (PHE), Barney Graham (NIH), Jürgen Richt (KSU), Robin Levis (FDA)

Moderator: Vaseeharan Sathiyamoorthy (WHO)

Meeting number (access code): 145 274 5012
Meeting password: r2Gq3BhFUP4

Thursday, September 17, 2020
3:00 pm | (UTC+02:00) Brussels, Copenhagen, Madrid, Paris | 1 hr 30 mins

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To: munoz-fontela@bnitm.de

Subject: [COVID-19] 29th WHO TC - Animal Models
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Start: 9/17/2020 8:00:00 AM
End: 9/17/2020 9:30:00 AM
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To: Albrecht, Randy[randy.albrecht@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Alyson Kelvin[AKelvin@dal.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; dbolton@hivresearch.org[dbolton@hivresearch.org]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; BRANGEL, Polina[brangelp@who.int]; Brasel, Trevor[trbrasel@UTMB.EDU]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; Cassels, Fred[fcassels@path.org]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; yu.cong@nih.gov[yu.cong@nih.gov]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; lisette.cornelissen[lisette.cornelissen@wur.nl]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; Damron, Fredrick[fdamron@hsc.wvu.edu]; que.dang@nih.gov[que.dang@nih.gov]; sodas[sodas@health.ucsd.edu]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; dgdiel@cornell.edu[dgdiel@cornell.edu]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Dohm, Erik Daniel[edohm@uab.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; Duprex, Paul[pduprex@pitt.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; Falzarano, Darryl[darryl.falzarano@usask.ca]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Flynn, Joanne L[joanne@pitt.edu]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Gerhards, Nora[nora.gerhards@wur.nl]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Griffiths, Anthony[ahgriff@bu.edu]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; rhakami@gmu.edu[rhakami@gmu.edu]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; S. Herfst[s.herfst@erasmusmc.nl]; seos@cnu.ac.kr[seos@cnu.ac.kr]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; jhogan@uga.edu[jhogan@uga.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Honko, Anna[honko@bu.edu]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; mito@ciea.or.jp[mito@ciea.or.jp]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; ajones[ajones@mail.rockefeller.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; KAZI, Fatema[kazif@who.int]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; alankhoo.imr[alankhoo.imr@gmail.com]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; Kobie, James J[jjkobie@uabmc.edu]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; Krammer, Florian[florian.krammer@mssm.edu]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; Krause, Philip[philip.krause@fda.hhs.gov]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; mary.lane@nih.gov[mary.lane@nih.gov]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; Levis, Robin[robin.levis@fda.hhs.gov]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; sean.li

(sean.li@canada.ca)[sean.li@canada.ca]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Idenisy (Idenisy@yahoo.com)[Idenisy@yahoo.com]; anice.lowen[anice.lowen@emory.edu]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; ivan.marazzi[ivan.marazzi@mssm.edu]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; marzia[marzia@niaid.nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; bobomok@hku.hk[bobomok@hku.hk]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; nnagata@niid.go.jp[nnagata@niid.go.jp]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; horer@ku.edu.tr[horer@ku.edu.tr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; mto@umn.edu[mto@umn.edu]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; peter.palese@mssm.edu[peter.palese@mssm.edu]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; PREZIOSI, Marie-pierre[preziosim@who.int]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; ravetch[ravetch@mail.rockefeller.edu]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; croy (croy@tulane.edu)[croy@tulane.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Carol.Sabourin@hhs.gov[Carol.Sabourin@hhs.gov]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; SALAMI, Kolawole[salamik@who.int]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; erica (erica@lji.org)[erica@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; res2025[res2025@med.cornell.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; sheahan[sheahan@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Sivko, Gloria S[sivkog@battelle.org]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; tcs38@psu.edu[tcs38@psu.edu]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; SWAMINATHAN, Soumya[swaminathans@who.int]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; tenoever@gmail.com[tenoever@gmail.com]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Vergara, Julia[julia.vergara@irta.cat]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; verstrepen@bprc.nl[verstrepen@bprc.nl]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; White, Alexander G[agw13@pitt.edu]; WOOD, David John[woodd@who.int]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp];

Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; ZHOU, Tiequn[ZhouT@who.int]; ZHU, Jin[Jin.Zhu@health.gov.au]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]
Cc: ibz1[ibz1@cdc.gov]; kyle.rosenke[kyle.rosenke@nih.gov]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 3/30/2021 4:35:03 PM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday April 1 3PM CET (Geneva time)

1. Andrew Jones & Jeffrey Ravetch (Rockefeller) - *Characterization of Syrian Hamster IgG Fc Receptors, a Small Animal Model of SARS-CoV-2 infection*
2. Emmie De wit (NIAID) - *Pathogenesis of VOC B.1.1.7 and B.1.351 in rhesus macaques*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, March 28, 2021 1:31 PM
To: randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; 'HENAO RESTREPO, Ana Maria'; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; philip.krause@fda.hhs.gov; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com;

Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts (johan.neyts@kuleuven.be); slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; 'WOOD, David John'; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov

Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, April 1, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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To: Albrecht, Randy[randy.albrecht@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Alyson Kelvin[AKelvin@dal.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; dbolton@hivresearch.org[dbolton@hivresearch.org]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; BRANGEL, Polina[brangelp@who.int]; Brasel, Trevor[trbrasel@UTMB.EDU]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; Cassels, Fred[fcassels@path.org]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; yu.cong@nih.gov[yu.cong@nih.gov]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; lisette.cornelissen[lisette.cornelissen@wur.nl]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; Damron, Fredrick[fdamron@hsc.wvu.edu]; que.dang@nih.gov[que.dang@nih.gov]; sodas[sodas@health.ucsd.edu]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; dgdiel@cornell.edu[dgdiel@cornell.edu]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Dohm, Erik Daniel[edohm@uab.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; Duprex, Paul[pduprex@pitt.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; Falzarano, Darryl[darryl.falzarano@usask.ca]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Flynn, Joanne L[joanne@pitt.edu]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Gerhards, Nora[nora.gerhards@wur.nl]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Griffiths, Anthony[ahgriff@bu.edu]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; rhakami@gmu.edu[rhakami@gmu.edu]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; S. Herfst[s.herfst@erasmusmc.nl]; seos@cnu.ac.kr[seos@cnu.ac.kr]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; jhogan@uga.edu[jhogan@uga.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Honko, Anna[honko@bu.edu]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; mito@ciea.or.jp[mito@ciea.or.jp]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; ajones[ajones@mail.rockefeller.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; KAZI, Fatema[kazif@who.int]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; alankhoo.imr[alankhoo.imr@gmail.com]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; Kobie, James J[jjkobie@uabmc.edu]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; Krammer, Florian[florian.krammer@mssm.edu]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; Krause, Philip[philip.krause@fda.hhs.gov]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; mary.lane@nih.gov[mary.lane@nih.gov]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; Levis, Robin[robin.levis@fda.hhs.gov]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; sean.li

(sean.li@canada.ca)[sean.li@canada.ca]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Idenisy (Idenisy@yahoo.com)[Idenisy@yahoo.com]; anice.lowen[anice.lowen@emory.edu]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; ivan.marazzi[ivan.marazzi@mssm.edu]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; marzia[marzia@niaid.nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; bobomok@hku.hk[bobomok@hku.hk]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; nnagata@niid.go.jp[nnagata@niid.go.jp]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; horer@ku.edu.tr[horer@ku.edu.tr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; mto@umn.edu[mto@umn.edu]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; peter.palese@mssm.edu[peter.palese@mssm.edu]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; PREZIOSI, Marie-pierre[preziosim@who.int]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; ravetch[ravetch@mail.rockefeller.edu]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; croy (croy@tulane.edu)[croy@tulane.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; SALAMI, Kolawole[salamik@who.int]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; erica (erica@lji.org)[erica@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; res2025[res2025@med.cornell.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; sheahan[sheahan@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Sivko, Gloria S[sivkog@battelle.org]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; tcs38@psu.edu[tcs38@psu.edu]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; SWAMINATHAN, Soumya[swaminathans@who.int]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; tenoever@gmail.com[tenoever@gmail.com]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Vergara, Julia[julia.vergara@irta.cat]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; verstrepen@bprc.nl[verstrepen@bprc.nl]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; White, Alexander G[agw13@pitt.edu]; WOOD, David John[woodd@who.int]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp];

Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; ZHOU, Tiequn[ZhouT@who.int]; ZHU, Jin[Jin.Zhu@health.gov.au]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; kyle.rosenke[kyle.rosenke@nih.gov]; caroline.foo[caroline.foo@kuleuven.be]; t.sulpice[t.sulpice@physiogenex.com]; gabriella.worwa[gabriella.worwa@nih.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; f.briand[f.briand@physiogenex.com]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 4/14/2021 7:27:31 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday April 15 3PM CET (Geneva time)

1. Chris Miller (UC Davis)/Neeltje van Doremalen (RML): *Characterization of CA SARS-CoV-2 variants (B 1.427/1.429) in hamsters: A preliminary report from the NorCal SARS-CoV-2 VOC Assessment Group*
2. François Brand (Physiogenex): *SARS-CoV-2 infection induces greater disease severity in the free choice diet-induced obese NASH hamster, a metabolic comorbidities model of COVID-19*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, April 11, 2021 7:48 AM
To: SCHWARTZ, Lauren; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; Crozier, Ian (NIH) [C]; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; Krause, Philip; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca;

grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts@kuleuven.be; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov; ibz1@cdc.gov; kyle.rosenke@nih.gov; caroline.foo@kuleuven.be; t.sulpice; gabriella.worwa@nih.gov; Vidadi.Yusibov@hhs.gov; François Briand
Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, April 15, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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To: Albrecht, Randy[randy.albrecht@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Alyson Kelvin[AKelvin@dal.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; dbolton@hivresearch.org[dbolton@hivresearch.org]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; BRANGEL, Polina[brangelp@who.int]; Brasel, Trevor[trbrasel@UTMB.EDU]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; Cassels, Fred[fcassels@path.org]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; yu.cong@nih.gov[yu.cong@nih.gov]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; lisette.cornelissen[lisette.cornelissen@wur.nl]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; Damron, Fredrick[fdamron@hsc.wvu.edu]; que.dang@nih.gov[que.dang@nih.gov]; sodas[sodas@health.ucsd.edu]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; dgdiel@cornell.edu[dgdiel@cornell.edu]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Dohm, Erik Daniel[edohm@uab.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; Duprex, Paul[pduprex@pitt.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; Falzarano, Darryl[darryl.falzarano@usask.ca]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Flynn, Joanne L[joanne@pitt.edu]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Gerhards, Nora[nora.gerhards@wur.nl]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Griffiths, Anthony[ahgriff@bu.edu]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; rhakami@gmu.edu[rhakami@gmu.edu]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; S. Herfst[s.herfst@erasmusmc.nl]; seos@cnu.ac.kr[seos@cnu.ac.kr]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; jhogan@uga.edu[jhogan@uga.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Honko, Anna[honko@bu.edu]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; mito@ciea.or.jp[mito@ciea.or.jp]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; ajones[ajones@mail.rockefeller.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; KAZI, Fatema[kazif@who.int]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; alankhoo.imr[alankhoo.imr@gmail.com]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; Kobie, James J[jjkobie@uabmc.edu]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; Krammer, Florian[florian.krammer@mssm.edu]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; Krause, Philip[philip.krause@fda.hhs.gov]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; mary.lane@nih.gov[mary.lane@nih.gov]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; Levis, Robin[robin.levis@fda.hhs.gov]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; sean.li

(sean.li@canada.ca)[sean.li@canada.ca]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Idenisy (Idenisy@yahoo.com)[Idenisy@yahoo.com]; anice.lowen[anice.lowen@emory.edu]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; ivan.marazzi[ivan.marazzi@mssm.edu]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; marzia[marzia@niaid.nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; bobomok@hku.hk[bobomok@hku.hk]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; nnagata@niid.go.jp[nnagata@niid.go.jp]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; horer@ku.edu.tr[horer@ku.edu.tr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; mto@umn.edu[mto@umn.edu]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; peter.palese@mssm.edu[peter.palese@mssm.edu]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; PREZIOSI, Marie-pierre[preziosim@who.int]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; ravetch[ravetch@mail.rockefeller.edu]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; croy (croy@tulane.edu)[croy@tulane.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; SALAMI, Kolawole[salamik@who.int]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; erica (erica@lji.org)[erica@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; res2025[res2025@med.cornell.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; sheahan[sheahan@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Sivko, Gloria S[sivkog@battelle.org]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; tcs38@psu.edu[tcs38@psu.edu]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; SWAMINATHAN, Soumya[swaminathans@who.int]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; tenoever@gmail.com[tenoever@gmail.com]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Vergara, Julia[julia.vergara@irta.cat]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; verstrepen@bprc.nl[verstrepen@bprc.nl]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; White, Alexander G[agw13@pitt.edu]; WOOD, David John[woodd@who.int]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp];

Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; ZHOU, Tiequn[ZhouT@who.int]; ZHU, Jin[Jin.Zhu@health.gov.au]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; kyle.rosenke[kyle.rosenke@nih.gov]; caroline.foo[caroline.foo@kuleuven.be]; t.sulpice[t.sulpice@physiogenex.com]; gabriella.worwa[gabriella.worwa@nih.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; f.briand[f.briand@physiogenex.com]
Cc: Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Kishimori, Jennifer M COL USARMY OSD OUSD P-R (USA)[jennifer.m.kishimori.mil@mail.mil]; Beddingfield, Brandon J[bbedding@tulane.edu]; michael.hevey@ST.DHS.GOV[michael.hevey@ST.DHS.GOV]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 4/21/2021 8:35:20 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday April 22 3PM CET (Geneva time)

1. Brandon Beddingfield (Tulane) - *Nonhuman Primate COVID-19 Disease Model: Comparative Pathophysiology of Exposure Route and Species Selection*
2. Paul Dabisch (NBACC) - *Estimation of the infectious dose of inhaled SARS-CoV-2 in a nonhuman primate model of COVID-19*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, April 18, 2021 1:36 PM
To: SCHWARTZ, Lauren; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; trbrasel@UTMB.EDU; lisambrosseau@gmail.com; abukreye@utmb.edu; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; MONALISA.CHATTERJI@gatesfoundation.org; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; kai.dallmeier@kuleuven.be; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; CDillen@som.umaryland.edu; edohm@uab.edu; Ruben.Donis@hhs.gov; william.dowling@cepi.net; mariette.ducatez@envt.fr; pduprex@pitt.edu; mmeitzen@utmb.edu; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence@nih.gov; joanne@pitt.edu; thomasf@primate.wisc.edu; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Adolfo.Garcia-Sastre@mssm.edu; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; KAZI, Fatema; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline.Kirchner@gatesfoundation.org; Harry.Kleanthous@gatesfoundation.org; 'KNEZEVIC, Ivana'; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; Krause, Philip; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov;

langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; roger.le-grand@cea.fr; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; Karen.Makar@gatesfoundation.org; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; johan.neyts@kuleuven.be; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; RIVEROS BALTA, Ximena; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; 'SALAMI, Kolawole'; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; erica@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; SCHWARTZ, Lauren; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; peshi@UTMB.EDU; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; SWAMINATHAN, Soumya; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov; JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; sktseng@UTMB.EDU; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; Jin.Zhu@health.gov.au; bosioc@niaid.nih.gov; ibz1@cdc.gov; kyle.rosenke@nih.gov; caroline.foo@kuleuven.be; t.sulpice@physiogenex.com; gabriella.worwa@nih.gov; Vidadi.Yusibov@hhs.gov; François Briand
Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, April 22, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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To: 'SCHWARTZ, Lauren'[schwartzl@who.int]; Albrecht, Randy[randy.albrecht@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Alyson Kelvin[AKelvin@dal.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; dbolton@hivresearch.org[dbolton@hivresearch.org]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; BRANGEL, Polina[brangelp@who.int]; Brasel, Trevor[trbrasel@UTMB.EDU]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; Ricardo Carrion, Jr.[rcarrion@TxBiomed.org]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; Cassels, Fred[fcassels@path.org]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; yu.cong@nih.gov[yu.cong@nih.gov]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; lisette.cornelissen[lisette.cornelissen@wur.nl]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; Damron, Fredrick[fdamron@hsc.wvu.edu]; que.dang@nih.gov[que.dang@nih.gov]; sodas[sodas@health.ucsd.edu]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; dgdiel@cornell.edu[dgdiel@cornell.edu]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Dohm, Erik Daniel[edohm@uab.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; Duprex, Paul[pduprex@pitt.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; Falzarano, Darryl[darryl.falzarano@usask.ca]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Flynn, Joanne L[joanne@pitt.edu]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; Gerhards, Nora[nora.gerhards@wur.nl]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Griffiths, Anthony[ahgriff@bu.edu]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; rhakami@gmu.edu[rhakami@gmu.edu]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; S. Herfst[s.herfst@erasmusmc.nl]; seos@cnu.ac.kr[seos@cnu.ac.kr]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; jhogan@uga.edu[jhogan@uga.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Honko, Anna[honko@bu.edu]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; mito@ciea.or.jp[mito@ciea.or.jp]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; ajones[ajones@mail.rockefeller.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; KAZI, Fatema[kazif@who.int]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; alankhoo.imr[alankhoo.imr@gmail.com]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; KNEZEVIC, Ivana[knezevici@who.int]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; Kobie, James J[jjkobie@uabmc.edu]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; Krammer, Florian[florian.krammer@mssm.edu]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; Krause, Philip[philip.krause@fda.hhs.gov]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; mary.lane@nih.gov[mary.lane@nih.gov]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; Levis, Robin[robin.levis@fda.hhs.gov]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; sean.li

(sean.li@canada.ca)[sean.li@canada.ca]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Idenisy (Idenisy@yahoo.com)[Idenisy@yahoo.com]; anice.lowen[anice.lowen@emory.edu]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; ivan.marazzi[ivan.marazzi@mssm.edu]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; Luis Martinez[LMartinez@txbiomed.org]; marzia[marzia@niaid.nih.gov]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; bobomok@hku.hk[bobomok@hku.hk]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; nnagata@niid.go.jp[nnagata@niid.go.jp]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; horer@ku.edu.tr[horer@ku.edu.tr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; mto@umn.edu[mto@umn.edu]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; peter.palese@mssm.edu[peter.palese@mssm.edu]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; PREZIOSI, Marie-pierre[preziosim@who.int]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; ravetch[ravetch@mail.rockefeller.edu]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; croy (croy@tulane.edu)[croy@tulane.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; SALAMI, Kolawole[salamik@who.int]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; erica (erica@lji.org)[erica@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; res2025[res2025@med.cornell.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; sheahan[sheahan@email.unc.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; Sivko, Gloria S[sivkog@battelle.org]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; tcs38@psu.edu[tcs38@psu.edu]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; SWAMINATHAN, Soumya[swaminathans@who.int]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; tenoever@gmail.com[tenoever@gmail.com]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Vergara, Julia[julia.vergara@irta.cat]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; verstrepen@bprc.nl[verstrepen@bprc.nl]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; White, Alexander G[agw13@pitt.edu]; WOOD, David John[woodd@who.int]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; ZHOU, Tiequn[ZhouT@who.int];

ZHU, Jin[Jin.Zhu@health.gov.au]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; kyle.rosenke[kyle.rosenke@nih.gov]; caroline.foo[caroline.foo@kuleuven.be]; t.sulpice[t.sulpice@physiogenex.com]; gabriella.worwa[gabriella.worwa@nih.gov]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; f.briand[f.briand@physiogenex.com]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Kishimori, Jennifer M COL USARMY OSD OUSD P-R (USA)[jennifer.m.kishimori.mil@mail.mil]; Beddingfield, Brandon J[bbedding@tulane.edu]; michael.hevey@ST.DHS.GOV[michael.hevey@ST.DHS.GOV]
Cc: Larry Schlesinger[LSchlesinger@txbiomed.org]; Joanne Turner[joanneturner@txbiomed.org]; Akudo Anyanwu[AAnyanwu@txbiomed.org]; Cory Hallam[CHallam@txbiomed.org]; Lisa Cruz[lcruz@txbiomed.org]
From: Jordi Torrelles[JTorrelles@txbiomed.org]
Sent: Thur 4/22/2021 9:05:12 AM (UTC-05:00)
Subject: ANNOUNCEMENT: Texas Biomed Global Health Virtual Symposium

Dear all,

At Texas Biomedical Research Institute we are running a Global Health Symposium next week, where we will be tackling questions about how to handle the next pandemic, as well as we will have a video message from Dr. Tedros Adhanom Ghebreyesus and talks with the Pfizer vaccine development team among others. Attending this symposium is free. Please, feel free to past this announcement around your colleagues.

For your consideration, the announcement and link to register is below.

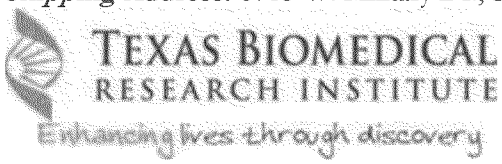
Thank you for your time reading this email and considering this invitation to attend this symposium.

Wishing you all a pleasant rest of the week,

Jordi

Jordi B. Torrelles, PhD
Professor
Lead, Population Health Program
Director, Biosafety Level 3 Program
Coordinator, Coronavirus Working Group
Texas Biomedical Research Institute
Office: (210) 258-9448
Email: jtorrelles@txbiomed.org
Web: http://www.txbiomed.org/

Mailing Address: P.O. Box 760549, San Antonio, TX 78245-0549
Shipping Address: 8715 W. Military Dr., San Antonio, TX 78227-5302



Celebrating the Institute's 80th anniversary, Texas Biomedical Research Institute is hosting the organization's first Virtual Global Health Symposium on April 29-30, featuring nearly 50 international scientists, global health and public policy leaders. #HealthStartsWithScience. Get registered today for this FREE event Here https://bit.ly/3vPkfEU

Subject: Texas Biomed's Global Health Symposium Announces Speaker Lineup

RSVP TODAY!

Welcome Speakers!

Texas Biomed is excited to announce its Global Health Virtual Symposium speaker lineup. Our program is set! We are gearing up for an exciting two days of science, policy and global health discussions!

Texas Biomed is Where Health Starts

Science that Inspires. Science that Delivers. Science that Heals.

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See what's happening on our social sites:

Texas Biomedical Research Institute | P.O. Box 760549, San Antonio, TX 78245-0549

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; Byrareddy, Siddappa

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port

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To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jennifer.m.kishimori.mil@mail.mil[jennifer.m.kishimori.mil@mail.mil]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan

García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara, Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall

(troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]
Cc: Wong, Lok-Yin Roy[lok-yinroy-wong@uiowa.edu]; Gerhards, Nora[nora.gerhards@wur.nl]; Port, Julia (NIH/NIAID) [F][julia.port@nih.gov]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 5/19/2021 9:48:24 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call. **Please note, you will have to download the most recent version of Zoom to attend the call.**

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday May 19 3PM CET (Geneva time)

1. Roy Wong (U. Iowa) - *Mouse adapted SARS-CoV-2 as a model for COVID-19*
2. Nora Gerhards (WUR) - *Efficient direct and limited indirect transmission of SARS-CoV-2 in cats*
3. Julia Port (NIH) - *Modelling aerosol transmission of SARS-CoV-2 in the Syrian hamster*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 16, 2021 8:14 AM
To: WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru;

ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion (rcarrion@TxBiomed.org); res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; Byrareddy, Siddappa

Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, May 20, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

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+1 253 215 8782 US (Tacoma)
+1 720 928 9299 US (Denver)
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To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jennifer.m.kishimori.mil@mail.mil[jennifer.m.kishimori.mil@mail.mil]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan

García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara, Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall

(troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]; lok-yinroy-wong[lok-yinroy-wong@uiowa.edu]; julia.port[julia.port@nih.gov]
Cc: Zahn, Roland [JRDNL][RZahn@its.jnj.com]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 5/26/2021 7:37:38 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday May 27 3PM CET (Geneva time)

1. Anja Kipar (U. Zurich) - *Viral neuroinvasion and neurotropism without neuronal damage in the hACE2 mouse model of COVID-19*
2. Dan Barouch (Harvard) - *Natural and Vaccine Immunity against SARS-CoV-2 Variants in Rhesus Macaques*
3. Antoine Nougairede (Aix Marseille Université) - *SARS-CoV-2 20I/501Y.V1 variant in a human reconstituted bronchial epithelium and in the hamster model*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 23, 2021 12:39 PM
To: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick;

feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; Port, Julia (NIH/NIAID) [F]
Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, May 27, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

Join Zoom Meeting
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+41225910005,,3612568290# Switzerland
+41225910156,,3612568290# Switzerland

Dial by your location
+41 22 591 00 05 Switzerland

+41 22 591 01 56 Switzerland
+41 31 528 09 88 Switzerland
+41 43 210 70 42 Switzerland
+41 43 210 71 08 Switzerland
+1 253 215 8782 US (Tacoma)
+1 720 928 9299 US (Denver)
+1 971 247 1195 US (Portland)
+1 213 338 8477 US (Los Angeles)
+1 346 248 7799 US (Houston)
+1 602 753 0140 US (Phoenix)
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+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 646 518 9805 US (New York)
+1 646 558 8656 US (New York)
+1 651 372 8299 US (Minnesota)
+1 786 635 1003 US (Miami)
+1 267 831 0333 US (Philadelphia)
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To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jennifer.m.kishimori.mil@mail.mil[jennifer.m.kishimori.mil@mail.mil]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan

García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara, Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall

(troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]; lok-yinroy-wong[lok-yinroy-wong@uiowa.edu]; julia.port[julia.port@nih.gov]; Benjamin Murrell[benjamin.murrell@ki.se]
Cc: Paul Medigen[paul@medigenvac.com]; ali.fattom@bluewillow.com[ali.fattom@bluewillow.com]; Allenlien@medigenvac.com[Allenlien@medigenvac.com]; chad.costley@bluewillow.com[chad.costley@bluewillow.com]; vira.bitko@bluewillow.com[vira.bitko@bluewillow.com]; Charles@medigenvac.com[Charles@medigenvac.com]; meeiyun@medigenvac.com[meeiyun@medigenvac.com]; AngieLin@medigenvac.com[AngieLin@medigenvac.com]; Yashan.Chuang@sbc-biotech.com[Yashan.Chuang@sbc-biotech.com]; michael.malison@gmail.com[michael.malison@gmail.com]; han.vandenbosch@vaxilon.nl[han.vandenbosch@vaxilon.nl]; vira.bitko@bluewillow.com[vira.bitko@bluewillow.com]; shyamala.ganesan@bluewillow.com[shyamala.ganesan@bluewillow.com]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 6/2/2021 10:33:37 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday June 3 3PM CET (Geneva time)

1. Ali Fattom (Blue Willow) & Allen Lien (MGV) - *Immunogenicity and efficacy of an Intranasal COVID-19 vaccine, S2-P/NE01, in mouse and Hamster animal model. An update and proposed path for clinical evaluation*
2. Benjamin Murrell (Karolinska Institute) - *VoC booster vaccines and nanobody therapies in K18 hACE2 mice*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, May 30, 2021 8:22 AM
To: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-

muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; Port, Julia (NIH/NIAID) [F]
Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, June 3, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; d.vanriel; Cherry, Sara

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Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

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Importance: Normal

Subject: Canceled: WHO COVID-19 Animal Models Group Call

Start Time: Thur 6/10/2021 8:00:00 AM (UTC-05:00)

End Time: Thur 6/10/2021 9:30:00 AM (UTC-05:00)

Required Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu;

Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert (Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; D.A.J. van Riel; Cherry, Sara

Due to a conflicting WHO meeting, we are cancelling the call this week.

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; D.A.J. van Riel; Cherry, Sara

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Agenda to follow.

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Meeting ID: 361 256 8290

From: Lisa CHAKRABARTI[lisa.chakrabarti@pasteur.fr]

Attendees: Tony.Schountz@colostate.edu; Techakitiroj Chatkul (tverakit@gmail.com); Segales, Joaquim; kupke (kupke@staff.uni-marburg.de); qinchuan (qinchuan@pumc.edu.cn); Karl.Erlandson (Karl.Erlandson@hhs.gov); erica (erica@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; mary.lane@nih.gov; Andrew.Phipps; Eitzen, Melissa M.; Florence, Clint (NIH/NIAID) [E]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Riccardo Russo; anja.kipar@uzh.ch; feldmannh@niaid.nih.gov; Levis, Robin; Hodgson, Paul; SBradfute@salud.unm.edu; wim.vanderpoel@wur.nl; Cartner, Samuel Corbin; lok-yinroy-wong; thomasf@primate.wisc.edu; danielle.anderson (danielle.anderson@duke-nus.edu.sg); sodas; BRANGEL, Polina; MNELSON@mail.dstl.gov.uk; William Dowling (william.dowling@cepi.net); Brasel, Trevor; RIVEROS BALTA, Ximena; sekim (sekim@krict.re.kr); estefania.rodriguez (estefania.rodriguez@bnitm.de); lgralins@email.unc.edu; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); De wit, Emmie (NIH/NIAID) [E]; Cherry, Sara; jeroen.kortekaas (jeroen.kortekaas@wur.nl); JOHN JAMES BACZENAS; Hwan K Kim (hwan.kim@stonybrook.edu); Neil Berry (Neil.Berry@nibsc.org); marlene.espinozamoraga; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Manki Song (mksong@ivi.int); Jason.Mott; DAVID H O'CONNOR (dhoconno@wisc.edu); hlchen (hlchen@hku.hk); Vandenberghe, Luk; MSLEVER (MSLEVER@dstl.gov.uk); Donis, Ruben (OS/ASPR/BARDA); Miles.Carroll (Miles.Carroll@phe.gov.uk); Perlman, Stanley; Bukreyev, Alexander; SHELBY L O'CONNOR; Kayvon Modjarrad (kmodjarrad@eidresearch.org); Romain Volmer (romain.volmer@envt.fr); langermans (langermans@bprc.nl); Dohm, Erik Daniel; bosioc@niaid.nih.gov; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); patrick.reid@unmc.edu; Seungtaek Kim (seungtaek.kim@ip-korea.org); john.c.trefry.civ (john.c.trefry.civ@mail.mil); dbolton@hivresearch.org; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); res2025; wenchun0617; Amelia Karlsson (amelia.karlsson@duke.edu); fkoide (fkoide@southernresearch.org); Hevey, Michael (CTR); Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); WaickmaA@upstate.edu; croy (croy@tulane.edu); Juan García Arriaza (jfgarcia@cnb.csic.es); sheahan; Tony.Wang (Tony.Wang@fda.hhs.gov); dean.smith (dean.smith@canada.ca); t.sulpice; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); horer@ku.edu.tr; Elliot Lilley - NC3Rs; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); HENAO RESTREPO, Ana Maria; dmissiak (dmissiak@bsd.uchicago.edu); bobomok@hku.hk; Falzarano, Darryl; kevinharrod (kevinharrod@uabmc.edu); Luis.Lugo.mil@afrims.org; Tadaki (tksuzuki@nih.go.jp); dgdiel@cornell.edu; kandeil_a@hotmail.com; Sivko, Gloria S; Krammer, Florian; Little, James (OS/ASPR/BARDA); Sally Sharpe (Sally.Sharpe@phe.gov.uk); Graham, Barney (NIH/VRC) [E]; anna (anna@thsti.res.in); Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); tenoever@gmail.com; JTorrelles@txbiomed.org; sean.li (sean.li@canada.ca); Frieman, Matthew; d.vanriel; KNEZEVIC, Ivana; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); lisambrosseau@gmail.com; verstrepen@bprc.nl; Albrecht, Randy; tcs38@psu.edu; sharon.daye2.mil@mail.mil; peter.palese@mssm.edu; PREZIOSI, Marie-pierre; tyamamoto@ciea.or.jp; Benjamin Murrell; Oreshkova, Nadia; Yper.Hall (Yper.Hall@phe.gov.uk); y.jacob.hou@unc.edu; WOOD, David John; Lee-Parritz, David; paul-mccray (paul-mccray@uiowa.edu); snumouse (snumouse@snu.ac.kr); kanta.subbarao (kanta.subbarao@influenzacentre.org); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); kyle.rosenke; Kobie, James J; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); seos@cnu.ac.kr; kai.dallmeier

(kai.dallmeier@kuleuven.be); salgampa (salgampa@njms.rutgers.edu); Stemmy, Erik (NIH/NIAID) [E]; Matthew.Reed.mil@afrims.org; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); l.enjuanes@cnb.csic.es; Volker.gerdts (Volker.gerdts@usask.ca); mariette.ducatez@envt.fr; Victoria.Wahl; que.dang@nih.gov; caroline.melo@rivm.nl; ygoez; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); David Vaughn (David.Vaughn@gatesfoundation.org); B.H.G. Rockx (b.rockx@erasmusmc.nl); SATHIYAMOORTHY, Vaseeharan; REIRELAND (REIRELAND@mail.dstl.gov.uk); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); CDillen@som.umaryland.edu; Munir, Muhammad; SPERGEL@email.chop.edu; YOO, Si Hyung; Stewart, James; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); Kristine Macartney (kristine.macartney@health.nsw.gov.au); daniel.martinez-arguelles; Pickett, Thames (NIH/NIAID) [E]; sutter (sutter@micro.vetmed.uni-muenchen.de); gustavo.palacios (gustavo.palacios@gmail.com); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); S. Herfst; Holbrook, Michael (NIH/NIAID) [C]; lisette.cornelissen; LESELLIER Sandrine (sandrine.lesellier@anses.fr); MacGill, Tracy; Schotsaert, Michael; Paul.Dabisch; Krause, Philip; angierasmussen@gmail.com; Barbara.Schnierle (Barbara.Schnierle@pei.de); grace.m.lidl.mil@mail.mil; antoine.nougairede; alankhoo.imr; JLPRIOR (JLPRIOR@dstl.gov.uk); LMartinez@txbiomed.org; caroline.foo; Vergara, Julia; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); Garcia-Sastre, Adolfo; Paul.Lambert (Paul.Lambert@unige.ch); Crozier, Ian (NIH) [C]; julia.port; Olinger, Gene; neeltje.vandoremalen@nih.gov; scordo (scordo@qb.fcen.uba.ar); Philip Minor (Philip.Minor2@gmail.com); Pauline Maisonnasse (pauline.maisonnasse@cea.fr); verschoor (verschoor@bprc.nl); ZHU, Jin; tomeri (tomeri@iibr.gov.il); ivan.marazzi; stittelaar (stittelaar@viroclinics.com); christian.c.hofer.mil@mail.mil; f.briand; Jayashankar, Lakshmi (OS/ASPR/BARDA); Damron, Fredrick; franck.TOURET@univ-amu.fr; ZHOU, Tiequn; mopargal (mopargal@rams.colostate.edu); Yusibov, Vidadi (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Roger Le Grand (roger.le-grand@cea.fr); Honko, Anna; Christiane GERKE; mdiamond (mdiamond@wustl.edu); rhakami@gmu.edu; dbarouch (dbarouch@bidmc.harvard.edu); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Shi, Pei yong; Simon Funnell (simon.funnell@phe.gov.uk); Nicola Rose (Nicola.Rose@nibsc.org); jfwchan (jfwchan@hku.hk); lawton.stubbert@canada.ca; jmkperrine; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); SWAMINATHAN, Soumya; troyrandall (troyrandall@uabmc.edu); marzia; SALAMI, Kolawole; ravetch; Vasan, Vasan (H&B, Geelong ACDP); gabriella.worwa; mito@ciea.or.jp; Chris Miller (cjmiller@ucdavis.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); rbaric (rbaric@email.unc.edu); dsreed@cvr.pitt.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); darwyn.kobasa@canada.ca; ramadany; GREY Finn (fgrey@exseed.ed.ac.uk); Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Tseng, Chien-Te K.; Gerhards, Nora; Treanor, John (OS/ASPR/BARDA) (CTR); Nadia KHELEF; Hensley, Lisa (NIH/NIAID) [E]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Griffiths, Anthony; Alyson Kelvin; rcarrion (rcarrion@TxBiomed.org); nnagata@niid.go.jp; Golding, Hana; sanath.rao; Javier Salguero (Javier.Salguero@phe.gov.uk); jhogan@uga.edu; nirp (nirp@iibr.gov.il); Karen Gooch; mto@umn.edu; Ann Rawkins (Ann.Rawkins@phe.gov.uk); sinabavari@comcast.net; Julia Tree (Julia.Tree@phe.gov.uk); Carolyn Clark (carolyn.clark@cepi.net); BAMFORD, Pearl; Duprex, Paul; White, Alexander G; IVMARTINEZ; anice.lowen; Munster,

Vincent (NIH/NIAID) [E]; Idenisy (Idenisy@yahoo.com); Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); Karen Makar (Karen.Makar@gatesfoundation.org); Flynn, Joanne L; Chi Van Dang (cdang@lcr.org); Russell.Ray@bcm.edu; Hild, Sheri (NIH/OD) [E]; Juergen Richt (jricht@vet.k-state.edu); Kathryn Ryan; shanchao (shanchao@wh.iov.cn); sid.byrareddy; johan.neyts (johan.neyts@kuleuven.be); mesteban (mesteban@cnb.csic.es); KAZI, Fatema; sbournazos@mail.rockefeller.edu; B.L. Haagmans (b.haagmans@erasmusmc.nl); Martin.Beer (Martin.Beer@fli.de); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); yu.cong@nih.gov; Mark Prescott - NC3Rs; mitchell.palmer@usda.gov; Asisa.Volz (Asisa.Volz@tiho-hannover.de); esulkowska@rics.bwh.harvard.edu; rkiatchula (rkiatchula@gmail.com); Mark Page (Mark.Page@nibsc.org); ajones; bradley.pickering (bradley.pickering@canada.ca); dustin.johnson (dustin.johnson@canada.ca); David Revelli (drevelli@lovelacebiomedical.org); mlewis (mlewis@bioqual.com); Flynn, Joanne L; Jeffrey V. Ravetch; Revelli, David; Griffiths, Anthony; THOMAS C FRIEDRICH (tfriedri@wisc.edu); Sinha, Tanima (OS/ASPR/BARDA); Stylianos Bournazos; Robert JEFF Hogan; Andrew Jones; Diane Bolton; Kortekaas, Jeroen

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Subject: Canceled: WHO COVID-19 Animal Models Group Call

Due to a conflicting WHO meeting, we are cancelling the call this week.

To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson (danielle.anderson@duke-nus.edu.sg)[danielle.anderson@duke-nus.edu.sg]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jmkperrine[jmkperrine@gmail.com]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara,

Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au];

SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]; lok-yinroy-wong[lok-yinroy-wong@uiowa.edu]; julia.port[julia.port@nih.gov]; Benjamin Murrell[benjamin.murrell@ki.se]; D.A.J. van Riel[d.vanriel@erasmusmc.nl]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]
Cc: Totura, Allison (OS/ASPR/BARDA)[Allison.Totura@hhs.gov]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Wed 6/16/2021 7:27:56 AM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday June 17 3PM CET (Geneva time)

1. Sara Cherry (U Penn) - *COVID-19 Antiviral Discovery Pipeline*
2. Allison Totura (BARDA) - *SARS-CoV-2 Vaccine Candidates: Correlates of Protection Study in Rhesus Macaque*
3. Juergen Richt (KSU) - *Susceptibility of wild and domestic ruminants to experimental SARS-CoV-2 infection*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, June 13, 2021 12:41 PM
To: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org;

James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jmkperrine@gmail.com; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; julia.port@nih.gov; benjamin.murrell@ki.se; d.vanriel@erasmusmc.nl; Cherry, Sara

Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, June 17, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

Join Zoom Meeting
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Meeting ID: 361 256 8290
One tap mobile
+41225910005,,3612568290# Switzerland
+41225910156,,3612568290# Switzerland

Dial by your location
+41 22 591 00 05 Switzerland
+41 22 591 01 56 Switzerland
+41 31 528 09 88 Switzerland

+41 43 210 70 42 Switzerland
+41 43 210 71 08 Switzerland
+1 253 215 8782 US (Tacoma)
+1 720 928 9299 US (Denver)
+1 971 247 1195 US (Portland)
+1 213 338 8477 US (Los Angeles)
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+1 602 753 0140 US (Phoenix)
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+1 669 900 9128 US (San Jose)
+1 470 250 9358 US (Atlanta)
+1 470 381 2552 US (Atlanta)
+1 646 518 9805 US (New York)
+1 646 558 8656 US (New York)
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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@duke-nus.edu.sg; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jennifer.m.kishimori.mil@mail.mil; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-

perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; Port, Julia (NIH/NIAID) [F]; Revelli, David; David Vaughn; Thomas Friedrich; Griffiths, Anthony; S. Herfst; Reed, Douglas S; Sinha, Tanima (OS/ASPR/BARDA); Stylianos Bournazos; Kortekaas, Jeroen; Jeffrey V. Ravetch; Diane Bolton; Unrath, Marya (ASPR/BARDA/NCD) (CTR); Malkevich, Nina (OS/ASPR/BARDA) (CTR); Andrew Jones

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); ldenisy (ldenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; d.vanriel; Cherry, Sara

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Subject: WHO COVID-19 Animal Models Group Call

Agenda to follow.

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69.174.57.160 (Canada)
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From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]

Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Location: GoToMeeting

Importance: Normal

Subject: A38 Task Order Bi-weekly Call

Start Time: Fri 4/24/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 4/24/2020 11:00:00 AM (UTC-05:00)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher

Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

****Updating our A38 task order update call frequency to biweekly instead of monthly due to the increase in model development studies and MCM studies****

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance: Normal

Start Time: Fri 4/24/2020 2:30:00 PM (UTC)

End Time: Fri 4/24/2020 4:00:00 PM (UTC)

Required Attendees: Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Pickett, Thames (NIH/NIAID) [E]; Liz.grinstead@colostate.edu; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]

Optional Attendees: Bouvier, Nicole; Zhongde Wang; Morrey, John; Richard Bowen

A38 Task Order Update_Template.docx

AGENDA for 4/24/2020:

1. **Updates from each site [CSU, UNC, USU, UTMB]:**

- **Current animal status**
- **Current study status**
- **Timelines for availability of MCM studies**
- **Any resources needed? Any hurdles/challenges?**

2. **Alternating bi-weekly email updates [due on: 5/8/2020, 6/5/2020, etc.] – please see attached template**

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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A38 Task Order Update

Establishment of Small Animal Models for Screening MCMs for the 2019 Novel Coronavirus (SARS-CoV-2)

Please include updates on the following:

- Current animal status (animal availability, colony expansion, actual numbers of animals available, etc.)
- Current study status
- Timelines for availability of MCM studies (should **emphasize** earliest possible date for study start)
- Any resources needed? Any hurdles/challenges?

Updates are required bi-weekly and will alternate between teleconference or email updates. The next alternating bi-weekly email updates are due by close of business on 5/8/2020, 6/5/2020, ... etc. Please email your site's update to Erik Stemmy ([HYPERLINK "mailto:erik.stemmy@nih.gov"]), Chelsea Lane ([HYPERLINK "mailto:mary.lane@nih.gov"]), and Thames Pickett ([HYPERLINK "mailto:pickettte@niaid.nih.gov"]).

Importance:	Normal
Start Time:	Fri 5/22/2020 2:30:00 PM (UTC)
End Time:	Fri 5/22/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 6/19/2020 2:30:00 PM (UTC)
End Time:	Fri 6/19/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]
Optional Attendees:	Richard Bowen; Bouvier, Nicole

Importance:	Normal
Start Time:	Fri 7/17/2020 2:30:00 PM (UTC)
End Time:	Fri 7/17/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Raul.Andino@ucsf.edu
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Elia Brodsky; Young, Jennifer (AE); Dang, Que (NIH/NIAID) [E]

Update for 7/17:
In addition to the A38 contractor updates, Dr. Raul Andino from UCSF will also provide a brief presentation on a new camera system that his laboratory is developing to measure non-traditional endpoints for SARS-CoV-2 in mice. We will follow Dr. Andio's presentation with updates from each A38 contractor.
Best,
Chelsea
****
Dear A38 Task Order Team,

Please find below the Zoom meeting information for the monthly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Erik and I will be updating the agenda shortly, so please stay tuned.

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 8/14/2020 2:30:00 PM (UTC)
End Time:	Fri 8/14/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Deye, Greg (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE)

Importance:	Normal
Start Time:	Fri 9/25/2020 2:30:00 PM (UTC)
End Time:	Fri 9/25/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Beasley, David W.; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Agenda 9/25:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (9/25: UNC; 10/9: UTMB; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Subject:	Canceled: A38 Task Order Bi-weekly Call
Start Time:	Fri 1/1/2021 3:30:00 PM (UTC)
End Time:	Fri 1/1/2021 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

Canceling our meeting on 1/1/2021 due to the holiday

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 10/9/2020 2:30:00 PM (UTC)
End Time:	Fri 10/9/2020 4:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/9/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~; **10/9: UTMB**; 10/23: USU; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

10/23/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~; **10/23: USU**; 11/6: CSU)

Dear A38 Task Order Team,

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Best,
Erik & Chelsea

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Importance:	Normal
Start Time:	Fri 11/6/2020 3:30:00 PM (UTC)
End Time:	Fri 11/6/2020 5:00:00 PM (UTC)
Required Attendees:	Lane, Chelsea (NIH/NIAID) [E]; Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; Bart Tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Baric, Toni C; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]

11/5/2020 Agenda:

- General Updates (Erik)
- A38 Sites Updates (CSU, USU, UNC, UTMB)
- Rotating check-in with individual sites (~~9/25: UNC~~;~~10/9: UTMB~~;~~10/23: USU~~; **11/6: CSU**)

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 887 1310
Password: **552.136**

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Toni C; Baric Toni; Baric, Ralph; Berhorst, Jackie; D. Menachery Vineet (vimenach@utmb.edu); Ferris Martin; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski Lisa; Heise Mark; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis; Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 9/10/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 9/10/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Toni C; Baric Toni; Baric, Ralph S; Berhorst, Jackie; D. Menachery Vineet (vimenach@utmb.edu); mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise Mark; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Resending the invitation.

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+13017158592,,95848751377#,,,,,,0#,, # US (Germantown)

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+1 346 248 7799 US (Houston)
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833 548 0276 US Toll-free
833 548 0282 US Toll-free
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Join by H.323
162.255.37.11 (US West)

162.255.36.11 (US East)
Meeting ID: 958 4875 1377
Passcode: **552.136**

Importance:	Normal
Subject:	Canceled: SIG U19 Monthly Meeting
Start Time:	Thur 10/8/2020 5:30:00 PM (UTC)
End Time:	Thur 10/8/2020 6:30:00 PM (UTC)
Required Attendees:	Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis
Optional Attendees:	Michael J Gale; Renee Ireton

Due to the annual Systems meeting, the October call will be cancelled.

Join Zoom Meeting
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Meeting ID: 958 4875 1377
Passcode: **552.136**

Importance:	Normal
Subject:	Canceled: SIG U19 Monthly Meeting
Start Time:	Thur 11/12/2020 6:30:00 PM (UTC)
End Time:	Thur 11/12/2020 7:30:00 PM (UTC)
Required Attendees:	Leist, Sarah; Heise Mark; D. Menachery Vineet (vimenach@utmb.edu); Baric Toni; Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis
Optional Attendees:	Michael J Gale; Renee Ireton; Graham PhD, Jessica B

The November call is cancelled due to a scheduling conflict.

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Meeting ID: 958 4875 1377
Passcode: **552.136**

Importance: Normal

Start Time: Thur 12/3/2020 6:30:00 PM (UTC)

End Time: Thur 12/3/2020 7:30:00 PM (UTC)

Required Attendees: Baric, Toni C; Baric Toni; Baric, Ralph S; Berhorst, Jackie; D. Menachery Vineet (vimenach@utmb.edu); mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise Mark; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Rescheduling December's SIG U19 call.

Thank you

Toni

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To: Logue, James[James.Logue@som.umaryland.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; sklein2[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; acox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 11/16/2020 10:13:23 AM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - November 17
nCoV PI call attendee list.xlsx

Hi Everyone,

On November 10th, Drs. Joachimiak and Fremont treated us to a double feature:

Dr. Andrzej Joachimiak
"**Structural studies of SARS-CoV-2 proteins and their complexes**"

Dr. Daved Fremont
"**Structural mechanisms of SARS-CoV-2 antibody neutralization"**

Thank you both for presenting and to those that were in attendance!

Tomorrow, November 17th, Dr. Russell Ray will be presenting on "**Leveraging genetic tools for functional neural circuit mapping in the control of breathing for COVID-19 studies**".

We are also looking for volunteers for next week, November 24th and for future calls starting December 8th. Please let me know if you are interested in presenting.

Thanks,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		13-Oct	20-Oct	27-Oct	3-Nov	11-Nov
Erik Stemmy	x	x	x	x	x	
Marciela DeGrace	x	x	x		x	
Rebecca Lampley	x	x	x	x	x	
Aditya Gaur						
Adolfo Garcia-Sastre	x	x	x	x	x	
Aisha Souquette						
Alan Embry				x		
Ali Ellebedy			x	x	x	
Alicia Fry				x		
Alison Augustine		x	x			
Alvaro Ordonez	x	x		x	x	
Amanda Perofsky						
Amy Krafft	x	x		x	x	
Andrea Pruijssers			x			
Andrea Sant	x	x		x		
Andrew Mesecar	x	x	x	x	x	
Andrew Pekosz		x	x	x	x	
Andy Mesecar						
Andrzej Joachimiak			x		x	
Aneesh Mehta						
Angela Rasmussen	x	x	x	x	x	
Ann Eakin						
Anice Lowen	x	x	x			
Anita McElroy	x		x	x		
Anne Piantadosi		x				
Aron Hall	x					
Atsuo Kuki		x	x		x	
Aubree Gordon				x		
Barry Rockx						
Becky Dutch						
Ben Cowling						
Ben Larman						
Benjamin Miller			x			
Ben Tenoever	x	x	x		x	
Bernard Lafont					x	
Bin Zhou		x	x	x	x	
Biao He						
Brooke Bozick	x	x		x		
Carly Dillen	x	x	x	x	x	
Carlie Williams		x		x		
Catherine Luke			x	x		
Claire Midgley				x	x	

Charles Russell			x	x	
Chelsea Lane		x		x	
Chris Brooke					
Christopher Hsu					
Chris Roberts					x
Clint Florence				x	
Conrad Mallia					
Colleen Jonsson	x	x		x	x
Connie Schmaljohn			x	x	x
Courtney Comar (Susan Weiss lab)					
Daved Fremont					x
David Martinez			x	x	
David Renner (Susan Weiss lab)					
David Topham					
David Wentworth			x	x	x
Deborah Lynn Fuller					
Diana Finzi		x			
Diane Post	x		x	x	
Diego Hijano					
Don Milton		x	x	x	x
Donna Neu	x	x	x	x	x
Elizabeth Fitzpatrick					
Erica Raterman					
Evans	x				
Eunchung Park	x	x	x		
Eun Mi Lee					
Florian Krammer	x	x	x	x	x
Francisco Chaves		x	x		
Frederic Bushman				x	
Gabriele Neumann	x	x	x	x	x
Gavin Smith					
Ghazi Kayali			x	x	
Glen Abedi					
Grace Tietz					
Greg Deye					
Hana Golding	x	x	x	x	x
Harm van Bakel	x			x	x
Holly Hammond					x
Hui-Ling Yen					x
Ian Crozier		x	x	x	x
Ian Plumb	x				
Isabelle Phan					
Ishwar Chandramouliswaran					
Ivan			x	x	
Jacob Hou	x	x	x	x	

Jae Jung			x		
James Hoffman					
James Kobie	x		x	x	
Jared Evans		x	x	x	x
Jean Patterson					
Jenni		x			
Jennifer German				x	
Jennifer Gordon	x			x	
Jennifer Hyde					x
Jens Wrammert					
Jeremy Crawford					
Jesse Erasmus					
Ji Lee					
Jimmy Logue					
Jim Chappell					
jmankow1					
Joe Breen	x				
Jonathan Runstadler	x	x	x	x	x
Joseph Mankowski					
Judy Hewitt					
Juergen Richt	x	x	x	x	x
Kanta Subbarao					
Katharina Koelle				x	
Katy Shaw-Saliba					
Katherine Fenstermacher	x		x	x	
Kimberly Coca					
Kimberly Stemple				x	x
Korin Bullen	x				
Kristina Lu					
Kris Emo					
Kris Lambert					
Kristen Hildebrand	x	x	x	x	x
Laura Hughes					
Lauren Sauer	x			x	
Larry Anderson	x	x	x	x	x
Larry Wolfraim				x	
Leo Poon					
Liliana Brown		x			
Lisa Hensley				x	x
Lisa Lindesmith		x			
Lisa Miorin					
Liz	x	x	x		x
Lori Newman	x			x	x
Lucy Cong	x	x	x	x	x
Mackenzie Zendt	x	x	x		

Malik Peiris	x	x			
Marie Killerby					
Mark Challberg					
Mark Denison			x		
Mark Heism			x		
Mark Pallansch		x			
Mark Sangster	x	x	x	x	x
Mark Williams			x	x	
Marlene Espinoza	x	x	x	x	x
Marta Gaglia		x	x	x	
Martha Nelson					
Martin Linster	x	x	x		
Masato Hatta (UW)					
Matt Frieman	x	x	x		x
Maureen McGargill		x	x	x	x
Mehul Suttar			x	x	
Melissa Uccellini	x	x	x		
Mercy Prabhudas					
Michael Bryan					
Michael Chan					
Michael Martin				x	
Mike Cooper				x	
Mike Holbrook	x	x		x	
Mindy Davis					
Missy				x	x
Nat Moorman			x		
Natalie Thornburg			x	x	
newmanlm			x		
Nidia Trovao				x	
Pamela McKenzie	x	x			
Patrice Becker					
Paul McCray	x	x	x	x	x
Paul Jacob Bueno de Mesquita				x	
Paul Thomas					
Peter Daszak	x	x		x	
Peter Halfmann	x		x	x	x
Peter Myler					
Peter Palese			x	x	x
Phuong Nguyen-Contant	x			x	
Punam Mathur		x	x	x	x
Rachel Graham	x	x			
Ralph Baric			x		
Randall Tressler					
Raul Andino					
Rebecca Dutch		x	x	x	

Reed Johnson		x		x	x
Reed Shabman				x	x
Richard Rothman	x				
Richard Sciotti					
Richard Webby	x				x
Rick Bushman					
Robert Johnson					x
Ron Fouchier	x	x		x	
Rudra Goudavet					
Russell Ray	x	x	x	x	x
Ryan Langlois					
Sabra Klein			x	x	
Sander Herfst				x	
Sanjay Jain	x	x	x	x	x
Sanmi Adenaiye				x	x
Samantha Loeber					
Sara Cherry			x	x	
Sara Woodson		x		x	
Scott Hensley					
Scott Strome	x	x	x	x	x
Seema Lakdawala					
Sharon Saydah					
Sheldon Tai					x
Shiho Chiba	x	x	x	x	x
Simon Anthony	x	x	x	x	
Sook Ho			x		
Sonnie Kim				x	
Stacey Schultz-Cherry	x		x	x	
Stanley Perlman			x		x
Stephen Tompkins		x			
Steve Smiley					
Surender Khurana	x	x	x	x	x
Susan Gerber					
Susan Weiss			x		x
Teresa Hauguel				x	
Thames P			x		
Theresa Fitzgerald	x	x			
Timothy Sheahan			x	x	
Troy Sutton		x		x	
Tom Fabrizio					
Tori Baxter			x		
Vineet Menachery	x	x		x	x
Viviana Simon					
Walt Orenstein	x		x		
Weina Sun		x	x		x

Wesley C Van Voorhis	x			x	x
William Karesh					
William Florence					x
William Morgenlander					x
Willy Valdivia					
Wolfgang Leitner					
Xizhi Guo					
Yoshihiro Kawaoka	x	x	x	x	x

To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; emma.hodcroft@ispm.unibe.ch[emma.hodcroft@ispm.unibe.ch]; emmahodcroft@gmail.com[emmahodcroft@gmail.com]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves,

Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; sklein2[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; acox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 11/19/2020 10:42:58 AM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - November 24th
nCoV PI call attendee list.xlsx

Hi Everyone,

On November 17th, Dr. Russell Ray presented on "**Leveraging genetic tools for functional neural circuit mapping in the control of breathing for COVID-19 studies**". Thank you to our presenter and those that attended.

Dr. Emma Hodcroft will be giving a presentation titled "**A Brief Overview of the 'Cluster 5' 'Mink Mutation' from Denmark**" on Tuesday, November 24th.

Hope everyone can join!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	11-Nov	17-Nov
Erik Stemmy	x	x
Marciela DeGrace	x	x
Rebecca Lampley	x	x
Aditya Gaur		
Adolfo Garcia-Sastre	x	
Aisha Souquette		
Alan Embry		
Ali Ellebedy	x	x
Alicia Fry		
Alison Augustine		x
Alvaro Ordonez	x	x
Amanda Perofsky		
Amy Kuehn		x
Amy Krafft	x	x
Andrea Pruijssers		
Andrea Sant		
Andrew Mesecar	x	x
Andrew Pekosz	x	x
Andy Mesecar		
Andrzej Joachimiak	x	x
Aneesh Mehta		
Angela Rasmussen	x	x
Ann Eakin		
Anice Lowen		x
Anita McElroy		
Anne Piantadosi		
Aron Hall		
Atsuo Kuki	x	
Aubree Gordon		x
Barry Rockx		
Becky Dutch		
Ben Cowling		
Ben Larman		
Benjamin Miller		
Ben Tenoever	x	
Bernard Lafont	x	
Bin Zhou	x	
Biao He		
Brooke Bozick		
Carly Dillen	x	x
Carlie Williams		x
Catherine Luke		

Claire Midgley	x	x
Charles Russell		
Chelsea Lane		
Chris Brooke		
Christopher Hsu		
Chris Roberts	x	
Clint Florence		
Conrad Mallia		
Colleen Jonsson	x	x
Connie Schmaljohn	x	x
Courtney Comar (Susan Weiss lab)		
Daved Fremont	x	
David Martinez		
David Renner (Susan Weiss lab)		
David Topham		x
David Wentworth	x	
Deborah Lynn Fuller		
Diana Finzi		
Diane Post		
Diego Hijano		
Don Milton	x	
Donna Neu	x	x
Elizabeth Fitzpatrick		
Erica Raterman		
Evans		
Eunchung Park		
Eun Mi Lee		
Florian Krammer	x	
Francisco Chaves		x
Frederic Bushman		
Gabriele Neumann	x	x
Gavin Smith		
Ghazi Kayali		x
Glen Abedi		
Grace Tietz		
Greg Deye		
Hana Golding	x	x
Harm van Bakel	x	x
Holly Hammond	x	
Hui-Ling Yen	x	
Ian Crozier	x	x
Ian Plumb		
Isabelle Phan		
Ishwar Chandramouliswaran		
Ivan		

Jacob Hou		
Jae Jung		
James Hoffman		
James Kobie		x
Jared Evans	x	
Jean Patterson		
Jenni		
Jennifer German		
Jennifer Gordon		
Jennifer Hyde	x	
Jens Wrammert		
Jeremy Crawford		
Jesse Erasmus		
Ji Lee		
Jimmy Logue		
Jim Chappell		
jmankow1		
Joe Breen		
Jonathan Runstadler	x	
Joseph Mankowski		x
Judy Hewitt		
Juergen Richt	x	x
Kanta Subbarao		
Katharina Koelle		
Katy Shaw-Saliba		
Katherine Fenstermacher		x
Kimberly Coca		
Kimberly Stemple	x	x
Korin Bullen		
Kristina Lu		
Kris Emo		
Kris Lambert		
Kristen Hildebrand	x	x
Laura Hughes		
Lauren Sauer		
Larry Anderson	x	x
Larry Wolfraim		x
Leo Poon		
Liliana Brown		x
Lisa Hensley	x	
Lisa Lindesmith		
Lisa Miorin		
Liz	x	
Lori Newman	x	
Lucy Cong	x	x

Mackenzie Zendt		
Malik Peiris		x
Marie Killerby		
Mark Challberg		
Mark Denison		
Mark Heism		
Mark Pallansch		
Mark Sangster	x	x
Mark Williams		
Marlene Espinoza	x	x
Marta Gaglia		
Martha Nelson		
Martin Linster		
Masato Hatta (UW)		
Matt Frieman	x	
Maureen McGargill	x	x
Mehul Suttar		
Melissa Uccellini		x
Mercy Prabhudas		
Michael Bryan		
Michael Chan		
Michael Martin		
Mike Cooper		
Mike Holbrook		
Mindy Davis		
Missy	x	
Nat Moorman		
Natalie Thornburg		
newmanlm		
Nidia Trovao		
Pamela McKenzie		
Patrice Becker		
Paul McCray	x	x
Paul Jacob Bueno de Mesquita		
Paul Thomas		
Peter Daszak		x
Peter Halfmann	x	x
Peter Myler		
Peter Palese	x	
Phuong Nguyen-Contant		
Punam Mathur	x	
Rachel Graham		
Ralph Baric		
Randall Tressler		
Raul Andino		

Rebecca Dutch		
Reed Johnson	x	
Reed Shabman	x	x
Richard Rothman		
Richard Sciotti		
Richard Webby	x	
Rick Bushman		
Robert Johnson	x	
Ron Fouchier		x
Rudra Goudavet		
Russell Ray	x	x
Ryan Langlois		
Sabra Klein		x
Sander Herfst		
Sanjay Jain	x	
Sanmi Adenaiye	x	
Samantha Loeber		
Sara Cherry		
Sara Woodson		
Scott Hensley		
Scott Strome	x	x
Seema Lakdawala		
Sharon Saydah		
Sheldon Tai	x	x
Shiho Chiba	x	x
Simon Anthony		
Sook Ho		
Sonnie Kim		
Stacey Schultz-Cherry		
Stacy Ferguson		x
Stanley Perlman	x	x
Stephen Tompkins		
Steve Smiley		
Surender Khurana	x	x
Susan Gerber		
Susan Weiss	x	
Teresa Hauguel		
Thames P		x
Theresa Fitzgerald		
Timothy Sheahan		x
Troy Sutton		
Tom Fabrizio		
Tori Baxter		
Vineet Menachery	x	
Viviana Simon		

Walt Orenstein		x
Weina Sun	x	
Wesley C Van Voorhis	x	
William Karesh		
William Florence	x	x
William Morgenlander	x	
Willy Valdivia		
Wolfgang Leitner		
Xizhi Guo		
Yoshihiro Kawaoka	x	

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Location: https://zoom.us/j/99540451771?pwd= **552.136**

Importance: Normal

Subject: SIG U19 December call

Start Time: Thur 12/3/2020 12:30:00 PM (UTC-06:00)

End Time: Thur 12/3/2020 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

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Importance: Normal

Subject: SIG U19 December call

Start Time: Thur 12/3/2020 12:30:00 PM (UTC-06:00)

End Time: Thur 12/3/2020 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Hi All,

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Toni

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Meeting ID: 995 4045 1771
Passcode: **552.136**

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Aneesh Mehta; Baric, Toni C; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; jmankows; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/FIC) [E]; Jennifer Hyde; Marshall Strome; RDBViral

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 5/19/2020 8:00:00 AM (UTC-05:00)

End Time: Tue 5/19/2020 9:00:00 AM (UTC-05:00)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel,

Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; jmankows; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/FIC) [E]; Jennifer Hyde; Marshall Strome; RDBViral

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 8/4/2020 1:00:00 PM (UTC)

End Time: Tue 8/4/2020 2:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein

Optional Attendees: Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance: Normal

Start Time: Tue 10/6/2020 1:00:00 PM (UTC)

End Time: Tue 10/6/2020 2:00:00 PM (UTC)

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Importance:	Normal
Start Time:	Tue 1/12/2021 2:00:00 PM (UTC)
End Time:	Tue 1/12/2021 3:00:00 PM (UTC)
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From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

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Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Biggins, Julia E CTR (USA); miguela.caniza@stjude.org; Fulkerson, Patricia (NIH/NIAID) [E]; Olson, Dan; asmonto@umich.edu; edwin.asturias@childrenscolorado.org; Ranallo, Ryan (NIH/NIAID) [E]; Kim, Sonnie (NIH/NIAID) [E]; rmedinas@med.puc.cl; csutcli1@jhu.edu; annette.fox@unimelb.edu.au; wkilembe@rzhrg-mail.org; Mark Mulligan; Sheena.Sullivan@influenzacentre.org; martin.blaser@cabm.rutgers.edu; bondoc@cabm.rutgers.edu; Garcia-Sastre, Adolfo; Thompson, Mark (CDC/DDID/NCIRD/ID); Dawood, Fatimah S. (CDC/DDID/NCIRD/ID); Randolph, Adrienne; dxc44@case.edu; Cassetti, Cristina (NIH/NIAID) [E]; Robien, Mark (NIH/NIAID) [E]; Gergen, Peter (NIH/NIAID) [E]; Mejias, Asuncion; Siriruk Changrob; Halasa, Natasha; rvandoorn@oucru.org; jbloom@fredhutch.org; francesco.berlanda-scorza@gatesfoundation.org; Taia T. Wang; lixiaoming@mailbox.sc.edu; asiegle@emory.edu; pssulli@emory.edu; rdmoore@jhmi.edu; LI, XIAOMING; Timothy Burgess; edward.mitre@usuhs.edu; dtribble@idcrp.org; Lee, Marina (NIH/NIAID) [E]; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rolfes, Melissa (CDC/DDID/NCIRD/ID); Adam Kucharski (adam.kucharski@lshtm.ac.uk); ahujas@uthscsa.edu; Sangster, Mark; Madhura Rane; Marc Choisy; Christian Grov; Jacques.banchereau@jax.org; mary.staat@cchmc.org; singsing.way@cchmc.org; ZHANG, JIAJIA; Monica McNeal

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Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi Everyone,

We will be incorporating COVID-19 Cohort presentations to our arsenal of talks. As a reminder, the goal for the weekly SARS-CoV-2 Investigators meeting is to provide a platform that is informative and encourages collaboration.

If you would like to present your research, please let me know. *

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: R.A.M. Fouchier; Read, Sarah (NIH/NIAID) [E]; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Miller, Benjamin; Matthew Frieman; Sabra Klein; Aubree Gordon; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Newman, Lori (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Qifang Bi; Olson, Daniel; Biggins, Julia E CTR (USA); Hou, Yixuan Jacob; Graham, Rachel; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT); Sarah Cobey; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; miguela.caniza@stjude.org; Fulkerson, Patricia (NIH/NIAID) [E]; Olson, Dan; asmonto@umich.edu; edwin.asturias@childrenscolorado.org; Ranallo, Ryan (NIH/NIAID) [E]; Kim, Sonnie (NIH/NIAID) [E]; rmedinas@med.puc.cl; csutcli1@jhu.edu; annette.fox@unimelb.edu.au; wkilembe@rzhrg-mail.org; Mark Mulligan; Sheena.Sullivan@influenzacentre.org; martin.blaser@cabm.rutgers.edu; bondoc@cabm.rutgers.edu; Garcia-Sastre, Adolfo; Thompson, Mark (CDC/DDID/NCIRD/ID); Dawood, Fatimah S. (CDC/DDID/NCIRD/ID); Randolph, Adrienne; dxc44@case.edu; Cassetti, Cristina (NIH/NIAID) [E]; Robien, Mark (NIH/NIAID) [E]; Gergen, Peter (NIH/NIAID) [E]; Mejias, Asuncion; Siriruk Changrob; Halasa, Natasha; rvandoorn@oucru.org; jbloom@fredhutch.org; francesco.berlanda-scorza@gatesfoundation.org; Taia T. Wang; lixiaoming@mailbox.sc.edu; asiegle@emory.edu; pssulli@emory.edu; rdmoore@jhmi.edu; LI, XIAOMING; Timothy Burgess; edward.mitre@usuhs.edu; dtribble@idcrp.org; Lee, Marina (NIH/NIAID) [E]; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rolfes, Melissa (CDC/DDID/NCIRD/ID); Adam Kucharski (adam.kucharski@lshtm.ac.uk); ahujas@uthscsa.edu; Sangster, Mark; Madhura Rane; Marc Choisy; Christian Grov; Jacques.banchereau@jax.org; mary.staat@cchmc.org; singsing.way@cchmc.org; ZHANG, JIAJIA; Monica McNeal; jheath@systemsbiology.org; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Ferguson, Stacy (NIH/NIAID) [E]; ODSET Pro; Lockmuller, Jane (NIH/NIAID) [E]; Marcum, Chris (NIH/NHGRI) [E]

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Subject: SARS-CoV-2 Weekly Investigators Meeting

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager

Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Location: https://zoom.us/j/94857161546?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly call-replacement link

Start Time: Thur 1/14/2021 12:30:00 PM (UTC-06:00)

End Time: Thur 1/14/2021 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Toni C; tcbaric@med.unc.edu; Baric, Ralph S; Berhorst, Jackie; vimenach@utmb.edu; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; heisem@med.unc.edu; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); 5f56638d66b14da0bc216c2f3e33b8d8-Sarah Rebec; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Hi All,

For some reason, people are having trouble accessing the call with the existing link. I am sending a new link for today's call only.

Toni

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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric

Location: https://zoom.us/j/99380423092?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 2/25/2021 12:30:00 PM (UTC-06:00)

End Time: Thur 2/25/2021 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric

This invitation replaces any previous invitation.

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From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: Second Webinar for Systems Immunology Program

Start Time: Tue 3/23/2021 2:00:00 PM (UTC-06:00)

End Time: Tue 3/23/2021 3:00:00 PM (UTC-06:00)

Required Attendees: Liu, Joy (NIH/NIAID) [E]; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Hi All,
This year's Systems Immunology meeting will be split in 3 separate 1 hour sessions. I will be forwarding 3 invitations. Our group presents on March 23.
Best regards,
Toni

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 9:56 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Diercks, Alan; Bruce Beutler; Leitner, Wolfgang (NIH/NIAID) [E]
Subject: Second Webinar for Systems Immunology Program
When: Tuesday, March 23, 2021 4:00 PM-5:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

According to your availability, our second webinar will be held from 4:00 to 5:00 PM EDT on March 23th. **Ralph Baric's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

Join ZoomGov Meeting
https://nih.zoomgov.com/j/1602362422?pwd **552.136**

Meeting ID: 160 236 2422
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Join by H.323
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161.199.136.10 (US East)
Meeting ID: 160 236 2422
Passcode: 552.136

.....

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 4/6/2020 9:37:30 AM (UTC-05:00)
Subject: SIG U19 call cancelled for this month

Hi Everyone,
We are going to cancel the SIG U19 monthly call this month. Stay safe and healthy!

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]

Location: GoToWebinar

Importance: Normal

Subject: Canceled: nCoV weekly investigators meeting

Start Time: Tue 1/28/2020 8:00:00 AM (UTC-06:00)

End Time: Tue 1/28/2020 9:00:00 AM (UTC-06:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott

Optional Attendees: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join/888107805

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code: **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

Importance: Normal
Start Time: Tue 2/11/2020 2:00:00 PM (UTC)
End Time: Tue 2/11/2020 3:00:00 PM (UTC)
Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: aneesh.mehta@emory.edu; R.A.M. Fouchier; Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]
Cc: Bozick, Brooke (NIH/OD) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com
Subject: nCoV weekly investigators meeting
When: Tuesday, February 11, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code: **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

To: Rbaric@email.unc.edu[Rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Josip Strčić[jstrcic@unicath.hr]
Sent: Sat 5/9/2020 2:31:53 AM (UTC-05:00)
Subject: Question, data sharing in manuscript shared on a preprint server
Details about study protocol.pdf

Dear Prof/Dr. Ralph S. Baric and Vineet D. Menachery,

We hope this message finds you well. We are contacting you regarding the article posted on the preprint server, titled: Mucin 4 Protects Female Mice from Coronavirus Pathogenesis.

We are conducting a study about data sharing in manuscripts about COVID-19 shared on medRxiv and bioRxiv, and we would be very grateful if you could answer one question. Your response to this email will be considered as informed consent to participate. More details about the study protocol, principal investigator and approval of the ethics committee are provided in the attachment.

We could not find in your manuscript any statement regarding availability of raw data. Considering the importance of data sharing in a public health crisis such as COVID-19 pandemic, could you please let us know whether you have considered sharing publicly raw data generated within your study?

Thank you for considering participation in our study.

Sincerely,

Josip Strcic

A study about data sharing in manuscripts about COVID-19 published on preprint servers

This study is conducted by principal investigator Prof. Livia Puljak, MD, PhD, affiliated with the Center for Evidence-Based Medicine and Healthcare, at the Catholic University of Croatia.

The aim of the study is to explore raw data sharing in manuscripts about COVID-19 posted on preprint servers medRxiv and bioRxiv. Within the study, we have analyzed whether manuscripts about COVID-19 posted on preprint servers medRxiv and bioRxiv mention public raw data (or code) sharing. Subsequently, we are contacting corresponding authors of those manuscripts to clarify location of shared data (if authors wrote that data are publicly available, but we are unable to locate data), circumstances for sharing data if the authors indicated that data will be made available on request, and whether the authors have considered publicly sharing raw data if they did not mention anything about that in their manuscript.

The study protocol was approved by the Ethics Committee of the Catholic University of Croatia (approval number: XYXY). Participants in the study are corresponding authors of manuscripts about COVID-19 posted on preprint servers medRxiv and bioRxiv. There will be no harms and no incentives for participation in this study. Invited participants are free to refuse participation in the study. Response to our questions will be considered as informed consent for participation in our study.

All responses will be anonymized and coded, and only one investigator (who is contacting the corresponding authors) will be aware of the identity of individuals responding to the question. All other team members will receive anonymized responses.

We kindly ask participants to consent to the collection, storing and processing of data they provide. The participants are kindly informed that: (i) that they have right to demand that their data is subsequently deleted, except for the data already analyzed or published; (ii) that the data will be used for research purposes only; (iii) that they have right to ask which data were collected and ask for revisions; (iv) that all information will be analyzed in anonymous or pseudonymous mode; (v) that the principal investigator is in charge of the project management; (vi) that their data will be permanently deleted ten years after completion of the project, and (vii) that principal investigator may share fully anonymized individual participant data for research purposes, in line with the FAIR data principles (findable, accessible, interoperable and re-usable) of the EU research framework (https://bit.ly/1Y0OMaI).

Contact of the principal investigator is:

Prof. Livia Puljak, MD, PhD

livia.puljak@unicath.hr

Please contact the principal investigator if you have any questions about the study, or if you need any additional clarifications.

Thank you for considering participation in our study

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 5/19/2020 8:00:00 AM (UTC-05:00)

End Time: Tue 5/19/2020 9:00:00 AM (UTC-05:00)

Required Attendees: Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved

Hi Everyone,

Below you will find the updated meeting link for our weekly investigators call regarding COVID-19.

Our tentative agendas will be:

- COVID-19 research presentation given by PI
- Animal Model updates
- Assay discussion
- Other Needs/Issues
- Call for presenters

ZoomGov Meeting:
https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Meeting ID: 160 971 1373
Password: **552.136**

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
833 568 8864 US Toll-free
+61 2 9158 3402 Australia
+55 11 4118 6875 Brazil
+56 44 208 1249 Chile
+81 3 4571 1977 Japan
+31 20 794 7340 Netherlands
+64 9 925 0388 New Zealand
+65 3163 2929 Singapore
+44 203 514 1879 United Kingdom
+44 203 481 1686 United Kingdom
Find your local number: https://www.zoomgov.com/u/abZFb1stu0

If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Jacob Kocher[jake.kocher22@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Fri 1/3/2020 11:04:46 AM (UTC-06:00)
Subject: Re:

Hey Ralph and Jake,

Happy new year. Congrats on the baby, Jake.

Do you have a response to review for JVI or the original reviewer comments? I will look to see if I have them.

I'll take a look over the weekend/early next week and get comments back. Just glancing at the figures, still think they need some work for clarity.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, January 2, 2020 12:15 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Jacob Kocher <jake.kocher22@gmail.com>
Subject:

Hi Jacob and Vineet, Here is the version of Anne's B cell paper with her final comments. Jake, can you take a look to make sure the new data you generated is appropriately presented. Vineet, I appreciate your comments. I'd also like your thoughts on where to submit this. Its been a year plus since it was reviewed at JV-should we go back or chase a sure thing. Jake, congrats on the new baby! Hope you both had a Happy Holiday and New Year. Ralph

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Renee Ireton; Graham PhD, Jessica B

Location: https://zoom.us/j/91792514323?pwd= **552.136**

Importance: Normal

Subject: SIG U19 recurring monthly call

Start Time: Thur 6/11/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 6/11/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Renee Ireton; Graham PhD, Jessica B

SIG U19 monthly calling information

Join Zoom Meeting
https://zoom.us/j/91792514323?pwd= **552.136**

Meeting ID: 917 9251 4323
Password: **552.136**
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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Schughart, Klaus; Graham, Rachel; Pardo Manuel de Villena, Fernando; Shaw, Ginger; Fischer, William A. II; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Graham, Jessica ; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Noll, Kelsey; Schaefer, Alexandra; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

Location: https://zoom.us/j/91792514323?pwd= **552.136**

Importance: Normal

Subject: SIG U19 recurring monthly call

Start Time: Thur 6/11/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 6/11/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Schughart, Klaus; Graham, Rachel; Pardo Manuel de Villena, Fernando; Shaw, Ginger; Fischer, William A. II; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Graham, Jessica ; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Noll, Kelsey; Schaefer, Alexandra; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

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Importance: Normal

Subject: SIG U19 recurring monthly call

Start Time: Thur 7/2/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 7/2/2020 1:45:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; McWeeney, Shannon ; mgale@u.washington.edu; Miller, Darla; Mooney, Michael ; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

SIG U19 monthly calling information- Change of date for the July call.

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Optional Attendees: Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

Good morning everyone,

Sending out a reminder for Thursday's call. Have a happy 4th!

Toni

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To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 7/30/2020 9:49:15 AM (UTC-05:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - August 4, 2020
nCoV PI call attendee list.xlsx

Hi Everyone,

Thank you to all who called in to listen to the presentation given by Dr. Wrammert on July 28th. I've attached the attendance list for everyone's review. I have provided an update at the end of this email regarding the question if contractors are able to apply to the PPE FOA – the answer is YES! Keep reading for details.

Next Tuesday, August 4th, we will have two presenters:

Dr. Katia Koelle
"Defining the causes of heterogeneity in antibody responses against SAR-CoV-2"

-and-

Dr. Weina Sun

"Newcastle disease viruses (NDV) expressing the spike protein of SARS-CoV-2 as vaccine candidates"

Update regarding the PPE FOA: https://grants.nih.gov/grants/guide/pa-files/PAR-20-256.html . Contractors are allowed to apply. Contractors could source the PPE they need for COVID-19 work under contracts and direct charge the contract. Alternatively, if you need or would like to use this FOA to attempt to secure PPE, do not double charge the government for the PPE that is received. There will be additional reporting responsibilities for those receiving PPE under this FOA.

Have a great rest of the week!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		

David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x

Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
mprabhudas						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sander Herfst		x	x	x	x	x

Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
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x					x			
			x	x	x	x	x	x
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To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; 'Marta Gaglia'[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 7/30/2020 10:21:29 AM (UTC-05:00)

Subject: RE: SARS-CoV-2 Weekly Investigators Meeting - August 4, 2020

CORRECTION

Hi Everyone,

Thank you to all who called in to listen to the presentation given by Dr. Wrammert on July 28th. I've attached the attendance list for everyone's review. I have provided an update at the end of this email regarding the question if contractors are able to apply to the PPE FOA – the answer is YES! Keep reading for details.

Next Tuesday, August 4th, we will have two presenters:

Dr. Sabra Klein
"Defining the causes of heterogeneity in antibody responses against SAR-CoV-2"

-and-

Dr. Weina Sun

"Newcastle disease viruses (NDV) expressing the spike protein of SARS-CoV-2 as vaccine candidates"

Update regarding the PPE FOA: https://grants.nih.gov/grants/guide/pa-files/PAR-20-256.html . Contractors are allowed to apply. Contractors could source the PPE they need for COVID-19 work under contracts and direct charge the contract. Alternatively, if you need or would like to use this FOA to attempt to secure PPE, do not double charge the government for the PPE that is received. There will be additional reporting responsibilities for those receiving PPE under this FOA.

Have a great rest of the week!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/91792514323?pwd=WUxQYnBPelZ6U3dXSUd6ZWUxVEN4UT09
Importance:	Normal
Subject:	Canceled: SIG U19 recurring monthly call Cancelled for August
Start Time:	Thur 8/13/2020 12:30:00 PM (UTC-05:00)
End Time:	Thur 8/13/2020 1:30:00 PM (UTC-05:00)
Required Attendees:	Schughart, Klaus; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Optional Attendees:	Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

SIG U19 monthly calling is cancelled for the month of August. See you in September.

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From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 8/18/2020 8:00:00 AM (UTC-05:00)

End Time: Tue 8/18/2020 9:00:00 AM (UTC-05:00)

Required Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID); Kirking, Hannah L. (CDC/DDPHSIS/CGH/DGHT); Plumb, Ian (CDC/DDID/NCEZID/DFWED)

nCoV PI call attendee list.xlsx

Hi All,

I'm canceling the SARS-CoV-2 Weekly Investigators Meeting for August 18th only. We will resume on August 25th with Dr. Mehul Suthar as our presenter.

Thank you Dr. Cherry for your presentation today! I have attached the attendee list for everyone's review.

See you all in two weeks!
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

liability for any statements made that are sender's own and not expressly made on behalf of the NIAID by one of its representatives.

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							

David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						

Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						

Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
William Florence						
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
x	x	x	x	x	x	x	x	x
x	x	x	x					
x	x	x	x	x	x	x	x	x
					x			
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From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd=

552.136

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 8/4/2020 8:00:00 AM (UTC-05:00)

End Time: Tue 8/4/2020 9:00:00 AM (UTC-05:00)

Required Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala;

amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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+64 9 801 0144 New Zealand
+65 3163 2929 Singapore
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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: antoinette_baric@med.unc.edu[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Virtual Zoom meeting

Importance: Normal

Subject: FW: Systems Immunology U19 Program Annual Meeting on Oct 9th, 2020

Start Time: Fri 10/9/2020 9:30:00 AM (UTC-05:00)

End Time: Fri 10/9/2020 4:30:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Systems Immun_2020_Agenda_draft3.pdf

Sorry all. Just got a revision to the original invitation expanding the time.

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Thursday, September 3, 2020 9:53 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Richard Ulevitch; Baric, Ralph S; Heise, Mark T; Jonathan Kagan; Bruce Beutler; Garry Nolan; Diercks, Alan; Aderem, Alan; Michael J Gale; Jennifer Lund; John Doench; Vijay Kuchroo; Liu, Joy (NIH/NIAID) [E]
Cc: Gralinski, Lisa E; mtferris; Baric, Toni C; Suthar, Mehul; Schughart, Klaus; Pardo Manuel de Villena, Fernando; Garry Nolan (gnolan@stanford.edu)
Subject: Systems Immunology U19 Program Annual Meeting on Oct 9th, 2020
When: Friday, October 9, 2020 10:30 AM-5:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Virtual Zoom meeting

Dear All,

Thank you all for your help. Please see the updated agenda for our annual meeting. **Please note that the meeting will start 8:00 AM PST.** If you have any questions, please let me know ASAP. The Zoom link and the registration site will be sent out later. I look forward to meeting you in the virtual conference.

Best regards,
Joy Liu

Systems Immunology U19 Annual Meeting

Division of Allergy, Immunology and Transplantation
National Institutes of Allergy and Infectious Diseases
Friday, October 9th, 2020
Virtual Meeting via Zoom
All Times EDT

Agenda

10:30 – 11:00 AM	Check-in & A/V testing
11:00 – 11:10 AM	**Welcome/Introductory Remarks** **Joy Liu/Daniel Rotrosen,** NIAID
11:10 – 12:40 PM	**Systems Approach to Immunity and Inflammation**
11:10 – 11:40 AM	*Germline Mutagenesis with Automated Meiotic Mapping to Study Immunity in Mice* **Bruce Beutler**, UT Southwestern Medical Center
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12:05 – 12:35 PM	*The Hierarchical Structures of Immune Neighborhoods* **Garry Nolan**, Stanford University
12:35 – 12:40 PM	*Inflammasomes and Inflammation in Health and Disease* **Richard Ulevitch,** The Scripps Research Institute
12:40 – 1:00 PM	**Break**
1:00 – 2:30 PM	**Systems Immunogenetics of Biodefense and Emerging Pathogens in the Collaborative Cross**
1:00 – 1:40 PM	*Introduction + Project 1: SIG U19 and the Collaborative Cross, Emerging Coronaviruses and SARS-CoV2* **Ralph Baric**, University of North Carolina at Chapel Hill
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4:20 – 4:25 PM	**Adjourn General Meeting**
4:20 – 5:20 PM	**Systems Immunology Steering Committee Meeting** **(closed session, Steering Committee members and NIAID staff only)**
5:20 PM	**End of Meeting**

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Attendees: Ralph Baric; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Virtual Zoom meeting

Importance: Normal

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I am forwarding the information just in case any of you were left off the email. Please not that this meeting changed from a 2 day meeting to a 1 day meeting.

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Best regards,
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Division of Allergy, Immunology and Transplantation
National Institutes of Allergy and Infectious Diseases
Wednesday, October 9th, 2020
Virtual Meeting via Zoom
All Times EDT

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From: antoinette_baric@med.unc.edu[antoinette_baric@med.unc.edu]

Attendees: Ralph Baric; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Virtual Zoom meeting

Importance: Normal

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Cc: Gralinski, Lisa E; mtferris; Baric, Toni C; Suthar, Mehul; Schughart, Klaus; Pardo Manuel de Villena, Fernando; Garry Nolan (gnolan@stanford.edu)
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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Schughart, Klaus; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

Location: https://zoom.us/j/91792514323?pwd= **552.136**

Importance: Normal

Subject: SIG U19 recurring monthly call

Start Time: Thur 9/10/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 9/10/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Schughart, Klaus; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy

Reminder that we will have our monthly SIG U19 call. The topic of discussion is the upcoming October meeting.

SIG U19 monthly calling information

Join Zoom Meeting
https://zoom.us/j/91792514323?pwd= **552.136**

Meeting ID: 917 9251 4323
Password: **552.136**
One tap mobile
+19292056099,,91792514323#,,1#, **552.136** US (New York)
+13017158592,,91792514323#,,1#, US (Germantown)

Dial by your location
+1 929 205 6099 US (New York)
+1 301 715 8592 US (Germantown)
+1 312 626 6799 US (Chicago)
+1 669 900 6833 US (San Jose)
+1 253 215 8782 US (Tacoma)
+1 346 248 7799 US (Houston)
Meeting ID: 917 9251 4323
Password: **552.136**
Find your local number: https://zoom.us/u/a5ntKItyA

Join by SIP
91792514323@zoomcrc.com

Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
Meeting ID: 917 9251 4323

Password: **552.136**

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 9/10/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 9/10/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Resending the invitation.

Join Zoom Meeting
https://zoom.us/j/95848751377?pwd= **552.136**

Meeting ID: 958 4875 1377
Passcode: **552.136**
One tap mobile
+19292056099,,95848751377#,,,,,,0#,, **552.136** # US (New York)
+13017158592,,95848751377#,,,,,,0#,, **552.136** # US (Germantown)

Dial by your location
+1 929 205 6099 US (New York)
+1 301 715 8592 US (Germantown)
+1 312 626 6799 US (Chicago)
+1 669 900 6833 US (San Jose)
+1 253 215 8782 US (Tacoma)
+1 346 248 7799 US (Houston)
888 475 4499 US Toll-free
833 548 0276 US Toll-free
833 548 0282 US Toll-free
877 853 5257 US Toll-free
Meeting ID: 958 4875 1377
Passcode: **552.136**
Find your local number: https://zoom.us/u/asQIWxs9V

Join by SIP
95848751377@zoomcrc.com

Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
Meeting ID: 958 4875 1377

Passcode: **552.136**

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Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Virtual Zoom meeting

Importance: Normal

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Toni

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Dear All,

The Systems Immunology U19 Program Annual Meeting is approaching. There are a few things I want to remind you:

1. To ensure a seamless and smooth meeting, **please send your slides to me by COB, Oct 7.**
2. To save everyone's time, we will not have a Zoom rehearsal before the meeting. Please **log on the meeting an half hour early before the meeting to work with the NIAID MEET staff to make sure your slides are correctly uploaded.** The Zoom link will be open at least 45 minutes before the meeting.
3. **Please note that the meeting will start 8:00 AM PST.**
4. **We will use chat box for Q&As.**
5. **If you don't present, please mute yourself.**
6. **The information for the Zoom is:**

Join ZoomGov Meeting

https://www.zoomgov.com/j/1600539251
Meeting ID: 160 053 9251

One tap mobile

+16692545252,,1600539251# US (San Jose)

+16468287666,,1600539251# US (New York)

Dial by your location

+1 669 254 5252 US (San Jose)

+1 646 828 7666 US (New York)

833. 8 8864 US Toll-free

Meeting ID: 160 053 9251

Find your local number: https://www.zoomgov.com/u/abKgOC1LtB

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Best regards,
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1:00 – 1:40 PM	*Introduction + Project 1: SIG U19 and the Collaborative Cross, Emerging Coronaviruses and SARS-CoV2* **Ralph Baric**, University of North Carolina at Chapel Hill
1:40 – 2:05 PM	*Project 2: Influenza Virus* **Mark Heise**, University of North Carolina at Chapel Hill
2:05 – 2:30 PM	*Project 3: West Nile Virus* **Michael Gale**, University of Washington
2:30 – 2:45 PM	**Break**
2:45 – 4:15 PM	**Defining Regulators of Immunity to Acute Infection Using CRISPR Screens**

2:45 – 2:55 PM	*Program Overview and Updates* **Arlene Sharpe**, Harvard University Medical School
2:55 – 3:05 PM	*Core C: CRISPR Library + Technology Development* **John Doench,** The Board Institute
3:05 – 3:15 PM	*Core B: Bioinformatics and Data Management* **Orr Ashenberg,** The Board Institute
3:15 – 3:30 PM	*Core D + Project 1: CRISPR Screens to Discover Regulators of CD8 T cells* **Martin LaFleur**, Harvard University Medical School
3:30 – 3:45 PM	*Project 1: CRISPR Screens to Discover Regulators of CD4 T cells* **Vijay Kuchroo**, Brigham and Women's Hospital
3:45 – 4:00 PM	*Project 2: CRISPR Screens to Discover Regulators of DC* **Jonathan Kagan,** Children's Hospital Corporation
4:00 – 4:15 PM	*Project 2: CRISPR Screens to Discover Regulators of DC/T Cell Interactions* **Nir Hacohen,** The Board Institute
4:15 – 4:20 PM	**Closing Remarks** **Joy Liu,** NIAID
4:20 – 4:25 PM	**Adjourn General Meeting**
4:20 – 5:20 PM	**Systems Immunology Steering Committee Meeting** **(closed session, Steering Committee members and NIAID staff only)**
5:20 PM	**End of Meeting**

To: Orenstein, Walter[worenst@emory.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph

Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Biao He[bhe@uga.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; Biao He[bhe@uga.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 9/16/2020 3:05:50 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - September 22nd

Hi All,

Thank you all for attending the Dr. Heath's presentation on Tuesday, September 15th and to Jim for presenting.

On Tuesday, September 22nd, Dr. Biao He will be giving a presentation titled: "**A single dose intranasal immunization with parainfluenza virus 5-based COVID-19 vaccine generates sterilizing immunity in nasal cavities of ferrets and cats**".

Hope you all can attend!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: R.A.M. Fouchier; Read, Sarah (NIH/NIAID) [E]; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Aneesh Mehta; Baric, Toni C; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; jmankows; Hildebrand, Kristen; Newman, Lori (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/FIC) [E]; Jennifer Hyde; Marshall Strome; RDBViral; jheath@systemsbiology.org; Krafft, Amy (NIH/NIAID) [E]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 1/12/2021 9:00:00 AM (UTC-05:00)

End Time: Tue 1/12/2021 10:00:00 AM (UTC-05:00)

Required Attendees: R.A.M. Fouchier; Read, Sarah (NIH/NIAID) [E]; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Stacey Schultz-Cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Aneesh Mehta; Baric, Toni C; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly

(NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; jmankows; Hildebrand, Kristen; Newman, Lori (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/FIC) [E]; Jennifer Hyde; Marshall Strome; RDBViral

Rebecca Lampley is inviting you to a scheduled ZoomGov meeting.

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: antoinette_baric@med.unc.edu[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Virtual Zoom meeting

Importance: Normal

Subject: FW: Systems Immunology U19 Program Annual Meeting on Oct 9th, 2020

Start Time: Fri 10/9/2020 9:00:00 AM (UTC-05:00)

End Time: Fri 10/9/2020 4:00:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Systems Immun_2020_Agenda_draft3.pdf

Systems Immunology U19 steering committee meeting.pdf

Hi All,
The meeting officially starts at 8am PT/11 am ET. The link will be open to upload your slides. See below for more specific details.
Toni

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Thursday, September 3, 2020 9:53 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Richard Ulevitch; Baric, Ralph S; Heise, Mark T; Jonathan Kagan; Bruce Beutler; Garry Nolan; Diercks, Alan; Aderem, Alan; Michael J Gale; Jennifer Lund; John Doench; Vijay Kuchroo; Leitner, Wolfgang (NIH/NIAID) [E]
Cc: Gralinski, Lisa E; mtferris; Baric, Toni C; Suthar, Mehul; Schughart, Klaus; Pardo Manuel de Villena, Fernando; Garry Nolan (gnolan@stanford.edu); Shannon McWeeney; Steven Chamberlin
Subject: Systems Immunology U19 Program Annual Meeting on Oct 9th, 2020
When: Friday, October 9, 2020 10:00 AM-5:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Virtual Zoom meeting

Dear All,

Attached please see the final agendas for Systems Immunology U19 Program Annual Meeting and the following Steering Committee Meeting. Please keep in mind for the followings:

1. To ensure a seamless and smooth meeting, **please send your slides to me by COB, Oct 7.**
2. Please **log on the meeting early to work with the NIAID MEET staff to make sure your slides are correctly uploaded.** The Zoom link will be open 1 hour early before the meeting.
3. **Please note that the meeting will start at 11AM EST that is 8:00 AM PST.**
4. Please **introduce next speaker** in your session after your presentation.
5. **We will use chat box for Q&As. So please check chat box periodically to answer any questions.**
6. **Please don't use "Raise Hand" function, as we will not monitor it.**
7. According to the definition of FOA, **Steering Committee members include Arlene Sharpe, Orr Ashenberg, Ralph Baric, Mark Heise, Shannon McWeeney, Richard Ulevitch, Alan Aderem, Garry Nolan. After the general meeting, NIAID staff will introduce you to a break room for Steering Committee Meeting.**
8. **The information for the Zoom is:.**

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Find your local number: https://www.zoomgov.com/u/abKgOC1LtB

Please feel free to let me know if you have any questions.

I look forward to meeting you virtually on Friday.

Best regards,
Joy Liu

Systems Immunology U19 Annual Meeting

Division of Allergy, Immunology and Transplantation
National Institutes of Allergy and Infectious Diseases
Friday, October 9th, 2020
Virtual Meeting via Zoom
All Times EDT

Agenda

10:00 – 11:00 AM	Check-in & A/V testing
11:00 – 11:10 AM	**Welcome / Introductory Remarks** **Joy Liu / Daniel Rotrosen,** NIAID
11:10 – 12:40 PM	**Systems Approach to Immunity and Inflammation**
11:10 – 11:40 AM	*Germline Mutagenesis with Automated Meiotic Mapping to Study Immunity in Mice* **Bruce Beutler**, UT Southwestern Medical Center
11:40 – 12:05 PM	*Systems Analysis of Innate Immune Responses to Infection* **Alan Diercks**, Seattle Children's Research Institute
12:05 – 12:35 PM	*The Hierarchical Structures of Immune Neighborhoods* **Garry Nolan**, Stanford University
12:35 – 12:40 PM	*From the bench to the bedside: CD14* **Richard Ulevitch,** The Scripps Research Institute
12:40 – 1:00 PM	**Break**
1:00 – 2:30 PM	**Systems Immunogenetics of Biodefense and Emerging Pathogens in the Collaborative Cross**
1:00 – 1:40 PM	*Introduction + Project 1: SIG U19 and the Collaborative Cross, Emerging Coronaviruses and SARS-CoV2* **Ralph Baric**, University of North Carolina at Chapel Hill
1:40 – 2:05 PM	*Project 2: Influenza Virus* **Mark Heise**, University of North Carolina at Chapel Hill
2:05 – 2:30 PM	*Project 3: West Nile Virus* **Michael Gale**, University of Washington
2:30 – 2:45 PM	**Break**
2:45 – 4:15 PM	**Defining Regulators of Immunity to Acute Infection Using CRISPR Screens**

2:45 – 2:55 PM	*Program Overview and Updates* **Arlene Sharpe**, Harvard University Medical School
2:55 – 3:05 PM	*Core C: CRISPR Library + Technology Development* **John Doench,** The Broad Institute
3:05 – 3:15 PM	*Core B: Bioinformatics and Data Management* **Orr Ashenberg,** The Broad Institute
3:15 – 3:30 PM	*Core D + Project 1: CRISPR Screens to Discover Regulators of CD8 T cells* **Martin LaFleur**, Harvard University Medical School
3:30 – 3:45 PM	*Project 1: CRISPR Screens to Discover Regulators of CD4 T cells* **Vijay Kuchroo**, Brigham and Women's Hospital
3:45 – 4:00 PM	*Project 2: CRISPR Screens to Discover Regulators of DC* **Jonathan Kagan,** Children's Hospital Corporation
4:00 – 4:15 PM	*Project 2: CRISPR Screens to Discover Regulators of DC/T Cell Interactions* **Nir Hacohen,** The Broad Institute
4:15 – 4:20 PM	**Closing Remarks** **Joy Liu,** NIAID
4:20 – 4:25 PM	**Adjourn General Meeting**
4:20 – 5:20 PM	**Systems Immunology Steering Committee Meeting** **(closed session, Steering Committee members and NIAID staff only)**
5:20 PM	**End of Meeting**

Systems Immunology U19 Annual Meeting

Steering Committee Meeting

Division of Allergy, Immunology and Transplantation
National Institutes of Allergy and Infectious Diseases
Friday, October 9th, 2020
Virtual Meeting via Zoom
All Times EDT

Agenda

4:20 – 4:25 PM Welcome/Introduction---Joy Liu / Richard Ulevitch

4:25 – 4:35 PM Follow up of action items from last meeting
- Collaboration between three U19 groups---Mark Heise
- Webinars--- Richard Ulevitch and Alene Sharpe
- Update of data deposition into ImmPort---Patrick Dun

4:35 – 4:50 PM Updates on COVID-19 research
- The Scripps U19 group --- Richard Ulevitch & Garry Nolan
- The UNC U19 group --- Ralph Baric & Mark Heise
- The Harvard U19 group --- Arlene Sharpe

4:50 – 4:55 PM Review issues and solutions

4:55 – 5:05 PM Plan for next steps
- Set up webinars
- Promote data deposition into ImmPort
- Set up a COVID-19 interest group
- Use Microsoft Teams to share data
- Other ideas

5:05 – 5:15 PM Feedbacks from NIAID leaders ---Daniel Rotrosen, Chuck Hackett, Alison Deckhut, Wolfgang Leitner

5:15 – 5:20 PM Wrap up---Joy Liu

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: Canceled: SIG U19 Monthly Meeting

Start Time: Thur 10/8/2020 12:30:00 PM (UTC-05:00)

End Time: Thur 10/8/2020 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton

Due to the annual Systems meeting, the October call will be cancelled.

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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis; Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 12/3/2020 12:30:00 PM (UTC-06:00)

End Time: Thur 12/3/2020 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Rescheduling December's SIG U19 call.

Thank you

Toni

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To: Lund, Jennifer[jlund@fredhutch.org]; Baric, Ralph S[rbaric@email.unc.edu]
Cc: Gralinski, Lisa E[lgralins@email.unc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 4/11/2019 11:45:38 AM (UTC-05:00)
Subject: RE: Paper idea - immune predictors of mortality following infection

---

From: Menachery, Vineet
Sent: Tuesday, April 02, 2019 1:21 PM
To: Lund, Jennifer; Baric, Ralph S
Cc: Gralinski, Lisa E; Leist, Sarah Rebecca; Schaefer, Alexandra
Subject: RE: Paper idea - immune predictors of mortality following infection

I'll take a look. Might not be until next week that I can get it back to you.
VDM

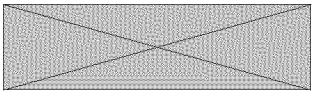
From: Lund, Jennifer [jlund@fredhutch.org]
Sent: Tuesday, April 02, 2019 12:58 PM
To: Baric, Ralph S
Cc: Menachery, Vineet; Gralinski, Lisa E; Leist, Sarah Rebecca; Schaefer, Alexandra
Subject: Re: Paper idea - immune predictors of mortality following infection

Thanks, Ralph. I agree with you that there are likely more papers possible here, but for now. We've done a similar analysis already for just WNV (published last year in JID), but would be happy to work with the other groups using the different pathogens one-by-one.

Lisa, Alex, Vineet, and Sarah, can you read through the manuscript and add any comments/edits that you may have?

Thanks,
Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org



Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Tuesday, April 2, 2019 at 6:21 AM
To: "Lund, Jennifer" <jlund@fredhutch.org>
Subject: RE: Paper idea - immune predictors of mortality following infection

Nice paper, my comments. ralph

From: Lund, Jennifer <jlund@fredhutch.org>

Sent: Wednesday, March 27, 2019 12:03 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; mtferris <mtferris@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Michael J Gale <mgale@uw.edu>; Miller, Darla <darla_miller@med.unc.edu>
Cc: Graham, Jessica B <jgraham@fredhutch.org>
Subject: Re: Paper idea - immune predictors of mortality following infection

Hi all,

Just a reminder to kindly look over this manuscript draft and add authors from your groups. It would be great if I could submit this in the next week or so.

Thanks,
Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Lund, Jennifer" <jlund@fredhutch.org>
Date: Tuesday, March 12, 2019 at 9:39 AM
To: "Baric, Ralph S" <rbaric@email.unc.edu>, "Heise, Mark T" <mark_heisem@med.unc.edu>, mtferris <mtferris@email.unc.edu>, "Pardo Manuel de Villena, Fernando" <fernando_pardo-manuel@med.unc.edu>, "McWeeney, Shannon" <mcweeney@ohsu.edu>, Michael J Gale <mgale@uw.edu>, Michael Mooney <mooneymi@ohsu.edu>, "Miller, Darla" <darla_miller@med.unc.edu>
Cc: "Graham, Jessica B" <jgraham@fredhutch.org>
Subject: Re: Paper idea - immune predictors of mortality following infection

Hi all,

Attached please find a draft of the manuscript we wrote up entitled “Universal predictors of mortality following virus infection”. I’m thinking of submitting it to the Journal of Clinical Investigation as a Concise Communication.

I’d be grateful for any feedback you may have, as well as a list of authors & affiliations from each of your groups to include. If you could get back to me by the end of the month at the latest, then I can get this submitted without delay. If you don’t want to be included as an author, please do let me know that too.

Thanks!
Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Saturday, March 2, 2019 at 7:16 AM
To: "Heise, Mark T" <mark_heisem@med.unc.edu>, "Lund, Jennifer" <jlund@fredhutch.org>, mtferris <mtferris@email.unc.edu>, "Pardo Manuel de Villena, Fernando" <fernando_pardo-manuel@med.unc.edu>, "McWeeney, Shannon" <mcweeney@ohsu.edu>
Cc: "Graham, Jessica B" <jgraham@fredhutch.org>
Subject: RE: Paper idea - immune predictors of mortality following infection

Hi Jenny, Project 1 is also on board. I'll discuss with group to work out a list of people who were involved. Great idea and original thinking!
ralph

From: Heise, Mark T <mark_heisem@med.unc.edu>
Sent: Friday, March 1, 2019 3:59 PM
To: Lund, Jennifer <jlund@fredhutch.org>; Baric, Ralph S <rbaric@email.unc.edu>; mtferris <mtferris@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>
Cc: Graham, Jessica B <jgraham@fredhutch.org>
Subject: RE: Paper idea - immune predictors of mortality following infection

Hi Jenny,
That is super interesting and I think that a joint paper is a great idea. So, Project 2 is on board. I will consult with Marty, and we will figure out a list of the people form Project 2 who should be included.
It would be great if you could present this at the next call.
Thanks and have a good weekend.
Mark

From: Lund, Jennifer <jlund@fredhutch.org>
Sent: Friday, March 1, 2019 3:04 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; mtferris <mtferris@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>
Cc: Graham, Jessica B <jgraham@fredhutch.org>
Subject: Paper idea - immune predictors of mortality following infection

Hi all,

Jess and I have been working on a project to correlate baseline splenic T cell frequencies and phenotypes with mortality following each of the infections used in the U19 screen. The punch line is that we can use this data to identify global baseline immune correlates or immune predictors of mortality to virus infection.

In short, we got the cleaned mortality data from Michael Mooney from each of the projects and selected lines that either: 1. Had no mortality following any of the 3 infections compared to lines that had mortality to all 3 of the infections, or 2. Had no mortality to either of the respiratory viruses compared to lines that had mortality to both of the respiratory viruses (Tables 1 and 2 in the attached document). We then graphed our flow cytometry data from spleens of uninfected mice from each of these lines to correlate T cell frequency and phenotype with protection from mortality (pages 4-6 of the attachment).

Attached are some of our findings, but overall, we've found that having more Tregs and more activated T cells prior to infection correlates with protection from lethality. I was thinking that we could write this up for a journal such as The Journal of Clinical Investigation. It's rare to have prospectively collected samples in human cohorts of infection, and so I think the CC is a really useful tool for this, provided you've done a big screen like we have.

Since this uses data from all of you, would you be willing in principle for us to go ahead with writing this up? If so, could you let me know who else should be an author from each of your groups? We'll try to present this briefly on the next call too.

I hope everyone has a nice weekend.

Jenny

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 5/23/2019 12:47:20 PM (UTC-05:00)
Subject: RE: Uganda Draft

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Thursday, May 23, 2019 11:03 AM
To: Menachery, Vineet
Subject: RE: Uganda Draft

I placed my comments onto Kenny's draft. Have sent stuff to barney for guidance. ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, May 21, 2019 4:58 PM
To: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: Uganda Draft

I think asking Barney for guidance is best idea. I am fine adding whoever is appropriate from VIC.

May need to consider same for Simon and Lipkin, not sure if their collaborators in Africa shoudl be included or not. Small price to pay if it facilitates future collaborations.

I assume Corti sent the antibody so include him.

I'll plan on working on the draft when I get it back and will try and get a cover letter to you by tomorrow. Plaese and Saif for Editorial board members?

From: Dinnon, Kenneth Harold III [kdinnon@email.unc.edu]
Sent: Tuesday, May 21, 2019 3:19 PM
To: Menachery, Vineet; Baric, Ralph S
Subject: Re: Uganda Draft

I am reworking the model figure today. I will send it back out to both of you and some additional comments on the draft late tonight.

Kenny

From: "Menachery, Vineet" <vimenach@UTMB.EDU>
Date: Tuesday, May 21, 2019 at 4:08 PM
To: "Baric, Ralph S" <rbaric@email.unc.edu>
Cc: "Dinnon, Kenneth Harold III" <kdinnon@email.unc.edu>
Subject: RE: Uganda Draft

Agreed on authors seeing it. Do you want David Corti or just reference the papers and have him in acknowledgment, what about Barney graham?

Kenny still working on figures; would like to send to authors by end of week, submit next week if possible.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Tuesday, May 21, 2019 3:00 PM
To: Menachery, Vineet
Subject: RE: Uganda Draft

Other authors need to take a look I think as well before you submit.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, May 16, 2019 4:38 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Uganda Draft

Here is the latest version of the draft.

Kenny, please edit the figure legends as needed. I didn't know the time points and did them fairlly quick.

Ralph, I added David Corti and left lanzevechia on, let me know if I should take them off.

I ran it through the PNAS generator, it is over the 6 page limit, but we can submit to PNAS plus which is online only. I am fine with that.

I will send Kenny notes on the figures to change in a separate document. If we want paper down to 6 page limit, likely need to cut model slide.

I'll work on a cover letter, but i have dept. retreat Monday. Our BSL3 is shut down next week too, so I'd like to get this paper submitted next week if possible.

VDM

To: Randell, Scott H.[scott_randell@med.unc.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; Dinnon, Kenneth Harold III[kdinnon@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 9/23/2019 10:29:03 AM (UTC-05:00)
Subject: Re: MERS-Uganda Draft

From: Randell, Scott H. <scott_randell@med.unc.edu>
Sent: Thursday, May 30, 2019 10:04 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Re: MERS-Uganda Draft

Vineet, I took a good read focusing on points related to HAE cultures and it all looks fine to me. Thanks for including me and good luck with PNAS. Best, Scott

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, May 28, 2019 7:35:24 PM
To: Randell, Scott H.
Cc: Baric, Ralph S; Dinnon, Kenneth Harold III
Subject: MERS-Uganda Draft

Hey Scott,
Please find attached the following manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection." The manuscript describes our efforts to recover a virus expressing the bat spike protein from PDF2180-CoV. You contributed to this work with provision of HAE cultures and we have included you as an author.

We are planning to submit the manuscript to PNAS in the next few weeks. Please take a look over it, paying close attention to the accuracy of your name and affiliation. Also, please add any authors that might be missing and their email contact information.

We would like to have the comments this week by Friday to try and send out next week. With the busy time of year, we understand if you require more time to look over it; please just let us know that you need more time.

If I do not hear from you by Friday, I will assume you are satisfied with the manuscript in its current state.

Thank you again for your contributions to this work. We look forward to hearing from you.

Vineet D. Menachery

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 9/10/2019 2:43:00 PM (UTC-05:00)
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Tuesday, September 10, 2019 2:27 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

mBIO sounds safer to me than Cell Reports—Emily had a great experience there without all the problems you mentioned. ralph

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, September 10, 2019 12:09 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I chatted with a few people about Cell Reports, and they said it has same issues as Nat. Com. with self importance and taking a long time to decide and then asking for more and more stuff.

Think Mbio might be best bet at this point. I called this morning, but didn't get through. I can chat this afternoon if you want. Otherwise, I'll start prepping for Mbio.

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, September 9, 2019 10:52 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I'm fine if you don't want it on a preprint. As long as it gets accepted by teh Feb Review cycle.

I guess I'd lean Cell Reports at this point. I haven't had any experience there, so not sure how it goes. I would like the variety in my CV. That being said, I also don't want them to sit on it for >60 days like Nat. Com did.

I'll work on the cover letter today and get it submitted this week at Cell Reports; happy to talk about it if you think Mbio is the better spot for it.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, September 6, 2019 7:04 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

Cell reports or mbio—I'm getting to the point where it is time to move on to other things, so maybe mbio is best. Reviewer number 1 is a real ass wipe. I would like to find out who they are so that I can start reviewing their papers-sounds like one of the damn dutch. I would prefer to stay out of a preprint server at this point. However, if you feel its important for your grant

submissions or in your best interest..... make the call. Be glad to chat if you want to talk about journal choices. Overall, I think Nature Communication is a shit whole of a journal. Tim's paper had also got beat to shit there by an ass reviewer with strong opinions on little issues. While I wish he would just go straight to cell reports (I think he feels the same way), we are going to send the resubmission back as he did a lot of the requested work for the second time (different set of requests both times). Personnally, I think his reviewer is just looking to kill a paper. Ralph

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, September 6, 2019 6:52 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: Decision on manuscript NCOMMS-19-23910-T

These reviews are petty and dumb.

At this point I think we should put on a preprint server.

Cell reports, plos path or mbio?

_____

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: sonja.schmid@us.nature.com <sonja.schmid@us.nature.com>
Sent: Friday, September 6, 2019 4:23:33 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Decision on manuscript NCOMMS-19-23910-T

Dear Dr Menachery,

Your manuscript entitled "Trypsin treatment unlocks barrier for zoonotic coronavirus infection" has now been seen by 2 referees, whose comments are appended below. In the light of their advice I regret to inform you that we cannot publish your manuscript in Nature Communications.

You will see that, while the reviewers find your work of some potential interest, they raise substantive concerns that cast doubt on the advance your findings represent over earlier work and the strength of the novel conclusions that can be drawn at this stage. In particular, reviewers are not convinced that the manuscript provides a sufficient conceptual advance without additional experiments providing insights into the mechanism underlying the observations. Unfortunately, these reservations are sufficiently important to preclude publication of this study in Nature Communications.

If you opted into the journal hosting details of a preprint version of your manuscript via a link on our dedicated website (https://nature-research-under-consideration.nature.com), please note that we will now remove these details as your manuscript is no longer under consideration at Nature Communications. For more information, please refer to our FAQ page at https://nature-research-under-consideration.nature.com/posts/19641-frequently-asked-questions

I am sorry that we cannot be more positive on this occasion and thank you for the opportunity to consider your work.

Best regards,
Sonja Schmid, PhD
Senior Editor
Nature Communications

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

The manuscript by Menachery et al. deals with the role of trypsin-dependent protease activation on coronavirus (CoV) infections in cell cultures.
The authors used a previously generated chimeric MERS-CoV carrying the Spike gene of a MERS-CoV conspecific bat-related Coronavirus (PDF2180-CoV from Uganda) and performed cell culture experiments with and without trypsin treatment.
The finding that trypsin treatment influences cell susceptibility and probably organ tropism of MERS-related CoV is interesting, however, not overly innovative and surprising.

I have several remarks.

1. It is an intriguing but not very surprising finding that protease activation by trypsin influences CoV cell entry. Coronaviruses enter cells by receptor-mediated endocytosis using different exopeptidases (e.g. DPP4, ACE2) or by protease-mediated (HAT, TMPRSS2) direct fusion of virus particle membranes with the cellular plasma membrane. The present study shows that trypsin-treatment facilitates virus replication of bat-derived CoV but does not present a single experiment on the mechanistic details. Neither do the authors analyze the effect and mechanistic consequences of trypsin on the Spike proteins nor do they identify the proposed alternative receptor.

2. Throughout the manuscript important controls are missing.
a) The authors should confirm correct transcript sequence and expression of DPP4 in both trypsin-adapted Vero and Huh7 cell lines. These are important controls, as aberrant expression of DPP4 in immortalized cell lines may affect the conclusions.
b) The authors should show for all applied CoV that the activated protease has a direct effect on the virus (and not on a putatively new host cell receptor): the authors could e.g. “prime” virus stocks with trypsin, neutralize trypsin after incubation, then infect cells with the primed stock. Figure 5B is not sufficient and shows only HKU5-CoV infection in Vero cells co-treated with trypsin.
c) Using HAE cells the authors claim that chimeric “MERS-Uganda” does not infect the respiratory tracts of humans. How often was this experiment repeated? Were different donors tested? Again, I would expect different set-ups like virus pre-treated with trypsin, cells pre-treated with trypsin and co-treatment. The timing and the concentration of the trypsin-treatment is essential. What about other differentiated permanent cells lines like Calu-3?
d) The authors should sequence the HKU5-CoV and MERS-Uganda genomes (or at least the spike gene) after infection on trypsin-treated cells to confirm that both viruses are stable and to evaluate whether DPP4 host-adaptation (as in Letko et al., 2018) remains a contributing factor in the increased infectivity they observed.
e) The authors used an already existing MERS clone with a full-length Spike of the con-specific PDF2180-CoV. It would be important to show that the proposed recombination event led to the putative change of tropism. Different variants e.g. a MERS-CoV spike with only the S1 domain of PDF2180-CoV ,with and without the sialic acid binding domain (S1A) would be important controls.
f) What about sialic acid binding in general? Since it was shown that MERS-CoV attachment is facilitated by sialic binding I would expect that the authors show the sialic binding capacity of PDF2180-CoV to investigate how the trypsin treatment influences the attachment.
g) Another important control would be to check the susceptibility/permissiveness of bat cells (lung vs intestine) to support the hypothesis of a switch in organ tropism from bats to humans.
h) To rule out that other viral co-factors influence the entry process (and the use of DPP4) it would be beneficial to use a full-length PDF2180-CoV infectious virus.
i) Generally it would be important to titrate supernatants in order to see the influence on infectious particle production.

3. The quality of the Figures is insufficient. The immunofluorescence pictures in all of the Figures are not suitable for publication. The cells look apoptotic and there is no counterstaining to see how many cells are on the pictures. Without counterstaining the reader cannot evaluate the negative controls. There are no scale bars. I am aware that trypsin-treatment may cause these artifacts but the authors should then try to reduce trypsin concentrations or work with pretreatment of

cells and /or virus stocks instead of continuous trypsin-treatment.

4. The Western blot in Fig. 3B and the fluorescence microscopy in Fig. 3A do not correspond. The WB shows a much stronger N protein band for trypsin-negative MERS-CoV infection, whereas in Fig. 3A the RFP assay the signals appear much brighter for trypsin-positive MERS-CoV infection.

5. General remark: Instead of just saying higher and lower, please indicate x-fold or percentage when discussing differences.

Reviewer #2 (Remarks to the Author):

This submission demonstrates that two potentially zoonotic coronaviruses, MERS-Uganda and MERS-like HKU5, will infect otherwise resistant cells if trypsin protease is supplied. The conclusions, therefore, are that trypsin protease "unlocks a barrier for zoonotic coronavirus infection". These results are of interest to the field because they highlight proteases as central host susceptibility factors in zoonotic coronavirus infection. As such, they move the field beyond a focus on receptors as the most relevant host susceptibility factors. Both virus receptors and proteases must now be simultaneously considered in evaluating susceptibility to zoonotic infections. Additionally, the findings in the paper are clear and convincing, and the results support the conclusions that are put forward. Finally, the paper is very well-written.

Comments for the authors:

1. Although the report has solid findings and credible interpretations of data, in some instances it does not make particularly novel insights. It is fairly well-known that some coronaviruses can be activated for cell entry by trypsin. Furthermore, the detailed architecture of the MERS spike : human DPP4 interaction is known, and it is understood that the MERS-Uganda and the MERS-like HKU5 spike proteins do not have complete hDPP4 receptor-binding motifs in their S1 domains. This latter point predicts the results shown in Fig 3, so much so that the results do not come across as especially novel. It is recommended that the authors further emphasize the novel features in this report.

2. The report could be strengthened, with potentially novel results, by further exploring the trypsin cleavage patterns of the Uganda and HKU5 spike proteins. The results shown in Fig 5B are a good start, but more could be presented. Many additional questions could be considered. What is the cleavage status of spike proteins on MERS-Uganda and HKU5 virus particles, before and after trypsin treatment? Does trypsin prime "free" virus particles for subsequent cell entry? Or does trypsin inactivate free virus particles? Put another way, do viruses have to first be attached to cells for trypsin to activate infection? Typically, there are two cleavages in the beta-coronavirus spikes that are relevant to cell entry, a priming S1/S2 cleavage and an activating S2prime cleavage. How do these substrate sites differ between MERS spikes, PDF2180/Uganda spikes and HKU5 spikes? Which of these substrate sites are cleaved by trypsin? If trypsin only cleaves at S1/S2, then what are
the proteases cleaving at S2prime? Are there Uganda spike-cleaving proteases that are present in Caco-2 cells but absent from primary HAE? To potentially elevate the novelty of the report, some or all of these questions should be addressed.

To: Logue, James[James.Logue@som.umaryland.edu]; Orenstein, Walter[worenst@emory.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 11/9/2020 3:32:33 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - November 10th
nCoV PI call attendee list.xlsx

Hi All,

On November 3rd, Dr. Bin Zhou gave a wonderful presentation titled "**SARS-CoV-2 spike D614G variant confers enhanced replication and transmissibility**". Thank you Dr. Zhou and those that were in attendance.

Tomorrow, November 10th, we will have a double feature brought to you by:

Dr. Andrzej Joachimiak
"**Structural studies of SARS-CoV-2 proteins and their complexes**"

Dr. Daved Fremont
"**Structural mechanisms of SARS-CoV-2 antibody neutralization"**

Looking forward to seeing everyone tomorrow!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	13-Oct	20-Oct	27-Oct	3-Nov
Erik Stemmy	x	x	x	x
Marciela DeGrace	x	x	x	
Rebecca Lampley	x	x	x	x
Aditya Gaur				
Adolfo Garcia-Sastre	x	x	x	x
Aisha Souquette				
Alan Embry				x
Ali Ellebedy			x	x
Alicia Fry				x
Alison Augustine		x	x	
Alvaro Ordonez	x	x		x
Amanda Perofsky				
Amy Krafft	x	x		x
Andrea Pruijssers			x	
Andrea Sant	x	x		x
Andrew Mesecar	x	x	x	x
Andrew Pekosz		x	x	x
Andy Mesecar				
Andrzej Joachimiak			x	
Aneesh Mehta				
Angela Rasmussen	x	x	x	x
Ann Eakin				
Anice Lowen	x	x	x	
Anita McElroy	x		x	x
Anne Piantadosi		x		
Aron Hall	x			
Atsuo Kuki		x	x	
Aubree Gordon				x
Barry Rockx				
Becky Dutch				
Ben Cowling				
Ben Larman				
Benjamin Miller			x	
Ben Tenoever	x	x	x	
Bin Zhou		x	x	x
Biao He				
Brooke Bozick	x	x		x
Carly Dillen	x	x	x	x
Carlie Williams		x		x
Catherine Luke			x	x
Claire Midgley				x
Charles Russell			x	x

Chelsea Lane		x		x
Chris Brooke				
Christopher Hsu				
Chris Roberts				
Clint Florence				x
Conrad Mallia				
Colleen Jonsson	x	x		x
Connie Schmaljohn			x	x
Courtney Comar (Susan Weiss lab)				
Daved Fremont				
David Martinez			x	x
David Renner (Susan Weiss lab)				
David Topham				
David Wentworth			x	x
Deborah Lynn Fuller				
Diana Finzi		x		
Diane Post	x		x	x
Diego Hijano				
Don Milton		x	x	x
Donna Neu	x	x	x	x
Elizabeth Fitzpatrick				
Erica Raterman				
Evans	x			
Eunchung Park	x	x	x	
Eun Mi Lee				
Florian Krammer	x	x	x	x
Francisco Chaves		x	x	
Frederic Bushman				x
Gabriele Neumann	x	x	x	x
Gavin Smith				
Ghazi Kayali			x	x
Glen Abedi				
Grace Tietz				
Greg Deye				
Hana Golding	x	x	x	x
Harm van Bakel	x			x
Holly Hammond				
Hui-Ling Yen				
Ian Crozier		x	x	x
Ian Plumb	x			
Isabelle Phan				
Ishwar Chandramouliswaran				
Ivan			x	x
Jacob Hou	x	x	x	x
Jae Jung			x	

James Hoffman				
James Kobie	x		x	x
Jared Evans		x	x	x
Jean Patterson				
Jenni		x		
Jennifer German				x
Jennifer Gordon	x			x
Jens Wrammert				
Jeremy Crawford				
Jesse Erasmus				
Ji Lee				
Jimmy Logue				
Jim Chappell				
jmankow1				
Joe Breen	x			
Jonathan Runstadler	x	x	x	x
Joseph Mankowski				
Judy Hewitt				
Juergen Richt	x	x	x	x
Kanta Subbarao				
Katharina Koelle				x
Katy Shaw-Saliba				
Katherine Fenstermacher	x		x	x
Kimberly Coca				
Kimberly Stemple				x
Korin Bullen	x			
Kristina Lu				
Kris Emo				
Kris Lambert				
Kristen Hildebrand	x	x	x	x
Laura Hughes				
Lauren Sauer	x			x
Larry Anderson	x	x	x	x
Larry Wolfraim				x
Leo Poon				
Liliana Brown		x		
Lisa Hensley				x
Lisa Lindesmith		x		
Lisa Miorin				
Liz	x	x	x	
Lori Newman	x			x
Lucy Cong	x	x	x	x
Mackenzie Zendt	x	x	x	
Malik Peiris	x	x		
Marie Killerby				

Mark Challberg				
Mark Denison			x	
Mark Heism			x	
Mark Pallansch		x		
Mark Sangster	x	x	x	x
Mark Williams			x	x
Marlene Espinoza	x	x	x	x
Marta Gaglia		x	x	x
Martha Nelson				
Martin Linster	x	x	x	
Masato Hatta (UW)				
Matt Frieman	x	x	x	
Maureen McGargill		x	x	x
Mehul Suttar			x	x
Melissa Uccellini	x	x	x	
Mercy Prabhudas				
Michael Bryan				
Michael Chan				
Michael Martin				x
Mike Cooper				x
Mike Holbrook	x	x		x
Mindy Davis				
Missy				x
Nat Moorman			x	
Natalie Thornburg			x	x
newmanlm			x	
Nidia Trovao				x
Pamela McKenzie	x	x		
Patrice Becker				
Paul McCray	x	x	x	x
Paul Jacob Bueno de Mesquita				x
Paul Thomas				
Peter Daszak	x	x		x
Peter Halfmann	x		x	x
Peter Myler				
Peter Palese			x	x
Phuong Nguyen-Contant	x			x
Punam Mathur		x	x	x
Rachel Graham	x	x		
Ralph Baric			x	
Randall Tressler				
Raul Andino				
Rebecca Dutch		x	x	x
Reed Johnson		x		x
Reed Shabman				x

Richard Rothman	x			
Richard Sciotti				
Richard Webby	x			
Rick Bushman				
Robert Johnson				
Ron Fouchier	x	x		x
Rudra Goudavet				
Russell Ray	x	x	x	x
Ryan Langlois				
Sabra Klein			x	x
Sander Herfst				x
Sanjay Jain	x	x	x	x
Sanmi Adenaiye				x
Samantha Loeber				
Sara Cherry			x	x
Sara Woodson		x		x
Scott Hensley				
Scott Strome	x	x	x	x
Seema Lakdawala				
Sharon Saydah				
Shiho Chiba	x	x	x	x
Simon Anthony	x	x	x	x
Sook Ho			x	
Sonnie Kim				x
Stacey Schultz-Cherry	x		x	x
Stanley Perlman			x	
Stephen Tompkins		x		
Steve Smiley				
Surender Khurana	x	x	x	x
Susan Gerber				
Susan Weiss			x	
Teresa Hauguel				x
Thames P			x	
Theresa Fitzgerald	x	x		
Timothy Sheahan			x	x
Troy Sutton		x		x
Tom Fabrizio				
Tori Baxter			x	
Vineet Menachery	x	x		x
Viviana Simon				
Walt Orenstein	x		x	
Weina Sun		x	x	
Wesley C Van Voorhis	x			x
William Karesh				
William Florence				

Willy Valdivia				
Wolfgang Leitner				
Xizhi Guo				
Yoshihiro Kawaoka	x	x	x	x

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Michael Davis[madphd@uw.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 11/11/2020 7:02:09 AM (UTC-06:00)
Subject: SIG U19 Call reminder

Hi everyone,
As a reminder, due to scheduling conflicts we have move/combined the SIG U19 Nov/Dec call to Dec 3 at 1:30 pm EST/10:30 PST. All calling information remains the same.

Have a great, safe and healthy Thanksgiving.
Toni
https://zoom.us/j/95848751377?pwd= **552.136**
Meeting ID: 958 4875 1377
Passcode: **552.136**
One tap mobile
+19292056099,,95848751377#,,,,,,0#,, **552.136** # US (New York)
+13017158592,,95848751377#,,,,,,0#,, # US (Germantown)
Dial by your location
+1 929 205 6099 US (New York)
+1 301 715 8592 US (Germantown)
+1 312 626 6799 US (Chicago)
+1 669 900 6833 US (San Jose)
+1 253 215 8782 US (Tacoma)
+1 346 248 7799 US (Houston)
888 475 4499 US Toll-free
833 548 0276 US Toll-free
833 548 0282 US Toll-free
877 853 5257 US Toll-free
Meeting ID: 958 4875 1377
Passcode: **552.136**
Find your local number: https://zoom.us/u/asQIWxs9V
Join by SIP
95848751377@zoomcrc.com
Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
Meeting ID: 958 4875 1377
Passcode: **552.136**

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Qifang Bi[qbi@uchicago.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; acox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; cobeywork@gmail.com[cobeywork@gmail.com]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Tue 11/24/2020 2:34:29 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - December 1
nCoV PI call attendee list.xlsx

Hi Everyone,

Thank you for joining today's presentation, "**A Brief Overview of the 'Cluster 5' 'Mink Mutation' from Denmark**" given by Dr. Emma Hodcroft.

The links below were provided by Dr. Hodcroft:

Here's a link which will go to all of the dedicated builds:
https://nextstrain.org/groups/neherlab

Here's the individual ones that was referenced in the talk:
nextstrain.org/groups/neherlab/ncov/S.Y453F
nextstrain.org/groups/neherlab/ncov/S.N439K
nextstrain.org/groups/neherlab/ncov/denmark
nextstrain.org/groups/neherlab/ncov/S.N501/2020-11-10

On Tuesday, December 1st, Dr. Karla Satchell will be giving a presentation on "**Structural Biology of the nsp16/nsp10 2'-O-methyltransferase: Impact for Structure based Drug Design**."

Hope everyone has a great rest of the week.
For those in the US, have a wonderful Thanksgiving!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384

Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	11-Nov	17-Nov	24-Nov
Erik Stemmy	x	x	x
Marciela DeGrace	x	x	x
Rebecca Lampley	x	x	x
Aditya Gaur			
Adolfo Garcia-Sastre	x		x
Aisha Souquette			
Alan Embry			x
Ali Ellebedy	x	x	
Alicia Fry			x
Alison Augustine		x	x
Alvaro Ordonez	x	x	x
Amanda Perofsky			
Amy Kuehn		x	x
Amy Krafft	x	x	x
Andrea Pruijssers			
Andrea Sant			
Andrew Mesecar	x	x	x
Andrew Pekosz	x	x	x
Andy Mesecar			
Andrzej Joachimiak	x	x	
Aneesh Mehta			
Angela Rasmussen	x	x	
Ann Eakin			
Anice Lowen		x	x
Anita McElroy			
Anne Piantadosi			
Aron Hall			
Atsuo Kuki	x		
Aubree Gordon		x	x
Barry Rockx			
Becky Dutch			
Ben Cowling			
Ben Larman			
Benjamin Miller			x
Ben Tenoever	x		
Bernard Lafont	x		
Bin Zhou	x		x
Biao He			
Brooke Bozick			
Carly Dillen	x	x	x
Carlie Williams		x	x
Catherine Luke			

Claire Midgley	x	x	x
Charles Russell			
Chelsea Lane			
Chris Brooke			
Christopher Hsu			
Chris Roberts	x		
Clint Florence			
Conrad Mallia			
Colleen Jonsson	x	x	x
Connie Schmaljohn	x	x	x
Courtney Comar (Susan Weiss lab)			
Daved Fremont	x		
David Martinez			x
David Renner (Susan Weiss lab)			
David Topham		x	x
David Wentworth	x		x
Deborah Lynn Fuller			
Diana Finzi			
Diane Post			x
Diego Hijano			
Don Milton	x		x
Donna Neu	x	x	
Elizabeth Fitzpatrick			
Emma Hodcroft			x
Erica Raterman			
Evans			
Eunchung Park			
Eun Mi Lee			
Florian Krammer	x		x
Francisco Chaves		x	
Frederic Bushman			
Gabriele Neumann	x	x	x
Gavin Smith			x
Ghazi Kayali		x	
Glen Abedi			
Grace Tietz			
Greg Deye			
Hana Golding	x	x	x
Harm van Bakel	x	x	x
Holly Hammond	x		
Hui-Ling Yen	x		x
Ian Crozier	x	x	
Ian Plumb			
Isabelle Phan			
Ishwar Chandramouliswaran			

Ivan			
Jacob Hou			
Jae Jung			
James Hoffman			
James Kobie		x	x
Jared Evans	x		x
Jason Goldstein			x
Jean Patterson			
Jenni			
Jennifer German			
Jennifer Gordon			
Jennifer Hyde	x		
Jens Wrammert			
Jeremy Crawford			
Jesse Erasmus			
Ji Lee			
Jimmy Logue			
Jim Chappell			
jmankow1			
Joe Breen			x
Jonathan Runstadler	x		x
Joseph Mankowski		x	x
Judy Hewitt			
Juergen Richt	x	x	x
Kanta Subbarao			
Katharina Koelle			x
Katy Shaw-Saliba			
Katherine Fenstermacher		x	
Kimberly Coca			
Kimberly Stemple	x	x	
Korin Bullen			
Kristina Lu			
Kris Emo			
Kris Lambert			
Kristen Hildebrand	x	x	
Laura Hughes			
Lauren Sauer			
Larry Anderson	x	x	x
Larry Wolfraim		x	
Leo Poon			
Liliana Brown		x	x
Lisa Hensley	x		x
Lisa Lindesmith			
Lisa Miorin			
Liz	x		

Lori Newman	x		x
Lucy Cong	x	x	
Mackenzie Zendt			x
Malik Peiris		x	x
Marie Killerby			
Mark Challberg			
Mark Denison			
Mark Heism			
Mark Pallansch			
Mark Sangster	x	x	x
Mark Williams			x
Marlene Espinoza	x	x	x
Marta Gaglia			
Martha Nelson			
Martin Linster			x
Masato Hatta (UW)			
Matt Frieman	x		x
Maureen McGargill	x	x	
Mehul Suttar			
Melissa Uccellini		x	x
Mercy Prabhudas			
Michael Bryan			
Michael Chan			
Michael Martin			
Mike Cooper			
Mike Holbrook			
Mindy Davis			
Missy	x		
Nat Moorman			
Natalie Thornburg			
newmanlm			
Nidia Trovao			
Pamela McKenzie			
Patrice Becker			
Paul McCray	x	x	x
Paul Jacob Bueno de Mesquita			
Paul Thomas			
Peter Daszak		x	
Peter Halfmann	x	x	x
Peter Myler			
Peter Palese	x		x
Phuong Nguyen-Contant			
Punam Mathur	x		x
Rachel Graham			
Ralph Baric			

Randall Tressler			
Raul Andino			
Rebecca Dutch			
Reed Johnson	x		x
Reed Shabman	x	x	x
Richard Rothman			
Richard Sciotti			
Richard Webby	x		
Rick Bushman			
Robert Johnson	x		
Ron Fouchier		x	x
Rudra Goudavet			
Russell Ray	x	x	x
Ryan Langlois			
Sabra Klein		x	
Sander Herfst			
Sanjay Jain	x		
Sanmi Adenaiye	x		x
Samantha Loeber			
Sara Cherry			x
Sara Woodson			x
Scott Hensley			
Scott Strome	x	x	x
Seema Lakdawala			
Sharon Saydah			
Sheldon Tai	x	x	x
Shiho Chiba	x	x	x
Simon Anthony			x
Sook Ho			
Sonnie Kim			
Stacey Schultz-Cherry			x
Stacy Ferguson		x	x
Stanley Perlman	x	x	x
Stephen Tompkins			x
Steve Smiley			
Surender Khurana	x	x	x
Susan Gerber			
Susan Weiss	x		x
Teresa Hauguel			
Thames P		x	x
Theresa Fitzgerald			x
Timothy Sheahan		x	
Troy Sutton			
Tom Fabrizio			
Tori Baxter			

Vineet Menachery	x		
Viviana Simon			
Walt Orenstein		x	x
Weina Sun	x		
Wesley C Van Voorhis	x		x
William Karesh			
William Florence	x	x	
William Morgenlander	x		
Willy Valdivia			
Wiriya Rutvisuttinunt			x
Wolfgang Leitner			
Xizhi Guo			
Yoshihiro Kawaoka	x		

To: rbaric@email.unc.edu[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Linyou Cao[lcao2@ncsu.edu]
Sent: Wed 2/5/2020 5:39:15 PM (UTC-06:00)
Subject: Re: Inquiry of your Nature Medicine paper on CoronaVirus

Dear Prof. Baric and Menachery,
I am writing to kindly follow up my inquiry, and would appreciate any clarification at your earliest convenience if at all possible. Otherwise I would have to bring this issue to the attention of your university administration, related funding agencies, and law enforcement.

Many thanks,

Linyou

On Tue, Feb 4, 2020 at 12:23 AM Linyou Cao <lcao2@ncsu.edu> wrote:

> Dear Prof. Baric and Prof. Menachery,
> I am writing to kindly seek some clarification about the paper you published at Nature Medicine as attached. In particular, I was hoping to know if the CoronaVirus now widely spreading in China and worldwide is the same or any format of mutation of the virus studied in the paper. This information would be extremely important for the development of efficient strategy to control or eventual stop the spreading and also for the development of medical treatment . I would truly appreciate your response for the well being of billions of people in China whose are suffering tremendous mental and physical pain even loss of life.
>
> Many thanks,
>
> Linyou
>
> --
> ----------
> Linyou Cao, PhD
> Associate Professor
> Department of Materials Science and Engineering
> Department of Electrical and Computer Engineering(Affiliated)
> Department of Physics (Affiliated)
> North Carolina State University
> 911 Partners Way
> Rm. 3070A, EB1
> Tel. 919-515-5407
> lcao2@ncsu.edu
> https://www.mse.ncsu.edu/cao/

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Linyou Cao, PhD
Associate Professor
Department of Materials Science and Engineering
Department of Electrical and Computer Engineering(Affiliated)
Department of Physics (Affiliated)
North Carolina State University
911 Partners Way
Rm. 3070A, EB1
Tel. 919-515-5407

lcao2@ncsu.edu
https://www.mse.ncsu.edu/cao/

To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Qifang Bi[qbi@uchicago.edu]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen,

Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; acox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Sarah Cobey[cobey@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; ODSET Pro[ODSETPro@mail.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Oki, Noffisat (NIH/OD) [E][noffisat.oki@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 12/2/2020 3:20:55 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - December 8th
nCoV PI call attendee list.xlsx

Hi Everyone,

On Tuesday, December 1st, Dr. Karla Satchell gave a presentation on "**Structural Biology of the nsp16/nsp10 2'-O-methyltransferase: Impact for Structure based Drug Design**." Thanks to our presenter and those that were able to join.

Next week, on Tuesday, December 8th, Dr. Ben Tenoever will be giving a seminar on **"Single virion tracking of SARS-CoV-2 in vivo to better understand systemic inflammation associated with COVID-19".**

If you are interested in presenting during future meetings, please reach out to me regarding your interest.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Nov	1-Dec
Erik Stemmy	x	x
Marciela DeGrace	x	x
Rebecca Lampley	x	x
Aditya Gaur		
Adolfo Garcia-Sastre	x	x
Aisha Souquette		
Alan Embry	x	
Ali Ellebedy		
Alicia Fry	x	
Alison Augustine	x	x
Alvaro Ordonez	x	
Amanda Perofsky		
Amy Kuehn	x	x
Amy Krafft	x	
Andrea Pruijssers		
Andrea Sant		
Andrew Mesecar	x	
Andrew Pekosz	x	x
Andy Mesecar		
Andrzej Joachimiak		
Aneesh Mehta		
Angela Rasmussen		
Ann Eakin		
Anice Lowen	x	x
Anita McElroy		
Anne Piantadosi		
Aron Hall		
Atsuo Kuki		
Aubree Gordon	x	x
Barry Rockx		
Becky Dutch		
Ben Cowling		
Ben Larman		
Benjamin Miller	x	
Ben Tenoever		x
Bernard Lafont		x
Bin Zhou	x	
Biao He		
Brooke Bozick		
Carly Dillen	x	x
Carlie Williams	x	
Catherine Luke		

Claire Midgley	x	x
Charles Russell		x
Chelsea Lane		
Chris Brooke		
Christopher Hsu		
Chris Roberts		
Clint Florence		x
Conrad Mallia		
Colleen Jonsson	x	x
Connie Schmaljohn	x	x
Courtney Comar (Susan Weiss lab)		
Daved Fremont		
David Martinez	x	
David Renner (Susan Weiss lab)		
David Topham	x	
David Wentworth	x	x
Deborah Lynn Fuller		
Diana Finzi		
Diane Post	x	x
Diego Hijano		
Don Milton	x	
Donna Neu		x
Elizabeth Fitzpatrick		
Emma Hodcroft	x	
Erica Raterman		
Evans		
Eunchung Park		x
Eun Mi Lee		
Florian Krammer	x	
Francisco Chaves		
Frederic Bushman		
Gabriele Neumann	x	x
Gavin Smith	x	
Ghazi Kayali		
Glen Abedi		
Grace Tietz		
Greg Deye		
Hana Golding	x	
Harm van Bakel	x	
Holly Hammond		x
Hui-Ling Yen	x	x
Ian Crozier		x
Ian Plumb		
Isabelle Phan		
Ishwar Chandramouliswaran		

Ivan		x
Jacob Hou		
Jae Jung		
James Hoffman		
James Kobie	x	
Jared Evans	x	x
Jason Goldstein	x	
Jean Patterson		
Jenni		
Jennifer German		
Jennifer Gordon		
Jennifer Hyde		x
Jens Wrammert		
Jeremy Crawford		
Jesse Erasmus		
Ji Lee		
Jimmy Logue		
Jim Chappell		
jmankow1		
Joe Breen	x	
Jonathan Runstadler	x	
Joseph Mankowski	x	
Judy Hewitt		
Juergen Richt	x	x
Kanta Subbarao		
Karla Satchell		x
Katharina Koelle	x	
Katy Shaw-Saliba		
Katherine Fenstermacher		x
Kimberly Coca		
Kimberly Stemple		x
Korin Bullen		
Kristina Lu		
Kris Emo		
Kris Lambert		
Kristen Hildebrand		x
Laura Hughes		
Lauren Sauer		
Larry Anderson	x	x
Larry Wolfraim		
Leo Poon		
Liliana Brown	x	x
Lisa Hensley	x	
Lisa Lindesmith		
Lisa Miorin		

Liz		x
Lori Newman	x	
Lucy Cong		
Mackenzie Zendt	x	
Malik Peiris	x	
Marie Killerby		
Mark Challberg		
Mark Denison		
Mark Heism		
Mark Pallansch		
Mark Sangster	x	x
Mark Williams	x	
Marlene Espinoza	x	x
Marta Gaglia		
Martha Nelson		
Martin Linster	x	
Masato Hatta (UW)		
Matt Frieman	x	
Maureen McGargill		x
Mehul Suttar		
Melissa Uccellini	x	x
Mercy Prabhudas		
Michael Bryan		
Michael Chan		
Michael Martin		
Mike Cooper		
Mike Holbrook		x
Mindy Davis		x
Missy		
Nat Moorman		
Natalie Thornburg		
newmanlm		
Nidia Trovao		
Noffisat Oki		x
Pamela McKenzie		x
Patrice Becker		
Paul McCray	x	x
Paul Jacob Bueno de Mesquita		
Paul Thomas		
Peter Daszak		
Peter Halfmann	x	x
Peter Myler		
Peter Palese	x	
Phuong Nguyen-Contant		
Punam Mathur	x	x

Qifang Bi		x
Rachel Graham		
Ralph Baric		
Randall Tressler		
Raul Andino		
Rebecca Dutch		
Reed Johnson	x	
Reed Shabman	x	
Richard Rothman		
Richard Sciotti		
Richard Webby		
Rick Bushman		
Robert Johnson		x
Ron Fouchier	x	x
Rudra Goudavet		
Russell Ray	x	x
Ryan Langlois		
Sabra Klein		x
Sander Herfst		
Sanjay Jain		
Sanmi Adenaiye	x	
Samantha Loeber		
Sara Cherry	x	x
Sara Woodson	x	
Scott Hensley		
Scott Strome	x	x
Seema Lakdawala		
Sharon Saydah		
Sheldon Tai	x	
Shiho Chiba	x	x
Simon Anthony	x	x
Sook Ho		
Sonnie Kim		
Stacey Schultz-Cherry	x	
Stacy Ferguson	x	
Stanley Perlman	x	
Stephen Tompkins	x	
Steve Smiley		
Steve Tsang		x
Surender Khurana	x	x
Susan Gerber		
Susan Weiss	x	
Teresa Hauguel		
Thames P	x	x
Theresa Fitzgerald	x	

Timothy Sheahan		
Troy Sutton		
Tom Fabrizio		
Tori Baxter		
Vineet Menachery		
Viviana Simon		
Walt Orenstein	x	x
Weina Sun		
Wesley C Van Voorhis	x	x
William Karesh		
William Florence		
William Morgenlander		
Willy Valdivia		
Wiriya Rutvisuttinunt	x	x
Wolfgang Leitner		
Xizhi Guo		
Yoshihiro Kawaoka		

To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Tristan Jordan[tristanxjordan@gmail.com]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Qifang Bi[qbi@uchicago.edu]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Sarah Cobey[cobey@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]
Cc: Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; ODSET Pro[ODSETPro@mail.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Oki, Noffisat (NIH/OD) [E][noffisat.oki@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 12/7/2020 10:03:57 AM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi All,

Apologies for any confusion my meeting invite might have caused. The meeting is still being conducted.

The update was to make everyone aware that we will be incorporating COVID-19 Cohort presentations to the series and to welcome the newly added investigators. As always, I will send out weekly emails with the upcoming presentation for everyone's awareness.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Baric, Ralph S[rbaric@email.unc.edu]
From: Peter Halfmann[peter.halfmann@wisc.edu]
Sent: Thur 2/6/2020 9:29:29 PM (UTC-06:00)
Subject: Re: Trypsin - Gibco

Thanks for the information.

On Feb 6, 2020, at 2:48 PM, Menachery, Vineet <vimenach@utmb.edu> wrote:

Just regular 0.5Trypsin/EDTA.

From: Peter Halfmann <peter.halfmann@wisc.edu>
Sent: Thursday, February 6, 2020 2:46 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: Trypsin - Gibco

Hi Ralph and Vineet,

With the nCoV case in Wisconsin, Yoshi and I were curious about the trypsin you use in your bat coronavirus manuscript.

It mentions trypsin Gibco, CA, but I am unsure of the exact product.

If you have a cat# to share, I would appreciate it!

Thanks,

Peter

To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; SAMANTHA LOEBER[sloeber@wisc.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Sabra Klein[sklein2@JHU.EDU]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Jennifer Hyde[jlhyde4@uw.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Emma Hodcroft[emmahodcroft@gmail.com]; Robert E. Schwartz[res2025@med.cornell.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID)

[E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]

Cc: Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Timothy Burgess[timothy.burgess@usuhs.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Graham, Rachel[rlgraham@ad.unc.edu]; Rafael Medina Silva[rmedinas@med.puc.cl]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; psichone@rzhrg-mail.org[psichone@rzhrg-mail.org]; Sullivan, Patrick S[pssulli@emory.edu]; Mark Mulligan[Mark.Mulligan@nyulangone.org]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 12/31/2020 3:14:04 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - January 5, 2021

Happy New Year, Everyone!

Dr. Ghazi Kayali will help kick off the 2021 SARS-CoV-2 Investigators Meeting by giving a presentation on **"Incidence, household transmission, and neutralizing antibody seroprevalence of COVID-19 in Egypt: Results of a community-based cohort".** His presentation will be on Tuesday, January 5th from 9:00 – 10:00 am EST.

As a reminder, this meeting will be canceled on Tuesday, January 12th and will resume Tuesday, January 19th.

Cheers,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 2/12/2020 2:58:52 PM (UTC-06:00)
Subject: SIG U19 call cancelled

Hi All,
Due to conflicting travel schedules, the February SIG U19 call has been cancelled.
Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Menachery, Vineet[vimenach@UTMB.EDU]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Mark Denison[mark.denison@vumc.org]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]
Cc: Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Wed 2/12/2020 8:58:37 AM (UTC-06:00)
Subject: nCoV investigator call - follow up resources
200_Protocol_v28_0.pdf

Hi everyone,

It was great speaking to you yesterday. Thank you for sharing your updates. As promised, here's some information for those unable to join yesterday's call so you can stay in the loop.

Funding: While we currently do not have any new funds designated for nCoV, we are collecting supplement requests so we can be ready if/when funds arrive.

Grantees: To submit a supplement request, please follow the instructions of this NOSI. The appropriate PA to use for submission is here.

CEIRS: Please send the CEIRS concept form to me and to the Prime PI of the Center you are working with.
If you are currently funded by CEIRS and have an urgent need for nCoV funds, write me an email and we can discuss. If you have both CEIRS and grant funding, please do not submit the same work to both as we will be reviewing all requests together.

Reagents: Currently BEI has one virus isolate available and is working on making genomic RNA available. We're also aware that the European Virus archive has an isolate and RNA. We are trying to get more isolates from multiple countries into BEI – please keep me informed if you know of connections we can reach out to about this. As you develop reagents, Erik and I will work with you to help expedite their deposit into BEI, so please keep us posted on your progress.

We are also working to see if the Ad-ACE2 vector can be deposited and I'll try to update by next week. If there are other high priority reagents you would like to see in BEI, please email me so I can curate a list.

Patient Samples: CDC teams still working on outreach and consent, so we expect an extremely limited supply of PBMCs, sera and blood from US patients. For those interested in setting up a protocol for collection of samples from patients at their institution or with a collaborator abroad, a template that the NIH Vaccine Research Center uses is attached. Please keep Erik and I informed if you decide to pursue this.

Thank you all! Please don't hesitate to email with any questions and we will talk next Tuesday! Looking forward to updates from those of you doing animal model testing.

Marciela

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March 19, 2019

Vaccine Research Center
VRC 200
(03-I-0263)

A Multicenter Specimen Collection Protocol to Obtain Human Biological Samples for Research Studies

Protocol Sponsored by:

Vaccine Research Center (VRC)
National Institute of Allergy and Infectious Diseases (NIAID)
National Institutes of Health (NIH)
Bethesda, Maryland

VRC Principal Investigator/Protocol Chair:

Grace Chen, M.D.
VRC, NIAID, NIH
Bethesda, MD 20892

IRB Initial Review: June 2, 2003

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TABLE OF ABBREVIATIONS

AE	Adverse Event
CBC	Complete Blood Count
CD4	Cluster of Differentiation Antigen 4
CLIA	Clinical Laboratory Improvement Act
DTM	Department of Transfusion Medicine
EDC	Electronic Data Capture
ELISA	Enzyme-linked Immunosorbent Assay
FDA	US Food and Drug Administration
GCP	Good Clinical Practices
HIV	Human Immunodeficiency Virus
HLA	Human Leukocyte Antigen
HRPP	Human Research Protection Program
IoR	Investigator of Record / Site Principle Investigator
IRB	Institutional Review Board
LIMS	Laboratory Information Management System
NIAID	National Institute of Allergy and Infectious Diseases
NIH	National Institutes of Health
PBMCs	Peripheral Blood Mononuclear Cells
PCR	Polymerase Chain Reaction
PI	Principal Investigator
PT	Prothrombin Time
PTT	Partial Thromboplastin Time
RNA	Ribonucleic Acid
SAE	Serious Adverse Event
SOPs	Standard Operating Procedures
UP	Unanticipated Problem
VITL	Vaccine Immunology Testing Laboratory
VRC	Vaccine Research Center
WBC	White Blood Cell

PRÉCIS

VRC 200: A Multicenter Specimen Collection Protocol to Obtain Human Biological Specimens for Research Studies

Protocol Design: This protocol is designed to perform collection of human specimens, such as blood, mucosal secretions, skin swabs, skin biopsy, or body fluids to support research studies. These samples will be used by researchers in their work on the development of vaccines, to study the correlates of immunity related to infectious diseases and in laboratory work related to the development and/or validation of immunological assays. Standard phlebotomy and apheresis procedures will be utilized to safely obtain necessary quantities of blood and cells.

Subjects: Adults ages 18 years and older.

Protocol Plan: Subjects who consent to participate will undergo standard medical procedures to obtain biological specimens. The signed informed consent is valid for one year; at least once per year, the subject must re-consent and eligibility should be re-confirmed.

Duration: Individual subjects may donate samples as often as permitted by their institution's guidelines. The IRB-approved protocol will remain open and undergo annual continuing review by the IRB as long as there continues to be a need for human biological specimens for research studies.

Endpoints: There is no analysis plan for this protocol. This protocol will be conducted in accordance with Good Clinical Practices for human research solely for the purpose of obtaining samples for research laboratories. Samples will be identified only by protocol identification number. Subject data, such as demographic information, aspects of medical history, laboratory parameters, recent immunizations or medications, HLA type, genetic tests and other medical information may be provided (identified by study number, but not subject name) to researchers if needed to support the objectives of the laboratory research.

1. INTRODUCTION AND RATIONALE

Research at the Vaccine Research Center (VRC) is ongoing to investigate different aspects of HIV and other infectious diseases as well as to elucidate human immunology. Frequently these laboratory studies require serum, plasma, peripheral blood mononuclear cells (PBMCs) and other types of human biological specimens, such as mucosal secretions (collected by swabs), body fluids, skin swabs or skin biopsy. This protocol allows for subjects to undergo a variety of routine specimen collection procedures to obtain biological samples that will be used by laboratory researchers in their work to develop vaccines and monoclonal antibodies, to study the correlates of immunity related to infectious diseases, and to develop and/or validate immunological assays.

2. DESCRIPTION OF SPECIMEN COLLECTION PROCEDURES

2.1 SPECIMEN COLLECTION PROCEDURES

Specimens will be obtained by routine medical practice methods.

- Blood samples will be collected from a vein by standard phlebotomy techniques.
- Body fluid samples including urine, semen, saliva, skin swabs, and/or mucosal secretions will be collected by standard clinical techniques. Mucosal secretions that may be collected include nasal, oral, pharyngeal, aural, conjunctival, vaginal, cervical, rectal and penile secretions.
- Skin biopsy samples will be collected by standard biopsy technique using local anesthesia. If a subject is willing to undergo a skin biopsy, then a separate consent process for this procedure will be completed. The sample collected will not routinely be sent for a formal pathology review, but may be sent at the discretion of the clinician if there is suspicion of an undiagnosed condition.

The results of testing performed by research laboratories will not be part of the subject's medical record. This protocol alone is not intended for general longitudinal study of subjects.

Specimens collected for standard diagnostic testing (e.g., swab for diagnosis of a skin infection, urine for pregnancy testing/urinalysis, blood for HIV testing, complete blood count, chemistry panel, lipid panel, hepatic panel, hepatitis screening, PT, PTT, HLA and lymphocyte phenotyping) may be collected for documentation of medical status when needed to either support a research project or assess well-being of the subject with regard to undergoing sample collection procedures. Results of such tests are available in the subject's medical record. Other standard medical tests may be obtained as well. Study subjects will be informed of any results that suggest a new diagnosis.

2.2 APHERESIS PROCEDURES AT NIH

Each apheresis procedure will be carried out by trained members of the NIH Clinical Center Apheresis Clinic under the supervision of the medical staff of the Department of Transfusion Medicine (DTM) by recommended methods [1]. Apheresis will be done using devices and procedures that conform to standard DTM guidelines and Standard Operating Procedures (SOPs). The plasma or peripheral blood mononuclear cells (PBMCs), or both, as requested, will be harvested. The red blood cells will be returned to the subject during all procedures and the plasma will be returned when PBMCs alone are the collected sample.

Blood from apheresis donors may also be tested for hepatitis A-G as part of the research investigation. HLA typing, genetic tests and HIV testing may also be performed. Stored samples may be used later to further evaluate immune responses and to elucidate genetic factors associated with immune response.

Approximately 1.0 – 3.0 x 10^9 cells will be collected per lymphapheresis procedure. The interval between successive apheresis procedures should be 21 or more days. In addition, the following guidelines apply to HIV positive subjects:

a) Subjects with CD4 <200 cells/μL are restricted to 3 apheresis sessions/year.
b) Subjects with CD4 >200 cells/μL are restricted to 6 apheresis sessions/year.

Subjects may be asked to undergo repetitive apheresis procedures depending upon the requirements of the particular research project for which the cells or plasma are being collected. Except under special circumstances (i.e. to be decided on a case-by-case basis), no subject should be asked to undergo more than six procedures per year. The DTM omnibus protocol for collection of mononuclear cells for research use by NIH investigators (protocol #99-CC-0168) allows performance of leukapheresis every 3 weeks in healthy subjects, not to exceed 17 donations per year. The U.S. Food and Drug Administration (FDA) regulations allow cytapheresis donations at a frequency of 24 donations per year, and plasmapheresis donations twice weekly [2]. With appropriate monitoring, at these frequencies, no detrimental long-term effects on healthy donors have been documented [3-6]. Since some of the subjects on the current protocol will have HIV infection, a more conservative upper limit of six donations per year was chosen.

Physicians or other staff ordering serial apheresis procedures are responsible for monitoring the immunologic and hematologic parameters of the subjects during these procedures. Declines in CD4 count, platelet counts, etc. that are potentially procedure-related will be considered when scheduling the interval for a subsequent apheresis procedure.

All exceptions to the above guidelines need to be discussed with and cleared by the PI (or designee) and must be reviewed and approved by the NIAID IRB beforehand. Apheresis of subjects in violation of the above guidelines may result in loss of access to this protocol.

2.3 APHERESIS PROCEDURES AT EXTERNAL RESEARCH SITES

If an apheresis procedure is performed at other sites outside of NIH, local site SOPs and guidelines will be followed.

3. PROTOCOL OBJECTIVES

To obtain human biological specimens such as blood (via phlebotomy), plasma or PBMC samples (via apheresis), mucosal secretions, skin swabs, body fluids or skin biopsy to support medical research.

4. PROTOCOL DESIGN AND CLINICAL PROCEDURES

Informed consent using a site-specific IRB-approved informed consent form will be obtained by all subjects prior to participation in this protocol. This protocol also allows for remote enrollment and sample collection, with the option for remote informed consent process being conducted by telephone (see Appendix IV).

4.1 ELIGIBILITY CRITERIA

Criteria for enrollment are minimal; however, additional eligibility requirements will be confirmed by a study clinician before scheduling a subject for apheresis or skin biopsy.

4.1.1 Inclusion Criteria

A subject must meet all of the inclusion criteria, as follows:

1. Age 18 years or older
2. Able and willing to complete the informed consent process
3. Willing to provide blood or other samples that will be stored for future research
4. Able to provide proof of identity to the acceptance of the clinician completing the enrollment process; when the telephone consent process is used, the clinician performing the sample collection will review and confirm the proof of identity

4.1.2 Exclusion Criteria

A subject will be excluded from protocol participation if there is presence of a condition that the attending physician considers to be a contraindication to the specimen collection procedures.

4.2 SCREENING AND ANNUAL ELIGIBILITY VISITS

Prescreening will include education about study procedures and a discussion of the eligibility criteria and purpose of the sample collections. If the subject is willing to participate, the informed consent will be signed and eligibility criteria documented. Subjects can participate in this protocol for one year using a single consent document. The informed consent will be reviewed and signed again if it has been more than one per year since the last prior specimen collection.

Screening evaluations that are required for determining specimen collection procedural eligibility must be completed within the 56 days prior to the procedure being performed. If the required evaluations are already available in the subject's medical record within the required timeframe, they do not have to be repeated for this protocol.

Screening and specimen collection procedures may all be performed in one visit or may be split into more than one visit, as needed, to meet the needs of an individual subject or the research study.

4.2.1 Schedule of Evaluations

1. Informed Consent process and signature of consent
2. Medical History; this may be limited to information relevant to the sample collection procedures or laboratory research for which the sample will be used. If a skin biopsy is to be collected, then the subject will be asked about a history of keloid scar formation and allergies to local anesthetic medications.
3. Physical Examination; this may be limited to blood pressure, temperature, heart rate, height and weight. A more extensive physical exam is not required, but may be performed based on the medical judgment of the clinician completing the screening process, needs of the research for which the sample is being collected or if requested by the subject.

4. CBC with differential and platelets: This evaluation is typically done but may be deemed as "not required" by a study physician or advanced practitioner based upon the circumstances and type of sample collection.
5. HIV-1 Serology: This evaluation is typically done as an HIV ELISA, with confirmatory testing needed to document HIV status; sites may use HIV tests that meet local institutional policy.

   For subjects already documented in the medical record to be HIV positive a quantitative viral load measurement alone may be done. When HIV status is not considered relevant to the research sample use, it is not a required evaluation.
6. CD4 count is optional, but usually obtained for subjects already documented in the medical record to be HIV positive; CD4 count may be done, but is not required for other study subjects.
7. Collection of samples to be stored for subsequent testing for hepatitis, other pathogens, and/or genetic tests/HLA type if needed for research use of the sample.
8. Other laboratory tests, as needed, to provide medical status information to support the research study or to assess the subject's well-being.

4.3 APHERESIS

In order to undergo apheresis procedures, a subject must have no medical contraindications. All apheresis procedures performed under this protocol are solely for research purposes. Subjects participating in an active clinical research protocol may participate in the apheresis protocol if the total amount of blood drawn does not exceed NIH guidelines or a site's institutional guidelines. A study clinician will complete a checklist for apheresis eligibility before referring a subject for apheresis. At the NIH, prior to scheduled procedure, the subject must have a venous assessment performed by the Apheresis staff to determine suitability for apheresis.

4.3.1 Apheresis Eligibility Criteria

For Healthy Volunteer

A healthy volunteer must meet all of the following criteria:

1. Afebrile (temperature $\leq 37.5^0$C)
2. Weight $\geq$110 pounds
3. Adequate bilateral antecubital venous access
4. Hemoglobin $\geq$ 12.5 g/dL for females; $\geq$ 13.0 g/dL for men
5. Platelets > 150,000 K/uL
6. No cardiovascular instability as indicated by a) history of medically significant cardiac arrhythmia within the last 12 months, or b) ischemic cardiovascular disease within the last 12 months, or c) heart rate outside of the 50 - 100 beats/minute interval (on 3 successive readings), or d) blood pressure greater than 180 mmHg (systolic) or 100 mmHg (diastolic) on 3 successive readings
7. No current lung or kidney disease
8. No known coagulation disorder

9. No sickle cell disease
10. No active or chronic hepatitis
11. No intravenous injection drug use in the past 5 years
12. Not breast feeding
13. Negative beta-human chorionic gonadotropin (β-HCG) pregnancy test (urine or serum) performed by a VRC study clinician within 72 hours prior to the apheresis procedure

Infectious Disease Patient

A patient with an infectious disease must meet all of the following criteria:

1. Weight ≥ 110 pounds
2. Afebrile (temperature ≤ 37.5° C)
3. Adequate bilateral antecubital venous access
4. No cardiovascular instability as indicated by a) history of medically significant cardiac arrhythmia within the last 12 months, or b) ischemic cardiovascular disease within the last 12 months, or c) heart rate outside of the 50 - 100 beats/minute (on 3 successive readings), or d) blood pressure greater than 180/100 mmHg (on 3 successive readings)
5. No current lung or kidney disease
6. No known coagulation disorder
7. No receipt of clotting factor concentrates in the past 5 years
8. Hemoglobin ≥ 9.0 g/dL
9. Platelets ≥50,000 K/uL
10. WBC ≥ 2.0 K/uL
11. Not breast feeding
12. Negative beta-human chorionic gonadotropin (β-HCG) pregnancy test (urine or serum) performed by a VRC study clinician within 72 hours prior to the apheresis procedure

4.3.2 Apheresis Procedures

Subjects must have initial apheresis procedure within 56 days of eligibility screening. Once determined eligible for apheresis, subjects do not need to be re-screened for each subsequent apheresis procedure unless deferred by the apheresis unit.

For women of reproductive potential, a pregnancy test by blood or urine will be performed by a VRC study clinician within 72 hours prior to the apheresis procedure. Results must be negative to proceed with apheresis.

Prior to beginning the apheresis procedure, a study clinician may request in advance that other laboratory tests be collected, such as CD4+ T cell count, PCR viral load, liver function panel or other tests as needed to monitor the well-being of the subjects or samples as needed by a research laboratory. The total volume of blood samples and types of specimens collected will be recorded in the records kept for each protocol visit.

Apheresis will require two antecubital venous access sites and will involve processing of less or equal to 5 liters of whole blood. When PBMC are collected, the expected mononuclear cell yield is approximately 0.5 to 1.0 x 10^9 cells per liter processed, and the apheresis device can process about 2-3 liters per hour. Thus, 1 to 2 hours are required to process 1 to 4 liters of blood and obtain about 1 to 4 x 10^9 leukocytes.

The volume of plasma removed during an apheresis procedure may range from 100 to 600 mL, depending on the procedure. The plasma volume is not replaced per regulatory standards. Subjects will be advised to drink a 12-oz glass of a decaffeinated beverage prior to the procedure.

About 6 mL of red blood cells will also be lost through the apheresis procedure. To account for this, a volume of 6 mL will be included when calculating the total whole blood sample volumes collected per apheresis visit. The clinic staff will take into account all samples collected for this and other protocols in which the subject may be participating.

During or following an apheresis visit, if there is any concern about the well-being of the subject, the clinic may conduct appropriate medical evaluations by history-taking, physical examination, laboratory tests, and/ or other testing.

NIH Clinic Site only:

All study subjects will be treated according to standard whole blood and apheresis donation policies and procedures operative in the Department of Transfusion Medicine (DTM). The Dowling Apheresis Clinic staff at the NIH Clinical Center routinely performs a hemoglobin test prior to initiating apheresis. If a subject is found to have a hemoglobin value less than permitted by the Apheresis Clinic, then the apheresis will not be initiated and the ordering provider will be notified. The VRC Study Coordinator will provide the Apheresis center with a request for numbers and types of tubes of blood to be collected prior to beginning the apheresis.

4.4 SKIN BIOPSY

The skin biopsies will be performed by a trained professional under universal antiseptic norms. The procedure may be done using local anesthesia. In order to undergo a skin biopsy, a subject must have no medical contraindications. The clinician will complete a checklist for skin biopsy eligibility before the procedure is performed. The skin biopsy eligibility includes the following:

1. No known allergies to the local anesthetic to be used
2. No history of keloid formation
3. No known coagulation disorders
4. Not pregnant or breast feeding

Subjects will have no more than 2 skin biopsies in the same visit and no more than 6 biopsies in a 1-year period.

Formal pathology review in a CLIA certified laboratory will not be performed unless the clinician assesses that there may be a medical condition not previously diagnosed.

4.5 BODY FLUID SAMPLES

For males providing a semen specimen in clinic, a private room will be given for the donation. Semen will be collected into a clinical container made for this purpose.

Urine samples, oral secretions, swabs of mucosa (e.g. gingiva, pharynx, penis, rectum, vagina) will be collected by standard clinical techniques.

These samples may be used for routine clinical testing or delivered to investigators or collaborators for research assays or storage for future research.

4.6 CRITERIA FOR DISCONTINUING PARTICIPATION

A subject may be discontinued from protocol participation for the following reasons:

1. Subject decides to discontinue participation
2. Subject has not had any protocol visits for 1 year
3. Subject has a serious adverse event related to study procedures that is a contraindication to future specimen collection procedures
4. Subject develops a medical condition that is a contraindication to continuing study participation
5. Subject becomes pregnant
6. Subject has repeatedly fails to comply with protocol requirements
7. The site Principal Investigator, Protocol Chair, or IRB decide to stop the protocol
8. The site Principal Investigator or Protocol Chair assesses that it is not in the best interest of the subject for the subject to continue participation

Subjects discontinued from participation may return to active status at a later date provided they are determined to be eligible by undergoing the screening process again and signing a new consent. Such subjects should be returned to active status using the same study identification number assigned previously for this protocol.

4.7 CRITERIA FOR STOPPING THE PROTOCOL

This study will be stopped if the Investigators decide that no additional subjects are needed or if regulatory authorities require discontinuation of the study.

5. SAFETY AND EVENT REPORTING

5.1 DEFINITIONS

5.1.1 Adverse Event

An adverse event (AE) is any untoward or unfavorable medical occurrence in a human subject, including any abnormal sign (for example, abnormal physical exam or laboratory finding), symptom, or disease, temporally associated with the subject's participation in the research, whether or not considered related to the subject's participation in the research.

The risks of the study procedures are minimal and are generally confined to the period of the actual study visit itself. In this protocol, AEs that are non-serious will not be routinely recorded in the protocol database.

5.1.2 Serious Adverse Event

An AE is designated a Serious Adverse Event (SAE) if it has any of the following outcomes:

- results in death;
- is life-threatening (i.e., places the subject at immediate risk of death);
- results in inpatient hospitalization or prolongation of an existing hospitalization;
- results in a congenital anomaly/birth defect; **or**
- based upon appropriate medical judgment, may jeopardize the subject's health and may require medical or surgical intervention to prevent one of the outcomes listed above in this definition

For this sample collection protocol, only SAEs that occur during or within 24 hours after a protocol visit will be recorded in the study database. In this regard, the outcome of any pregnancies identified during participation in this screening protocol will **not** be followed for collection of data about possible congenital anomalies or birth defects as there are no investigational treatments or procedures associated with this screening protocol.

5.1.3 Unanticipated Problem

An Unanticipated Problem (UP) is defined as any incident, experience, or outcome that meets **all three** of the following criteria:

- is unexpected in nature, severity, or frequency in relation to the research risks that are described in the protocol, informed consent, Investigator's Brochure, other study documents or in consideration of the characteristics of the subject population being studied; **and**
- is related to participation in the research; **and**
- suggests that the research places subjects or others at a greater risk of harm (including physical, psychological, economic, or social harm) than was previously known or recognized.

Serious UP: An UP that meets the definition of an SAE or compromises the safety, welfare or rights of subjects or others.

An UP that is not an AE (UPnonAE) is an UP that does not fit the definition of an AE, but which may, in the opinion of the investigator, involve risk to the subject, affect others in the research study, or significantly impact the integrity of research data. Such events would be considered a non-serious UP. For example, for this study, we will report occurrences of breaches of confidentiality or accidental destruction of study records.

5.1.4 Protocol Deviation Definition

A Protocol Deviation is defined as any change, divergence, or departure from the IRB-approved study procedures in a research protocol that has a major impact on the subject's rights, safety, or well-being and/or the completeness, accuracy or reliability of the study data.

Non-serious Protocol deviations are characterized as:

- Those that occur because a member of the research team deviates from the protocol.
- Those that are identified before they occur, but cannot be prevented.
- Those that are discovered after they occur.

Serious Protocol Deviation: A deviation that meets the definition of a SAE or compromises the safety, welfare or rights of subjects or others.

5.1.5 Non-Compliance Definition

Non-compliance is the failure to comply with applicable NIH HRPP policies, IRB requirements, site-specific regulatory requirements or regulatory requirements for the protection of human subjects. Non-compliance is further characterized as serious, continuing or minor.

"Serious non-compliance" is defined as non-compliance that:

- Increases risks, or causes harm, to participants
- Decreases potential benefits to participants
- Compromises the integrity of the NIH-HRPP
- Invalidates the study data

"Continuing non-compliance" is non-compliance that is recurring.

"Minor non-compliance" is non-compliance that is neither serious nor continuing.

5.2 REPORTING TO THE NIAID IRB

Refer to the NIAID IRB website for the forms, procedures and most current guidance to use when reporting to the IRB.

The following will be reported within 7 calendar days of investigator awareness:

- Serious and non-serious UP
- Deaths
- Serious protocol deviations
- Serious or continuing non-compliance
- SAEs that are possibly, probably, or definitely related to the research regardless of expectedness. Only SAEs that occur during or within 24 hours after the protocol visit will be reported.

The following waiver applies to reporting anticipated protocol deviations and expected UPnonAEs: Anticipated deviations in the conduct of the protocol will not be reported to the IRB unless they occur at a rate greater than anticipated by the study team. Expected AEs will not be reported to the IRB unless they occur at a rate greater than that known to occur in healthy adults. If the rate of these events exceeds the rate expected by the study team, the events will be classified and reported as though they are unanticipated problems.

5.2.1 Annual Reporting to the IRB

The following will be reported to the IRB in summary at the time of Continuing Review:

- Serious and non-serious UP
- Expected SAEs that are possibly, probably, or definitely related to the research
- SAEs that are not related to the research
- All AEs, except expected AEs granted a waiver of reporting
- Serious and Non-Serious Protocol Deviations
- Serious, continuing, and minor non-compliance
- Any trends or events which in the opinion of the investigator should be reported

5.3 REPORTING TO A NON-NIH IRB

Each site IoR is responsible for reporting AEs, unanticipated problems, protocol deviations and non-compliance to the site IRB and other relevant local regulatory authorities in accordance with their institutional and country requirements for reporting.

Site-specific data reports will be made available through the data management contractor to facilitate expedited and continuing review reporting requirements.

5.4 DATA AND SAFETY MONITORING PLAN

The risk level of this protocol is low. The Principal Investigator and designees will monitor study data and subject safety.

6. STATISTICAL CONSIDERATIONS

This protocol does not require a statistical endpoint analysis. Data and blood samples collected as part of the protocol will be provided to laboratory investigators as needed for laboratory research analyses in a manner that does not reveal the identity of the subject.

7. STORED SAMPLES, HEPATITIS AND HIV SCREENING, AND GENETIC TESTING

To be eligible for the protocol, participants must be willing to allow stored specimens to be used in the future for studying HIV disease, immune function, and other medical conditions, and to have viral hepatitis screening, HIV testing, and genetic tests, including HLA typing, performed. If tests show evidence of any acute or chronic condition, subjects will be informed of the results and advised to seek appropriate medical care for the condition.

Intended use of the samples/specimens/data:

Samples, specimens and data collected under this protocol may be used to study HIV and other diseases, the immune system, other medical conditions, and for research assay validation. Genetic testing may be performed in accordance with the genetic testing information that was included in the study informed consent.

How stored samples, specimens and data from sample use will be stored:

All of the stored study research samples are labeled by a code (such as a number) that only the study team can link to the subject. Samples are stored at the Vaccine Immunology Testing Laboratory (VITL) in Gaithersburg, MD, at VRC laboratories, or at approved research

collaborator laboratories, which are all secure facilities with limited access. Skin biopsy samples collected for research may be stored at an approved collaborating laboratory (refer to Appendix II). Data will be kept in password-protected computers. Only investigators or their designees will have access to the stored samples and data.

How samples/specimens/data will be tracked:

Samples used by VITL will be tracked in the Laboratory Information Management System (LIMS) database. Research samples collected at each study visit will be recorded in the Advantage EDC database.

What will happen to the samples/specimens/data at the completion of the protocol:

In the future, other investigators (both at NIH and at external sites) may wish to study these samples and/or data. IRB approval must be sought prior to any sharing of samples. Any clinical information shared about those samples would similarly require prior IRB approval. The research use of stored, unlinked or unidentified samples may be exempt from the need for prospective IRB review and approval. Exemption requests will be submitted in writing to the NIH Office of Human Subjects Research, which is authorized to determine whether a research activity is exempt.

At the time of protocol termination, samples will remain in the VITL facility, VRC laboratories or approved collaborator's laboratory (refer to Appendix II). With IRB approval, stored samples may be transferred to another repository. Data will be archived by the VRC in compliance with regulatory requirements for retention of research records, or after IRB approval, records may be either destroyed or transferred to another repository.

Circumstances that would prompt the PI to report loss or destruction of samples/specimens/data to the IRB:

The NIH Intramural Protocol Violation definition related to loss of or destruction of samples will be followed in reporting to the IRB. Any loss or unanticipated destruction of samples (for example, due to freezer malfunction) or data (for example, misplacing a printout of data with identifiers) that compromises the scientific integrity of the study will be reported to the IRB. The PI will also notify the IRB if the decision is made to destroy the remaining samples.

8. HUMAN SUBJECT PROTECTIONS

This research study will be conducted in compliance with the protocol, Good Clinical Practices (GCP), and all applicable regulatory requirements.

8.1 INSTITUTIONAL REVIEW BOARD

A copy of the protocol, proposed informed consent document, other written information that is given to subjects, and any proposed advertising material will be submitted to the IRB for written approval.

The investigator will submit and, where necessary, obtain approval from the IRB for all subsequent protocol amendments and changes to the informed consent document. The investigator will notify the IRB of deviations from the protocol or serious AEs occurring at the site and other AE reports received from NIAID, VRC, in accordance with local procedures. The investigator will be responsible for obtaining annual IRB approval/renewal throughout the duration of the protocol.

8.2 SUBJECT IDENTIFICATION AND ENROLLMENT OF SUBJECTS

Participants may be subjects participating solely in this protocol or may be subjects in other VRC studies from whom more cells are needed for research than can be collected by routine phlebotomy. This is not research protocol that requires a fixed schedule of evaluations or a population in which all participants have particular health characteristics in common.

8.2.1 Participation of Children

Children are not eligible to participate in this clinical trial. The guidelines for the participation of children are in 45 CFR 46, Subpart D, 401-409. Under the Department of Health and Human Services protections for children, generally, healthy children can be studied when the research is considered as "not greater than minimal risk." Children can be involved in research with greater than minimal risk only when it presents the prospect of direct benefit to the individual child or is likely to yield generalizable knowledge about the child's disorder or condition.

8.2.2 Participation of Site Employees

Each study site will follow institutional policies regarding participation of site employees in VRC 200. Site specific policies related to employee involvement in research protocols have been provided to NIAID IRB.

NIH Clinic Site Specific:

At the VRC site, NIH employees and members of their immediate families may participate in this protocol. The VRC site will follow the Guidelines for the Inclusion of Employees in NIH Research Studies and will give each employee a copy of the "NIH Information Sheet on Employee Research Participation" and a copy of the "Leave Policy for NIH Employees Participating in NIH Medical Research Studies."

Neither participation nor refusal to participate will have an effect, either beneficial or adverse, on the participant's employment or work situation. The NIH information sheet regarding NIH employee research participation will be distributed to all potential subjects who are NIH employees. The employee subject's privacy and confidentiality will be preserved in accordance with NIH Clinical Center and NIAID policies. For the NIH employee subjects, consent will be obtained by an individual who is independent of the employee's team. If the individual obtaining consent is a co-worker to the subject, independent monitoring of the consent process will be included through the Bioethics Consultation Service. Protocol study staff will be trained on obtaining potentially sensitive and private information from co-workers or subordinates.

University of Puerto Rico Medical Sciences Campus (UPR MSC) Site Specific:

At the UPR MSC site, UPR MSC employees and students will not be enrolled in this protocol. The UPR MSC site will only enroll subjects from the community.

8.3 INFORMED CONSENT

The study informed consent form template is provided in Appendix I. The written informed consent document should be prepared in the language(s) of the potential subject population. Before a subject's participation in the protocol, it is the investigator's responsibility to ensure that written informed consent is obtained from the subject after adequate explanation of the aims, methods, anticipated benefits, and potential hazards of the protocol and before any protocol-specific screening procedures.

The acquisition of informed consent should be documented in the subject's medical records, as required by 45 CFR 46.117 and the informed consent form should be signed and personally dated by the subject and by the person who conducted the informed consent discussion. The original signed informed consent document should be retained in the medical chart and a copy of the consent form should be provided to the subject.

8.4 SUBJECT CONFIDENTIALITY

The investigator will ensure that the subject's anonymity is maintained in any reports. All records will be kept confidential to the extent provided by federal, state and local law. Medical records are made available for review within the guidelines set by the Federal Privacy Act. Direct access includes examining, analyzing, verifying, and reproducing any records and reports that are important to the evaluation of the protocol.

8.5 EVALUATION OF BENEFITS AND RISKS/DISCOMFORTS

There is no benefit to the subject for participating in this protocol, but society may benefit from knowledge gained from research on the specimen donations.

Risks of Specimen Collections: All specimen collection procedures used are common in routine medical practice.

- *Blood drawing*: The risks of blood sample collection are minimal and consist of mild discomfort at the sample collection site. The procedure may cause pain, bruising, and, rarely, infection at the site where the blood is taken.
- *Collection of samples by swabs*: rubbing swabs over the mucosal surfaces can cause momentary discomfort.
- *Skin biopsy*: any time the skin is opened, such as occurs with a skin biopsy, there is a chance of infection. Infection after a skin biopsy is rare and care will be taken to try to prevent infection. There may be pain or discomfort during the skin biopsy or while it is healing. There may be a small amount of bleeding after the skin biopsy. There is the risk of a small scar. Subjects known to form "keloid" scars are not eligible for a skin biopsy performed solely for research purposes. Rarely, the local anesthetic medicine used to numb the skin may cause an allergic reaction.
- *Apheresis*: donations may cause pain, bruising, and discomfort in the arms where the needles are placed. It may also cause chills, nausea, heartburn, mild muscle cramps and tingling sensation around the mouth or in the fingers, however this can usually be relieved by slowing or temporarily interrupting the apheresis or taking a calcium containing antacid, such as Tums®. Other possible side effects are anxiety, vomiting and lightheadedness. Temporary lowering of the blood pressure may develop. There is the rare possibility of infection, fainting or seizure. Very rarely a nerve problem at the needle placement site may occur. Also, very rarely, a machine malfunction may occur, resulting in the loss of about one unit of blood. There may be additional risks of apheresis that are unknown at this time.
- *New Diagnoses*: It is possible that the standard medical tests performed as part of this research protocol will result in new diagnoses. Depending upon the medical findings and

consequences of being provided with the new medical information about health status, the study subject may view this aspect of study participation as either a risk or a benefit.

Expected Adverse Events Associated with Apheresis:

All study subjects will be treated according to standard whole blood and apheresis donation policies and procedures operative in the DTM. Adverse reactions to apheresis procedures are rare. They include pain and bruising at needle placement sites and the loss of less than a pint of blood due to rare cases of apheresis device malfunction. Vasovagal episodes, characterized by transient hypotension, dizziness, nausea, and rarely syncope, are seen in less than 5% of procedures. Citrate toxicity, consisting of cutaneous paresthesia's, chills, nausea, and rarely muscle spasms, is caused by the citrate anticoagulant used to prevent the extracorporeal circuit from clotting, and may be seen to a mild degree in 30-50% of donations. Postural manipulation and fluid administration are used to manage vasovagal reactions. Citrate reactions are usually relieved by slowing the rate of the anticoagulant infusion and by administering oral calcium carbonate tablets.

The plastic kits used to collect the blood and apheresis products are sterilized, single-use, disposable sets. No blood products are given during these donations and procedures. A DTM physician is available in or near the Apheresis Donor Area at all times to provide short term medical care for complications or reactions resulting from the donation procedures.

Rarely, machine malfunction may results in loss of as much as a half-unit (250 mL) of whole blood.

Subjects may rarely sustain a drop in total lymphocyte count (and CD4+ T cell count) when lymphapheresis is performed frequently over a short period of time[5, 6]. The extent and duration of this drop appears to be variable and not necessarily predictable; therefore there are no absolute guidelines as to what may constitute an excessive number or frequency of procedures under these circumstances. Further, the long-term consequences, if any, of this drop are unknown, but presumably could be more significant in subjects with pre-existing baseline abnormalities in total lymphocyte or CD4+ T cell numbers, such as those with advanced HIV-1 disease or other causes of lymphocytopenia. As a safeguard, the Apheresis Clinic has guidelines to assist in determining whether it is both safe and appropriate for a given subject to undergo serial apheresis procedures. However, these guidelines are general rules that are not meant to take the place of the clinical judgment of the Principal Investigator in reviewing a subject's clinical history and deciding independently whether a subject remains eligible to undergo additional apheresis procedures. Individual scientists or other protocol personnel requesting apheresis of particular subjects are also responsible for ensuring that serial measurements of CD4+ T cell counts, platelet numbers, and other safety parameters as indicated, are performed appropriately. This is particularly important if individual subjects are having apheresis procedures performed for more than one research protocol.

8.6 COMPENSATION

Subjects will be compensated for time and inconvenience in accordance with the standards for compensation at each site. The total compensation for the subject is based on the number of study clinic visits and sample collections performed.

Compensation rates are based on site policy and are consistent with similar protocols conducted at these sites. Sites rates are as follows:

Site	Apheresis Procedures	Clinic Visits Involving Needle-stick Procedures (excluding apheresis)	Clinic Visits Without Needle-stick Procedures	Skin Biopsy	Timeline for providing compensation
VRC	$250	$175	$75	$200	After each completed clinic visit by direct deposit
UPR MSC	N/A	$100	$50	N/A	After each completed clinic visit by cash

The approximate total compensation is included in each site informed consent document. Compensation may need to be reported to the Internal Revenue Service (IRS) as taxable income.

9. ADMINISTRATIVE AND LEGAL OBLIGATIONS

9.1 PROTOCOL DOCUMENTATION AND STORAGE

The principal investigator will maintain a list of appropriately qualified persons to whom trial duties are delegated.

Source documents are original documents, data, and records from which the subject's data are obtained. These include but are not limited to hospital records, clinical and office charts, laboratory and pharmacy records, diaries, and correspondence.

The investigator and staff are responsible for maintaining a comprehensive and centralized filing system of all protocol-related essential documentation, suitable for inspection at any time by representatives from NIAID, VRC and/or applicable regulatory authorities. Elements include:

- Subject files containing completed informed consent documents, and supporting copies of source documentation
- Files containing the protocol with all amendments, copies of all correspondence with the IRB and the National Institute of Allergy and Infectious Diseases, Vaccine Research Center.

In addition, all original source documentation will be maintained and be readily available.

All essential documentation will be retained by the institution for the same period of time required for medical records retention. No protocol document will be destroyed without prior written agreement between the National Institute of Allergy and Infectious Diseases, Vaccine Research Center and the investigator.

9.2 Monitoring and Data Collection

The National Institute of Allergy and Infectious Diseases, Vaccine Research Center, regulatory authority inspectors or their authorized representatives are responsible for contacting and visiting the investigator for the purpose of inspecting the facilities and, upon request, inspecting the various records of the trial, provided that subject confidentiality is respected.

Clinical research data will be collected in a secure electronic data management system maintained by the VRC. Source documentation is entered into the subject's medical chart.

9.3 Policy Regarding Research-Related Injury

The study site will provide short-term medical care for any injury resulting from participation in this protocol. In general, no long-term medical care or financial compensation for research-related injuries will be provided by the study sites, the National Institutes of Health, or the United States Federal Government.

9.4 Multi-site Management

The Vaccine Research Center, NIAID, NIH is the coordinating center as well as a site for this protocol. Each site that will be participating will have a site Principal Investigator and Associate Investigators (see Appendix II) who have parallel roles at their respective institutions in managing the conduct of the study at their sites in compliance with all applicable regulations and good clinical practices. The protocol plan is to establish a Reliance Agreement with each collaborating study site such that the NIAID IRB is the IRB of Record for the conduct of the protocol. If a reliance agreement is not established, the site will be required to obtain a local IRB review.

9.5 Language

All written information and other material to be used by subjects and investigative staff must use vocabulary and language that are clearly understood.

9.6 Publications Resulting from this Protocol

The specimens collected through this research protocol have been used in the support of assay development and validation which does not typically result in a publication of results, as well as laboratory research studies that have been published [7-24].

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APPENDIX I: INFORMED CONSENT FORM

The template informed consent forms are provided to guide development of a site-specific consent form. Only IRB-approved consent forms will be used to consent subjects for study participation.

Title: VRC 200: A Multicenter Specimen Collection Protocol to Obtain Human Biological Samples for Research Studies

VRC 200 Standard Informed Consent Form Template

INTRODUCTION

We invite you to take part in a research study at the [insert name of institution].

First, we want you to know that:

Taking part in [insert name of institution] research is entirely voluntary.

You may choose not to take part, or you may withdraw from the study at any time. In either case, you will not lose any benefits to which you are otherwise entitled. However, to receive care at the [insert name of institution], you must be taking part in a study or be under evaluation for study participation.

You may receive no benefit from taking part. The research may give us knowledge that may help people in the future.

Second, some people have personal, religious or ethical beliefs that may limit the kinds of medical or research treatments they would want to receive (such as blood transfusions). If you have such beliefs, please discuss them with your [insert name of institution] doctors or research team before you agree to the study.

Now we will describe this research study. Before you decide to take part, please take as much time as you need to ask any questions and discuss this study with anyone at [insert name of institution], or with family, friends or your personal physician or other health professional.

PURPOSE AND PROCEDURES

The purpose of this study is to collect biological specimens for research purposes. Parts of the blood are often needed in research studies. Other types of specimens sometimes needed for research are other blood components, body fluids (such as semen or urine), or secretions (for example, from the nose, mouth, or different skin areas). A skin sample (biopsy) is another type of specimen that is sometimes useful for research.

Scientists at the Vaccine Research Center (VRC) will use these samples for research studies of different diseases and immune system responses, including HIV, hepatitis, responses to infections, vaccinations and other medical research. Even if you do not have a disease, your samples can be used to try to discover ways to prevent or treat medical conditions. Standard approved medical procedures will be used to collect these samples.

The following must be true for you to be eligible for the study:

- You must be age 18 years or older
- You must be able and willing to complete the informed consent process
- You must be willing to provide samples that will be stored for future research

- You must be able to provide proof of your identity

You must sign this consent before we can begin screening. Signing this form indicates that you are willing to be screened and, if eligible, you may enroll. If the screening shows that you are not eligible for the study, you will not be enrolled. A doctor or nurse will ask you some questions about your medical history and perform a physical exam.

You have the right to refuse any of the types of samples collections procedures at any time. You may not be offered certain types of sample collections if there is not a need for such samples by any research laboratories at the time of your visit. You may not be eligible for some types of sample collections. A study nurse or physician will check for your eligibility for the sample collections that have special requirements.

Your consent to enroll will be consent to collect samples for up to a one-year period. After that, if more samples are needed and you wish to continue participating in this protocol, you must sign a new consent form each year.

As many as 3,000 people may participate in this study. The actual number may be lower or be higher, depending on the need for research samples and the willingness of subjects to participate. Most subjects will have only one or a few samples collected. Different types of samples are discussed in the consent, but only certain types of sample types may be collected from you. This will be discussed in advance before the sample is collected.

BLOOD SAMPLES

Blood will be drawn by standard phlebotomy techniques from veins in the arms or hands only. Typically, about 100 mL (about 6 tablespoons) of blood will be drawn from your arm for testing. More or less may be drawn depending upon the research needs. The study staff will discuss the blood draw plan with you before starting.

URINE, SEMEN, SALIVA OR SWAB SAMPLES

If applicable and needed, samples of urine, semen, or saliva may also be collected for research use.

For urine and semen samples, you will collect the sample in private by yourself with a cup.

Some samples will be collected by a swab, a nurse or doctor will use a swab (like a Q-tip) to brush a part of your body, such as over a skin area or inside the nose, the mouth, vagina, or penis. For certain types of swab samples, for example around the anal area, you may collect the sample yourself, in private.

SKIN BIOPSY

If you are willing and eligible, and a skin sample is needed for research, then a separate consent will be signed, which explains the procedure and risks.

APHERESIS

We may ask you to provide blood samples collected by a procedure called "apheresis." To be eligible for apheresis:

- You must not have an unstable heart as indicated by your medical history and test results
- You must not have blood pressure greater than 180/100
- You must not have a known blood clotting disorder

- You must not be breast feeding
- If you are a woman who could get pregnant, you will have a urine or blood pregnancy test within 72 hours before the apheresis procedure. The test must show that you are not pregnant
- You must not to have a condition that the attending physician or the apheresis clinic staff considers a reason to not do an apheresis procedure

Before an apheresis is done, your weight, pulse and blood pressure will be checked, and you will have a blood test to be sure you are healthy enough to donate blood cells. You will be asked questions about your general health and medical history. You will be asked to lie on a recliner or couch.

The procedure is done using one needle placed into each arm. The kits used to collect the apheresis products are sterilized, single-use, disposable sets that are not in contact with any person's body fluids other than yours. No blood products are given to you during these procedures.

In the apheresis procedure, blood is removed through a needle in the vein of one arm, spun in a machine that permits separation of the desired blood component (white blood cells or plasma), and then the remainder is returned through a needle in the other arm. Citrate, a medication to prevent blood from clotting, is added to the blood while in the machine to prevent it from clotting.

The purpose of this procedure is to allow the investigator to obtain and study a larger number of white blood cells or plasma than would otherwise be possible by simple blood drawing. The number of white blood cells or plasma collected is a small fraction of the total amount in your body. The body quickly replaces removed cells and plasma. Similar procedures are used on a daily basis in the Blood Bank of the [insert name of institution] and by other blood banks as a means of obtaining blood products from normal donors and as a form of therapy for certain diseases. Your samples will not be used for transfusion or therapy, however. The procedure will take approximately 1-3 hours.

HEPATITIS SCREENING

Some of the blood drawn from you as part of this study may be used to screen for different types of viral liver infections, such as hepatitis. If the tests show evidence of hepatitis or other medical conditions, you will be informed of the results. If you do not have a regular physician, the study team will assist in referring you to an appropriate physician for evaluation.

GENETIC TESTING

Some of the blood drawn from you as part of this study will be used for genetic tests. Some genetic tests are done in research studies to see if genetic differences in people cause different types of immune responses. Your blood sample used in these genetic tests will not have your name on it, and the results will not be in your medical record. These tests are not used to check your health, and we will not tell you the results.

NIH Site only: A special genetic test, called HLA typing, may be done by the NIH Clinical Center medical laboratory. These results will be in your medical record, but they will not be used to check your health. Any genetic testing, including HLA typing, is for research purposes only. Any genetic information collected or learned about you will be kept confidential. Medical

records, including HLA test results, are kept securely. We will not give any genetic information that is in your medical record to anyone without your permission.

If HLA typing is done in a research laboratory, the result will not be included in your medical record.

HIV TESTING

As part of this study, we will test you for infection with the Human Immunodeficiency Virus (HIV), the virus that causes AIDS. If you are infected with HIV, you will still be able to participate in this study. We will tell you what the results mean, how to find care, how to avoid infecting others, how we report HIV infection, and the importance of informing your partners at possible risk because of your HIV infection.

STORED SAMPLES

To be eligible for the study, you must also be willing to allow some of your blood and other samples to be stored for future research on HIV disease, the immune system, or other medical conditions.

Generally, the results from the research done with your stored samples will not be given to your private doctor and will not be put in your medical record. This is because the test results, unlike routine medical testing, may be experimental or preliminary. The relevance of these tests to your care may be unknown. However, at your request, the results of any research tests will be discussed with you or your physician by one of the investigators.

Labeling of stored samples: Your stored samples will be labeled with a code (such as a number) that only the study team can link to you. Any identifying information about you will be kept confidential to the extent permitted by law.

Future studies: Your samples may be kept in storage for a long time and used in the future by medical researchers. When the study team shares your samples, they will share it with only a code on it. Some information about you, such as your gender, age, health history, or ethnicity may also be shared with other investigators.

Your stored materials will be used only for research and will not be sold or used for treating other people. The research done with your materials may be used to develop new products in the future, but you will not receive payment for such products.

RISKS

Blood drawing may cause pain, bruising, and, rarely, infection at the site where the blood is taken.

Collection of samples by swabs rubbing over the inside of the nose, inside the mouth, vagina, penis or skin can cause temporary discomfort.

Apheresis Procedure Risks: Apheresis donations are generally safe and side effects are rare. Pain, bruising or discomfort at the needle placement site may occur. Sometimes apheresis causes a tingling sensation around the mouth or in the finger, chills, nausea, heartburn or mild muscle cramps. This can usually be relieved by slowing or temporarily interrupting the apheresis or taking a calcium containing antacid, such as Tums®. Other possible side effects are anxiety, vomiting, and lightheadedness. Temporary lowering of the blood pressure may develop. There is the rare possibility of infection, fainting or seizure. There may also be a slightly increased

bleeding tendency for a few hours after the procedure due to the temporary presence of the anticoagulant. Very rarely a nerve problem at the needle placement site may occur. There are theoretical risks from re-infusion of the blood after processing by the machine such as infection or an adverse reaction to the blood components. However, these risks must be exceedingly rare if they occur, since they have not been seen in many thousands of subjects who have undergone this or similar procedures to date. Rarely the performance of frequent apheresis procedures over a short period of time can result in a drop in total blood cell counts, including the absolute CD4+ T cell count (a type of blood cell that fights infection), or a drop in the platelet count (a type of blood cell that helps blood to clot). The extent or duration of the drop in these cell counts may be unpredictable and vary from person to person. The short or long-term risks associated with these drops are also unknown, and they could possibly be more serious in those individuals whose blood counts are already below the normal range as a result of HIV-1 infection or other medical conditions.

Based upon your blood cell counts or other medical conditions, we may limit the number of times that you are eligible to undergo apheresis over a set period of time. Blood cell counts and other safety blood studies may be checked periodically during the time that you are enrolled on this protocol. You will be informed about the results of the type of routine blood tests that are done to check on the state of your health. There may be additional risks of apheresis that are unknown at this time. Any new information that may affect your willingness to participate in this study will be disclosed to you.

BENEFITS

There will be no direct benefit to you for participating in this protocol. The knowledge gained through this research may benefit others in the future.

UNKNOWN RISKS or BENEFITS

Some routine medical tests may be performed during study participation. You may learn new information about your health. Receiving a new diagnosis may be stressful. You may feel that learning new information about your health is a benefit of study participation. Or you may feel this is risk of study participation.

ALTERNATIVES

This study procedures are not being done to treat a medical condition. You may choose to not participate in any or all of the procedures discussed.

COMPENSATION

[Site specific information]

You will be compensated [insert amount] for each visit than includes an apheresis procedure, [insert amount] for each visit (without apheresis) that includes procedures that require a needle-stick, and [insert amount] for clinic visits in which there is no needle-stick. If a skin biopsy is performed, extra compensation is provided and this is discussed in the skin biopsy consent.

Compensation will be provided [add site-specific time for when compensation will be provided].

Total compensation is based on the number of study clinic visits and the type of sample collection performed. Your compensation may need to be reported to the Internal Revenue Service (IRS) as taxable income.

REASONS FOR REMOVING YOU FROM THE STUDY WITHOUT YOUR CONSENT

You may be removed from the study without your consent for the following reasons:

- The NIH doctor feels that staying in the study is harmful to you.
- The study is cancelled or stopped.
- You don't keep appointments or follow study procedures.

COSTS TO YOU FOR YOUR PARTICIPATION

There will be no charge to you or your health insurance company for any of the costs that are directly related to this study. However, the costs of any other medical care you may need during this period will be your responsibility.

OTHER PERTINENT INFORMATION

1. Confidentiality. When results of an NIH research study are reported in medical journals or at scientific meetings, the people who take part are not named and identified. In most cases, the [insert name of institution] will not release any information about your research involvement without your written permission. However, if you sign a release of information form, for example, for an insurance company, the [insert name of institution] will give the insurance company information from your medical record. This information might affect (either favorably or unfavorably) the willingness of the insurance company to sell you insurance.

The Federal Privacy Act protects the confidentiality of your [insert name of institution] medical records. However, you should know that the Act allows release of some information from your medical record without your permission, for example, if it is required by the Food and Drug Administration (FDA), members of Congress, law enforcement officials, or other authorized hospital accreditation organizations.

2. Policy Regarding Research-Related Injuries. The [insert name of institution] will provide short-term medical care for any injury resulting from your participation in research here. In general, no long-term medical care or financial compensation for research-related injuries will be provided by the National Institutes of Health, [insert name of institution] or the Federal Government. However, you have the right to pursue legal remedy if you believe that your injury justifies such action.

3. Payments. The amount of payment to research volunteers is guided by the [insert name of institution] policies. In general, patients are not paid for taking part in research studies at the [insert name of institution]. Reimbursement of travel and subsistence will be offered consistent with [insert name of institution] guidelines.

4. Problems or Questions. If you have any problems or questions about this study, or about your rights as a research participant, or about any research-related injury, contact the principal investigator, [insert name] at [insert number], or Study Coordinator, [insert name] at [insert phone number]. You may also call the Clinical Center Patient Representative at 301-496-2626.

5. Consent Document. Please keep a copy of this document in case you want to read it again.

COMPLETE APPROPRIATE ITEM(S) BELOW:

Adult Patient's Consent

I have read the explanation about this study and have been given the opportunity to discuss it and to ask questions. I hereby consent to take part in this study.

Signature of Adult Patient/Legal Representative	Date	Print Name

THIS CONSENT DOCUMENT HAS BEEN APPROVED FOR USE FROM [insert date] THROUGH [insert date].

Signature of Investigator	Date	Signature of Witness	Date

Print Name	Print Name

APPENDIX II: CONTACT INFORMATION

Study Chair and VRC Site Principal Investigator:
Grace Chen, M.D., M.P.H. 240-669-2809
Vaccine Research Center, NIAID, NIH
40 Convent Drive
Bethesda, MD 20892

VRC Associate Investigators:
Barney Graham, M.D., Ph.D., 301-594-8468
Joseph Casazza, M.D., 301-594-8627
Cynthia Starr Hendel, CRNP 301-451-8715
Lasonji Holman, FNP 301-402-8641
Sarah Plummer, RN, MSN, NP 301-402-8640
Martin Gaudinski, M.D., 301-648-1149
Abidemi .O. Ola, MSN, FNP., 301-761-7641
Cristina A. Carter, M.D., 301-496-7196
Allison Beck, PA-C, MPAS, 301-761-7158
Alicia Widge, M.D., M.S., 301-761-7968

VRC Study Coordinators / Research Nurses:
Ingelise Gordon, RN, Study Coordinator
All Clinic Staff: 301-451-8715
Pamela Costner, RN, BSN
Jennifer Cunningham, RN, BSN
Brenda Larkin, RN, BSN, MBA
Floreliz Mendoza, RN
Laura Novik, RN, BSN, MA
Jamie Saunders, RN, BSN
William Whalen, RN, BSN
Xioalin Wang, RN, BSN
Aba Mensima Eshun, RN, BSN
Anita Arthur, RN, BSN

VRC Study Site:
National Institutes of Health Clinical Center
5NES Vaccine Evaluation Clinic
Bethesda, MD 20892

Data Coordinating Center
EMMES Corporation: 301-251-1161
Rockville, MD 20850

Scientific Collaborators:
Robert Bailer, Ph.D., 301-594-8481
Daniel Douek, M.D, Ph.D., 301-594-8484
Richard Koup, M.D., 301-594-8585
Peter Kwong, Ph.D., 301-594-8685
John Mascola, M.D., 301-594-8490
Mario Roederer, Ph.D., 301-594-8491
Richard Schwartz, Ph.D., 301-594-8485
Robert Seder, M.D., 301-594-8483
Nancy Sullivan, Ph.D., 301-435-7853
Emily Coates, Ph.D., 301-402-4581
Josephine Cox, PhD., 301-594-8468
Katherine Houser, PhD., 301-761-7658
Adrian McDermott, Ph.D., 301-761-6963
Eli Boritz, M.D., Ph.D., 301-443-5398
Julie Ledgerwood, D.O., 301-594-8502

Research Immunology Central Laboratory:
VITL (Vaccine Immunology Testing Laboratory)
9 West Watkins Mill Road, Suite 150
Gaithersburg, MD 20878

NIH Apheresis Clinic
Kamille A. West, MD
Chief, Blood Services Section
Department of Transfusion Medicine
NIH Clinical Center
Bldg 10 Room 1C711E
Bethesda, MD 20892
Phone: 301-594-5357
kamille.west@nih.gov

VRC Protocol Operations:
Maria C. Burgos Florez, M.Sc., 301-761-7338
Galina Yamshchikov, M.S., 301-761-7056
Nina M. Berkowitz, M.P.H., 240-747-7940
Olga Vasilenko, M.S., 301-761-7171
Iris Pittman, BA, CCRP, 301-761-6994
Ro Shauna S. Rothwell, Ph.D., 301-761-746
Lam Ngan Le, MBA, CCRP., 240-319-3824
Somia Hickman, Ph.D., 301-761-7884
Eugeania Burch, M.P.H., 301-761-7836
Olga Trofymenko, MD., 240-292-0684

VRC Recruitment Team: 301-402-8604 / 866-833-5433 Preeti Apte, MHA, BA Cora Trelles Cartagena, BSW Renunda Hicks	

Collaborating Sites	Site Investigators of Record
Site: The University of Puerto Rico - Medical Science Campus (UPR MSC) Puerto Rico Clinical and Translational Research Consortium (PRCTRC)	
Clinic Location:	1st Floor University Hospital San Juan, Puerto Rico 00936-5067
Principal Investigator:	Clemente Diaz, M.D., 787-381-6246 1st Floor University Hospital P.O. Box 365067 San Juan, Puerto Rico 00936-5067 clemente.diaz@upr.edu
Associate Investigators:	Irma Febo, MD
Study Coordinators:	Aileen Rivera Maldonado, RN, MSN Carmen M Rivera Torres, RN, MPH Lizzie Ramos Tolinchi, MPH
Research Nurses:	Barbara Guzmán, RN, MPH Sheyla Garced, RN, MS

Contact information for collaborations added after VRC 200, Version 1.0 approval:

Contact	Research Collaboration
Antonio Lanzavecchia, M.D. Institute for Research in Biomedicine Via Vincenzo Vela 6 CH-6500 Bellinzona Switzerland 41-91-8200310 lanzavecchia@irb.unisi.ch	Approved as Amendment L (OPS approval 4/11/07) The VRC will send stored specimens to a non-NIH collaborator for laboratory research related to immune responses to antigens associated with filoviruses (e.g., Ebola, Marburg) and arenaviruses (e.g. Lassa fever virus). This immunological research will include isolation of human monoclonal antibodies. The laboratory data will then be provided to VRC in support of VRC vaccine research. Hybridomas secreting the monoclonal antibodies identified through this collaboration will also be provided back to VRC as part of this collaboration.
Georgia Tomaras, Ph.D. Duke Human Vaccine Institute 106 Research Drive MSRB II, 4th Floor Duke University Medical Center 103020 Durham, NC 27710 919-684-5384 gdt@duke.edu	Approved as Version 6.0, Letter of Amendment #1 (OPS Amendment P approval 1/17/08) Coded blood samples, without personal identifying information, will be sent to the Duke Human Vaccine Institute for the conduct of *in vitro* assays that are based on previously published methods and evaluate for the viral suppression activity of activated T cells. The VRC will collaborate with this research group to use these data, as well as other measures of immunogenicity, towards the goal of better understanding of immune responses to vaccines and viral pathogens.
Rafik Sekaly, M.D. Université de Montréal, CR-CHUM Institut National de la Santé et de la Recherche Médical, U743 Montréal, Québec, H2X1P1 Canada rafick-pierre.sekaly@umontreal.ca 514-890-8000, x0728	Approved as Version 6.0, Letter of Amendment #2 (OPS Amendment R approval 2/29/08) Coded peripheral mononuclear blood cell samples, without personal identifying information, will be sent to Montreal University to perform *in vitro* gene array assays towards the goal of better understanding host genetic factors that affect immune responses.
Jacob D. Estes, Ph.D. The AIDS and Cancer Virus Program SAIC-Frederick, Inc. NCI-Frederick Fort Detrick Campus Bldg. 535, Rm. 413b Frederick, MD 21702 301-846-7641 estesj@mail.nih.gov	New in Version 7.0 Coded skin biopsy samples may be sent to the AIDS and Cancer Virus program for immunohistochemistry; evaluations may include assessments for neutrophils, B cells, T lymphocytes [including retinoid-related orphan receptor gamma t (RORgt) and interleukin 17 to assess for Th17 cells], defensins and other immunohistochemistry parameters. Microarrays may be performed on the tissue, and if sufficient quantity is available, flow cytometry to look at T cell subsets and cytokine expression.
Clemencia Pinilla, Ph.D. Torrey Pines Institute for Molecular Studies 3550 General Atomics Court San Diego, CA 92121 858-455-3783	Approved as Version 7.0, Letter of Amendment #1 (OPS Amendment X approval 9/9/08) Coded PBMC samples, without personal identifying information, will be sent to the Torrey Pines Institute for

cpinilla@tpims.org	Molecular Studies to identify new epitopes within vaccinia. These epitopes may be relevant vaccine targets and they will make possible new analyses of immune responses in vaccine evaluation and studies of disease pathogenesis.
Stephen De Rosa, Ph.D. HVTN Laboratory Program Fred Hutchinson Cancer Res Ctr 1100 Fairview Ave. North, LE-200 Seattle, WA 98109-1024 Phone: 206-667-1681 Fax: 206-667-6608 Email: sderosa@fhcrc.org Guido Ferrari, M.D. CHAVI Duke Repository Assistant Research Professor Department of Surgery Duke University Medical Center DUMC Box 2926 Durham, NC 27710 Phone: 919-684-3042 Fax: 919-684-4288 Email: gflmp@duke.edu Jill Gilmour, Ph.D. Senior Director, Clinical Research IAVI Core Laboratory 5th floor, St. Stephens Centre Chelsea and Westminster Hosp. 369 Fulham Road London, SW 10 England 9NH Phone: 44-208-746-5098 Email: jgilmour@iavi.org	Approved as Version 7.0, Letter of Amendment #2 (OPS Amendment Z approval 12/17/08) Coded blood samples, without personal identifying information, will be sent to the three research laboratories listed for work on the development of immunological assays, including virus suppression assays and a new intracellular cytokine staining method.
Terence M. Tumpey, Ph.D. Centers for Disease Control and Prevention Influenza Division, Mail Stop G-16 1600 Clifton Road N.E. Atlanta, GA 30333 Phone: 404-639-5444 Fax: 404-639-2530	Approved as Version 8, Letter of Amendment #1 (OPS Amendment CC approval 5/20/09) Coded blood samples, without personal identifying information, will be sent to Dr. Tumpey for work on the assessment of influenza immune responses.
HVTN Laboratory Program University of Washington Virology Specialty Laboratory Seattle, WA	New in Version 9.0; updated in Version 10, Letter of Amendment#2 (OPS LL approval 6/18/13) Coded blood samples, without personal identifying information, from prior HVTN study participants who need long-term follow-up HIV testing will be sent to the HVTN Laboratory. This laboratory may also collaborate on a variety of virologic assays using coded samples from VRC 200 subjects (whether or not a prior HVTN study participant).
James Crowe, M.D. Vanderbilt University, Pediatrics and Infectious Disease 1161 21st Ave South D-7240 MCN	Approved as Version 9, Letter of Amendment #1 (OPS Amendment II approval 11/29/10)

Nashville, TN 37232-2581 Phone: 615-343-8064 Email: james.crowe@vanderbilt.edu	Coded blood samples, without personal identifying information will be sent for laboratory research related to immune responses to antigens associated with filoviruses (e.g., Ebola, Marburg) and other pathogens. This immunological research will include isolation of human monoclonal antibodies. The laboratory data will then be provided to VRC in support of VRC vaccine research. Hybridomas secreting the monoclonal antibodies identified through this collaboration will also be provided back to VRC as part of this collaboration.
Joseph J. Mattapallil, D.V.M., Ph.D. Dept. of Microbiol. & Immunology F. Edward Herbert Schl. of Med. Uniformed Services University 4301 Jones Bridge Road Bethesda, MD 20814 Telephone: 301-295-3737 e-mail: joseph.mattapallil@usuhs.edu	Approved as Version 10, Letter of Amendment #1 (OPS Amendment KK. approval 4/30/12) Coded stored specimens will be provided for laboratory research related to regulation of immune responses in HIV-infected subjects. Non-identifying demographic data and antiretroviral therapy (ART) status may be provided to facilitate the analysis. The laboratory data will also be provided back to VRC as part of this collaboration.
Jason Brenchley, Ph.D. Senior Investigator NIAID, Viral Pathogenesis and Vaccine Section Laboratory of Molecular Microbiology 4 Center Drive, Room 201 Bethesda, MD 20892-0460 Phone: 301-496-1498 Email: jbrenchl@niaid.nih.gov	Approved as Version 10, Letter of Amendment #3 (OPS Amendment MM. approval 7/31/13) The VRC will send coded blood/PBMC specimens to this NIH collaborator for laboratory research related to the level of transcription factors known to be important for CD4/CD8 differentiation in sorted subsets of PBMC. Non-identifying demographic data may be provided to facilitate the data analysis.
Cristine Kinross, Ph.D. Sr. Product Manager Epicentre, an Illumina company 5602 Research Park Blvd, Suite 200 Madison, WI 53719 Phone: 608-442-6111 Email: Cristine.Kinross@epicentre.com	New in Version 11.0 The VRC will send coded specimens which will be used to sequence all HIV transcript molecules derived from cellular samples of a group of HIV-infected donors using the Illumina next generation deep sequencing platform. Epicentre's novel technology specifically removes host cell-associated transcripts from total RNA specimens, leaving only pathogen-derived material for deep sequencing. This technology will allow characterization of HIV gene expression in individual samples and comparison across samples to reveal any variation in the way the virus expresses its genes in different cells types, and in different donors.
Mary N. Carrington, Ph.D. Laboratory of Experimental Immunology Head, HLA Typing Section Center for Cancer Research National Cancer Institute Building 560, Room 21-89 Frederick, MD 21702-1201	Approved as Version 11, Letter of Amendment #1 (OPS Amendment OO. approval 2/20/14) The VRC will send coded specimens for HLA type and related immunological assessments. Non-identifying demographic data may be provided to facilitate the data analysis.

Ted C. Pierson, Ph.D. Senior Investigator Chief, Viral Pathogenesis Section Laboratory of Viral Diseases, NIAID, NIH 33 North Drive Building 33, Room 2E19A.2 Bethesda, MD 20892 301-451-7977	New in Version 12.0 The VRC will send coded specimens for neutralization assay and related immunological assessments. Non-identifying demographic data may be provided to facilitate the data analysis.
Chih-Jen Wei, Ph.D. Director, Synthetic & Immune Biology Bio-Innovation, Global Bio-Therapeutics Sanofi US 270 Albany Street Cambridge, MA 02139 Tel.: 617.665.4791 Cell: 617.571.4374 Email: chih-jen.wei@sanofi.com	Approved as Version 14.0, Letter of Amendment #1 (OPS Amendment TT. Approval 03/9/2016) The VRC will send coded blood/serum specimens to the scientific collaborator for research related to the development of a Zika virus vaccine. Non-identifying demographic data may be provided to facilitate the data analysis.
Sujatha Rashid, MS, PhD, PMP Senior Scientist, Virology BEI Resources www.beiresources.org 10801 University Boulevard Manassas, VA 20110-2209 Tel: (703) 365-2700 ext. 2660 Email: srashid@atcc.org	Approved as Version 14.0, Letter of Amendment #2 (OPS Amendment UU. Approval 03/23/2016) As requested by DMID/NIAID, the VRC will send coded blood/serum specimens to the BEI repository (https://www.beiresources.org/) and the contact person there to receive the samples is noted below. The samples will be used for Zika virus related research. Only non-identifying demographic data may be provided to facilitate the data analysis.
Joseph Campo, Ph.D. Antigen Discovery, Inc. 1 Technology Drive, STE E 309 Irvine, CA 92618 Tel: (949) 679-4068 David M. Koelle, M.D. University of Washington School of Medicine 750 Republican St, Room E651 Seattle, WA 98109 Tel: (206) 616-1940	Approved as Version 14.0, Letter of Amendment #3 (OPS Amendment VV. Approval 05/11/2016) The VRC will send coded PBMCs specimens to Antigen Discovery, Inc. and University of Washington, the contact persons there to receive the samples are noted below. The samples will be used to isolate Pf-specific T cell responses and characterize antigen specificity. Only non-identifying demographic data may be provided to facilitate the data analysis.

Dan Barouch, MD, PhD Beth Israel Deaconess Medical Center E/CLS-1047 330 Brookline Ave Boston, MA 02215 Tel: 617-735-4485 Fax: 617-735-4566 Email: dbarouch@bidmc.harvard.edu Stephen S. Whitehead, PhD Laboratory of Infectious Diseases, NIAID, NIH Bldg 33, Room 3W10A 33 North Drive, MSC 3203 Bethesda, MD 20892-3203 Telephone: 301-496-7692 Fax: 301-480-4873 Email: whitehead@niaid.nih.gov	Version 14.0, Letter of Amendment #4 The VRC will send coded blood/serum specimens to the scientific collaborators for research related to the development of a Zika virus vaccine. Only non-identifying demographic data may be provided to facilitate the data analysis.
Mark Page, PhD Division of Virology National Institute for Biological Standards and Control (NIBSC) Blanche Lane, South Mimms, Potters Bar, Hertfordshire, EN6 3QG UK Tel: 01707 641 283 Email: mark.page@nibsc.org	As part of the global initiative for assay standardization, NIBSC in conjunction with its partners (such as National Control Laboratories and WHO Collaborating Centers) will collect and analyze Zika antibody positive serum and plasma in an international collaborative study. All study data will be anonymized and statistically analyzed by NIBSC in accordance with the WHO guidelines on biological standardization. A formal report will be submitted to the WHO Expert Committee for Biological Standardization for endorsement as an International Standard.
Matthew Bonaparte, Ph.D. Sanofi Pasteur Deputy Director Project Representation Global Clinical Immunology 1 Discovery Drive Swiftwater, PA 18370 Telephone: 570-957-2493| Email: Matthew.Bonaparte@sanofipasteur.com	These serum samples will be used for development of research level serological assays to assess immune response to Zika vaccination and/or infection, and evaluation of assay specificity in the case that prior exposure to Dengue virus can be demonstrated.
Jonathan F. Smith, Ph.D. Chief Scientific Officer PaxVax 3985-A Sorrento Valley Blvd San Diego, CA 92121 Telephone: 919-622-3374 Email: jsmith@paxvax.com	The VRC will send coded blood/serum specimens to the scientific collaborator for passive transfer protection studies in non-human primates, and for the assessment of vaccine - induced immune response.

Alessandro Sette, Dr. Biol. Sci. Center Head, Division Head, and Professor Center for Infectious Disease, Division of Vaccine Discovery La Jolla Institute for Allergy and Immunology 9420 Athena Circle La Jolla, California USA Telephone: 858-752-6916 Email: alex@lji.org	The VRC will send coded blood samples to the scientific collaborator at the La Jolla institute. These samples will be used to characterize T-cell reactivity and the immune response to Zika. Only non-identifying demographic data may be provided to facilitate the data analysis.
James Rogers, PhD Manager Battelle Biomedical Research Center www.battelle.org 1425 Plain City-Georgesville Rd (St Rt 142) West Jefferson, OH 43162 Telephone: 614-424-5428 Email: rogersjv@battelle.org	The VRC will send coded blood/serum specimens to Battelle. The samples will be used for Zika virus related research and assay development. Only non-identifying demographic data may be provided to facilitate the data analysis.
David I Watkins, Ph.D. Professor of Pathology Vice-Chair Research Dept. Pathology University of Miami Leonard M. Miller School of Medicine Life Sciences Technology Park 1951 NW 7th Avenue, Suite 2340 Miami, FL 33136 Telephone: (305)243-0405 Cell: (786)879-9926 E-mail: dwatkins@med.miami.edu	The VRC will send coded serum and/or plasma samples to the scientific collaborator at the University of Miami Leonard M. Miller School of Medicine. The serum and/or plasma samples will be used for development of serological assays to assess immune response to Zika infection and/or vaccination.
Kayvon Modjarrad, M.D., Ph.D. Associate Director, Emerging Infectious Disease Threats Military HIV Research Program / Walter Reed Army Institute of Research 6720A Rockledge Drive, Suite 400, Bethesda, MD 20817 USA Telephone: 1-301-500-3623 Cell: 301-335-4707 Email: kmodjarrad@hivresearch.org	The VRC will send coded serum or plasma samples to the scientific collaborator at the Walter Reed Army Institute of Research. The serum or plasma samples will be used for the evaluation of Zika immune responses.

Marc Fischer, MD, MPH Arboviral Diseases Branch Centers for Disease Control and Prevention 970-221-6489 mfischer@cdc.gov	The VRC will send coded serum and/or plasma samples to the scientific collaborator at the Centers for Disease Control and Prevention. The serum and/or plasma samples will be used for development of serological assays to assess immune response to Zika infection and/or vaccination.
Manoj K. Pastey DVM, MS, PhD Associate Professor Head, Molecular Diagnostic Laboratory 105 Magruder Hall College of Veterinary Medicine Oregon State University Corvallis, OR 97331 Telephone: (541) 737-3940 Email: Manoj.Pastey@oregonstate.edu	The VRC will send coded samples to the scientific collaborator at OSU. The samples from HIV infected individuals will be used to identify antibodies against HIV NS2 protein by ELISA assay.
Hansi Dean, PhD Vice President and Head Discovery Research Takeda Pharmaceuticals 40 Landsdowne Street Office: 75 Sidney-3062 Cambridge, MA 02139 Telephone: (617)761-6860 Email: hansi.dean@takeda.com	The VRC will send coded serum and/or plasma samples to the scientific collaborator at Takeda Inc. The serum and/or plasma samples will be used for development of serological assays such as ELISA and neutralizing antibody assays.
Anuja Matthew, PhD, M.Sc. Research Associate Professor Institute for Immunology and Informatics University of Rhode Island 80 Washington St. Room 334B Providence, RI 02903 Tel: (401) 277-5309 Email: mathewa@uri.edu	The VRC will send coded blood/PBMCs specimens to Anuja Mathew at the University of Rhode Island. The samples will be used to assess adaptive immunity to flaviviruses including ZIKV. Dr. Matthew and her group will assess B cell and antibody responses (in supernatants) and characterize Flavivirus specificity. Only non-identifying demographic data may be provided to facilitate the data analysis.
Gregory A. Poland, M.D., MACP, FIDSA, FRCP Director, Mayo Vaccine Research Group 611C Guggenheim Building Mayo Clinic and Foundation 200 First Street, SW Rochester, MN 55905 Tel: (507) 284-4968 Email: poland.gregory@mayo.edu	The VRC will send coded blood/PBMCs specimens to the Mayo Vaccine Research Center. These samples will be used to characterize T-cell and immunologic responses to Zika. Only non-identifying demographic data may be provided to facilitate the data analysis.

Allison M.W. Malloy, MD, MSc Department of Pediatrics Infectious Disease Faculty F. Edward Hebert School of Medicine - "America's Medical School" Uniformed Services University of the Health Sciences (USU) 4301 Jones Bridge Road Rm A3028 Bethesda, Maryland, 20814 301-295-3733 allison.malloy@usuhs.edu	The VRC will send coded blood specimens to Allison Malloy at the Uniformed Services University of the Health Sciences. These samples will be used for analysis of T cells and dendritic cells from healthy volunteers for response to natural influenza virus infection. Only non-identifying demographic data may be provided to facilitate the data analysis.
Andrew Ward, Ph.D. Department of Integrative Structural and Computational Biology The Scripps Research Institute 10550 North Torrey Pines Road, La Jolla, CA 92037 (858) 784-7320 andrew@scripps.edu	The VRC will send coded serum samples to Andrew Ward at the Scripps Research Institute. These samples will be used to determine the epitopes on the HKU-1 coronavirus spike protein that are bound by polyclonal antibodies. Only non-identifying demographic data may be provided to facilitate the data analysis.
Surender Khurana, Ph.D. Div. of Viral Products Center for Biologics Evaluation and Research (CBER) US Food and Drug Administration (FDA) Bldg-52/72, Rm-1230 10903 New Hampshire Avenue Silver Spring, MD-20993 (240) 402-9632 Surender.Khurana@fda.hhs.gov	The VRC will send coded serum samples to Surender Khurana at CBER. These samples will be used for antibody analysis. Only non-identifying demographic data may be provided to facilitate the data analysis.
Carl Hansen, Ph.D. Director & CEO AbCellera Biologics Inc. 2215 Yukon Street Vancouver, BC V5Y 0A1 (778) 945-8384 carl.hansen@abcellera.com	The VRC will send coded blood samples to Carl Hansen at AbCellera. These samples will be used for antibody identification analysis. Only non-identifying demographic data may be provided to facilitate the data analysis.

APPENDIX III: TEMPLATE SKIN BIOPSY CONSENT

The sample informed consent forms are provided to guide development of a site-specific consent form. Only IRB-approved consent forms will be used to consent subjects for study participation.

Title: VRC 200: A Multicenter Specimen Collection Protocol to Obtain Human Biological Samples for Research Studies

Skin Biopsy Consent

INTRODUCTION

We invite you to take part in a research study at the [insert name of institution].

First, we want you to know that:

Taking part in [insert name of institution] research is entirely voluntary.

You may choose not to take part, or you may withdraw from the study at any time. In either case, you will not lose any benefits to which you are otherwise entitled. However, to receive care at the [insert name of institution], you must be taking part in a study or be under evaluation for study participation.

You may receive no benefit from taking part. The research may give us knowledge that may help people in the future.

Second, some people have personal, religious or ethical beliefs that may limit the kinds of medical or research treatments they would want to receive (such as blood transfusions). If you have such beliefs, please discuss them with your [insert name of institution] doctors or research team before you agree to the study.

Now we will describe this research study. Before you decide to take part, please take as much time as you need to ask any questions and discuss this study with anyone at [insert name of institution], or with family, friends or your personal physician or other health professional.

PURPOSE OF THE STUDY

You are participating in a protocol for the donation of blood, tissue, or other samples for laboratory research. This consent is to offer you the choice of making a skin biopsy donation. Skin biopsy samples can be useful in laboratory research.

A skin biopsy is a medical procedure that removes a small piece of skin. A separate consent for the skin biopsy is needed for two reasons. First, you may choose not to have a skin biopsy. Second, you should understand the way a skin biopsy is done and the risks of a skin biopsy before deciding whether to have one.

If you have a skin biopsy, it will be done at the [insert name of institution]. You will also be treated there if any side effects of the skin biopsy occur.

You will be told of any new information learned during this study that might cause you to change your mind about having a skin biopsy. When a skin biopsy is collected for research in this study, it is usually not sent to the regular hospital lab for a "pathology" report. If it is sent to see if there are any abnormal medical conditions, then you will be told before it is sent and will be informed of the result. The report will be in your medical record. Samples given to research labs and results of any test performed will be labeled only with your study identification number. The results of any tests done by research laboratories with your skin sample will <u>not</u> be in your medical record.

STUDY PROCEDURES

A skin biopsy is done in an outpatient clinic. You will receive a medicine such as lidocaine with epinephrine to reduce pain and bleeding. Medicine to reduce pain is called an anesthetic. The anesthetic may be given by injection or applied to the skin at the place where the skin biopsy will

be done. The anesthetic may sting briefly. If you have ever had an allergic reaction to a numbing medicine, such as novocaine or lidocaine, which are commonly used by dentists or surgeons, do not sign this consent until the details of your allergic reaction have been discussed with a study doctor.
After the skin is numb, a sharp, hollow instrument will be used to remove a small, circular piece of skin. The circle will be about the size of a pencil eraser. This biopsy method is called a "punch biopsy." After the punch biopsy, the skin may be closed with one or two stitches. You must follow the directions given to you for keeping the area clean until it heals. You must return to the clinic for the appointment given to you to have the stitches removed several days later. Careful methods and clean equipment will be used to prevent infection.
If you are invited to have a skin biopsy for research because it is known to be an area being treated for a local infection, then photos may be taken. You must inform the clinic promptly if you have any fever, swelling, increased pain or increased area of infection.

RISKS OF SKIN BIOPSY
Any time the skin is opened there is a chance of infection. If there is a known infection at the biopsy site then healing may take longer. Infection after a skin biopsy is rare and care will be taken to try to prevent infection. You may have pain or discomfort during the skin biopsy or while it is healing. You may have a very small amount of bleeding right after the skin biopsy. You will have a small scar. If you have skin that tends to form large scars of the type called "keloids," then you will have risk of a keloid forming at the biopsy area. A history of keloid formation increases the risk for keloid scarring from the skin biopsy. If you have a known history of keloid scarring you are advised to inform the study staff and not have a skin biopsy that is only for research purposes.
Rarely, the anesthetic medicine used to numb the skin may cause an allergic reaction. In rare cases allergic reactions to medications can be life threatening. In rare cases anesthetic medications can cause an abnormal heart rhythm. The anesthetic may also interact with certain other medicines to cause serious side effects. Be sure to review all your medications and drug use with the study staff before agreeing to have a local anesthetic. Certain antidepressant medicines and illicit drugs such as cocaine are among the drugs that can react with anesthetics to cause side effects.

BENEFITS
You may have no benefit from the skin biopsy. If your skin has a medical condition you may learn more about the cause of the problem.

COSTS TO YOU FOR YOUR PARTICIPATION
There will be no charge to you or your health insurance company for the skin biopsy or care of the skin biopsy. However, the costs of any other medical care during the period will be charged to you or your insurance company.

PAYMENT TO YOU FOR YOUR PARTICIPATION

[Site specific information]

You will be paid [insert amount] above the usual compensation for a visit that includes a skin biopsy. The skin biopsy stitches will be removed about 7-10 days later.

Compensation will be provided [add site-specific time for when compensation will be provided].

Total compensation is based on the number of study clinic visits and the type of sample collection performed. Your compensation may need to be reported to the Internal Revenue Service (IRS) as taxable income.

ALTERNATIVES

You may choose to not have a skin biopsy.

OTHER PERTINENT INFORMATION

1. Confidentiality. When results of an NIH research study are reported in medical journals or at scientific meetings, the people who take part are not named and identified. In most cases, the [insert name of institution] will not release any information about your research involvement without your written permission. However, if you sign a release of information form, for example, for an insurance company, the [insert name of institution] will give the insurance company information from your medical record. This information might affect (either favorably or unfavorably) the willingness of the insurance company to sell you insurance.

The Federal Privacy Act protects the confidentiality of your [insert name of institution] medical records. However, you should know that the Act allows release of some information from your medical record without your permission, for example, if it is required by the Food and Drug Administration (FDA), members of Congress, law enforcement officials, or authorized hospital accreditation organizations.

2. Policy Regarding Research-Related Injuries. The [insert name of institution] will provide short-term medical care for any injury resulting from your participation in research here. In general, no long-term medical care or financial compensation for research-related injuries will be provided by the National Institutes of Health, [insert name of institution], or the Federal Government. However, you have the right to pursue legal remedy if you believe that your injury justifies such action.

3. Payments. The amount of payment to research volunteers is guided by the [insert name of institution] policies. In general, patients are not paid for taking part in research studies at the [insert name of institution]. Reimbursement of travel and subsistence will be offered consistent with [insert name of institution] guidelines.

4. Problems or Questions. If you have any problems or questions about this study, or about your rights as a research participant, or about any research-related injury, contact the Principal Investigator, [insert name], at [insert phone number], or Study Coordinator [insert name] at [insert phone number].

You may also call the Clinical Center Patient Representative at (301) 496-2626.

5. Consent Document. Please keep a copy of this document in case you want to read it again.

COMPLETE APPROPRIATE ITEM(S) BELOW:

Adult Patient's Consent

I have read the explanation about this study and have been given the opportunity to discuss it and to ask questions. I hereby consent to take part in this study.

Signature of Adult Patient/Legal Representative	Date	Print Name

THIS CONSENT DOCUMENT HAS BEEN APPROVED FOR USE FROM [insert date] THROUGH [insert date].

Signature of Investigator	Date	Signature of Witness	Date
Print Name		Print Name	

APPENDIX IV: REMOTE SAMPLE COLLECTION PROCEDURES

Procedures for Obtaining Informed Consent Over the Telephone and Conducting a Remote Enrollment into VRC 200 (03-I-0263)

Obtaining consent by telephone may be used for this protocol when a subject with unusual or difficult to find characteristics that are key to research being conducted does not reside locally and is willing to have a medical care provider collect research blood samples for shipment to the VRC.

The process for obtaining consent by telephone is as follows:

- The Clinical Staff will provide forms needed for the offsite admissions process, if needed, and a current copy of the protocol consent document for remote enrollments. The Clinical Staff will also provide appropriate return-addressed shipper(s) for returning the admissions forms, signed consent document and samples collected.
- After allowing time for receipt and review of the consent document, a Clinical Staff member who is authorized to obtain consent for the protocol will contact the subject by telephone at a mutually agreeable time to discuss the consent in the presence of a witness who is with the subject.
- The Clinical Staff will ask the subject to verify his/her identity by stating their first and last name, and date of birth.
- Once verification is determined, the Clinical Staff will review the elements of the consent with the subject.
- The Clinical Staff will allow the subject to verbalize any questions or concerns and will answer all questions to the satisfaction of the subject.
- If the subject agrees to consent, the Clinical Staff will inform the subject that he/she will be placed on a speakerphone so that the audible consent can be witnessed by a witness present with the staff member.
- Each witness will state his/her name. Each witness must be an adult. The witness present in the room with the Clinical Staff member will be another Clinical Trials Core staff member.
- For the witnesses, the subject will repeat his/her own first and last name, date of birth, and read the protocol name and number from the consent document.
- The subject will sign, date and time his/her copy of the consent document. The witness with the subject will also sign and date the consent document.
- The manner of obtaining consent, date, time and the names of the person administering the consent, providing consent and the name of the witness will be documented in the research record.
- Once the consent document is received by the site and checked for accuracy, it will be signed and dated with the day the consent process was conducted; typically this will be a date prior to when the original is received. The date the original is received by the site will be documented in the research record. The original document will be filed in the

medical record and a copy of the signed consent document will be mailed back to the subject.

The procedure for assignment of a study identification number, sample processing, and sample use is as follows:

The enrollment in the study database may be completed after the offsite admissions is completed and the telephone portion of the consenting is done and the subject and witness have verified verbally that the consent document is signed. Similarly, the blood samples may be collected by a qualified medical care provider that is with the subject after the telephone portion of the consenting is done. The offsite admissions form, consent document and sample may be sent in the same shipper or separate shippers as convenient to the persons involved. Before being sent to a research laboratory for processing, any label with a subject name or personal identifier will be removed and replaced with a label using the study identification number. The blood sample may be processed for proper storage upon arrival; however, it may not be used for research purposes until the signed consent document is received by the site.

INFORMED CONSENT FORM FOR REMOTE SAMPLE COLLECTION

The template informed consent forms are provided to guide development of a site-specific consent form. Only IRB-approved consent forms will be used to consent subjects for study participation.

Title: VRC 200: A Multicenter Specimen Collection Protocol to Obtain Human Biological Samples for Research Studies

VRC 200 Standard, for Consent by Telephone

INTRODUCTION

We invite you to take part in a research study at the [insert name of institution].

First, we want you to know that:

Taking part in [insert name of institution] research is entirely voluntary.

You may choose not to take part, or you may withdraw from the study at any time. In either case, you will not lose any benefits to which you are otherwise entitled. However, to receive care at the [insert name of institution], you must be taking part in a study or be under evaluation for study participation.

You may receive no benefit from taking part. The research may give us knowledge that may help people in the future.

Second, some people have personal, religious or ethical beliefs that may limit the kinds of medical or research treatments they would want to receive (such as blood transfusions). If you have such beliefs, please discuss them with your [insert name of institution] doctors or research team before you agree to the study.

Now we will describe this research study. Before you decide to take part, please take as much time as you need to ask any questions and discuss this study with anyone at [insert name of institution], or with family, friends or your personal physician or other health professional.

PURPOSE AND PROCEDURES

The purpose of this study is to collect biological specimens for research purposes. Parts of the blood are often needed in research studies. Other types of specimens sometimes needed for research are other blood components, body fluids (such as semen or urine), or secretions (for example, from the nose, mouth, vagina, penis or different skin areas). A skin sample (biopsy) is another type of specimen that is sometimes useful for research. .

Scientists at the Vaccine Research Center will use the samples collected for research studies of different diseases and immune system responses, including HIV, hepatitis, responses to infections, vaccinations and other medical research. Even if you do not have a disease, your samples can be used to try to discover ways to prevent or treat medical conditions. Standard approved medical procedures will be used to collect these samples.

The following must be true for you to be eligible for the study:

- You must be age 18 years or older
- You must be able and willing to complete the informed consent process
- You must be willing to provide samples that will be stored for future research
- You must be able to provide proof of your identity

You must sign this consent before a research sample can be collected. This consent is for participants who are enrolling in the study through a consent process done over the telephone or

if already enrolled, having a sample collected remotely for shipment to the Vaccine Research Center at the NIH. The blood sample will be collected by a local medical care provider for this shipment.

Your consent to enroll will be consent to collect samples for up to a one-year period. After that, if more samples are needed and you wish to continue participating in this protocol, you must sign a new consent form each year.

As many as 3,000 people may participate in this study. The actual number may be lower or be higher, depending on the need for research samples and the willingness of subjects to participate. Most subjects will have only one or a few samples collected.

BLOOD SAMPLES

Blood will be drawn by standard phlebotomy techniques from veins in the arms only. Typically, about 100 mL (about 6 tablespoons) of blood will be drawn from your arm for testing. More or less may be drawn depending upon the research needs. The study staff will discuss the blood draw plan with you before starting.

HEPATITIS SCREENING

Some of the blood drawn from you as part of this study may be used to screen for different types of viral liver infections, such as hepatitis. If the tests show evidence of hepatitis or other medical conditions, you will be informed of the results. If you do not have a regular physician, the study team will assist in referring you to an appropriate physician for evaluation.

GENETIC TESTING

Some of the blood drawn from you as part of this study will be used for genetic tests. Some genetic tests are done in research studies to see if genetic differences in people cause different types of immune responses. Your blood sample used in these genetic tests will not have your name on it and the results will not be in your medical record. These tests are not used to check your health and we will not tell you the results.

NIH Site only: A special genetic test, called HLA typing, may be done by the NIH Clinical Center medical laboratory. These results will be in your medical record but they will not be used to check your health. Any genetic testing, including HLA typing, is for research purposes only. Any genetic information collected or learned about you will be kept confidential. Medical records, including HLA test results, are kept securely. We will not give any genetic information that is in your medical record to anyone without your permission.

If HLA typing is done in a research laboratory, the result will not be included in your medical record.

HIV TESTING

As part of this study, we will test you for infection with the Human Immunodeficiency Virus (HIV), the virus that causes AIDS. If you are infected with HIV you will still be able to participate in this study. We will tell you what the results mean, how to find care, how to avoid infecting others, how we report HIV infection, and the importance of informing your partners at possible risk because of your HIV infection.

STORED SAMPLES

To be eligible for the study, you must also be willing to allow some of your blood samples to be stored for future research on HIV disease, the immune system, or other medical conditions.

Generally, the results from the research done with your stored samples will not be given to your private doctor and will not be put in your medical record. This is because the test results, unlike routine medical testing, may be experimental or preliminary. The relevance of these tests to your care may be unknown. However, at your request, the results of any research tests will be discussed with you or your physician by one of the investigators.

Labeling of stored samples

Your stored samples will be labeled with a code (such as a number) that only the study team can link to you. Any identifying information about you will be kept confidential to the extent permitted by law.

Future studies

Your samples may be kept in storage for a long time and used in the future by medical researchers. When the study team shares your samples, they will share it with only a code on it. Some information about you, such as your gender, age, health history, or ethnicity may also be shared with other investigators.

Your stored materials will be used only for research and will not be sold or used for treating other people. The research done with your materials may be used to develop new products in the future, but you will not receive payment for such products.

RISKS

Blood drawing may cause pain, bruising, and, rarely, infection at the site where the blood is taken.

Collection of samples by swabs rubbing over the inside of the nose, inside the mouth vagina, penis or skin can cause temporary discomfort.

BENEFITS

There will be no direct benefit to you for participating in this protocol. The knowledge gained through this research may benefit others in the future.

UNKNOWN RISKS OR BENEFITS

Some routine medical tests may be performed during study participation. You may learn new information about your health. Receiving a new diagnosis may be stressful. You may feel that learning new information about your health is a benefit of study participation. Or you may feel this is a risk of study participation.

ALTERNATIVES

The study procedures are not being done to treat a medical condition. You may choose not to participate in any or all of the procedures discussed.

COMPENSATION

[Site specific information]

You will be compensated [insert amount] for blood samples collected by needle stick. Other payments for time and inconvenience of study visits may be offered in accordance with [insert institution] guidelines.

Compensation will be provided [add site-specific time for when compensation will be provided].

Total compensation is based on the number of study clinic visits and the type of sample collection performed. Your compensation may need to be reported to the Internal Revenue Service (IRS) as taxable income.

REASONS FOR REMOVING YOU FROM THE STUDY WITHOUT YOUR CONSENT

You may be removed from the study without your consent for the following reasons:

- The NIH doctor feels that staying in the study is harmful to you.
- The study is canceled or stopped.
- You don't keep appointments or follow study procedures.

COSTS TO YOU FOR YOUR PARTICIPATION

There will be no charge to you or your health insurance company for any of the costs that are directly related to this study. However, the costs of any other medical care you may need during this period will be your responsibility. You will not have to pay the cost of shipping the sample or completed forms.

OTHER PERTINENT INFORMATION

1. Confidentiality. When results of an NIH research study are reported in medical journals or at scientific meetings, the people who take part are not named and identified. In most cases, the [insert name of institution] will not release any information about your research involvement without your written permission. However, if you sign a release of information form, for example, for an insurance company, the [insert name of institution] will give the insurance company information from your medical record. This information might affect (either favorably or unfavorably) the willingness of the insurance company to sell you insurance.

The Federal Privacy Act protects the confidentiality of your [insert name of institution] medical records. However, you should know that the Act allows release of some information from your medical record without your permission, for example, if it is required by the Food and Drug Administration (FDA), members of Congress, law enforcement officials, or authorized hospital accreditation organizations.

2. Policy Regarding Research-Related Injuries. The [insert name of institution] will provide short-term medical care for any injury resulting from your participation in research here. In general, no long-term medical care or financial compensation for research-related injuries will be provided by the National Institutes of Health, [insert name of institution], or the Federal Government. However, you have the right to pursue legal remedy if you believe that your injury justifies such action.

3. Payments. The amount of payment to research volunteers is guided by the [insert name of institution] policies. In general, patients are not paid for taking part in research studies at the [insert name of institution]. Reimbursement of travel and subsistence will be offered consistent with [insert name of institution] guidelines.

4. Problems or Questions. If you have any problems or questions about this study, or about your rights as a research participant, or about any research-related injury, contact the principal investigator, [insert name] at [insert phone number], or Study Coordinator [insert name] at [insert phone number].
You may also call the Clinical Center Patient Representative at (301) 496-2626.

5. Consent Document. Please keep a copy of this document in case you want to read it again.

COMPLETE APPROPRIATE ITEM(S) BELOW:

Adult Patient's Consent
I have read the explanation about this study and have been given the opportunity to discuss it and to ask questions. I hereby consent to take part in this study.

Signature of Adult Patient/Legal Representative	Date	Print Name

THIS CONSENT DOCUMENT HAS BEEN APPROVED FOR USE FROM [insert date] THROUGH [insert date].

Signature of Investigator	Date	Signature of Witness	Date
Print Name		Print Name	

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves,

Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Katie Clepp[katie.clepp@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 1/7/2021 12:31:13 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - January 19th

Hi Everyone,

On Tuesday, January 5th, Dr. Ghazi Kayali kicked off the New Year by giving a wonderful presentation on **"Incidence, household transmission, and neutralizing antibody seroprevalence of COVID-19 in Egypt: Results of a community-based cohort".** Thank you to our presenter and to those that were able to join.

As a reminder, this meeting will be canceled on Tuesday, January 12th and will resume Tuesday, January 19th with Dr. Rogan Grant giving a presentation on "**Self-sustaining circuits between infected alveolar macrophages and T cells in severe SARS-CoV-2 pneumonia".**

Have a wonderful weekend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch

DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Location: https://zoom.us/j/94857161546?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly call-replacement link

Start Time: Thur 1/14/2021 12:30:00 PM (UTC-06:00)

End Time: Thur 1/14/2021 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Hi All,

For some reason, people are having trouble accessing the call with the existing link. I am sending a new link for today's call only.

Toni

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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Ferris, Martin Thomas[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Michael Davis[madphd@uw.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Fri 1/15/2021 1:51:39 PM (UTC-06:00)
Subject: Changing day of SIG U19 call

Hi Everyone,
NIH has scheduled a recurring call that causes a conflict for Ralph on our SIG U19 call. I propose we change the Thursday calls, same time , but on the 1st, 3rd, or 4th Thursday of the month. Can you let me know which would work best for you.
Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; 'Marta Gaglia'[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves,

Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Katie Clepp[katie.clepp@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 1/14/2021 2:02:41 PM (UTC-06:00)
Subject: RE: SARS-CoV-2 Weekly Investigators Meeting - January 19th

Happy Thursday almost Fri-Yay!

Just a reminder that we will be meeting on Tuesday, January 19th with Dr. Rogan Grant giving a presentation on "**Self-sustaining circuits between infected alveolar macrophages and T cells in severe SARS-CoV-2 pneumonia".**

If you are interested in presenting, please reach out to me. I know there's some really important research being conducted by this group and would like encourage you all to highlight your data.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS

5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C]
Sent: Thursday, January 7, 2021 1:31 PM
Subject: SARS-CoV-2 Weekly Investigators Meeting - January 19th

Hi Everyone,

On Tuesday, January 5th, Dr. Ghazi Kayali kicked off the New Year by giving a wonderful presentation on **"Incidence, household transmission, and neutralizing antibody seroprevalence of COVID-19 in Egypt: Results of a community-based cohort".** Thank you to our presenter and to those that were able to join.

As a reminder, this meeting will be canceled on Tuesday, January 12th and will resume Tuesday, January 19th with Dr. Rogan Grant giving a presentation on "**Self-sustaining circuits between infected alveolar macrophages and T cells in severe SARS-CoV-2 pneumonia".**

Have a wonderful weekend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C

(CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]
Cc: Caniza, Miguela[Miguela.Caniza@STJUDE.ORG]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 1/25/2021 3:35:31 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - January 26th
nCoV PI call attendee list.xlsx

Hi Everyone!

On Tuesday, January 19th, Rogan Grant gave a wonderful presentation on "**Self-sustaining circuits between infected alveolar macrophages and T cells in severe SARS-CoV-2 pneumonia".** Thank you to our presenter and to those that attended.

Tomorrow, January 26th, Dr. Thomas Friedrich will be sharing some information on "**SARS-CoV-2 variants in Wisconsin**". Hope you all are able to join!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch

DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	5-Jan	19-Jan
Erik Stemmy	x	x
Marciela DeGrace	x	
Rebecca Lampley	x	x
Aditya Gaur		
Adolfo Garcia-Sastre	x	x
Adrienne Randolph		
Aisha Souquette		
Alan Embry		
Alexander Misharin		x
Ali Ellebedy	x	
Alicia Fry	x	
Alison Augustine		
Alvaro Ordonez		x
Amanda Perofsky		
Amy Kuehn	x	x
Amy Krafft		
Andrea Pruijssers		
Andrea Sant		
Andrew Mesecar		
Andrew Pekosz	x	x
Andy Mesecar		
Andrzej Joachimiak	x	x
Aneesh Mehta		
Angela Rasmussen		
Ann Eakin		
Anice Lowen	x	
Anita McElroy		
Anne Piantadosi		
Aron Hall	x	x
Asun Mejias	x	
Atsuo Kuki		x
Aubree Gordon	x	x
Barry Rockx		
Becky Dutch		
Ben Cowling		
Ben Larman		
Benjamin Miller		x
Ben Singer		x
Ben Tenoever		x
Bernard Lafont		
Bin Zhou		
Biao He		

Brooke Bozick	x	
Carly Dillen	x	x
Carlie Williams		x
Catherine Luke		
Catherine Sutcliffe	x	
Claire Midgley	x	
Charles Russell	x	x
Chelsea Lane	x	
Chris Brooke		
Christopher Hsu		
Chris Roberts		
Clint Florence		
Conrad Mallia		
Colleen Jonsson	x	x
Connie Schmaljohn	x	x
Courtney Comar (Susan Weiss lab)		
Daniel Blanco-Melo		
Daniel Olson	x	
Daved Fremont		
David Martinez		
David Renner (Susan Weiss lab)		
David Topham		x
David Tribble		
David Wentworth		
Deborah Lynn Fuller		
Denis Nash	x	
Derek Eisnor		x
Diana Finzi		
Diane Post		
Diego Hijano		
Don Milton	x	x
Donna Neu	x	x
Doris Strome		
Edwin Asturias		x
Elizabeth Bartom		x
Elizabeth Fitzpatrick	x	
Emma Hodcroft		
Erica Raterman		
Evans		
Eunchung Park	x	x
Eun Mi Lee		
Florian Krammer	x	x
Francisco Chaves	x	
Frederic Bushman		
Gabriele Neumann	x	x

Gage Moreno		
Gavin Smith		
Ghazi Kayali	x	
Glen Abedi		
Grace Tietz		
Greg Deye		
Hana Golding		x
Harm van Bakel		
Holly Hammond		x
Hui-Ling Yen		
Ian Crozier	x	x
Ian Plumb		
Isabelle Phan		
Ishwar Chandramouliswaran		
Ivan Marazzi		
Jacob Hou		
Jacques Banchereau		
Jae Jung		
James Hoffman		
James Kobie	x	x
Jared Evans	x	
Jason Goldstein		
Jayeeta Dutta		
Jean Patterson		
Jenni		
Jennifer German		
Jennifer Gordon		
Jennifer Hyde		
Jennifer Kishimori		
Jens Wrammert		
Jeremy Crawford		
Jesse Erasmus		
Jessica Ho		
Ji Lee		
Jimmy Logue		
Jim Chappell		
jmankow1		
Joe Breen		
Jonathan Runstadler	x	x
Joseph Mankowski		x
Judy Hewitt		
Juergen Richt	x	
Julia Biggins		x
Kanta Subbarao		
Karla Satchell		

Katarina Braun		
Katharina Koelle	x	
Katie Mulka		x
Katy Shaw-Saliba		
Katherine Fenstermacher	x	x
Kimberly Coca		
Kimberly Stemple		
Korin Bullen		
Kristina Lu		
Kris Emo		
Kris Lambert		
Kristen Hildebrand	x	x
Laura Hughes		
Lauren Sauer		
Larry Anderson		x
Larry Wolfraim		
Leo Poon		
Liliana Brown	x	
Lisa Hensley		
Lisa Lindesmith		
Lisa Miorin		
Liz		
Lori Newman		
Lucy Cong		x
Luis Martinez-Sobrido	x	
Mackenzie Zendt		
Malik Peiris		
Marie Killerby		
Marina Lee	x	
Mark Challberg		
Mark Denison	x	x
Mark Heism		
Mark Pallansch		
Mark Robien	x	x
Mark Sangster		x
Mark Simons		
Mark Williams		x
Marlene Espinoza	x	x
Marta Gaglia		x
Martha Nelson		
Martin Blaser	x	x
Martin Linster		x
Mary Allen Staat	x	x
Masato Hatta (UW)		
Mathew Esona		

Matt Frieman	x	x
Maureen McGargill	x	x
Mehul Suttar		
Melissa Rolfes		
Melissa Uccellini	x	x
Mercy Prabhudas		
Michael Bryan		
Michael Chan		
Michael Martin		
Mike Cooper		
Mike Holbrook	x	x
Mindy Davis		
Missy		
Monica McNeal		x
Nat Moorman		
Nasia Safdar		x
Natalie Thornburg		
newmanlm		
Nidia Trovao		
Noffisat Oki		
Octavio Ramilo	x	
Oluwasanmi Adenaiye	x	x
Pamela McKenzie	x	x
Patrice Becker	x	
Paul McCray	x	x
Paul Jacob Bueno de Mesquita	x	
Paul Thomas		
Peter Daszak		
Peter Halfmann		
Peter Myler		
Peter Palese		x
Phuong Nguyen-Contant		
Punam Mathur	x	x
Qifang Bi		
Rachel Graham		
Rafael Medina		x
Ralph Baric		
Randall Tressler		
Raul Andino		
Rebecca Dutch		x
Reed Johnson	x	
Reed Shabman	x	x
Richard Rothman		
Richard Sciotti		
Richard Webby	x	

Rick Bushman		
Robert Johnson		x
Robert Schwartz	x	
Ron Fouchier		
Rudra Goudavet		
Russell Ray		x
Ryan Langlois		
Ryan Ranallo	x	x
Sabra Klein	x	
Sander Herfst		
Sanjay Jain		x
Sanmi Adenaiye		
Samantha Loeber		
Sara Cherry	x	x
Sara Woodson		
Scott Hensley		
Scott Strome	x	x
Sean Whelan		x
Seema Lakdawala		
Shahida Baqar	x	x
Sharon Saydah		
Sheldon Tai	x	x
Shiho Chiba		x
Simon Anthony		
Sing Sing	x	
Sook Ho		
Sonnie Kim	x	x
Stacey Schultz-Cherry	x	x
Stacy Ferguson	x	x
Stanley Perlman		x
Stephen Tompkins		
Steve Smiley		
Steve Tsang		
Sue Cammarata		x
Surender Khurana		x
Susan Gerber		
Susan Weiss		x
Teresa Hauguel	x	
Thames P	x	x
Theresa Fitzgerald		
Thomas Friedrich	x	
Tim Burgess		x
Timothy Sheahan		
Tristan		
Troy Sutton	x	x

Tom Fabrizio	x	
Tori Baxter		
Vanessa Merino		
Vernon Musale		
Vineet Menachery		
Viviana Simon		
Walt Orenstein		x
Weina Sun		
Wesley C Van Voorhis	x	x
William Karesh		
William Kilembe		
William Florence		
William Morgenlander		
Willy Valdivia		
Wiriya Rutvisuttinunt	x	
Wolfgang Leitner		
Xizhi Guo		
Yoshihiro Kawaoka		

To: Thomas Friedrich[tfriedri@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Simons, Mark[mark.simons@usuhs.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu];

asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Sara Monteiro Pires[smpi@food.dtu.dk]; José Luis Peñalvo[jpenalvo@itg.be]; Edmond Ng[Edmond.Ng@lshtm.ac.uk]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [F][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]

Cc: Jacques Banchereau[Jacques.Banchereau@jax.org]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Marcum, Chris (NIH/NHGRI) [E][chris.marcum@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Thur 2/4/2021 1:22:23 PM (UTC-06:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting - February 9th

nCoV PI call attendee list.xlsx

Hi Everyone,

I hope you all enjoyed both of the presentation on Tuesday, February 2nd.

Our double feature included:

Drs. Dave O'Connor and Thomas Friedrich

"COVID on campus: investigating links between SARS-CoV-2 transmission among college students and the broader community"

And

Dr. Denis Nash
"Serologic outcomes in a national, community-based cohort of U.S. adults: the CHASING COVID Cohort Study"

Thank you to all of out presenters and those in attendance.

Next Tuesday, February 9th, Dr. Sara Monteiro Pires will give a presentation on **"European Burden of Disease Network's COVID-19 activities: Fostering collaboration and methodological development".**

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	2-Feb
Erik Stemmy	x
Marciela DeGrace	
Rebecca Lampley	x
Aditya Gaur	
Adolfo Garcia-Sastre	x
Adrienne Randolph	
Aisha Souquette	
Alan Embry	
Alexander Misharin	
Ali Ellebedy	
Alicia Fry	
Alison Augustine	x
Allison Cline	x
Alvaro Ordonez	x
Amanda Perofsky	
Amy Kuehn	x
Amy Krafft	x
Andrea Pruijssers	
Andrea Sant	
Andrew Mesecar	
Andrew Pekosz	x
Andy Mesecar	
Andrzej Joachimiak	x
Aneesh Mehta	
Angela Rasmussen	
Ann Eakin	
Anice Lowen	x
Anita McElroy	
Anne Piantadosi	
Aron Hall	
Asun Mejias	x
Atsuo Kuki	
Aubree Gordon	
Barry Rockx	
Becky Dutch	
Ben Cowling	
Ben Larman	
Benjamin Miller	
Ben Singer	
Ben Tenoever	
Bernard Lafont	x
Betty Poon	x

Bin Zhou	
Biao He	
Brooke Bozick	
Carly Dillen	x
Carlie Williams	x
Catherine Luke	
Catherine Sutcliffe	x
Claire Midgley	x
Charles Russell	x
Chelsea Lane	x
Chris Brooke	
Christopher Hsu	
Chris Marcum	x
Chris Roberts	
Clint Florence	
Conrad Mallia	
Colleen Jonsson	x
Connie Schmaljohn	x
Courtney Comar (Susan Weiss lab)	
Daniel Blanco-Melo	
Daniel Olson	x
Daved Fremont	
David Haslam	x
David Martinez	
David McDonald	x
David Meekins	
David O'Connor	x
David Renner (Susan Weiss lab)	
David Topham	x
David Tribble	x
David Wentworth	
Deborah Lynn Fuller	
Denis Nash	x
Derek Eisnor	x
Diana Finzi	
Diane Post	
Diego Hijano	
Don Milton	x
Donna Neu	x
Doris Strome	
Dustin Currie	x
Edwin Asturias	
Elizabeth Bartom	
Elizabeth Fitzpatrick	
Emma Hodcroft	

Erica Raterman	
Evans	
Eunchung Park	x
Eun Mi Lee	
Florian Krammer	x
Francisco Chaves	x
Frederic Bushman	
Gabriele Neumann	x
Gage Moreno	x
Gavin Smith	
Gene Millar	x
Geoffrey Gottlieb	x
Ghazi Kayali	x
Glen Abedi	
Grace Tietz	
Greg Deye	
Hana Golding	x
Hannah Segaloff	x
Harm van Bakel	x
Holly Hammond	
Hui-Ling Yen	
Ian Crozier	x
Ian Plumb	
Isabelle Phan	
Ishwar Chandramouliswaran	
Ivan Marazzi	
Jacob Hou	
Jacques Banchereau	
Jae Jung	
James Hoffman	
James Kobie	x
James Mancuso	x
Jared Evans	x
Jason Goldstein	x
Jason Hataye	x
Jayeeta Dutta	
Jean Patterson	
Jeffrey Herrmann	x
Jenni	
Jennifer German	
Jennifer Gordon	
Jennifer Hyde	
Jennifer Kishimori	
Jens Wrammert	
Jeremy Crawford	

Jesse Erasmus	
Jessica Ho	
Ji Lee	
Jimmy Logue	
Jim Chappell	
jmankow1	
Joana	x
Joe Breen	x
Jonathan Runstadler	x
Joseph Mankowski	
Judy Hewitt	
Juergen Richt	x
Julia Biggins	
Kanta Subbarao	
Karla Satchell	
Katarina Braun	x
Katharina Koelle	x
Katie Mulka	
Katy Shaw-Saliba	
Katherine Fenstermacher	
Keri Althoff	
Kimberly Coca	
Kimberly Stemple	x
Korin Bullen	
Kristina Lu	
Kris Emo	
Kris Lambert	
Kristen Hildebrand	x
Laura Hughes	
Lauren Sauer	
Larry Anderson	x
Larry Wolfraim	
Leo Poon	
Liliana Brown	x
Lisa Hensley	
Lisa Lindesmith	
Lisa Miorin	
Liz	
Lori Newman	
Lucy Cong	x
Luis Martinez-Sobrido	
Mackenzie Zendt	
Malik Peiris	
Marie Killerby	x
Marina Lee	x

Mark Challberg	
Mark Denison	x
Mark Heism	
Mark Pallansch	
Mark Robien	x
Mark Sangster	x
Mark Simons	x
Mark Williams	
Marlene Espinoza	x
Marta Gaglia	
Martha Nelson	x
Martin Blaser	x
Martin Linster	
Mary Allen Staat	x
Masato Hatta (UW)	
Mathew Esona	
Matt Frieman	x
Maureen McGargill	x
Mehul Suttar	
Melissa Rolfes	
Melissa Uccellini	
Mercy Prabhudas	x
Michael Bryan	
Michael Chan	
Michael Martin	
Mike Cooper	
Mike Holbrook	x
Mindy Davis	
Missy	
Monica McNeal	x
Nat Moorman	
Nasia Safdar	x
Natalie Thornburg	
newmanlm	
Nidia Trovao	
Noffisat Oki	
Octavio Ramilo	
Oluwasanmi Adenaiye	
Pamela McKenzie	x
Patrice Becker	
Paul McCray	x
Paul Jacob Bueno de Mesquita	
Paul Thomas	
Peter Daszak	
Peter Halfmann	

Peter Myler	
Peter Palese	
Phuong Nguyen-Contant	
Punam Mathur	x
Qifang Bi	
Rachel Graham	
Rafael Medina	x
Ralph Baric	
Randall Tressler	
Raul Andino	
Rebecca Dutch	x
Reed Johnson	
Reed Shabman	
Richard Rothman	
Richard Sciotti	
Richard Webby	
Richard Wunderink	x
Rick Bushman	
Robert Bruno	
Robert Johnson	
Robert Schwartz	x
Rogier van Doorn	x
Ron Fouchier	x
Rosemary McKaig	x
Rudra Goudavet	
Russell Ray	x
Ryan Langlois	
Ryan Ranallo	
Sabra Klein	x
Sander Herfst	
Sanjay Jain	
Sanmi Adenaiye	
Samantha Loeber	
Sara Cherry	
Sarah Cobey	x
Sara Woodson	
Scott Hensley	x
Scott Strome	x
Sean Whelan	
Seema Lakdawala	
Shahida Baqar	
Sharon Saydah	
Shelby O'Connor	
Sheldon Tai	x
Shiho Chiba	

Simon Anthony	
Sing Sing	
Sook Ho	
Sonnie Kim	
Stacey Schultz-Cherry	
Stacy Ferguson	x
Stanley Perlman	
Stephen Tompkins	x
Steve Smiley	
Steve Tsang	
Sue Cammarata	x
Surender Khurana	x
Susan Gerber	
Susan Weiss	x
Teresa Hauguel	
Thames P	x
Theresa Fitzgerald	
Thomas Friedrich	x
Tim Burgess	x
Timothy Sheahan	
Tristan	
Troy Sutton	x
Tom Fabrizio	
Tori Baxter	
Vanessa Merino	
Vernon Musale	
Vineet Menachery	
Viviana Simon	
Walt Orenstein	x
Weina Sun	
Wesley C Van Voorhis	x
William Karesh	
William Kilembe	x
William Florence	
William Morgenlander	
Willy Valdivia	
Wiriya Rutvisuttinunt	x
Wolfgang Leitner	
Xizhi Guo	
Yoshihiro Kawaoka	
Zach Pope	x

To: Mark Denison[mark.denison@vumc.org]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/VRC) [F][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Thur 2/20/2020 7:18:23 AM (UTC-06:00)
Subject: RE: nCoV weekly investigators meeting

Hello everyone,

As we discussed on the last call, it could be useful to share information certain experimental results, especially animal model work, in as close to real time as possible enable better planning of experiments by the entire group.

During the Zika response, the portal that was used for this was LabKey's Open Research Portal: https://openresearch.labkey.com/project/home/begin.view. This is a fully public portal.

Please consider if this platform might work, and we can discuss on our next call including any logistics and support needed for setting up accounts.

Thank you!

Marciela

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: Mark Denison; aneesh.mehta@emory.edu; Johnson, Reed (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg
Subject: nCoV weekly investigators meeting
When: Tuesday, February 18, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code: **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: Third Webinar for Systems Immunology Program

Start Time: Thur 4/1/2021 12:00:00 PM (UTC-06:00)

End Time: Thur 4/1/2021 1:00:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 10:01 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Leitner, Wolfgang (NIH/NIAID) [E]; Diercks, Alan; Bruce Beutler
Subject: Third Webinar for Systems Immunology Program
When: Thursday, April 1, 2021 2:00 PM-3:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

According to your availability, our third webinar will be held from 2:00 to 3:00 PM EDT on April 1st. **Richard Ulevitch's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

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From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: First Webinar for Systems Immunology Program

Start Time: Wed 3/17/2021 1:00:00 PM (UTC-06:00)

End Time: Wed 3/17/2021 2:00:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 9:51 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Diercks, Alan; Bruce Beutler; Leitner, Wolfgang (NIH/NIAID) [E]
Subject: First Webinar for Systems Immunology Program
When: Wednesday, March 17, 2021 3:00 PM-4:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

Thank you for your responses. I have set up the dates and times for our webinar according to your availability. The first webinar will be held from 3:00 to 4:00 PM EDT on March 17th. **Arlene Sharpe's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

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Meeting ID: 160 236 2422
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From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric; Graham PhD, Jessica B; Michael J Gale
Location:	https://zoom.us/j/99380423092?pwd=VS9iWnlZWDI0ZUppQ1VUVnVlWnc4dz09
Importance:	Normal
Subject:	SIG U19 Monthly Meeting
Start Time:	Thur 2/25/2021 12:30:00 PM (UTC-06:00)
End Time:	Thur 2/25/2021 1:30:00 PM (UTC-06:00)
Required Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Optional Attendees:	Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Good morning all,

The agenda for this call will be to discuss the upcoming Systems Immunogenetics annual meetings.

Best regards,
Toni

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Passcode: **552.136**

To: Rbaric@email.unc.edu[Rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Michael.Markie@F1000.com[Michael.Markie@F1000.com]
Sent: Sat 2/22/2020 7:19:38 AM (UTC-06:00)
Subject: your preprint on BioRxiv

Hi Ralph and Vincent,

I hope you are well.

I came across your preprint today (Mucin 4 Protects Female Mice from Coronavirus Pathogenesis) and thought that if you have yet to earmark it for publication in a specific journal then it would be a great fit for F1000Research. F1000Research is a post publication peer review journal that has a versioned publication system where any updates to studies can be made easily and keep readers up to date with any changes. All the peer review is open and we could publish the article formally as quickly as 7 days. We have a specific coronavirus area in our Disease Outbreaks gateway which is popular with the community due to our speed and transparency around research where it is vital to get the information out without haste.

If you think you might be interested in publishing with us, or if you have any questions then please do get in touch.

Regards

Michael Markie
Publishing Director, F1000 Platforms

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Location: https://zoom.us/j/99380423092?pwd= 552.101/CLP

Importance: Normal

Subject: Canceled: SIG U19 Monthly Meeting-Canceled

Start Time: Thur 4/22/2021 12:30:00 PM (UTC-05:00)

End Time: Thur 4/22/2021 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Today's call is canceled due to scheduling conflicts. We will resume calls in May.

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To: Diamond, Michael[mdiamond@wustl.edu]; Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; qtan@pathology.wustl.edu[qtan@pathology.wustl.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Cockrell, Adam[adam_cockrell@unc.edu]; Kocher, Jacob Frederick[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 5/5/2021 7:48:26 AM (UTC-05:00)
Subject: RE: hypergraphs paper accepted! need author approval

I agree. Please Add:
RSB has ongoing unrelated collaborations and/or sponsored research agreements with Moderna, VaxArt, Eli Lily, Pfizer, Takeda and Ridgeback Biosciences. Ralph

---

From: Diamond, Michael <mdiamond@wustl.edu>
Sent: Wednesday, May 5, 2021 7:47 AM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>; Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; qtan@pathology.wustl.edu; vimenach@utmb.edu; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Cockrell, Adam <adam_cockrell@unc.edu>; Kocher, Jacob Frederick <jacob.kocher@unc.edu>; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Baric, Ralph S <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>
Subject: Re: hypergraphs paper accepted! need author approval

We need to add a Conflict of Interests Statement

M.S.D. is a consultant for Inbios, Vir Biotechnology, and Fortressa Biotech and on the Scientific Advisory Boards of Moderna and Immunome. The Diamond laboratory has received unrelated funding support in sponsored research agreements from Moderna, Vir Biotechnology, Kaleido, and Emergent BioSolutions.

From: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Sent: Tuesday, May 4, 2021 5:57 PM
To: Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu <shufang.fan@wisc.edu>; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu <danielle.westhoffsmith@wisc.edu>; qtan@pathology.wustl.edu <qtan@pathology.wustl.edu>; vimenach@utmb.edu <vimenach@utmb.edu>; sheahan@email.unc.edu <sheahan@email.unc.edu>; adam_cockrell@unc.edu <adam_cockrell@unc.edu>; jacob.kocher@unc.edu <jacob.kocher@unc.edu>; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>
Subject: hypergraphs paper accepted! need author approval

Hello all,

I'm pleased to let you know that the paper "Hypergraph Models of Biological Networks to Identify Genes Critical to Pathogenic Viral Response" has been accepted to BMC Bioinformatics pending a couple of minor editorial fixes (e.g., numbering supplementary figures properly)! Thank you all for the work to get this research out! One of the final things that needs to be included in the paper is a statement that "all authors have read and approve this manuscript." That is what I'm writing about now. I've attached the version that's nearly final (I did already include that statement in the author contributions, so that I don't forget to get it in there). It's not terribly changed from the original version that you saw, and that is up on arXiv, but there were a few additions based on an initial round of revisions. Please read it through and let me know if you have any issues. Please reply back by the end of the week. If you're not able to read through it by then and would like more time let me know. If I don't hear from you I'll take that as approval.

Thank you again!

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Pacific Northwest National Laboratory
Phone: 206-528-3461

To: Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; qtan@pathology.wustl.edu[qtan@pathology.wustl.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]
From: Purvine, Emilie[Emilie.Purvine@pnnl.gov]
Sent: Tue 5/4/2021 5:57:17 PM (UTC-05:00)
Subject: hypergraphs paper accepted! need author approval
Hyperbio_centrality_paper (1).pdf

Hello all,

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From: Diamond, Michael[mdiamond@wustl.edu]
Sent: Wed 5/5/2021 6:47:17 AM (UTC-05:00)
Subject: Re: hypergraphs paper accepted! need author approval

We need to add a Conflict of Interests Statement

M.S.D. is a consultant for Inbios, Vir Biotechnology, and Fortressa Biotech and on the Scientific Advisory Boards of Moderna and Immunome. The Diamond laboratory has received unrelated funding support in sponsored research agreements from Moderna, Vir Biotechnology, Kaleido, and Emergent BioSolutions.

From: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Sent: Tuesday, May 4, 2021 5:57 PM
To: Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu <shufang.fan@wisc.edu>; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu <danielle.westhoffsmith@wisc.edu>; qtan@pathology.wustl.edu <qtan@pathology.wustl.edu>; vimenach@utmb.edu <vimenach@utmb.edu>; sheahan@email.unc.edu <sheahan@email.unc.edu>; adam_cockrell@unc.edu <adam_cockrell@unc.edu>; jacob.kocher@unc.edu <jacob.kocher@unc.edu>; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>
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Pacific Northwest National Laboratory

Phone: 206-528-3461

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 3/9/2020 2:18:27 PM (UTC-05:00)
Subject: FW: Sig Face to Face

Hello everyone,
With so many flights being cancelled, we decided to run this meeting virtually. It will be 11-5 ET and below is the link. I will be sending an agenda tomorrow.

Thank you
Toni

From: Graham, Rachel <rlgraham@email.unc.edu>
Sent: Monday, March 9, 2020 3:16 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>
Subject: RE: Sig Face to Face

Here is the call-in link:

SIG U19 Meeting

Wed, Mar 11, 2020 11:00 AM - 5:00 PM (EDT)

Please join my meeting from your computer, tablet or smartphone.
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Rachel Graham, Ph.D.
Assistant Professor
Baric Lab | UNC-Chapel Hill
(919) 966-4689

On Mar 9, 2020, 3:13 PM -0400, Baric, Toni C <antoinette_baric@med.unc.edu>, wrote:
~~~~~~~~~~~~

To: Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
Cc: Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]
From: Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]
Sent: Wed 6/2/2021 2:29:27 AM (UTC-05:00)
Subject: RE: Your article published in BMC Bioinformatics is now online

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From: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Sent: Tuesday, June 1, 2021 9:26 AM
To: Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; vimenach@utmb.edu; sheahan@email.unc.edu; adam_cockrell@unc.edu; jacob.kocher@unc.edu; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>; qingtan@wustl.edu
Subject: FW: Your article published in BMC Bioinformatics is now online

Hello all,

See below for our final published paper! Thanks again to you all!

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Pacific Northwest National Laboratory
Phone: 206-528-3461

From: Springer <SpringerAlerts@springeronline.com>
Sent: Monday, May 31, 2021 3:28 PM
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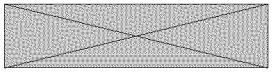
Subject: Your article published in BMC Bioinformatics is now online



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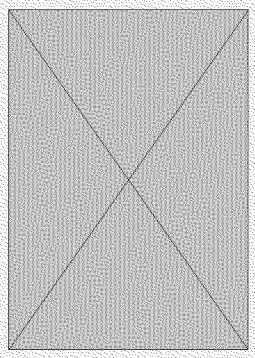

BMC Bioinformatics

Hypergraph models of biological networks to identify genes critical to pathogenic viral response

Song Feng, Emily Heath, Brett Jefferson, Cliff Joslyn, Henry Kvinge, Hugh D. Mitchell, Brenda Praggastis, Amie J. Eisfeld, Amy C. Sims, Larissa B. Thackray, Shufang Fan, Kevin B. Walters, Peter J. Halfmann, Danielle Westhoff-Smith, Qing Tan, Vineet D. Menachery, Timothy P. Sheahan, Adam S. Cockrell, Jacob F. Kocher, Kelly G. Stratton, Natalie C. Heller, Lisa M. Bramer, Michael S. Diamond, Ralph S. Baric, Katrina M. Waters, Yoshihiro Kawaoka, Jason E. McDermott, Emilie Purvine

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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Tue 3/10/2020 6:58:04 PM (UTC-05:00)
Subject: SIG Meeting agenda
Draft Schedule for March 2020 SIGU19 meeting mth.docx

Hi Everyone,
Attached is the agenda for tomorrow. I will start the meeting with some Core A updates.
Toni

SIG-U19 Teleconference

11:00-11:20 Welcome and Overview (Ralph and Mark)

11:20-12:20 Project 1: SARS-CoV (Ralph Baric) (20 mins each)

Sarah Leist: Flow F2

Alex Schaefer: SARS

Lisa Gralinski: CC Mouse Models

12:20-1:20 Project 2: Influenza A virus (Mark Heise and Klaus Schughart)

Integrating Phenotypes Across CC Studies (Heise)

An update on human IAV studies (Schughart):

1:20-1:30 Break

1:30-2:00 Project 3: West Nile virus (Mike Gale and Jenny Lund)

2:00-2:30 Core B: An Update on CC status (Marty Ferris and FPMV)

2:30-3:00 Core C: An Update on QTL Refinement (Mike Mooney and Shannon McWeeney)

3:00-4:00 Discussion

- Other data sets/collaboration opportunities
- Papers
- Other discussion items

To: Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
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And here:

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From: Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>
Sent: Wednesday, June 2, 2021 12:29 AM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>; Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; vimenach@utmb.edu; sheahan@email.unc.edu; adam_cockrell@unc.edu; jacob.kocher@unc.edu; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>; qingtan@wustl.edu
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Hello all,

See below for our final published paper! Thanks again to you all!

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Pacific Northwest National Laboratory
Phone: 206-528-3461

From: Springer <SpringerAlerts@springeronline.com>
Sent: Monday, May 31, 2021 3:28 PM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
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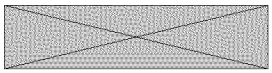

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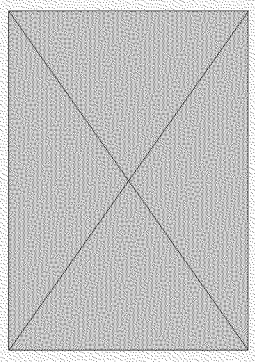

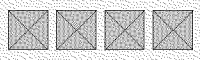

BMC Bioinformatics

Hypergraph models of biological networks to identify genes critical to pathogenic viral response

Song Feng, Emily Heath, Brett Jefferson, Cliff Joslyn, Henry Kvinge, Hugh D. Mitchell, Brenda Praggastis, Amie J. Eisfeld, Amy C. Sims, Larissa B. Thackray, Shufang Fan, Kevin B. Walters, Peter J. Halfmann, Danielle Westhoff-Smith, Qing Tan, Vineet D. Menachery, Timothy P. Sheahan, Adam S. Cockrell, Jacob F. Kocher, Kelly G. Stratton, Natalie C. Heller, Lisa M. Bramer, Michael S. Diamond, Ralph S. Baric, Katrina M. Waters, Yoshihiro Kawaoka, Jason E. McDermott, Emilie Purvine

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Best regards,
Your Marketing Team

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Tue 3/24/2020 2:51:08 PM (UTC-05:00)
Subject: April reverse site visit postponed

Hi everyone,
I hope you are all staying safe and healthy. NIH has responded to our request to postpone the Systems Immunogenetics reverse site visit scheduled at the end of April. At the moment they have not chosen a new date. I will let you know as soon as it has been decided.

Take care.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Matthew Frieman[mfrieman@som.umaryland.edu]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]
Cc: Erika Arch[earch@asu.edu]; Brenda Hogue[Brenda.Hogue@asu.edu]; Alexandra Lucas[arlucas5@asu.edu]; Ian Hogue[ihogue@asu.edu]; Julie Kurth[Julie.Kurth@asu.edu]; Dianne Price[Dianne.Price@asu.edu]; Kerri Robinson[Kerri.Robinson@asu.edu]; Stephen Munk[Stephen.Munk@asu.edu]; Oday Hana[Oday.Hana@asu.edu]; Neal Woodbury[NWoodbury@asu.edu]; Kenro Kusumi[Kenro.Kusumi@asu.edu]; Nancy Gonzales[nancy.gonzales@asu.edu]; Felicia Goodrum[fgoodrum@email.arizona.edu]; Paul Boehmer[boehmer@email.arizona.edu]; Steven Potts[sp@oncomyx.com]; Michael Wood[mw@oncomyx.com]; Leslie Sharp[leslie.sharp@oncomyx.com]
From: Grant McFadden[grantmcf@asu.edu]
Sent: Wed 3/25/2020 2:03:17 PM (UTC-05:00)
Subject: Friday Viroholics seminar series: the Zoom version

Matt, Darryl, Vineet, Marion, Adolfo, Ralph and Stan:

First, thank you all for tentatively agreeing to Zoom-speak in our Friday noon (PT) virology seminar series at ASU, that is now heavily focused on coronaviruses and treating respiratory virus diseases.

Second, I hope to have a tentative April-May speaker schedule for you by the end of this week, or early next week, but in the meantime, feel free to join us electronically for this Friday's Zoom seminar on coronavirus vaccines from Brenda Hogue (https://asu.zoom.us/j/ **552.136**

Brenda G. Hogue, PhD
Professor
Biodesign Center for Immunotherapy, Vaccines and Virotherapy (B-CIVV)
School of Life Sciences
Arizona State University

"Virus-like Particles - a platform for coronavirus vaccines"

Friday, March 27, 2020
Noon - 1:00 PM (MST/same as PT now in Arizona)
Join via Zoom: https://asu.zoom.us/j/ **552.136**

Or Telephone:
Dial(for higher quality, dial a number based on your current location):
US: +1 669 900 6833 or +1 346 248 7799 or +1 646 876 9923 or +1 253 215 8782 or +1 301 715 8592 or +1 312 626 6799
Meeting ID: 244 676 617
International numbers available: https://asu.zoom.us/ **552.136**

Or iPhone one-tap (US Toll): +16699006833, **552.136** or +13462487799,, **552.136**

We really appreciate your support!

Grant

Grant McFadden
Director, Center for Immunotherapy, Vaccines, and Virotherapy (B-CIVV)

Biodesign Institute
727 E Tyler Street, Room A330E
Arizona State University
Tempe, AZ, 85287

Ph: 480-727-3388
FAX: 480-965-1844
Cell: 352-672-2263
Email: grantmcf@asu.edu
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To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]
From: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Sent: Mon 3/30/2020 3:20:18 PM (UTC-05:00)
Subject: COVID-19 Investigator Call March 31

Hi Everyone,
It's hard to believe it has already been a week since our last call! My apologies for being slow to get this information out to you, but below is the attendee roster from last week. In the interest of time we will not plan to do an official roll call moving forward, except for asking if there are new attendees who haven't joined before. Note that there were several folks who were identified only as "Caller #," so please let me know (**do not reply to all**) if you're not on the list and I will add you. I have also pasted below a link to NIH's grant FAQ page regarding COVID-19 in case there is information there that is useful for you.

Moving forward we are going to change the format of the meeting a bit and have one or two short (~15 minute) presentations where someone can present a highlight of their COVID-19 work. Hopefully this will stimulate more discussion of specific topics. After those talks we will then run through a few updates on some standing agenda items. As always we would like this to be a useful venue to engage with the group, so please reach out if you have other suggestions for topics or would like to volunteer to give a short update at a future meeting. See below for an agenda for tomorrow's call.

Erik

March 31 Agenda
Short Highlight 1: Fouchier Group (Sander Herfst, EMC)
Short Highlight 2: Peiris Group (HKU)
Standing items
- Animal Models
- Reagents
- Assays

Open Discussion

NIH Grants COVID-19 FAQ: https://grants.nih.gov/grants/natural_disasters/corona-virus.htm

March 24 Attendee Roster

Erik Stemmy
Marciela DeGrace
Rebecca Lampley
Adolfo Garcia-Sastre
Andrew Pekosz
Annice Lowen
Aubree Gordon
Ben Cowling
Brooke Bozick
Courtney Comar (Susan Weiss lab)
David Topham
Mark Denison
Diane Post
Florian Krammer
Frederic Bushman
Gabriele Neumann
Ghazi Kayali
Harm van Bakel
Katy Shaw-Saliba
Kimberly Stemple
Larry Anderson
Lisa Hensley
Masato Hatta (UW)
Melissa Uccellini
Pamela McKenzie
Peter Palese
Punam Mathur
Reed Johnson
Richard Webby
Chris Roberts
Alan Embry
Charles Russell
Stacey Schultz-Cherry
Stephen Tompkins
Paul Thomas
Tom Fabrizio

To: Rbaric@email.unc.edu[Rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Koedi Lawley[koedilawley@tamu.edu]
Sent: Wed 4/1/2020 11:19:15 AM (UTC-05:00)
Subject: Supplemental Materials- Mucin 4 Protects Female Mice from Coronavirus Pathogenesis

Hello Dr. Baric and Dr. Menachery,
I am a graduate student in Dr. Candice Brinkmeyer-Langford's lab at Texas A&M University, and I came across your pre-print for "Mucin 4 Protects Female Mice from Coronavirus Pathogenesis". I am very intrigued by your paper and wanted to learn more, however, the supplemental materials referenced in the paper don't appear to be available online. Is there any way that I might obtain a copy of those supplemental materials?

Best Regards,

Koedi Lawley

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Tue 4/7/2020 7:09:59 AM (UTC-05:00)
Subject: Pilot reviews

Hi All,
I know that you are all incredibly busy but I needed to have the reviews on the pilots on March 31. Please send your reviews as soon as possible.

Thank you and stay safe.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]
Sent: Tue 4/7/2020 7:10:19 AM (UTC-05:00)
Subject: Re: Pilot reviews

will do

Fernando

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Tuesday, April 7, 2020 8:09 AM
To: Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; JACKIE V. BERHORST (jdao@uw.edu) <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Mike <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney (mcweeney@ohsu.edu) <mcweeney@ohsu.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>
Subject: Pilot reviews

Hi All,
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Thank you and stay safe.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][jjohnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]
From: Crozier, Ian (NIH) [C][ian.crozier@nih.gov]
Sent: Tue 4/14/2020 9:10:09 AM (UTC-05:00)
Subject: Re: nCoV weekly investigators meeting

Eric et al,
Link to ongoing IRF study: https://openresearch.labkey.com/project/Coven/COVID-001/begin.view?
Thanks for the invitation (and forgive a few extra minutes!)
Best,
Ian

Ian Crozier, MD [C]
Medical Affairs Scientist II
Clinical Monitoring Research Program Directorate (CMRPD)
Frederick National Laboratory for Cancer Research
Leidos Biomedical Research, Inc.
Support to: NIAID Integrated Research Facility at Fort Detrick
Phone: +1-301-631-7203
Cell: +1-240-825-5032
Email: ian.crozier@nih.gov

From: marciela.degrace@nih.gov

When: 9:00 AM - 10:00 AM April 14, 2020
Subject: nCoV weekly investigators meeting
Location: GoToWebinar

Adding Ian Crozier MD, NIAID IRF-Frederick

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>
Sent: Tuesday, February 11, 2020 7:26 AM
To: Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; Mark Denison; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; jmclellan@austin.utexas.edu
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]
Subject: nCoV weekly investigators meeting
When: Occurs every Tuesday effective 1/28/2020 from 9:00 AM to 10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/VRC) [F]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]
Subject: nCoV weekly investigators meeting
When: Occurs every Tuesday effective 1/28/2020 from 9:00 AM to 10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov)

know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join/ **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Mon 12/16/2019 10:32:49 AM (UTC-06:00)
Subject: RE: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!
JVI Spotlight Text-rsb.docx

Reads great, minor comment.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 16, 2019 10:43 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Re: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Here is the draft of the spotlight text. I'd like to have it sent to JV by the end of the day if possible.

Also, with Amy gone, who is handling the publication bills.

Thanks

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, December 11, 2019 2:07 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Fw: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

guess somebody thought it was interesting.

I"ll work on this and send you a draft by Friday.

VDM

From: Dutch, Rebecca <rebecca.dutch@uky.edu>
Sent: Wednesday, December 11, 2019 12:44 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Dear Vineet,

Congratulations! Your article, "Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection " (JVI01774-19) has been selected by the editors of the Journal of Virology for inclusion in "Spotlight," a feature in the Journal that highlights research articles of significant interest from the current issue. This section follows the table of contents and includes short descriptions of five especially meritorious articles.

If you wish your article to be included in this section, please draft a short, declarative title and a brief summary of your manuscript (between 50-100 words) and forward these to me. The summary should be composed in general terms, highlighting the broad biological significance of the work. Also, please select a panel of one figure from your paper to display alongside the text in the Spotlight section. Please crop the

figure file so that it includes only the portion of the figure to be published in the Spotlight, and send the resulting high-resolution (300dpi) TIF (preferred), EPS, or PPT file to me. The figure can convey the most important experimental result of your study or an interesting image. Do not send a multi-panel figure. We only have space for a single panel. Please include a short descriptive title for the figure. The title used in the legend for the chosen figure may suffice. You will find an example of what we are aiming for in this section, attached.

As our printing deadlines are very tight, we must receive your material – the headline, paragraph of text, cropped figure file, and brief figure legend by 5 pm (Eastern Standard Time) on Tuesday the 17th of December. Please let me know if I can help you with any questions. Thank you for contributing to the Journal of Virology Spotlight.

Sincerely,
Becky Dutch
Editor, Journal of Virology

Rebecca Dutch
Professor and Chair, Molecular and Cellular Biochemistry
University of Kentucky College of Medicine
143 BBSRB
741 S. Limestone St.
Lexington, KY 40536-0509

To: Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Graham, Rachel[rlgraham@email.unc.edu]
Cc: Edwards, Caitlin E[caitedw@unc.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Mon 12/16/2019 10:34:38 AM (UTC-06:00)
Subject: RE: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Thought I'd include cait. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 16, 2019 10:45 AM
To: Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Graham, Rachel <rlgraham@email.unc.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Hi Tim, Lisa, and Rachel,

Between the three of you, I imagine one of you knows who handles this invoice. I CCed Ralph too, but wasn't sure if you had someone in place doing this stuff yet or not.

Happy holidays.

VDM

From: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Sent: Monday, December 16, 2019 3:32 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Subject: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Dear Dr. Vineet Menachery,

Your article, Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection (Manuscript # JVI01774-19), is scheduled to be published in issue 5 of Journal of Virology.

To facilitate prompt publication of your article, please use this link to the Author Services system to do any of the following:

- Pay publication fees
- Pay additional fees (Open Access, supplemental materials, etc.)
- Order reprints or eprints

https://authorservices.cadmus.com/Shibboleth.sso/Login?entityID=https://login.asm.org/idp/shibboleth&target=/DRIPShopperWeb%2Foffer.do%3FarticleID%3D3096272%26emailAddress%3Dvimenach%40utmb.edu

You may pay by credit card, or purchase order. Doing so will create a printable invoice that you can include with your payment, or submit to your funding institution as a pro-forma invoice. The invoice you create will contain information

about payment by credit card, bank wire, or check. You must use this system to create an accurate invoice for payment.

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To join or renew your ASM membership, go to: www.asm.org/join.

If you experience problems with your fees or with the Author Services website, please email ASM.AuthorServicesSupport@cenveo.com.

Thank you,

ASM Reprint/Billing Account Manager.

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To: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; vincent.munster_nih.gov vincent.munster@nih.gov[vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; Saif, Linda[saif.2@osu.edu]; Wang, Qiuhong[wang.655@osu.edu]; vlasova.1@osu.edu[vlasova.1@osu.edu]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Tue 4/21/2020 8:56:57 AM (UTC-05:00)
Subject: Request from Linda Saif & her group at OSU

Dear All,

As I mentioned on the call, Linda Saif and her group (cc'd here) sent a request for reagents (below). If any of you can help, please contact her directly at the emails below…

From: Saif, Linda <saif.2@osu.edu> "Wang, Qiuhong" <wang.655@osu.edu> Anastasia Vlasova <vlasova.1@osu.edu
Sent: Friday, February 28, 2020 10:23 PM
To: Peter Daszak <daszak@ecohealthalliance.org>
Subject: Re: nature news request
Importance: High

A major component of my research has been using the pig as a model for human rotavirus vaccines since they are susceptible to disease and infection with human rotaviruses and I have long term NIH support for this research using a pig disease model (also for human noroviruses testing for antivrials!).

Do you know any source for the SARS-CoV-2 reagents I indicated below?

First: hyperimmune sera to SARS-CoV-2 nonstructural and structural proteins, respectively, for IHC and IFA assays.

Also:

1. SARS-CoV-2 S-pseudovirus;
2. Hyperimmune sera to SARS-CoV-2 nonstructural and structural proteins, respectively;
3. Human antiserum to SARS-CoV-2;
4. Human antiserum to SARS-CoV;
5. Human antiserum to MERS-CoV;
6. Human antiserum to HCoV-OC43;
7. Human antiserum to HCoV-HKU1;
8. Human antiserum to HCoV-229E;
9. Human antiserum to HCoV-NL63;

Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>
Sent: Monday, April 20, 2020 3:09 PM
To: Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>; Leo Poon <llmpoon@hku.hk>; Webby, Richard <Richard.Webby@STJUDE.ORG>; malik <malik@hku.hk>; Ghazi Kayali <ghazi@human-link.org>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; yguan@hku.hk; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@STJUDE.ORG>; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>; Baric, Ralph <rbaric@email.unc.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; zhu huachen <zhuhch@hku.hk>;

Aubree Gordon <gordonal@umich.edu>; vincent.munster_nih.gov vincent.munster@nih.gov <vincent.munster@nih.gov>; PETERPALESE <peter.palese@mssm.edu>; 'Krammer, Florian' <florian.krammer@mssm.edu>; Ben Cowling <bcowling@hku.hk>; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C <antoinette_baric@med.unc.edu>; MASATO HATTA <masato.hatta@wisc.edu>; Gabriele Neumann (gabriele.neumann@wisc.edu) <gabriele.neumann@wisc.edu>; Subbarao, Kanta <kanta.subbarao@influenzacentre.org>; Mathur, Punam (NIH/NIAID) [E] <mathurpu@niaid.nih.gov>; Mark Denison <mark.denison@vumc.org>; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E] <johnsonreed@niaid.nih.gov>; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E] <kstemple@niaid.nih.gov>; Sutton, Troy Clavell <tcs38@psu.edu>; marlene.espinozamoraga@mssm.edu; Simon, Viviana <viviana.simon@mssm.edu>; Van bakel, Harm <harm.vanbakel@mssm.edu>; McKenzie, Pamela <Pamela.McKenzie@STJUDE.ORG>; Deckhut, Alison (NIH/NIAID) [E] <augustine@niaid.nih.gov>; jmclellan@austin.utexas.edu
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID) <agf1@CDC.GOV>; Pallansch, Mark A. (CDC/DDID/NCIRD/OD) <map1@CDC.GOV>; Hall, Aron (CDC/DDID/NCIRD/DVD) <esg3@CDC.GOV>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Lampley, Rebecca (NIH/NIAID) [C] <rebecca.lampley@nih.gov>; Andy Pekosz <apekosz1@jhu.edu>; Topham, David <David_Topham@URMC.Rochester.edu>; Gerber, Susan I. (CDC/DDID/NCIRD/DVD) <bhx1@cdc.gov>; zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E] <brooke.bozick@nih.gov>; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Wentworth, David E. (CDC/DDID/NCIRD/ID) <gll9@cdc.gov>; Russell, Charles <Charles.Russell@STJUDE.ORG>; Cooper, Michael (NIH/NIAID) [E] <michael.cooper3@nih.gov>; Weiss, Susan <weisssr@pennmedicine.upenn.edu>; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina <weina.sun@mssm.edu>; Roberts, Chris (NIH/NIAID) [E] <paul.roberts@nih.gov>; Stephen M Tompkins <smt@uga.edu>; Uccellini, Melissa <melissa.uccellini@mssm.edu>; Thomas, Paul <Paul.Thomas@STJUDE.ORG>; B.H.G. Rockx <b.rockx@erasmusmc.nl>; Michael Chan <mchan@hku.hk>; S. Herfst <s.herfst@erasmusmc.nl>; Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>; Park, Eun-Chung (NIH/NIAID) [E] <epark@niaid.nih.gov>; Crozier, Ian (NIH) [C] <ian.crozier@nih.gov>; Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; andrea_sant@urmc.rochester.edu; Ellebedy, Ali <ellebedy@wustl.edu>; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E] <readsa@niaid.nih.gov>; Finzi, Diana (NIH/NIAID) [E] <dfinzi@niaid.nih.gov>; Turpin, Jim (NIH/NIAID) [E] <jturpin@niaid.nih.gov>
Subject: COVID-19 Weekly Investigator Call April 21

Hello Everyone,
On this week's call we'll have presentations from Matt Frieman from UMD on some of his ongoing drug testing work, and from Stanley Perlman on his model development work. As promised, below is the attendee list from last week. Note that if you had dialed in only via phone you were recorded as "Caller X," so let us know if your name is missing and we can add it to our records.

Please email Marciela and I if you would like to present on May 5th or 12th.

Thanks!
Erik

Attendees April 14th
Erik Stemmy

Marciela DeGrace

Rebecca Lampley

Adolfo Garcia-Sastre

Alan Embry

Alison Augustine

Andrea Sant

Andrew Pekosz

Annice Lowen

Aubree Gordon

Brooke Bozick

Charles Russell

Chelsea Lane

Chris Roberts

David Topham

David Wentworth

Diane Post

Donna Neu

Eunchung Park

Florian Krammer

Frederic Bushman

Gabriele Neumann

Ghazi Kayali

Harm van Bakel

Ian Crozier

Jim Chappell

Juergen Richt

Katy Shaw-Saliba

Kimberly Stemple

Larry Anderson

Lisa Hensley

Mark Denison

Mark Sangster

Marlene Espinoza

Martin Linster

Masato Hatta (UW)

Matt Frieman

Pamela McKenzie

Paul Thomas

Peter Daszak

Peter Palese

Punam Mathur

Reed Johnson

Richard Rothman

Ron Fouchier

Sander Herfst

Stacey Schultz-Cherry

Stephen Tompkins

Susan Gerber

Susan Weiss

Tom Fabrizio

Walt Orenstein

Weina Sun

Yoshihiro Kawaoka

To: Baric, Ralph S[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Gralinski, Lisa E[lgralins@email.unc.edu]; Graham, Rachel[rlgraham@email.unc.edu]
Cc: Edwards, Caitlin E[caitedw@unc.edu]
From: Sheahan, Timothy Patrick[sheahan@email.unc.edu]
Sent: Mon 12/16/2019 2:20:38 PM (UTC-06:00)
Subject: Re: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

I have this in the works. T

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Monday, December 16, 2019 at 11:34 AM
To: "Menachery, Vineet" <vimenach@UTMB.EDU>, "Sheahan, Timothy Patrick" <sheahan@email.unc.edu>, "Gralinski, Lisa E" <lgralins@email.unc.edu>, "Graham, Rachel" <rlgraham@email.unc.edu>
Cc: "Edwards, Caitlin E" <caitedw@unc.edu>
Subject: RE: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Thought I'd include cait. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 16, 2019 10:45 AM
To: Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Graham, Rachel <rlgraham@email.unc.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Hi Tim, Lisa, and Rachel,

Between the three of you, I imagine one of you knows who handles this invoice. I CCed Ralph too, but wasn't sure if you had someone in place doing this stuff yet or not.

Happy holidays.

VDM

From: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Sent: Monday, December 16, 2019 3:32 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: asm.authorservicessupport@cenveo.com <asm.authorservicessupport@cenveo.com>
Subject: Payment for your upcoming article in Journal of Virology , ms. JVI01774-19

Dear Dr. Vineet Menachery,

Your article, Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection (Manuscript # JVI01774-19), is scheduled to be published in issue 5 of Journal of Virology.

To facilitate prompt publication of your article, please use this link to the Author Services system to do any of the following:

- Pay publication fees
- Pay additional fees (Open Access, supplemental materials, etc.)
- Order reprints or eprints

https://authorservices.cadmus.com/Shibboleth.sso/Login?entityID=https://login.asm.org/idp/shibboleth&target=/DRIPShopperWeb%2Foffer.do%3FarticleID%3D3096272%26emailAddress%3Dvimenach%40utmb.edu

You may pay by credit card, or purchase order. Doing so will create a printable invoice that you can include with your payment, or submit to your funding institution as a pro-forma invoice. The invoice you create will contain information about payment by credit card, bank wire, or check. You must use this system to create an accurate invoice for payment.

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If you experience problems with your fees or with the Author Services website, please email ASM.AuthorServicesSupport@cenveo.com.

Thank you,

ASM Reprint/Billing Account Manager.

****

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Sekine, Aimee[aimeem@uw.edu]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; Thomas, Sunil[calvinho@uw.edu]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 1/9/2019 12:50:50 PM (UTC-06:00)
Subject: SIG U19 conference call

Hi All,
Just a reminder that we will have a short conference call for SIG U19 tomorrow at 1:30pm ET. Alex Schaefer will be presenting her data from Project 1. If you have any agenda items, please forward them to Mark. Calling numbers are the usual.

Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 1/9/2019 2:05:29 PM (UTC-06:00)
Subject: Fw: U19 flow gating strategies

I can't see this being in China, but wanted to keep you in the loop. I hope it looks interesting and we get something from all that flow data. looks like they are enthusiastic about at least one QTL, but have no idea how significant. hope your doing well. ralph

---

From: Michael Mooney <mooneymi@ohsu.edu>
Sent: Wednesday, January 9, 2019 2:26 PM
To: Jensen, Kara; Baric, Ralph S; Shannon McWeeney
Cc: Leist, Sarah Rebecca; Schaefer, Alexandra; Gralinski, Lisa E; Gabrielle Choonoo; Sophia Jeng
Subject: RE: U19 flow gating strategies

Hi all,
Plots and gene annotations for QTL candidates for the dendritic cell flow panel have been uploaded to Box. There are several peaks that pass the 0.5 genome-wide threshold. The peak on chr6: ~60-90Mb (for multiple phenotypes) looks particularly strong (CAST effect).

https://ohsu.box.com/s/a06uiwlm044hjt4dyxhrk6tci529dx6p

We are currently going through the other panels to identify any outliers and get the final sample sizes (we started with the dendritic panel because it had data for the most lines). Let us know if you have any questions.

Lisa, is there any update on the titer data? I think last email you mentioned there were ~30 samples that still needed to be done.

Regards,

Mike

From: Jensen, Kara [kara_jensen@med.unc.edu]
Sent: Monday, August 20, 2018 9:05 AM
To: Baric, Ralph S; Michael Mooney; Shannon McWeeney
Cc: Leist, Sarah Rebecca; Schaefer, Alexandra; Gralinski, Lisa E; Gabrielle Choonoo
Subject: U19 flow gating strategies

Hello all,

Attached are schematics of the gating strategies used for the three panels evaluated. Please let me know if you have any questions, or need clarification.

Thanks!

Kara

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Friday, August 3, 2018 at 1:48 PM
To: "Jensen, Kara" <kara_jensen@med.unc.edu>, "mooneymi@ohsu.edu" <mooneymi@ohsu.edu>, "mcweeney@ohsu.edu" <mcweeney@ohsu.edu>

Cc: "Leist, Sarah Rebecca" <leist@email.unc.edu>, "Schaefer, Alexandra" <aschaefe@email.unc.edu>, "Gralinski, Lisa E" <lgralins@email.unc.edu>, "Baric, Toni C" <antoinette_baric@med.unc.edu>
Subject: RE: U19 SARS flow analysis

Hi Shannon, hope your doing well. We should set up a time to talk about these flow datasets and there analyses. Talk with you soon. Ralph

---

From: Jensen, Kara
Sent: Friday, August 3, 2018 1:34 AM
To: mooneymi@ohsu.edu; mcweeney@ohsu.edu; Baric, Ralph S <rbaric@email.unc.edu>
Cc: Leist, Sarah Rebecca <leist@email.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>
Subject: U19 SARS flow analysis

Hi all,

Thanks for your patience. Attached is the final analysis of the SARS-infected CC mouse lines for the U19 project.

For orientation, there are 4 tabs. The first tab is a summary of the samples tested, and whether or not there were issues during the experimental and/or acquisition phases, and if these data were analyzable or not. The second, third and fourth tabs are the specific data across all animals for the lymphoid, myeloid, and dendritic cell panels, respectively. These samples are organized by date, and I have reported both the frequencies of each subpopulation as a percentage of total LCA+/CD45+ events, as well as the total cell counts. Keep in mind that there is high variability in the efficiency of the lung digestions, filter steps, staining, and acquisition that render cell counts alone as problematic. I've included them here more as secondary information to help inform how 'real' the frequencies are. For example, you might have 0.01% of total LCA events for a particular cell population, but if there are 350 events within that gate, it suggests that is a real population, and not just noise that can accompany flow experiments.

Note that there are a number of orange and yellow highlighted sample dates, and even specific data wells highlighted within certain dates. Yellow indicates those samples are not analyzable, and cannot be used for further analysis. The orange color indicates that there are issues that render that sample partially analyzable, and/or that I was not completely confident in the gates, but did the best I could to be consistent and accurate. For example, an orange sample might have a parameter that was not acquired when the flow was run, meaning that any cell population using that marker for definition can't be used, but that other markers acquired properly can still be used. Orange is also used to reference assay dates with other issues, such as parameters run partially off scale, or population frequencies that don't appear consistent with expected values. I'm happy to discuss this further, and provide visual examples to help illustrate the process I applied to analyze this data set since I realize this might be somewhat vague.

Would it be helpful to have a call to coordinate downstream QTL analysis efforts before getting in too deep? Specifically, I'd like to discuss how to approach the significant number of 'orange' samples- whether or not to leave them out of the first pass comparisons, and if it would be possible to run comparisons with and without the samples in which I have less confidence.

Thanks!

Kara

To: Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Ralph Baric[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Frieman, Matthew[MFrieman@som.umaryland.edu]
Sent: Thur 2/28/2019 9:08:34 AM (UTC-06:00)
Subject: The U.S. is funding dangerous experiments it doesn't want you to know about - The Washington Post

Did you guys read this yet?
Inglesby is pushing on the fact that its not reported what it was that was discussed/changed/agreed to during this new approval process that allowed the Yoshi and Fouchier experiments/grants to be approved again.

The details of the experiments are fine to keep protected, but I would think they had to agree to additional safeguards to be allowed to do the experiments again. Wouldn't you want to know what those are so that we can potentially incorporate them into our lab SOPs and safety rules?

I am not totally against this line of reasoning by them on this.

https://www.washingtonpost.com/opinions/the-us-is-funding-dangerous-experiments-it-doesnt-want-you-to-know-about/2019/02/27/5f60e934-38ae-11e9-a2cd-307b06d0257b_story.html?utm_term=.b71c0953c48e

Matthew Frieman, PhD
University of Maryland School of Medicine
685 West Baltimore St
Room 380
Baltimore, MD 21201

office: 410-706-2539
cell: 443-791-7600

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
Cc: Schaefer, Alexandra[aschaefe@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 2/18/2019 7:27:44 AM (UTC-06:00)
Subject: SIG U19 agenda
Systems Immun_2019_Agenda_draft20190215[1].docx

Hi Everyone,
We received an email from Chao with a draft agenda. Please see attached.
Thank you

Toni Baric
Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

Systems Immunology U19 Annual Meeting

April 11 – 12, 2019

National Institutes of Allergy and Infectious Diseases
5601 Fishers Lane, 1D06 Conference Room
Rockville, MD 20852

Agenda

Day 1

8:40 – 9:00AM	**Registration**
9:00 – 9:05AM	**Welcome/Introductory Remarks** **Chao Jiang,** NIAID
9:05 – 9:20AM	*Short talk 1*
9:20 – 12:05PM	(including a 15-min break) *Systems Approach to Immunity and Inflammation* **Richard Ulevitch**, The Scripps Research Institute
12:05 – 1:15PM	**Lunch break**
1:15 – 1:30PM	*Short talk 2*
1:30 – 4:15PM	(including a 15-min break) *Systems Immunogenetics of Biodefense and Emerging Pathogens in the Collaborative Cross* **Ralph Baric** and **Mark Heise,** University of North Carolina at Chapel Hill
4:15PM	**Adjourn Day 1**

Day 2

9:00 – 11:45AM	(including a 15-min break) *Defining Regulators of Immunity to Acute Infection Using CRISPR Screens* **Arlene Sharpe**, Harvard University Medical School
11:45AM	**Adjourn general meeting**
12:00 – 1:00 PM (TBD)	**Systems Immunology Steering Committee Meeting (closed session, Steering Committee members and NIAID staff only)**

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Sekine, Aimee[aimeem@uw.edu]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; Thomas, Sunil[calvinho@uw.edu]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 2/14/2019 12:55:22 PM (UTC-06:00)
Subject: SIG U19 Pilot project announcement
System Immunogenetics U19 Pilot Research Funds Available.docx

Hi All,
As promised, attached please find the announcement for the 2019-20 pilot project. My goal is to submit this as a subaward with our progress report so the recipient does not have to wait too long to get there funds.
Thanks

Toni Baric
Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

Pilot Research Funds Available.

The Center for Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross at the University of North Carolina at Chapel Hill conducts innovative research focused on the identification of immune regulatory genes and variant alleles that regulate disease outcomes following SARS-CoV, Ebola, Influenza, Chikungunya and West Nile Virus infections and/or vaccinations. The program uses systems genetic based approaches in the Collaborative Cross Genetic Reference Population to map genes that regulate protective or pathogenic immune outcomes following infection or vaccination. Pilot research program goals should fall within one or more of the following areas, including: building collaborative interactions with existing Projects that extend the breadth of the Program; developing new models of human immunity and/or disease; mapping novel immune regulatory genes; responding to emerging public health emergencies; and/or translating murine immune discoveries to human disease and improved public health. Approximately $115,000 total dollars will be available for a 1 year pilot program. Interested applicants are encouraged to submit specific aims (1 page), a two page grant application outlining research goals, an NIH Biosketch, Budget, Budget Justification and a one-half page Scope of Work. Budget period is anticipated from 9/1/2019-8/31/20. The candidate selected would need to submit a signed, PHS 398 face page. All interested parties should submit their grant applications to Antoinette Baric, Program Manager (antoinette_baric@med.unc.edu) by April 12, 2019 at 5 PM ET. For more information on the Systems Immunogenetics program, please visit the website [HYPERLINK "http://www.systemsimmunogenetics.org"]

To: Frieman, Matthew[MFrieman@som.umaryland.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 2/28/2019 1:45:39 PM (UTC-06:00)
Subject: RE: The U.S. is funding dangerous experiments it doesn't want you to know about - The Washington Post

Thanks for passing this on. It would be of value to hear about the additional safeguards, although I am overall uncertain as to what NIH is doing with SARS and MERS grants, beyond the "general" statement "no PC30 safety concerns".
ralph

From: Frieman, Matthew <MFrieman@som.umaryland.edu>
Sent: Thursday, February 28, 2019 10:09 AM
To: Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Menachery, Vineet <vimenach@UTMB.EDU>
Subject: The U.S. is funding dangerous experiments it doesn't want you to know about - The Washington Post

Did you guys read this yet?

Inglesby is pushing on the fact that its not reported what it was that was discussed/changed/agreed to during this new approval process that allowed the Yoshi and Fouchier experiments/grants to be approved again.

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I am not totally against this line of reasoning by them on this.

https://www.washingtonpost.com/opinions/the-us-is-funding-dangerous-experiments-it-doesnt-want-you-to-know-about/2019/02/27/5f60e934-38ae-11e9-a2cd-307b06d0257b_story.html?utm_term=.b71c0953c48e

Matthew Frieman, PhD
University of Maryland School of Medicine
685 West Baltimore St
Room 380
Baltimore, MD 21201

office: 410-706-2539
cell: 443-791-7600

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: 3/8/2019 12:18:39 AM
To: Menachery, Vineet [vimenach@UTMB.EDU]
Subject: RE: Darpa project

Well, the Autonomous website doesn't provide much insight into what they are doing or the molecular strategies. Great PR-the kind of stuff that DARPA would like--but I wonder if it has legs or is based on BS. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, March 7, 2019 6:27 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>
Subject: FW: Darpa project

Hey Ralph (and Toni),

I just chatted with guys from ATI (listed below). I told them that I don't have the capacity to do the quick turn around on in vivo mouse work and recommended that they talk to you. They prefer your model to Kent's.

I told them I would make an email introduction which I'll do in a few minutes.

I am under the impression that they think they will get this DARPA funding to do the MERS work. They want me to do the in vitro work and have you do mouse work and then work back to the marmoset model at UTMB.

If you aren't interested, no worries. I am not desperate for the money and based on our conversations with them, not sure I have the ability to be as responsive as they need the project to be. I'm happy to chat over the phone about it tonight or in the morning.

VDM

From: Menachery, Vineet
Sent: Thursday, March 07, 2019 2:20 PM
To: Baric, Ralph S
Subject: Darpa project

Hey Ralph,

I have been approached by a group to working with DARPA to do some MERS work. They are currently funded to do work on CCHF and some other tick viruses and DARPA has requested a proposal to apply their approach to MERS-CoV. Since they were already working with UTMB, I was suggested as a possible person to interact with.

I've had several conversations with them over the past few weeks. They are interested in both in vitro and in vivo validation. I am going to be talking with them further in the next few days, but I am not sure that I have the capacity/interest in doing all the mosue work. If it was at UTMB, it would be Kent's model. I had suggested the UNC DPP4 mice as an alternative.

Would you be interested in participating or even leading the mouse work? I am not sure where it is going, but after talking with Scott Weaver here, it can be a good bit of money, but it is essentially contract work. It does get you into the groups that work with DARPA, so you can get to network with them and carve out a place with the program officers. I know EcoHealth is involved heavily.

The website of the guys leading the project is below. I do not know them personally, and my interactions with them have been far from illuminating. https://www.autonomous.bio/https://www.autonomous.bio/

Anyway, let me know if you have a thought or suggestion. Happy to talk over the phone about this as well.

Hope you are well.

VDM

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Sekine, Aimee[aimeem@uw.edu]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; Thomas, Sunil[calvinho@uw.edu]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 2/13/2019 2:19:26 PM (UTC-06:00)
Subject: SIG U19 conference call

Hi All,
Just a reminder that we will have a short conference call for SIG U19 tomorrow at 1:30pm ET. If you have any agenda items, please forward them to Mark. Calling numbers are the usual.

Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Baric, Ralph S[rbaric@email.unc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Edwards, Caitlin E[caitedw@unc.edu]
From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Thur 3/14/2019 3:22:24 PM (UTC-05:00)
Subject: updated QTL table
SARS QTL table - current.xlsx

Hi all,

Here is the updated table of QTLs for Project 1. There are some extra notes to the right about details of the SARS QTLs but the left columns contain all of the important information for figures or slides. The three Ebola QTLs are in a second table below the SARS table. Please let me know if I missed anything or if you have any additional information that should be included.

thanks,

Lisa

SAR-CoV Host Susceptibility (HrS) QTL		
QTL	**Chromosome Region**	**Phenotype**
HrS1	Chr. 3: 18.2MB - 26.6Mb	D4 Perivascular Cuffing
HrS2	Chr. 16: 31.5Mb – 36.7Mb	D4 Titer
HrS3	Chr. 15: 72.1Mb – 75.8Mb	D4 Eosinophilia
HrS4	Chr. 13: 52.8Mb – 54.9Mb	D4 Perivascular Cuffing
HrS5	Chr.18: 42.8Mb – 55.6Mb	D3 WL, D4 WL, D4 Titer, D4 hemorrhage, D4 perivascular cuffing, D4 edema
HrS6	Chr. 9: 118.8Mb – End	D3 Weight Loss
HrS7	Chr. 7: 58.4Mb – 125.7Mb	D4 Titer
HsR8	Chr. 12	D4 Titer
HrS9	Chr. 15: 39.9Mb – 58.5Mb	D4 hemorrhage
HrS10	Chr. 13: 20Mb – 24Mb	HKU3-MA Mortality
HrS11	Chr. 5: 112Mb – 119Mb	HKU3-MA Mortality
HrS12	Chr. 15: 59Mb-68Mb	HKU3-MA Weight Loss
HrS13	Chr. 10: 87Mb-99Mb	HKU3-MA Weight Loss
HrS14	Chr. 1: 72Mb-118Mb	D2 titer
HrS15	Chr. 11: 13.5Mb-36Mb	D2 Penh
HrS16	Chr. 11: 3.5Mb-27Mb	D4 Rpef
HrS17	Chr. 15: 31.5Mb-81.4Mb	D4 weight loss
HrS18	Chr. 17:25MB-35Mb	D32 IgG1, D32 total IgG (N)

Hrs19	Chr. 16: 36.5Mb-41Mb	D32 total IgG (N)
HrS20	Chr. 10: 92Mb-100Mb	D32 total IgG (N)
HrS21	Chr. 3: 16Mb-23Mb	D32 total IgG (N)
HrS22	Chr. 16: 7Mb-41Mb	D15 IgG2ac (N)
HrS23	Chr. 6: 52M	eQTL
HrS24	Chr. 4: 111.7-.8	eQTL
HrS25	Chr. 4: 117M	eQTL
HrS26	Chr. 3: 101M	eQTL
HrS27	Chr. 6: 68Mb-85Mb	% D4 CD8+ DCs
HrS28	Chr. 15: 31.5Mb-81.4Mb	Hemorrhage

Relevant Ebola Host Susceptibility (HrE) QTL		
HrE1	Chr7: 100-109Mb	Mortality
HrE2	Chr7: 100-109Mb	Weight loss d5
HrE3	Chr8: 115-129Mb	D6 titer (blood)

Candidate Gene	published?	allele effects	gene target?	Status/notes
Trim55	PLoS Gen			
Muc4, Parp family	PLoS Gen			
Bai1	PLoS Gen			
Cdhr2	PLoS Gen			
Ticam2	G3		B6 drives WL	
	G3		WSB drives WL	
CD13	G3		complex	
	G3			
Enpp2	G3		CAST high	
Trim38			PWK high, Cast kind of high, others	
Git2				
Wisp1				
				also an antibody qtl near here
			NOD high, B6 slightly negative, most others neutral	
			NOD negative	
Sla				

Sirpb1-> Dap12		same region as Trim55		
		same region as HrS4	AJ high, PWK low	
Pon3		not indicated	CAST (Wild)	preCC
		AJ	Cast/PWK	preCC
		not indicated	Cast/PWK	preCC
		CAST	not indicated	preCC
	CAST			
Sla				

Trim12c, Trim6, Trim34
Trim67, Cdt1, Chmp1A

	LOD Score	% variation
antibody studies underway	7.799037251	0.26
	7.260722434	0.22
	7.433698891	0.26
	9.060194826	0.21
	4.5	6-13%
	4.5	0.07
Sarah working on CD13	8	0.123
	4.1	0.054
Lisa working on Enpp2	5	0.091
Lisa working on getting		
Sarah working on Git2		
Alex working on Wisp1		
Lisa Balb F2		

mini-F2 strategy
mini-F2 strategy
mini-F2 strategy
Lisa/Cait working on Pon3

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
Cc: Schaefer, Alexandra[aschaefe@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 3/21/2019 9:11:53 AM (UTC-05:00)
Subject: FW: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019
Systems Immun_2019_Agenda_draft20190319.docx

Hi Everyone,
Attached is the agenda for the Systems meeting in April.
Toni

From: Chao Jiang <chao.jiang@nih.gov>
Date: Thursday, March 21, 2019 at 10:04 AM
To: Richard Ulevitch <richard@5amventures.com>, "Heise, Mark T" <mark_heisem@med.unc.edu>, Arlene Sharpe <arlene_sharpe@hms.harvard.edu>, "Ulevitch, Richard" <Ulevitch@scripps.edu>, "Baric, Ralph" <rbaric@email.unc.edu>
Cc: "Leitner, Wolfgang (NIH/NIAID) [E]" <wleitner@niaid.nih.gov>, "Liu, Joy (NIH/NIAID) [E]" <liujoy@niaid.nih.gov>, "Tollini Farrell, Grace (NIH/NIAID) [C]" <grace.tollini@nih.gov>, Patricia Rutledge <pattyr@scripps.edu>, "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Hillman, Sarah Ellen" <Sarah_Hillman@hms.harvard.edu>
Subject: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019

Dear All,

Attached please find the updated agenda. Let me know if you have anything to add or change.

Here's the meeting registration link, https://palladianpartners.cvent.com/U19AnnualMeeting. For any logistic issues, please contact Grace Tollini (she is copied here).

Please let us know if you have any questions.

Thank you,
Chao

Chao Jiang, Ph.D.
Program Officer
Innate Immunity Section, Basic Immunology Branch
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases, NIH, DHHS
5601 Fishers Lane, Room 7B47, MSC 9828
Rockville, MD 20852
Bethesda, MD 20892
(FedEx/UPS delivery: Rockville, MD 20852)
Tel: 301-761-7802
Email: chao.jiang@nih.gov

Systems Immunology U19 Annual Meeting

April 11, 2019

National Institutes of Allergy and Infectious Diseases
5601 Fishers Lane, 1D06 Conference Room
Rockville, MD 20852

Agenda

8:20 – 8:45AM	**Registration**
8:45 – 8:50AM	**Welcome/Introductory Remarks** **Joy Liu**, NIAID
8:50 – 10:50 AM	*Systems Approach to Immunity and Inflammation*
8:50 – 9:25AM	*New proteins with immune function from random germline mutagenesis* **Bruce Beutler**, UT Southwestern Medical Center
9:25 – 10:00AM	*Systems biology analysis of the innate immune response to infectious disease* **Alan Diercks**, Center for Infectious Disease Research
10:00 – 10:35AM	*TBD* **Garry Nolan**, Stanford University
10:35 – 10:50AM	*Studies of NLRP3 inflammasomes* **Richard Ulevitch**, The Scripps Research Institute
10:50 – 11:00AM	**Break**
11:00AM – 1:00PM	*Systems Immunogenetics of Biodefense and Emerging Pathogens in the Collaborative Cross*
11:00 – 11:10AM	*UNC U19 Overview* - *Program Summary* - *Unique Programmatic Capabilities* **Ralph Baric**, University of North Carolina at Chapel Hill
11:10 – 11:30AM	*Project 1: SARS-CoV* **Ralph Baric**, University of North Carolina at Chapel Hill
11:30 – 11:50AM	*Project 2: Influenza A virus* **Mark Heise**, University of North Carolina at Chapel Hill

11:50AM – 12:20PM *Project 3: West Nile Virus*
Mike Gale, University of Washington
Jenny Lund, Fred Hutchinson Cancer Research Center

12:20 – 12:35PM *Core B: Mouse Genetics Core*
Marty Ferris, University of North Carolina at Chapel Hill
Fernando Pardo Manuel de Villena, University of North Carolina at Chapel Hill

12:35 – 12:50PM *Core C: Systems Genetics and Bioinformatics Core*
Shannon McWeeney, Oregon Health & Science University

12:50 – 1:00PM *Human Correlates Analysis*
Klaus Schughart, University of Tennessee Health Science Center

1:00 – 2:00PM **Lunch break**

2:00 – 4:00PM *Defining Regulators of Immunity to Acute Infection Using CRISPR Screens*

2:00 – 2:20PM *U19 overview and updates*
Arlene Sharpe, Harvard University Medical School

2:20 – 2:35PM *CRISPR/Cas9 gene perturbation technology (Core D and Project 1)*
Martin LaFleur, Harvard University Medical School

2:35 – 2:55PM *CRISPR screens to discover regulators of CD4 T cells (Project 1)*
Vijay Kuchroo, Brigham and Women's Hospital

2:55 – 3:15PM *CRISPR screens to discover regulators of DC (Project 2)*
Jon Kagan, Children's Hospital Corporation

3:15 – 3:35PM *CRISPR screens to discover regulators of DC (Project 2)*
Nir Hacohen, The Broad Institute

3:35 – 3:55PM *Bioinformatics and data management (Core B)*
Orr Ashenberg, The Broad Institute

3:55 – 4:00PM *Wrap-up*
Arlene Sharpe, Harvard University Medical School

4:00 PM **Adjourn general meeting**

4:15 – 5:00 PM **Systems Immunology Steering Committee Meeting**

(TBD) **(closed session, Steering Committee members and NIAID staff only)**

To: Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
Cc: Schaefer, Alexandra[aschaefe@email.unc.edu]
From: Heise, Mark T[mark_heisem@med.unc.edu]
Sent: Thur 3/28/2019 2:07:07 PM (UTC-05:00)
Subject: RE: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019

Hi Klaus,
The influenza related choices are perfect!
Thanks
Mark

From: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>
Sent: Thursday, March 28, 2019 11:17 AM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; JACKIE V. BERHORST (jdao@uw.edu) <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Mike <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Shannon McWeeney (mcweeney@ohsu.edu) <mcweeney@ohsu.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>
Cc: Schaefer, Alexandra <aschaefe@email.unc.edu>
Subject: AW: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019

Dear all,
I wanted to present the following hits in human DEGs in DC. Hope this is fine for you. If you have strong reservations with any of them, let me know.
Klaus

Prof. Dr. Klaus Schughart
Head of Dept. of Infection Genetics
Helmholtz Centre for Infection Research,
University of Veterinary Medicine Hannover,
University of Tennessee Health Science Center
Inhoffenstr. 7
D-38124 Braunschweig
Germany

E-mail : Klaus.Schughart@helmholtz-hzi.de
Phone: +49 531 6181 1100

Von: Baric, Toni C <antoinette_baric@med.unc.edu>
Gesendet: Donnerstag, 21. März 2019 15:11
An: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery Vineet (vimenach@utmb.edu); mgale@u.washington.edu; Miller, Darla; Mooney, Mike; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney (mcweeney@ohsu.edu); Suthar, Mehul S. (mehul.s.suthar@emory.edu)
Cc: Schaefer, Alexandra
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Cc: "Leitner, Wolfgang (NIH/NIAID) [E]" <wleitner@niaid.nih.gov>, "Liu, Joy (NIH/NIAID) [E]" <liujoy@niaid.nih.gov>, "Tollini Farrell, Grace (NIH/NIAID) [C]" <grace.tollini@nih.gov>, Patricia Rutledge <pattyr@scripps.edu>, "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Hillman, Sarah Ellen" <Sarah_Hillman@hms.harvard.edu>
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Please let us know if you have any questions.

Thank you,
Chao

Chao Jiang, Ph.D.
Program Officer
Innate Immunity Section, Basic Immunology Branch
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases, NIH, DHHS
5601 Fishers Lane, Room 7B47, MSC 9828
Rockville, MD 20852
Bethesda, MD 20892
(FedEx/UPS delivery: Rockville, MD 20852)
Tel: 301-761-7802
Email: chao.jiang@nih.gov

To: Menachery, Vineet[vimenach@UTMB.EDU]; Schaefer, Alexandra[aschaefe@email.unc.edu]
Cc: Katrina.waters@pnnl.gov[Katrina.Waters@pnnl.gov]; Michelle Craft[michelle.craft@wid.wisc.edu]; Baric, Ralph S[rbaric@email.unc.edu]
From: Amie Eisfeld[amie.eisfeld@wisc.edu]
Sent: Mon 3/18/2019 2:11:26 PM (UTC-05:00)
Subject: RE: MHC paper datasets

Hi Vineet,

Alex was/is in charge of data dissemination for this project, and has access to all the available ChIP-seq and MeDIP data.

She should be able to answer your questions.

Thank you,

Amie

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, March 13, 2019 2:52 PM
To: Schaefer, Alexandra <aschaefe@email.unc.edu>; Amie Eisfeld <amie.eisfeld@wisc.edu>
Cc: Katrina.waters@pnnl.gov; Michelle Craft <michelle.craft@wid.wisc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: MHC paper datasets

Hey all,

One of the PIs I know at UTMB is doing some CHIPseq and MeDIP analysis and was looking at the MHC paper. He said that when he downloaded the GEO files, it only had information for chromosome 6. Is that all we uploaded? He is interested in looking at all the sequencing data to compare changes after infection vs his HIV studies.

Is it possible to send the .bed files for the seq data? Is there a reason these data weren't included in the GEO submission?

Thanks

VDM

From: Schaefer, Alexandra [aschaefe@email.unc.edu]
Sent: Monday, January 08, 2018 12:19 PM
To: Amie Eisfeld; Menachery, Vineet
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: Re: MHC paper datasets

Hi all,

FYI:
I uploaded all necessary files to GEO on Friday--
waiting for them to get back to me with accession #, etc.

Thanks,
Alex

From: Amie Eisfeld <amie.eisfeld@wisc.edu>
Sent: Wednesday, January 3, 2018 1:41:41 PM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: RE: MHC paper datasets

FYI – the data is now available.

The four experiments are listed at the top of this page on the OMICs-LHV public site:
https://omics-lhv.org/data/

… and links go to mirrored pages from the OMICS-LHV LabKey site. I've just confirmed that everything is in working order.

Alex,

Please let us know when you have the GEO accession numbers for the deposited data and we will update the OMICS-LHV public site.

Thank you,

Amie

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Wednesday, January 03, 2018 11:30 AM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Ok, sounds good. I will finish up the proof and plan on submitting it this afternoon. Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Wednesday, January 03, 2018 11:29 AM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

It should be completed in the next 1-2 hours.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Wednesday, January 03, 2018 10:48 AM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Hey Amie,

Any update on the progress for this? I let Ralph and Yoshi know the delay.

Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Tuesday, January 02, 2018 9:21 AM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

I will work with Michelle to:

1. Move the files Alex uploaded to the appropriate pages on the LabKey server.
2. Make the LabKey pages open to the public.
3. Make links to the LabKey pages available from the OMICs public page.

How do you want the study labeled on the OMICs public page?

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Tuesday, January 02, 2018 9:10 AM
To: Schaefer, Alexandra <aschaefe@email.unc.edu>; Amie Eisfeld <amie.eisfeld@wisc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Hey All,

Can we get this resolved today so that I can upload the corrected proofs today?

It seems the best action would be to make the files available on the omics public site in the short term and then proceed with the Geo submission. Once completed, the omics site can link to the Geo submission.

I imagine Amie can help facilitate this through Michelle, but perhaps there is someone else that should be looped in.

Thanks

VDM

From: Schaefer, Alexandra [aschaefe@email.unc.edu]
Sent: Saturday, December 30, 2017 5:34 PM
To: Menachery, Vineet; Amie Eisfeld
Cc: Katrina.waters@pnnl.gov
Subject: Re: MHC paper datasets

Hi All,

I moved all relevant ChIP-Seq and MeDIP-seq files into the Dropbox in LabKey, they are in a folder named ChIP-MeDIP-Seq.

They are bed files (those are what NCBI GEO calls 'processed data files')--- they pretty much are the peak calling files; they are small enough and I hesitated to upload any seq. files. I also added an excel sheet which has all the information regarding samples, protocols, and pipelines used (this is a template which NCBI GEO provides for uploading NGS files).

I understand that I don't have admin rights to actually upload the data; so it would be great if somebody could help me here and upload them into the experimental folders in LabKey.

Amie,
you mentioned that this could be then opened for public access, is this correct?
This way we could keep the reference in the paper for submission and I can work this week on getting all the files, bed (or maybe wig files) and the raw sequencing files to NCBI Geo
-- I think I will need a day or 2 to look into the submission process; I have no experience with this; and then later we could link the GEO ID to the experiments on LabKey.

Please let me know if anything is missing and/or if you need any further information.

Thanks,
Alex

From: Schaefer, Alexandra
Sent: Friday, December 29, 2017 2:50:14 PM
To: Menachery, Vineet; Amie Eisfeld
Cc: Katrina.waters@pnnl.gov

Subject: Re: MHC paper datasets

Hi all,

I agree,
I'll move all relevant files into the dropbox at
https://omics-lhv.discovery.wisc.edu/project/home/begin.view?
to be moved into their permanent location tomorrow (Saturday).

Thanks,
Alex

OMICS-LHV: /home
omics-lhv.discovery.wisc.edu
The OMICS-LHV (Lethal Human Viruses) project aims to develop a comprehensive understanding of the host response to unique viruses that cause lethal infections in humans.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, December 29, 2017 2:39:38 PM
To: Amie Eisfeld; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

In terms of the only data I am not aware of being available is the CHIP data that Alex has and can send tomorrow (Saturday). Can we host it on the Systems site in the short term and submit to GEO thereafter. I prefer not to delay publication.

I have asked the ViPR information to be removed. Let me know if we can have the data available for submission of the proof Tuesday, Jan 2.

Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Thursday, December 28, 2017 5:19 PM
To: Menachery, Vineet; aschaefe@email.unc.edu
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Whoever has the data needs to make sure it is available.

Alex spoke to me briefly about where to deposit it about a year ago. My impression is that she was seeking a public database for deposition. NCBI GEO takes all kinds of sequence data, so I think this would be the most logical location for deposition, so that the data can be available in the long term.

Regarding the OMICS-LHV public page – we have not used this to make any data publicly available for any publication to date. We only list the location of data deposited into public databases.

If the data are posted to the LabKey web portal, we could make that page publicly available. None of the ChIP-seq or Me-DIP data has been posted to the LabKey portal to date, although we do have pages dedicated to these experiments (see https://omics-lhv.discovery.wisc.edu/project/OMICS-Data/ICL106/begin.view? and https://omics-lhv.discovery.wisc.edu/project/OMICS-Data/ICL105/begin.view?).

A few other things:

1. We are not using the PRIDE database anymore, so unless you are using data from Systems Virology, this is not correct. All proteomics data from the current contract have been made available in the MassIVE database. If you let me know which experiments you used for the paper, I can give you the accession number.

2. Katrina should probably comment on the availability of the data through PNNL sites – this is not something we have been reporting in other papers.

3. Data and datasets have not been submitted to ViPR, so this statement should be removed.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Thursday, December 28, 2017 4:15 PM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; aschaefe@email.unc.edu
Cc: Katrina.waters@pnnl.gov
Subject: MHC paper datasets

Hi Amie, Alex, and Katrina,

Not sure who would be responsible for this, but the PNAS paper requires availability of the raw data.

For the methylation data, we cited that it was available on the omics public page. When I clicked on the link, I saw no reference to the CHIP-SEQ data. I think Alex was working with Jason on this, but hopefully she can be provide clarity on this.

The proofs require a 48Hr turn around, although they may be more forgiving because of the holiday. Sorry for the late notice, but wanted to make sure it was all in place prior to submission.

CHIP-Seq, MeDIP-Seq, and raw proteomics data have been made available on the Omics-LHV web portal (https://omics-lhv.org/data/). Raw proteomics data corresponding to peptide identifications used to populate the AMT tag database are available at the PRoteomics IDEntification (PRIDE) database, https://www.ebi.ac.uk/pride/ (accession nos. 19,877–19,890). The raw quantitative proteomics data can be accessed at the Pacific Northwest National Laboratory Biological Mass Spectrometry Data and Software Distribution Center (omics.pnl.gov/) in the Systems Virology Contract Data folder within the Browse Available Data folder. All datasets and associated metadata have been submitted to the Virus Pathogen Resource (www.viprbrc.org/brc/home.spg?decorator=vipr).

Thanks

VDM

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
Cc: Schaefer, Alexandra[aschaefe@email.unc.edu]
From: Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]
Sent: Thur 3/28/2019 10:17:01 AM (UTC-05:00)
Subject: AW: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019
candidate genes NiAID_SIG_talk_kls_270319.pdf

Dear all,

I wanted to present the following hits in human DEGs in DC. Hope this is fine for you. If you have strong reservations with any of them, let me know.

Klaus

Prof. Dr. Klaus Schughart
Head of Dept. of Infection Genetics
Helmholtz Centre for Infection Research,

University of Veterinary Medicine Hannover,

University of Tennessee Health Science Center
Inhoffenstr. 7
D-38124 Braunschweig
Germany

E-mail : Klaus.Schughart@helmholtz-hzi.de
Phone: +49 531 6181 1100

Von: Baric, Toni C <antoinette_baric@med.unc.edu>
Gesendet: Donnerstag, 21. März 2019 15:11
An: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery Vineet (vimenach@utmb.edu); mgale@u.washington.edu; Miller, Darla; Mooney, Mike; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney (mcweeney@ohsu.edu); Suthar, Mehul S. (mehul.s.suthar@emory.edu)
Cc: Schaefer, Alexandra
Betreff: FW: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019

Hi Everyone,
Attached is the agenda for the Systems meeting in April.
Toni

From: Chao Jiang <chao.jiang@nih.gov>
Date: Thursday, March 21, 2019 at 10:04 AM
To: Richard Ulevitch <richard@5amventures.com>, "Heise, Mark T" <mark_heisem@med.unc.edu>, Arlene Sharpe

<arlene_sharpe@hms.harvard.edu>, "Ulevitch, Richard" <Ulevitch@scripps.edu>, "Baric, Ralph" <rbaric@email.unc.edu>
Cc: "Leitner, Wolfgang (NIH/NIAID) [E]" <wleitner@niaid.nih.gov>, "Liu, Joy (NIH/NIAID) [E]" <liujoy@niaid.nih.gov>, "Tollini Farrell, Grace (NIH/NIAID) [C]" <grace.tollini@nih.gov>, Patricia Rutledge <pattyr@scripps.edu>, "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Hillman, Sarah Ellen" <Sarah_Hillman@hms.harvard.edu>
Subject: Updated agenda and registration link for Systems Immunology U19 Annual Meeting - April 11, 2019

Dear All,

Attached please find the updated agenda. Let me know if you have anything to add or change.

Here's the meeting registration link, https://palladianpartners.cvent.com/U19AnnualMeeting. For any logistic issues, please contact Grace Tollini (she is copied here).

Please let us know if you have any questions.

Thank you,
Chao

Chao Jiang, Ph.D.
Program Officer
Innate Immunity Section, Basic Immunology Branch
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases, NIH, DHHS
5601 Fishers Lane, Room 7B47, MSC 9828
Rockville, MD 20852
Bethesda, MD 20892
(FedEx/UPS delivery: Rockville, MD 20852)
Tel: 301-761-7802
Email: chao.jiang@nih.gov

U19 genes / candidates

Project	scientist	Gene	comments	analysis
SARS	Leist	Anpep, Git2, Wisp1	abstract IMGC 2018	done
Ebola	Schaefer	Trim12xxx (human TRIM5)	abstract IMGC 2018	done
Influenza	Heise, Noll	Nlrp1b, Mbd1	SIG tel conf 8.11.18	done
WNV	Gale	Park2	SIG meetings	done
SARS	Gralinski	Ext1, Sla, Asap1	IMGC 2018	done
SARS	Baric	Trim38, Trim14	Tel conf. 20.12.2019	done
SARS	Leist/Schaefer	Ubl3		done
Ebola	Schaefer	Trim6, Trim34, Trim22, Trim67, Cdt1, Chmp1	UNC 120319	
SARS	Leist	Tlr4 pathway	UNC 110319	
Flu	Heise, Noll	Fcgr2a, C1qbp, Rpain	UNC 110319	
SARS	Gralinski	Lamp3, Enpp2	UNC 110319	

24 candiate genes

U19 genes / candidates
– word cloud by total hits

LAMP3

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      human_symbol mouse_symbol
20584        LAMP3         Lamp3
```

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43344	30_DEG_SIG_cells_FLU__A549_24h_inf_vs_ctrl_170119.txt
43347	33_DEG_SIG_cells_FLU__THP1_12h_inf_vs_ctrl_170119.txt
226102	**10_limma_DEG_HAE_FLU_late_mock_240818.txt**
43346	32_DEG_SIG_cells_FLU__THP1_8h_inf_vs_ctrl_170119.txt
226104	12_limma_DEG_HAE_SARS_subset2_late_dORF6_cntrl_240818.txt
226101	09_limma_DEG_HAE_FLU_early_mock_240818.txt
43343	29_DEG_SIG_cells_FLU__A549_8h_inf_vs_ctrl_170119.txt
226105	13_limma_DEG_HAE_SARS_subset2_late_icSARS_cntrl_240818.txt
168312	**21_limma_DEG_Tsalik_2017_viral_ctrl_151018.txt**
226103	11_limma_DEG_HAE_SARS_subset2_late_BAT_cntrl_240818.txt
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8340	19_limma_DEG_unpubl_Tang_FLU_svre_hlthy_291118.txt
27155	**24_limma_DEG_Zhai_2015_FLU_inf_ctrl_151018.txt**
46641	**06_limma_DEG_Dunning_FLU_subset1_mod_HC_151018.txt**
46642	08_limma_DEG_Dunning_FLU_subset1_svre_mod_151018.txt

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             gene  adj.p.value logFC_or_Rsq
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43344       LAMP3 6.331232e-05    6.3675833
43347       LAMP3 2.630623e-04    6.3552610
226102      LAMP3 8.076243e-52    5.4822505
43346       LAMP3 5.441630e-04    5.1011353
226104      LAMP3 8.004019e-30    3.7526172
226101      LAMP3 2.948873e-17    3.7232007
43343       LAMP3 6.958018e-03    3.2189183
226105      LAMP3 1.716637e-26    2.9496223
168312      LAMP3 2.171045e-19    2.6786810
226103      LAMP3 4.695754e-18    2.2599860
43345       LAMP3 3.101182e-02    2.2230603
27208       LAMP3 3.831368e-32    1.8167249
83401       LAMP3 1.950421e-06    1.4468891
4385        LAMP3 1.879095e-03    0.9066952
272091      LAMP3 6.432870e-12    0.8618113
22610       LAMP3 1.166494e-02    0.8502229
A_23_P29773 LAMP3 5.795648e-59    0.8262113
8340        LAMP3 1.908072e-03    0.7523317
27155       LAMP3 6.396265e-05    0.6308131
46641       LAMP3 4.403972e-07    0.6303440
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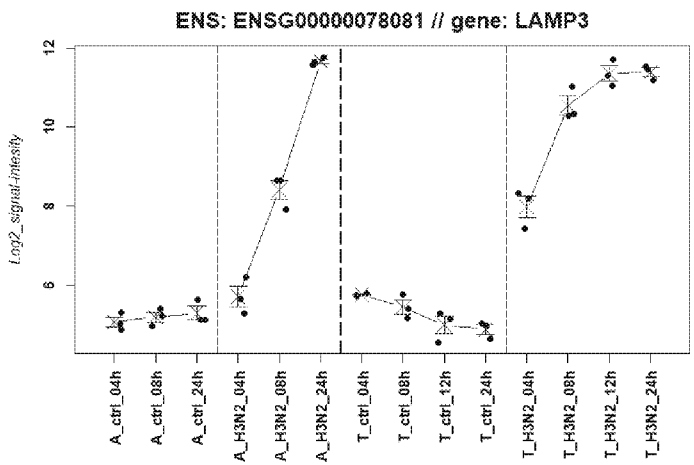
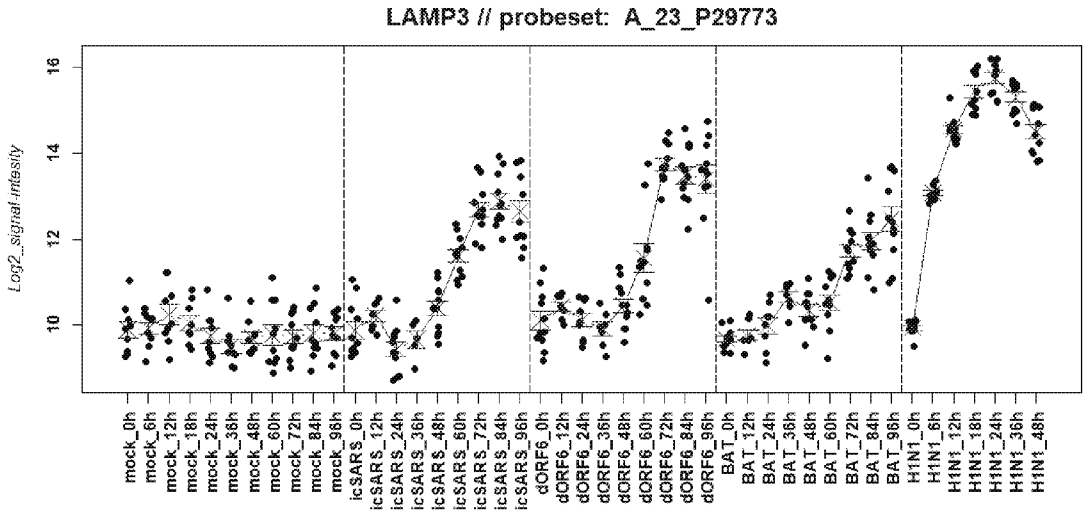
Hits in 7 datasets and 22 DEG lists.

LAMP3

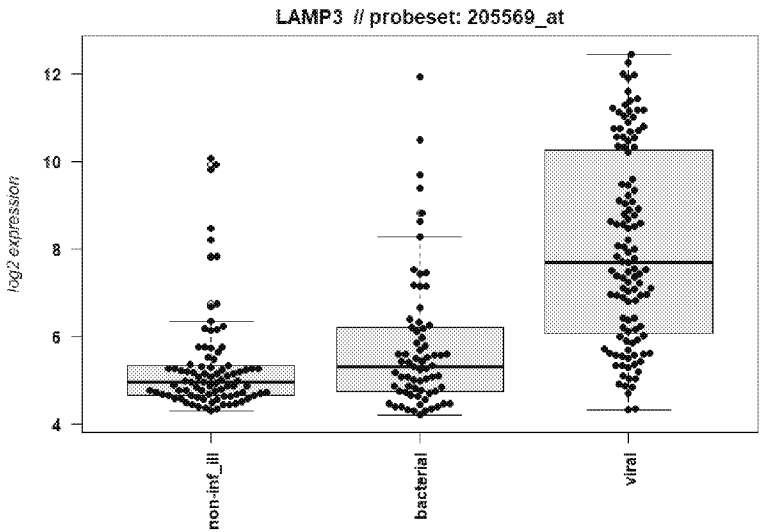
A549 THP1



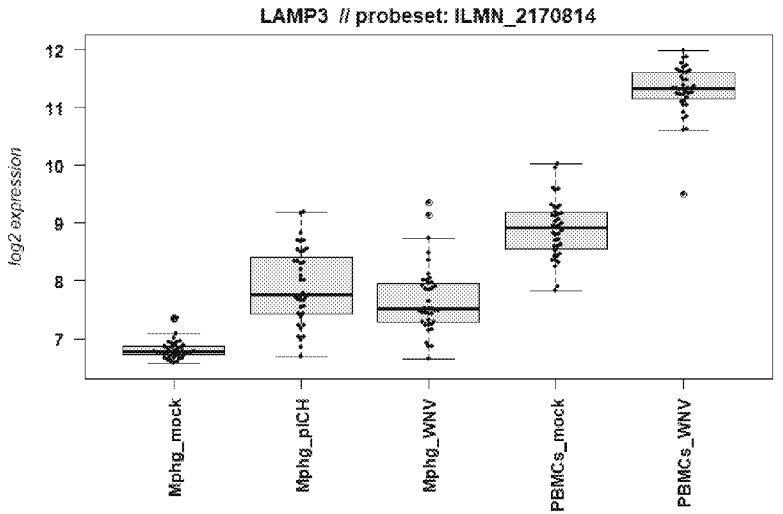
SIMS HAE



Tsalik

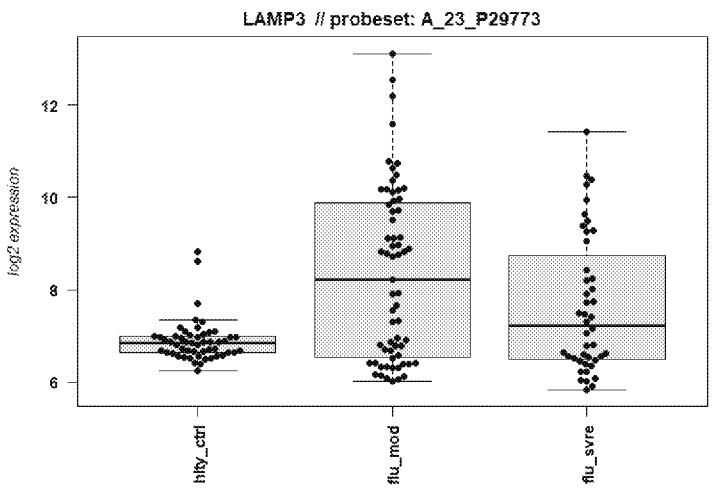


Quian WNV

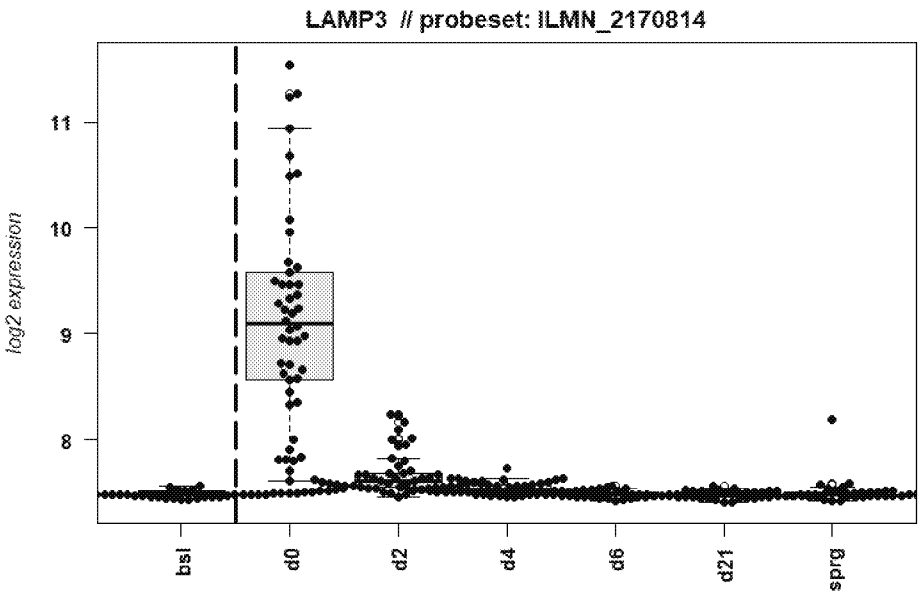


LAMP3

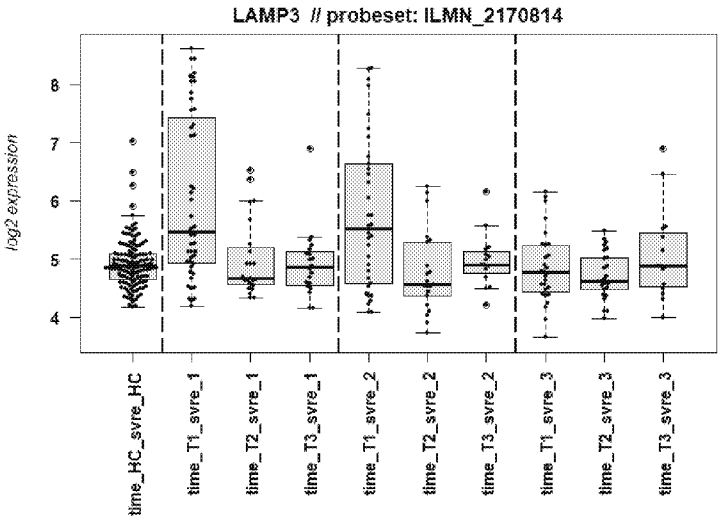
Tang unpubl

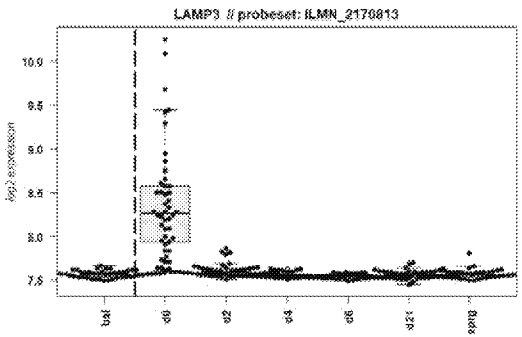


Zhai



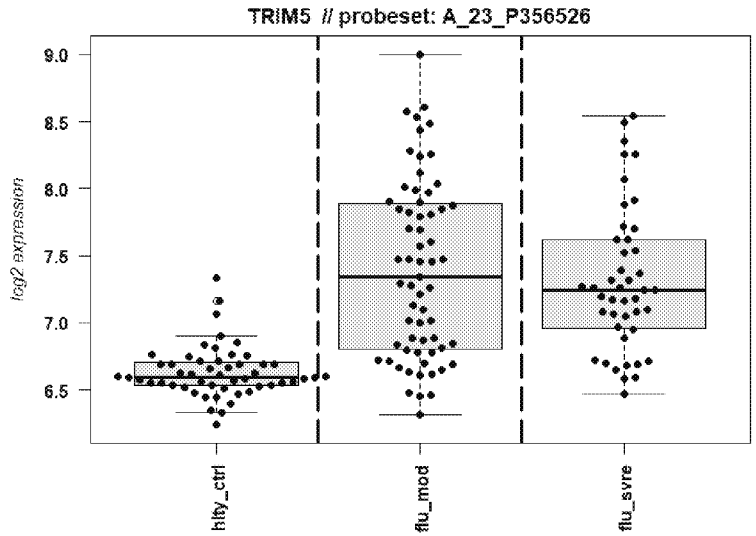
Dunning



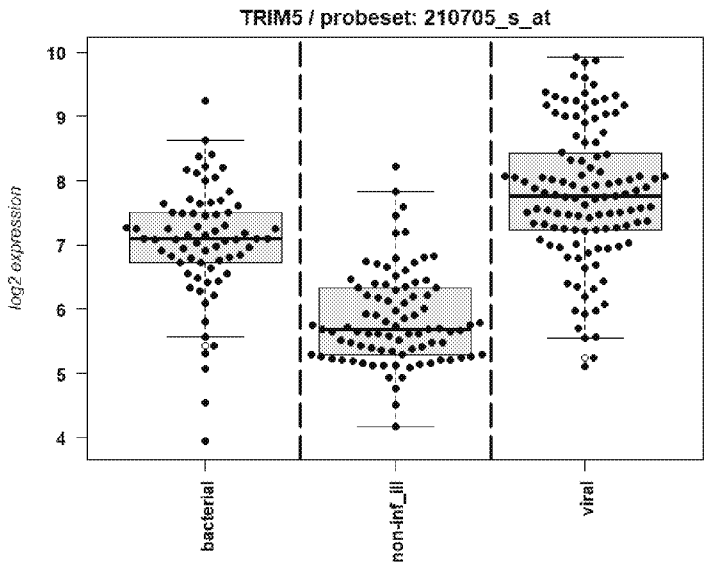


TRIM5

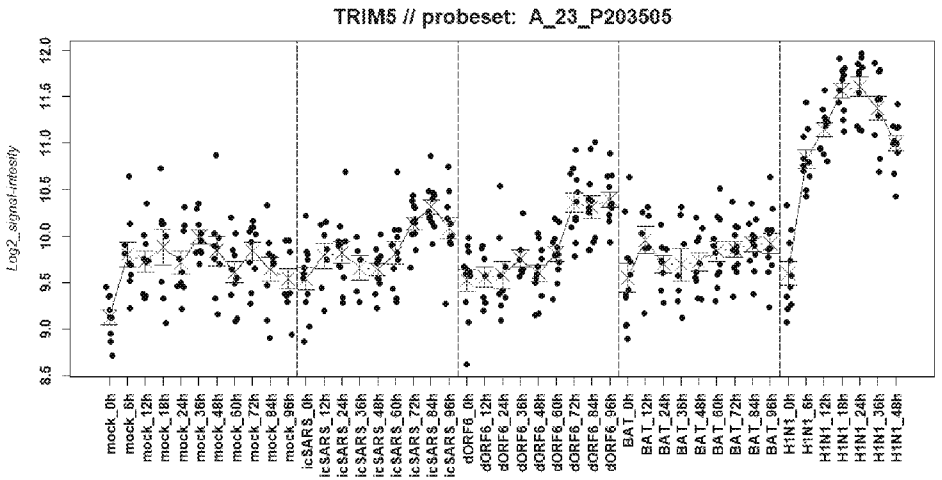
Tang - flu



Tsalik - flu

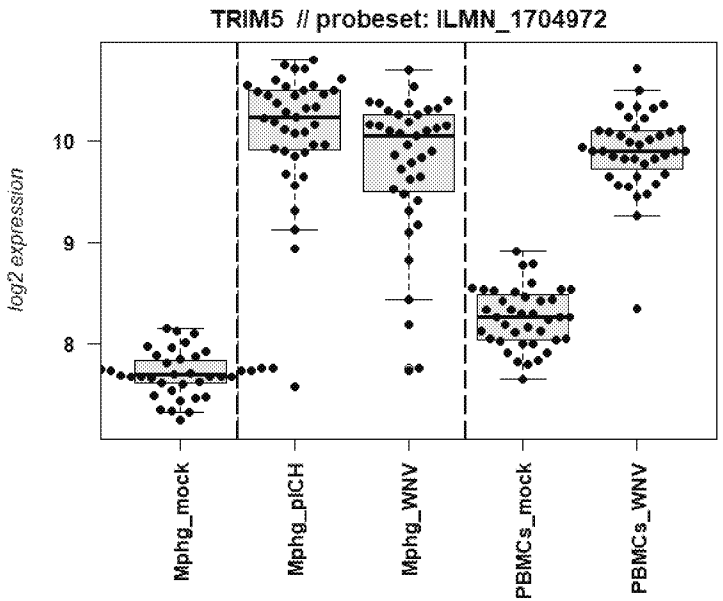


HAE

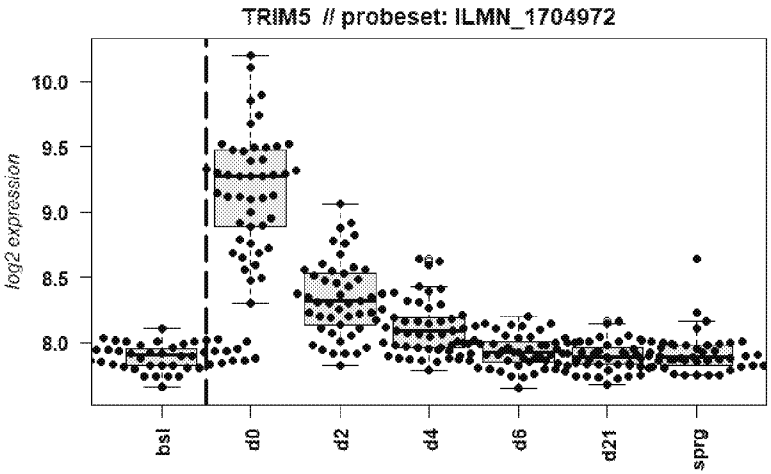


TRIM5

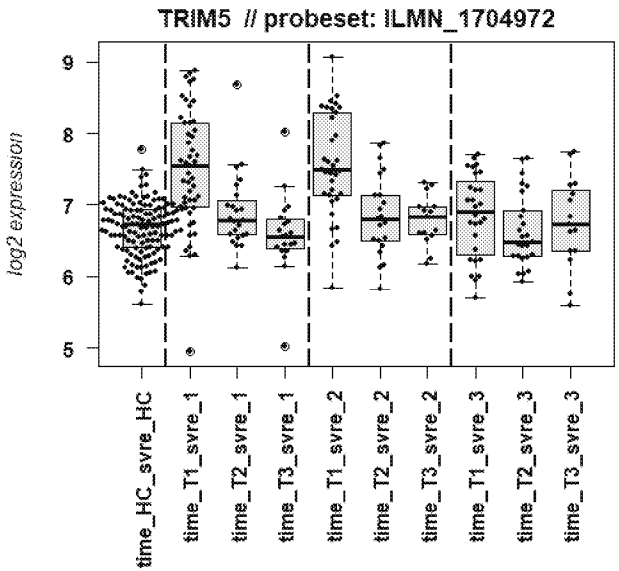
Quian - WNV



Zhai FLU

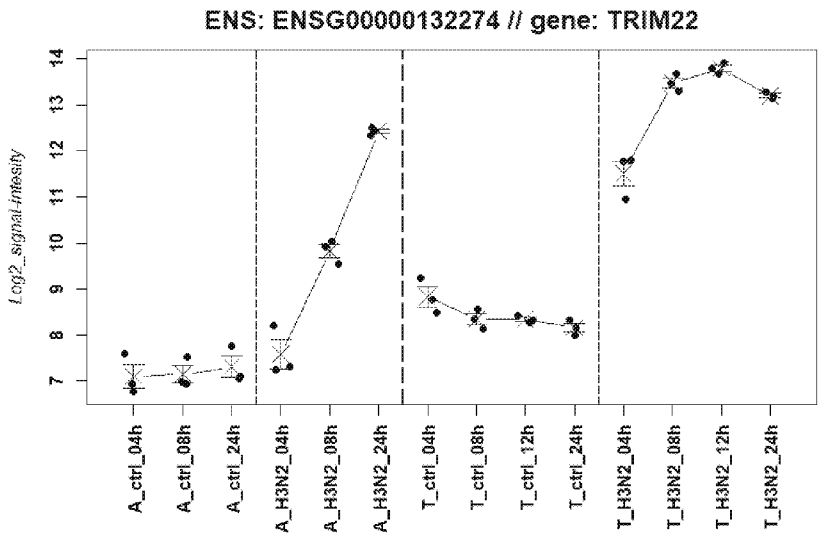


Dunning FLU

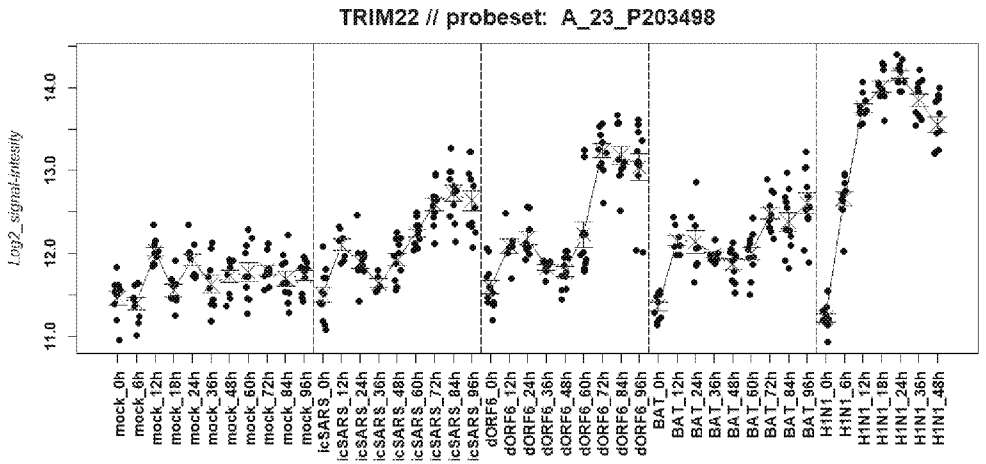


TRIM22

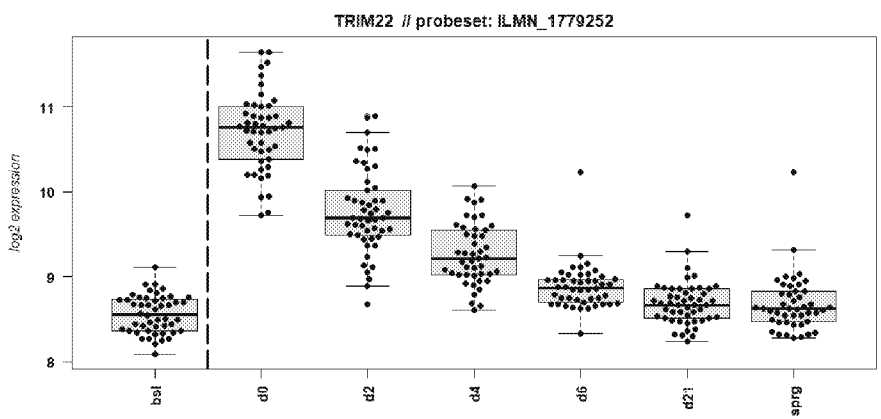
A549 THP1



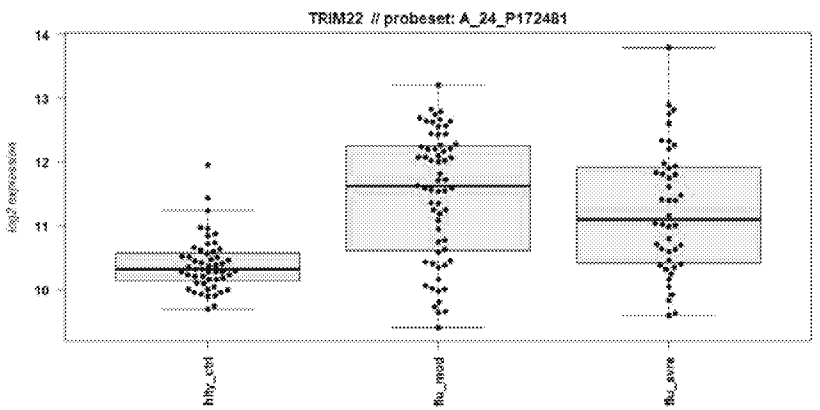
Sims HAE



Zhai

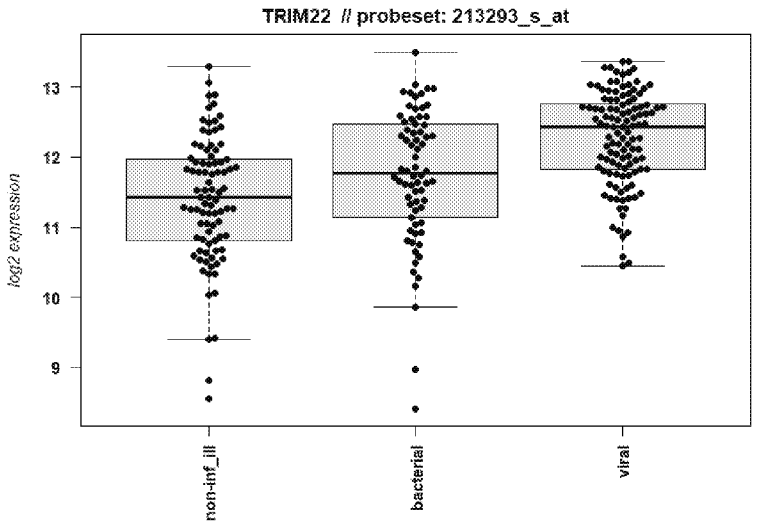


Tang unpubl

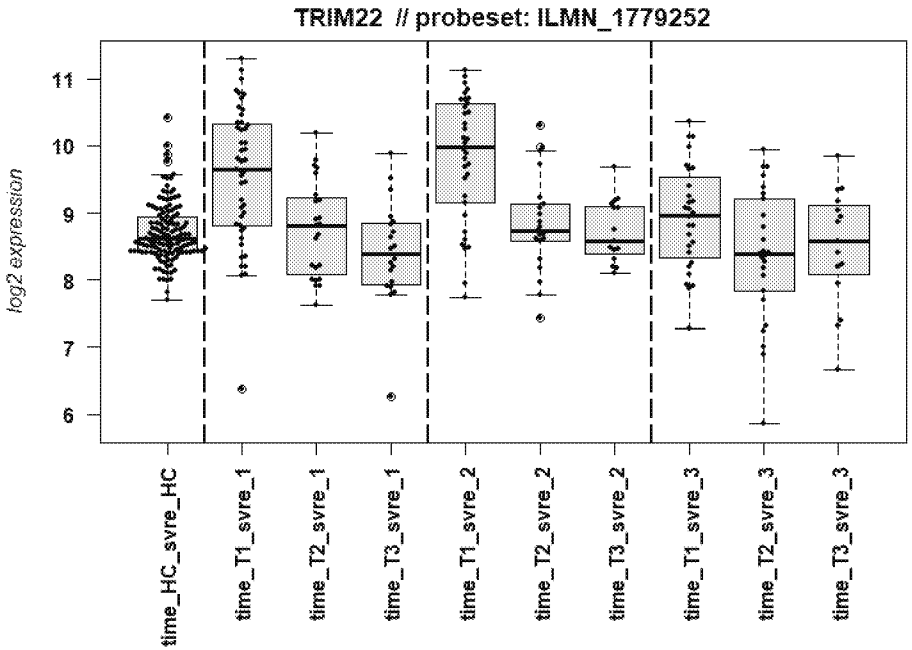


TRIM22

Tsalik



Dunning



To: Arlene Sharpe[arlene_sharpe@hms.harvard.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Baric, Ralph[rbaric@email.unc.edu]; Richard Ulevitch[richard@5amventures.com]; Garry Nolan (gnolan@stanford.edu)[gnolan@drowlab.com]; jonathan.kagan@childrens.harvard.edu[jonathan.kagan@childrens.harvard.edu]; alan.diercks@seattlechildrens.org[alan.diercks@seattlechildrens.org]; jgraham@fhcrc.org[jgraham@fhcrc.org]; lgralins@email.unc.edu[lgralins@email.unc.edu]; vkuchroo@evergrande.hms.harvard.edu[vkuchroo@evergrande.hms.harvard.edu]; lafleur@fas.harvard.edu[lafleur@fas.harvard.edu]; mcweeney@ohsu.edu[mcweeney@ohsu.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mooneymi@ohsu.edu[mooneymi@ohsu.edu]; fernando_pardo-manuel@med.unc.edu[fernando_pardo-manuel@med.unc.edu]; aschaefe@email.unc.edu[aschaefe@email.unc.edu]; kschugha@uthsc.edu[kschugha@uthsc.edu]; oashenbe@fhcrc.org[oashenbe@fhcrc.org]
Cc: Leitner, Wolfgang (NIH/NIAID) [E][wleitner@niaid.nih.gov]
From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]
Sent: Fri 4/12/2019 2:39:34 PM (UTC-05:00)
Subject: Thank you for attending the System Immunology Annual Meeting

Dear All,
Thank you very much for coming to this year's Systems Immunology U19 program annual meeting! It was my great pleasure meeting each of you.
After the meeting, I have received positive feedbacks from our Division Director and Branch Chief. The talks were really informative and interesting.
You have made amazing progress. We really enjoyed the meeting. The Steering Committee Meeting went well too. There were so many good ideas for
collaboration and resource sharing. We really appreciate your input. We look forward to meeting you next time.
Please feel free to talk to me if you have any feedbacks or questions.
Best regards,
Joy

Qian"Joy" Liu, MD, MSc
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases
5601 Fishers Lane, Rm 7B54, Rockville, MD 20852
(E) liujoy@mail.nih.gov| (P) 301-761-6621
(Cell) 301-828-7184

To: Menachery, Vineet[vimenach@UTMB.EDU]; Baric, Ralph S[rbaric@email.unc.edu]; Amie Eisfeld[amie.eisfeld@wisc.edu]
Cc: Katrina.waters@pnnl.gov[Katrina.Waters@pnnl.gov]; Michelle Craft[michelle.craft@wid.wisc.edu]
From: Schaefer, Alexandra[aschaefe@email.unc.edu]
Sent: Tue 3/19/2019 9:46:18 AM (UTC-05:00)
Subject: Re: MHC paper datasets

Hi All,

Just to clarify,
as Ralph said, all the underlying raw data files as well as the data files used for the key conclusion were submitted in January 2018 and are publicly available at GEO under the following accession numbers:

GSE108881: Chip-Seq
GSE108882: MeDIP-Seq

Best,
Alex

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, March 18, 2019 4:35:19 PM
To: Baric, Ralph S; Amie Eisfeld; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: RE: MHC paper datasets

So are the underlying files available somewhere publicly? If so, can I get the link to pass along.
Thanks

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Monday, March 18, 2019 3:16 PM
To: Amie Eisfeld; Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: RE: MHC paper datasets

Hi Vineet, all the datafiles were submitted on the MeDip and Chip seq data associated with the paper. in addition, they wanted the files highlighted as key for the paper which focused on chr 6. I think you have accessed only the chr 6 data, not the underling files for the remaining data. Alex submitted all the data. ralph

---

From: Amie Eisfeld <amie.eisfeld@wisc.edu>
Sent: Monday, March 18, 2019 3:11 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Katrina.waters@pnnl.gov; Michelle Craft <michelle.craft@wid.wisc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: MHC paper datasets

Hi Vineet,

Alex was/is in charge of data dissemination for this project, and has access to all the available ChIP-seq and MeDIP data.

She should be able to answer your questions.

Thank you,

Amie

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, March 13, 2019 2:52 PM
To: Schaefer, Alexandra <aschaefe@email.unc.edu>; Amie Eisfeld <amie.eisfeld@wisc.edu>
Cc: Katrina.waters@pnnl.gov; Michelle Craft <michelle.craft@wid.wisc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: MHC paper datasets

Hey all,

One of the PIs I know at UTMB is doing some CHIPseq and MeDIP analysis and was looking at the MHC paper. He said that when he downloaded the GEO files, it only had information for chromosome 6. Is that all we uploaded? He is interested in looking at all the sequencing data to compare changes after infection vs his HIV studies.

Is it possible to send the .bed files for the seq data? Is there a reason these data weren't included in the GEO submission?

Thanks

VDM

From: Schaefer, Alexandra [aschaefe@email.unc.edu]
Sent: Monday, January 08, 2018 12:19 PM
To: Amie Eisfeld; Menachery, Vineet
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: Re: MHC paper datasets

Hi all,

FYI:
I uploaded all necessary files to GEO on Friday--
waiting for them to get back to me with accession #, etc.

Thanks,
Alex

From: Amie Eisfeld <amie.eisfeld@wisc.edu>
Sent: Wednesday, January 3, 2018 1:41:41 PM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov; Michelle Craft
Subject: RE: MHC paper datasets

FYI – the data is now available.

The four experiments are listed at the top of this page on the OMICs-LHV public site:
https://omics-lhv.org/data/

… and links go to mirrored pages from the OMICS-LHV LabKey site. I've just confirmed that everything is in working order.

Alex,

Please let us know when you have the GEO accession numbers for the deposited data and we will update the OMICS-

LHV public site.

Thank you,

Amie

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Wednesday, January 03, 2018 11:30 AM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Ok, sounds good. I will finish up the proof and plan on submitting it this afternoon. Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Wednesday, January 03, 2018 11:29 AM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

It should be completed in the next 1-2 hours.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Wednesday, January 03, 2018 10:48 AM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Hey Amie,

Any update on the progress for this? I let Ralph and Yoshi know the delay.

Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Tuesday, January 02, 2018 9:21 AM
To: Menachery, Vineet; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

I will work with Michelle to:

1. Move the files Alex uploaded to the appropriate pages on the LabKey server.
2. Make the LabKey pages open to the public.
3. Make links to the LabKey pages available from the OMICs public page.

How do you want the study labeled on the OMICs public page?

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Tuesday, January 02, 2018 9:10 AM
To: Schaefer, Alexandra <aschaefe@email.unc.edu>; Amie Eisfeld <amie.eisfeld@wisc.edu>
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Hey All,

Can we get this resolved today so that I can upload the corrected proofs today?

It seems the best action would be to make the files available on the omics public site in the short term and then proceed with the Geo submission. Once completed, the omics site can link to the Geo submission.

I imagine Amie can help facilitate this through Michelle, but perhaps there is someone else that should be looped in.

Thanks

VDM

From: Schaefer, Alexandra [aschaefe@email.unc.edu]
Sent: Saturday, December 30, 2017 5:34 PM
To: Menachery, Vineet; Amie Eisfeld
Cc: Katrina.waters@pnnl.gov
Subject: Re: MHC paper datasets

Hi All,

I moved all relevant ChIP-Seq and MeDIP-seq files into the Dropbox in LabKey, they are in a folder named ChIP-MeDIP-Seq.

They are bed files (those are what NCBI GEO calls 'processed data files')--- they pretty much are the peak calling files; they are small enough and I hesitated to upload any seq. files. I also added an excel sheet which has all the information regarding samples, protocols, and pipelines used (this is a template which NCBI GEO provides for uploading NGS files).

I understand that I don't have admin rights to actually upload the data; so it would be great if somebody could help me here and upload them into the experimental folders in LabKey.

Amie,
you mentioned that this could be then opened for public access, is this correct?
This way we could keep the reference in the paper for submission and I can work this week on getting all the files, bed (or maybe wig files) and the raw sequencing files to NCBI Geo
-- I think I will need a day or 2 to look into the submission process; I have no experience with this; and then later we could link the GEO ID to the experiments on LabKey.

Please let me know if anything is missing and/or if you need any further information.

Thanks,
Alex

From: Schaefer, Alexandra
Sent: Friday, December 29, 2017 2:50:14 PM
To: Menachery, Vineet; Amie Eisfeld
Cc: Katrina.waters@pnnl.gov
Subject: Re: MHC paper datasets

Hi all,

I agree,
I'll move all relevant files into the dropbox at
https://omics-lhv.discovery.wisc.edu/project/home/begin.view?
to be moved into their permanent location tomorrow (Saturday).

Thanks,
Alex

OMICS-LHV: /home
omics-lhv.discovery.wisc.edu
The OMICS-LHV (Lethal Human Viruses) project aims to develop a comprehensive understanding of the host response to unique viruses that cause lethal infections in humans.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, December 29, 2017 2:39:38 PM
To: Amie Eisfeld; Schaefer, Alexandra
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

In terms of the only data I am not aware of being available is the CHIP data that Alex has and can send tomorrow (Saturday). Can we host it on the Systems site in the short term and submit to GEO thereafter. I prefer not to delay publication.

I have asked the ViPR information to be removed. Let me know if we can have the data available for submission of the proof Tuesday, Jan 2.

Thanks

VDM

From: Amie Eisfeld [amie.eisfeld@wisc.edu]
Sent: Thursday, December 28, 2017 5:19 PM
To: Menachery, Vineet; aschaefe@email.unc.edu
Cc: Katrina.waters@pnnl.gov
Subject: RE: MHC paper datasets

Whoever has the data needs to make sure it is available.

Alex spoke to me briefly about where to deposit it about a year ago. My impression is that she was seeking a public database for deposition. NCBI GEO takes all kinds of sequence data, so I think this would be the most logical location for deposition, so that the data can be available in the long term.

Regarding the OMICS-LHV public page – we have not used this to make any data publicly available for any publication to date. We only list the location of data deposited into public databases.

If the data are posted to the LabKey web portal, we could make that page publicly available. None of the ChIP-seq or Me-DIP data has been posted to the LabKey portal to date, although we do have pages dedicated to these experiments (see https://omics-lhv.discovery.wisc.edu/project/OMICS-Data/ICL106/begin.view? and https://omics-lhv.discovery.wisc.edu/project/OMICS-Data/ICL105/begin.view?).

A few other things:

1. We are not using the PRIDE database anymore, so unless you are using data from Systems Virology, this is not correct. All proteomics data from the current contract have been made available in the MassIVE database. If you let me know which experiments you used for the paper, I can give you the accession number.

2. Katrina should probably comment on the availability of the data through PNNL sites – this is not something we have been reporting in other papers.

3. Data and datasets have not been submitted to ViPR, so this statement should be removed.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]

Sent: Thursday, December 28, 2017 4:15 PM
To: Amie Eisfeld <amie.eisfeld@wisc.edu>; aschaefe@email.unc.edu
Cc: Katrina.waters@pnnl.gov
Subject: MHC paper datasets

Hi Amie, Alex, and Katrina,

Not sure who would be responsible for this, but the PNAS paper requires availability of the raw data.

For the methylation data, we cited that it was available on the omics public page. When I clicked on the link, I saw no reference to the CHIP-SEQ data. I think Alex was working with Jason on this, but hopefully she can be provide clarity on this.

The proofs require a 48Hr turn around, although they may be more forgiving because of the holiday. Sorry for the late notice, but wanted to make sure it was all in place prior to submission.

CHIP-Seq, MeDIP-Seq, and raw proteomics data have been made available on the Omics-LHV web portal (https://omics-lhv.org/data/). Raw proteomics data corresponding to peptide identifications used to populate the AMT tag database are available at the PRoteomics IDEntification (PRIDE) database, https://www.ebi.ac.uk/pride/ (accession nos. 19,877–19,890). The raw quantitative proteomics data can be accessed at the Pacific Northwest National Laboratory Biological Mass Spectrometry Data and Software Distribution Center (omics.pnl.gov/) in the Systems Virology Contract Data folder within the Browse Available Data folder. All datasets and associated metadata have been submitted to the Virus Pathogen Resource (www.viprbrc.org/brc/home.spg?decorator=vipr).

Thanks

VDM

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 3/7/2019 6:04:05 PM (UTC-06:00)
Subject: RE: Darpa project

Hi Vineet, I would be delighted to work with you on this project, especially if it helps your group get money as well. How do I find out more details? Is this vaccine or antiviral small molecule inhibitors, viral pathogenesis or immunomodulatory-based research? ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, March 7, 2019 6:27 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>
Subject: FW: Darpa project

Hey Ralph (and Toni),

I just chatted with guys from ATI (listed below). I told them that I don't have the capacity to do the quick turn around on in vivo mouse work and recommended that they talk to you. They prefer your model to Kent's.

I told them I would make an email introduction which I'll do in a few minutes.

I am under the impression that they think they will get this DARPA funding to do the MERS work. They want me to do the in vitro work and have you do mouse work and then work back to the marmoset model at UTMB.

If you aren't interested, no worries. I am not desperate for the money and based on our conversations with them, not sure I have the ability to be as responsive as they need the project to be. I'm happy to chat over the phone about it tonight or in the morning.

VDM

From: Menachery, Vineet
Sent: Thursday, March 07, 2019 2:20 PM
To: Baric, Ralph S
Subject: Darpa project

Hey Ralph,

I have been approached by a group to working with DARPA to do some MERS work. They are currently funded to do work on CCHF and some other tick viruses and DARPA has requested a proposal to apply their approach to MERS-CoV. Since they were already working with UTMB, I was suggested as a possible person to interact with.

I've had several conversations with them over the past few weeks. They are interested in both in vitro and in vivo validation. I am going to be talking with them further in the next few days, but I am not sure that I have the capacity/interest in doing all the mosue work. If it was at UTMB, it would be Kent's model. I had suggested the UNC DPP4 mice as an alternative.

Would you be interested in participating or even leading the mouse work? I am not sure where it is going, but after talking with Scott Weaver here, it can be a good bit of money, but it is essentially contract work. It does get you into the groups that work with DARPA, so you can get to network with them and carve out a place with the program officers. I know EcoHealth is involved heavily.

The website of the guys leading the project is below. I do not know them personally, and my interactions with them have been far from illuminating. https://www.autonomous.bio/https://www.autonomous.bio/

Anyway, let me know if you have a thought or suggestion. Happy to talk over the phone about this as well.

Hope you are well.

VDM

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 4/26/2019 5:53:03 AM (UTC-05:00)
Subject: RE:

Vineet, I appreciate the full story. However, your second paragraph is still at odds with your first sentence. If some data is shared without the courtesy of discussing it first with the lab that generated the data, it is flat out inappropriate. Consequently, I don't believe I accused you incorrectly, as you seem to be arguing scope. How can you offer their data for our U19 without discussing this with the PI who is directing the student? Why wasn't I brought into this discussion beforehand. If you can't understand my frustration, then you are correct and we have a problem.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, April 25, 2019 10:12 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE:

Ralph,

I don't appreciate being accused of things that I didn't do.

I did not share any QTL mapping or any other data from the U19 with them. I did share that Trim6 might be a target under the QTL for Ebola and that genetic diversity might be important. I did this in context of one of their students presenting their Ebola data on Trim6 KO mice. If that was inappropriate, I apologize.

I did share with Lisa that we have infected the Trim6KO mice with SARS and found a phenotype. Perhaps this was inappropriate as well. The researcher had offered their Ebola Trim6KO data as preliminary data if we wanted to use it in the U19 presentation. Again, perhaps this was inappropriate.

I agree that there are norms in behaviors to be followed, but accusing me of sharing data with direct competitors without knowing the full story also results in a loss of trust between members of the group.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Thursday, April 25, 2019 8:41 PM
To: Menachery, Vineet
Subject:

Hi Vineet, Lisa had mentioned that you had shared our Ebola Mapping data and candidate genes with researchers at UTMB who do Ebola research, and who also happen to have a Trim6 KO. If so, this is inappropriate. It was not your data and not yours to share. As a collaborator on the U19 there are norms in behavior that have to be followed or it results in a complete loss of trust between members of the group. Ralph

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 4/25/2019 8:41:46 PM (UTC-05:00)

Hi Vineet, Lisa had mentioned that you had shared our Ebola Mapping data and candidate genes with researchers at UTMB who do Ebola research, and who also happen to have a Trim6 KO. If so, this is inappropriate. It was not your data and not yours to share. As a collaborator on the U19 there are norms in behavior that have to be followed or it results in a complete loss of trust between members of the group. Ralph

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; Thomas, Sunil[calvinho@uw.edu]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 5/8/2019 6:44:34 PM (UTC-05:00)
Subject: SIG U19 call tomorrow

Hi all
We will have our regularly scheduled call tomorrow at 1:30 ET; 10:30 PT. The item on the agenda will be discussing the results of the pilots.

Phone: 1-800-747-5150
Passcode [redacted]
Germany, calling number below:
08001014525

access code [redacted]

552.136

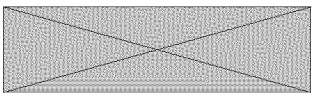
Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]; Graham, Jessica B[jgraham@fredhutch.org]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; lgralins@email.unc.edu[lgralins@email.unc.edu]
From: Lund, Jennifer[jlund@fredhutch.org]
Sent: Thur 4/11/2019 12:04:41 PM (UTC-05:00)
Subject: Re: All virus Paper

Thanks, Vineet!

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org



Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Menachery, Vineet" <vimenach@UTMB.EDU>
Date: Thursday, April 11, 2019 at 9:51 AM
To: "Graham, Jessica B" <jgraham@fredhutch.org>, "Lund, Jennifer" <jlund@fredhutch.org>
Cc: "Baric, Ralph S" <rbaric@email.unc.edu>, "lgralins@email.unc.edu" <lgralins@email.unc.edu>
Subject: All virus Paper

Hey Jenny and Jess,

I mentioned some of my thoughts to Jess at the meeting. I also cced Lisa so that she can comment on my comments.

Let me know if you want me to look at it again. I think its a nice study.

VDM

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]
From: Suthar, Mehul[mehul.s.suthar@emory.edu]
Sent: Thur 5/16/2019 12:59:08 PM (UTC-05:00)
Subject: RE: [External] FW: SIG U19 call tomorrow

I sent in my comments to Toni, but I did not receive a follow-up call-in information. Is there a call today?

Mehul

From: Baric, Toni C [mailto:antoinette_baric@med.unc.edu]
Sent: Monday, May 13, 2019 3:20 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; JACKIE V. BERHORST (jdao@uw.edu) <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Mike <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney (mcweeney@ohsu.edu) <mcweeney@ohsu.edu>; Suthar, Mehul <mehul.s.suthar@emory.edu>
Subject: [External] FW: SIG U19 call tomorrow

Hi All,
Can you make a call this Thursday May 16 at 1:30 ET?
Toni

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, May 09, 2019 8:24 AM
To: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Toni C <antoinette_baric@med.unc.edu>
Cc: Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Green, Richard <greener@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Schughart, Klaus Josef <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; Thomas, Sunil <calvinho@uw.edu>; West, Ande <westande@email.unc.edu>
Subject: RE: SIG U19 call tomorrow

Hi, the major goal for todays SIG U19 meeting was to discuss and select topic candidates for inclusion into the pilot program. As all the reviews aren't yet in and several can't make the call, I think we need to reschedule to next week at a time when a quorum of investigators are available for discussing the projects. We also need to make final decisions by next week for inclusion in the noncompeting renewal packet for year three of the grant. Toni can you search for a time? Please get the reviews in ASAP…thanking those who have already done so.
Ralph and Mark

From: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>
Sent: Wednesday, May 8, 2019 7:57 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>

Cc: Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Green, Richard <greener@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Schughart, Klaus Josef <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; Thomas, Sunil <calvinho@uw.edu>; West, Ande <westande@email.unc.edu>
Subject: Re: SIG U19 call tomorrow

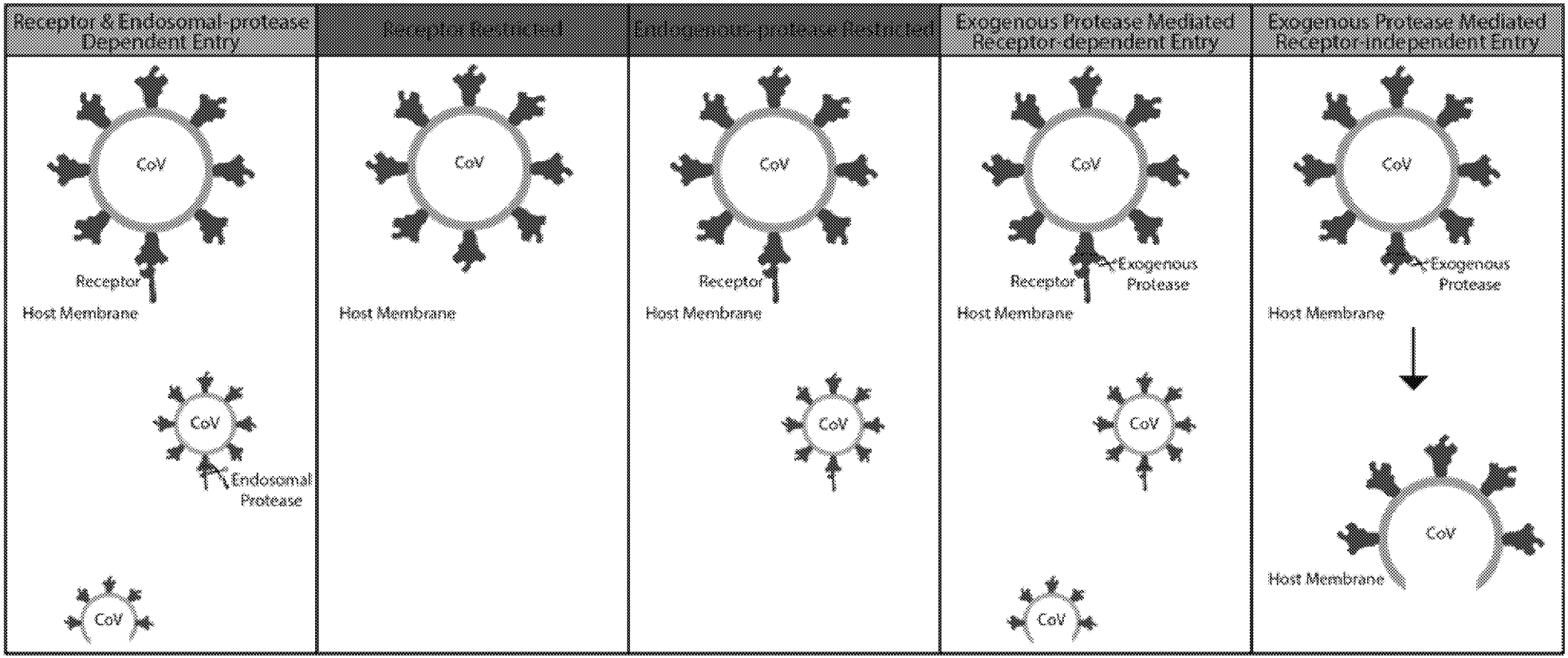
I will not be able to participate.
Sorry,
Klaus

Von meinem iPad gesendet
Am 09.05.2019 um 01:44 schrieb Baric, Toni C <antoinette_baric@med.unc.edu>:

> Hi all
> We will have our regularly scheduled call tomorrow at 1:30 ET; 10:30 PT. The item on the agenda will be discussing the results of the pilots.
>
> Phone: 1-800-747-5150
> Passcode: **552.136**
> Germany, calling number below:
> 08001014525
>
> access code: **552.136**

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu



To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 5/13/2019 2:19:37 PM (UTC-05:00)
Subject: FW: SIG U19 call tomorrow

Hi All,
Can you make a call this Thursday May 16 at 1:30 ET?
Toni

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, May 09, 2019 8:24 AM
To: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Toni C <antoinette_baric@med.unc.edu>
Cc: Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Green, Richard <greener@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Schughart, Klaus Josef <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; Thomas, Sunil <calvinho@uw.edu>; West, Ande <westande@email.unc.edu>
Subject: RE: SIG U19 call tomorrow

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Ralph and Mark

From: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>
Sent: Wednesday, May 8, 2019 7:57 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Green, Richard <greener@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Schughart, Klaus Josef <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; Thomas, Sunil <calvinho@uw.edu>; West, Ande <westande@email.unc.edu>
Subject: Re: SIG U19 call tomorrow

I will not be able to participate.
Sorry,

Klaus

Von meinem iPad gesendet
Am 09.05.2019 um 01:44 schrieb Baric, Toni C <antoinette_baric@med.unc.edu>:

> Hi all
> We will have our regularly scheduled call tomorrow at 1:30 ET; 10:30 PT. The item on the agenda will be discussing the results of the pilots.
>
> Phone: 1-800-747-5150
> Passcode: **552.136**
> Germany, calling number below:
> 08001014525
>
> access code **552.136**

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[klaus.schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 5/16/2019 1:13:23 PM (UTC-05:00)
Subject: Re: [External] FW: SIG U19 call tomorrow

We just had it. Sorry Mehul

Get Outlook for Android

From: Suthar, Mehul <mehul.s.suthar@emory.edu>
Sent: Thursday, May 16, 2019 1:59:08 PM
To: Baric, Toni C; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); mtferris; Menachery Vineet (vimenach@utmb.edu); mgale@u.washington.edu; Miller, Darla; Mooney, Mike; Pardo Manuel de Villena, Fernando; Schughart, Klaus; Shannon McWeeney (mcweeney@ohsu.edu)
Subject: RE: [External] FW: SIG U19 call tomorrow

I sent in my comments to Toni, but I did not receive a follow-up call-in information. Is there a call today?

Mehul

From: Baric, Toni C [mailto:antoinette_baric@med.unc.edu]
Sent: Monday, May 13, 2019 3:20 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; JACKIE V. BERHORST (jdao@uw.edu) <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Mike <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney (mcweeney@ohsu.edu) <mcweeney@ohsu.edu>; Suthar, Mehul <mehul.s.suthar@emory.edu>
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Cc: Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Green, Richard <greener@uw.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Schughart, Klaus Josef <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; Thomas, Sunil <calvinho@uw.edu>; West, Ande <westande@email.unc.edu>

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Klaus

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> Passcode: **552.136**
> Germany, calling number below:
> 08001014525
>
> access code **552.136**
>
> Toni Baric
> Department of Microbiology and Immunology
> 9025 Burnett Womack
> CB# 7292
> Chapel Hill, NC 27599-7292
> Office: 919-966-3507
> tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 5/10/2019 11:18:16 AM (UTC-05:00)
Subject: FW: MERS-Uganda draft
Spike processng Uganda figure.pptx

Hi Vineet, is this the other model for figure 6? ralph

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 6/4/2019 2:51:52 PM (UTC-05:00)
Subject: RE: Uganda Draft

If you can send along a paragraph for inclusion in the project 1 progress report, this would be helpful thanks. Hope you enjoy plus strand meeting. I would have liked to have attended.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 4, 2019 3:43 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: Uganda Draft

Still HumanAbs. I will check with him when I see him at the meeting. Assuming Barney and Lingshu don't have any further comments, I will plan to submit next week after I talk to him.

Also, do you need anything for the progress report for U19.

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Tuesday, June 04, 2019 2:04 PM
To: Menachery, Vineet
Subject: RE: Uganda Draft

That's a great plan, Is he still listed as working for humabs or does the meeting site provide his current email?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 4, 2019 2:53 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: Uganda Draft

I will send to her shortly and CC you and Barney.

As for Davide, he is registered to speak and attend plus strand, so I could ask him directly, but he's not scheduled to speak until later in the meeting.

We'd have to wait until next week to submit. Probably need to give Lingshu time to read the paper if she wanted, which probably pushes us to Friday. Up to you, I'm fine either way, but I don't have a relationship with him so it probably doesn't impact me going forward. I'll look and see if he's provided antibodies to others without authorship.

I'll email text to Lingshu and let me know if you want me to just talk to Corti directly next week.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Tuesday, June 04, 2019 1:36 PM
To: Menachery, Vineet

Subject: RE: Uganda Draft

Hi Vineet, finally heard from Barney-he was celebrating his 40th anniversary and was out of all electronic contact for 3 weeks or so. In any event, he suggested we add Lingshu (she made the antibodies under his direction). Wang, Lingshu (NIH/VRC) [E] wangling@niaid.nih.gov You should send her a copy to make sure she is on board, before pressing go. Regarding Davide, I think he left humabs and I have no idea where he is. He hasn't answered my last 4 emails, so I think maybe we should just thank him and lanzavecchia in the acknowledgements section—he has gotten about 5-6 papers out of us so I think we have been kind. thoughts? Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, June 3, 2019 12:05 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: RE: Uganda Draft

Everything is uploaded and ready to go at PNAS.

Immediate Open access is an extra $1150; I marked no for open access. All PNAS articles are free online after 6 months.

I have listed myself as corresponding author prior to submission, but put in the notes that after acceptance, you as the corresponding author and that should be indicated in the text.

Just let me know when you want me to submit.

VDM

From: Menachery, Vineet
Sent: Friday, May 31, 2019 3:28 PM
To: Baric, Ralph S
Cc: kdinnon@email.unc.edu
Subject: RE: Uganda Draft

I just saw the email to my UNC account with the text changes and letter.

I'll incorporate those changes in the text. I'll start uploading the files this weekend and will wait until next week to submit so we can try to hear from Barney again. Do you want to email Davide, I might not be in his address book. Only question is either of them have conflict of interest; last time Davide didn't for WIV1 paper, not sure for this antibody.

VDM

From: Menachery, Vineet
Sent: Friday, May 31, 2019 3:20 PM
To: Baric, Ralph S
Cc: kdinnon@email.unc.edu
Subject: Uganda Draft

Ralph,

I've attached the Uganda draft and final figures following comments from various authors. I did not hear from Davide or Barney. I added Scott Randell to the author line and he read over the manuscript.

I have also attached the cover letter if you want to modify; I was planning to ask for Enjuanes, Gallagher, and Baker for reviewers. Any other suggestions? Also need editors for the editorial board, was thinking palese or Oldstone.

It is otherwise ready to go in my mind.

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; Thomas, Sunil[calvinho@uw.edu]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 6/13/2019 11:22:54 AM (UTC-05:00)
Subject: SIG U119 call cancelled

Hi Everyone,
There will not be a call today. A few reminders, we are in the home stretch for year 7. Make sure all your funds are expended by August 31. Also I wanted to let you know that Helen Lazear was the successful candidate for this year's pilot award.

Thank you

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 6/25/2019 3:34:47 PM (UTC-05:00)
Subject: RE: presubmission draft

I think this is good!

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 4:31 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: presubmission draft

Dear Editors at Cell Host & Microbe:

Please find our presubmission inquiry for our manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection", by Menachery, Dinnon, et al.

In this work, we describe the restriction of two MERS-like bat coronaviruses and the use of exogenous trypsin to overcome this barrier. Employing a MERS-CoV reverse genetic system, we constructed a chimeric virus replacing the wild-type spike with the PDF2180-CoV spike, a MERS-like virus found in an Ugandan bat. While initially not viable, we found that the addition of exogenous trypsin rescued viral replication in Vero and human cells. The chimeric MERS virus could replicate in human gut cells, but not in human airway cells. Notably, blockade of MERS-CoV receptor DPP4 had no impact on chimeric virus replication, suggesting use of an alternate receptor. Testing of monoclonal antibodies designed against the RBD and S2 portions of the MERS-CoV spike showed no efficacy against the PDF2180-chimeric virus. Importantly, exogenous trypsin also rescued replication of a second group 2C CoV, full-length HKU5-CoV. These results indicate host protease cleavage of spike constitutes a primary barrier for group 2C CoV emergence. Coupled with receptor binding, spike activation offers a new parameter to evaluate emergence potential of coronavirus. In addition, the finding offers a means to recover previously uncultivable zoonotic coronavirus strains.

We have attached our abstract and a graphical description of our findings for you to review. WE look forward to your response.

Sincerely,

Vineet D. Menachery & Ralph S. Baric

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Baric, Ralph S[rbaric@email.unc.edu]
From: Cell Press Cell Host and Microbe[hostmicrobe@cell.com]
Sent: Tue 6/25/2019 3:49:05 PM (UTC-05:00)
Subject: RE: Presubmission Inquiry: Barrier to Coronavirus Emergence

Dear Dr. Menachery,

Thank you for your interest in Cell Host & Microbe. We have received your presubmission inquiry, and it has been passed to the editors for consideration. Please feel free to contact me should you have any questions.

Best regards,

Alex Dvorkin
Editorial Operations Associate, *Cell Host & Microbe*
50 Hampshire Street, 5th floor
Cambridge, MA 02139
+1(617) 397 2851
hostmicrobe@cell.com

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 4:40 PM
To: Cell Press Cell Host and Microbe <hostmicrobe@cell.com>
Cc: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Presubmission Inquiry: Barrier to Coronavirus Emergence

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Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 6/27/2019 11:14:41 AM (UTC-05:00)
Subject: RE: Presubmission Inquiry: Barrier to Coronavirus Emergence

Alsoconsider science advances, impact 12 before cell reports. My guess cell reports might be best guess, although science advances might bite.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, June 27, 2019 9:18 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: Presubmission Inquiry: Barrier to Coronavirus Emergence

I will go ahead and send the inquiry to Nat. Micro and start prepping manuscript it for Cell Reports. Assuming it doesn't get positive responses from Nat. Micro, I'll submit to Cell Reports next week.

The CHM editor that got it was not the one I met.

From: Cell Press Cell Host and Microbe [hostmicrobe@cell.com]
Sent: Wednesday, June 26, 2019 2:12 PM
To: Menachery, Vineet
Cc: Baric, Ralph S
Subject: RE: Presubmission Inquiry: Barrier to Coronavirus Emergence

Dear Dr. Menachery,

Thank you for your email and interest in submitting a paper to Cell Host & Microbe. We have read the details of the proposed submission and would like to suggest that submission to another journal would be more appropriate.
I am sorry not to be positive on this occasion but hope you will remain interested in the journal and will contact us again about other papers from your lab.
Best regards,
Caeul

Caeul Lim, PhD
Scientific Editor, Cell Host & Microbe & Trends Reviews
Interim Editor, Trends in Cell Biology
Cell Press | 50 Hampshire St. | Cambridge MA
Follow us on twitter @cellhostmicrobe

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 4:40 PM
To: Cell Press Cell Host and Microbe <hostmicrobe@cell.com>
Cc: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Presubmission Inquiry: Barrier to Coronavirus Emergence

Dear Editors at Cell Host & Microbe:

Please find our presubmission inquiry for our manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection", by Menachery, Dinnon, et al.

In this work, we describe the restriction of two MERS-like bat coronaviruses and the use of exogenous trypsin to overcome this barrier. Employing a MERS-CoV reverse genetic system, we constructed a chimeric virus replacing the wild-type spike with the PDF2180-CoV spike, a MERS-like virus found in an Ugandan bat. While initially not viable, we found that the addition of exogenous trypsin rescued viral replication in Vero and human cells. The chimeric MERS virus could replicate in human gut cells, but not in human airway cells. Notably, blockade of MERS-CoV receptor DPP4 had no impact on chimeric virus replication, suggesting use of an alternate receptor. Testing of monoclonal antibodies designed against the RBD and S2 portions of the MERS-CoV spike showed no efficacy against the PDF2180-chimeric virus. Importantly, exogenous trypsin also rescued replication of a second group 2C CoV, full-length HKU5-CoV. These results indicate host protease cleavage of spike constitutes a primary barrier for group 2C CoV emergence. Coupled with receptor binding, spike activation offers a new parameter to evaluate emergence potential of coronavirus. In addition, the finding offers a means to recover previously uncultivable zoonotic coronavirus strains.

We have attached our abstract and a graphical description of our findings for you to review. We look forward to your response.

Sincerely,

Vineet D. Menachery & Ralph S. Baric

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 6/25/2019 1:07:18 PM (UTC-05:00)
Subject: RE: PNAS MS# 2019-09188 Decision Notification

Cell host and microb?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 2:05 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: FW: PNAS MS# 2019-09188 Decision Notification

Such bull shit.

Where do you want to go? Nature Micro or Cell Host is my thought.

From: journalstaff@pnascentral.org [journalstaff@pnascentral.org]
Sent: Tuesday, June 25, 2019 10:48 AM
To: Menachery, Vineet
Cc: vineet@email.unc.edu
Subject: PNAS MS# 2019-09188 Decision Notification

June 25, 2019

Title: "**Trypsin treatment unlocks barrier for zoonotic coronaviruses infection.**"
Tracking #: 2019-09188
Authors: Menachery et al.

Dear Dr. Menachery,

I regret to inform you that the PNAS Editorial Board has declined your manuscript [MS# 2019-09188] for further consideration. We receive many more good papers than we can publish and the Board must carefully weigh which papers merit external review. The expert who served as editor concluded that although this work is interesting, it does not have the broad appeal needed for PNAS and is better suited for a more specialized journal.

Thank you for submitting your manuscript to PNAS. I am sorry we cannot be more encouraging this time, and I hope you will consider submitting future work to PNAS.

Sincerely yours,
May R. Berenbaum
Editor-in-Chief

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 7/5/2019 11:06:22 AM (UTC-05:00)
Subject: RE: ASM nomination

They (Mike and Yoshi) were both delighted to participate. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, July 1, 2019 11:30 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: ASM nomination

See attached CV.

From: Menachery, Vineet
Sent: Sunday, June 30, 2019 11:01 AM
To: Baric, Ralph S
Subject: RE: ASM nomination

I'll send the CV Monday or Tuesday.

Thanks again. Hopefully Diamond and Yoshi will do it. I know Mike has written most of my letters for this. Yoshi did the one for the Star award. They only have to write it if I make the first cut.

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Saturday, June 29, 2019 4:24 PM
To: Menachery, Vineet
Subject: RE: ASM nomination

Hi Vineet, Okay thisis very helpful. I will be delighted to lead it and get the nominating letter together, send cv next week. I had been concerned a bout contacting other referee's at the last minute and wasn't aware they had draft letters already available.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, June 28, 2019 11:26 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: ASM nomination

Hey Ralph,

The nomination is a webform (in the link) and has a slot (4000 characters) for defining why I am deserving of the award. They only contact the references (Diamond or Yoshi or Scott) if I am a finalist. Both have already written a letter on my behalf for the Texas Star award, so I think they have text already.

I can ask Scott, but based on what I have heard, it really needs to be someone that can put the nominee's accomplishments in the perspective of your field. The people who have won that I know (Nick Heaton and Stacy Horner) had their post-doc PI nominate (Gale and Palese) them.

It has been implied that the nomination is about your record, the stature of the people who are your references, and the nominator highlighting your importance to your specific field. I think you are probably most qualified to do that.

The award does not always get many people applying. The nomination is due almost a year before the next meeting and most people miss the deadline and forget. That being said, my biggest strike for the award will be not having an independent pub from my own lab. Best is the number of papers I've published. We got favorable reviews on our JVI paper this month, but won't be back

in til later in July.

I can send my CV next week, but you can also send it at a later date, that might help.

Thanks for participating.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Friday, June 28, 2019 2:58 PM
To: Menachery, Vineet
Subject: RE: ASM nomination

Hi Vineet, I'd be delighted to participate. Given the timeline, it might be better for me to write a letter and scott to nominate, as I can address why your deserving of this award for early career basic research, which I think you'd be competitive for. Not sure how quickly diamond and kawaoka can respond or whether they have made other commitments, although they are both familiar with your work. Does scott have a feel for the mechanism here? Is it better for your former mentor or current chair to nominate you for this award? Some insight into this would help. Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, June 27, 2019 10:07 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: ASM nomination

Hey Ralph,

Would you be willing to nominate me for the ASM early career award. https://www.asm.org/Academy/ASM-Award-for-Early-Career-Basic-Researchhttps://www.asm.org/Academy/ASM-Award-for-Early-Career-Basic-Research

The application requires 1 nominator and 2 references. I'd suggest that Mike Diamond and Yoshi would be good for the nomination. You could also use Scott Weaver. I put their emails down below. The hardest part of the form is the following prompt:

Describe the nominee's outstanding contributions to the microbial sciences. Please be as specific as possible, with particular focus on why the nominee is deserving of this specific award (*no more than 4000 characters*). For more information regarding specific awards descriptions, please visit: https://www.asm.org/Academy/ASM-Awards.

If you are willing, the nomination is due by July 9th. If you don't have time, I can ask Scott Weaver or another person to nominate me. Let me know and I will send you and updated CV.ThanksVDM

mdiamond@wustl.edu
yoshihiro.kawaoka@wisc.edu
sweaver@UTMB.EDU

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Green, Richard [greener@uw.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 7/10/2019 3:04:58 PM (UTC-05:00)
Subject: SIG U19 call canceled

Hi All,
Due to several key people being out of town, we cancel our July call. Please plan on a call in August. If you have anything specific you would like to cover at that time, please let me know.

Remember that the end of the budget period is August 31. Please make every effort to spend out all your funds. We will not be requesting carryover.
Thank you

Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 7/16/2019 12:36:15 PM (UTC-05:00)
Subject: RE: Decision on Nature Microbiology manuscript NMICROBIOL-19061557A

Sounds good!

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, July 16, 2019 10:00 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: FW: Decision on Nature Microbiology manuscript NMICROBIOL-19061557A

Rejected for Nat. Micro, but we can send to Nat. Com. I know the editor at Nat. Com. so they said they'll send it out. Figure this is easiest move.

Ok with you?

VDM

From: libera.presti@nature.com [libera.presti@nature.com]
Sent: Tuesday, July 16, 2019 8:57 AM
To: Menachery, Vineet
Subject: Decision on Nature Microbiology manuscript NMICROBIOL-19061557A

16th July 2019

Dear Professor Menachery,

Thank you for submitting your Letter entitled "Trypsin treatment unlocks barrier for zoonotic coronavirus infection" for consideration in Nature Microbiology. I regret to inform you that after careful consideration and discussion with my editorial colleagues, we have decided that we cannot consider it for publication here.

As you may know, we decline a substantial proportion of manuscripts without sending them to referees, so that they may be sent elsewhere without delay. In such cases, even if referees were to certify the manuscript as technically correct, we consider that the work does not represent the type of advance that Nature Microbiology seeks to publish. These editorial judgements are based on considerations such as the degree of conceptual advance provided, the breadth of potential interest to researchers and timeliness.

In this case, we appreciate your major findings that MERS-CoV engineered with the PDF-2180 spike protein is able to infect human cell lines in presence of exogenous trypsin and in a DPP4-independent manner and that antibodies targeted against MERS-CoV, even to regions in the highly conserved S2 domain, may be ineffective against viruses expressing the PDF-2180 spike. However given the modest insights provided here into the mechanisms behind trypsin-mediated entry, your study has not matched our criteria for further consideration. We therefore feel that the paper would find a more suitable outlet in another journal.

I am sorry to have invited you to submit the paper only to reach a decision which must inevitably be disappointing. While we endeavour to assess papers as best as possible at the presubmission stage, I am sure you will understand that it is not always possible to do so accurately, given the limited information available.

Although we cannot offer publication, I have discussed your manuscript with our colleagues at Nature Communications, and they would be happy to send it out for formal peer review if you transfer the manuscript. Should you wish to have your paper reviewed at Nature Communications, please use the link to the Springer Nature manuscript transfer service in the footnote. It is not necessary to reformat your paper at this point.

Your handling editor at Nature Communications would be Dr. Sonja Schmid (Sonja.schmid@us.nature.com). If there is anything you would like to discuss before transferring the paper, please don't hesitate to contact her by e-mail.

Please note that Nature Communications is a fully open access journal. For information about article processing charges, open access funding, and advice and support from Nature Research, please consult the Nature Communications Open Access page (www.nature.com/ncomms/open_access/index.html).

I am sorry that we cannot respond more positively on this occasion.

Yours sincerely

Libera

Libera Lo Presti, PhD
Associate Editor
Nature Microbiology
4 Crinan Street
London, N1 9XW

libera.presti@nature.com

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All Nature Research journals are editorially independent, and the decision to consider your manuscript will be taken by their own editorial staff. For more information, please see our manuscript transfer FAQ page.

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 7/30/2019 6:47:53 PM (UTC-05:00)
Subject: RE: Uganda Paper

Good news, of course go ahead

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, July 30, 2019 1:33 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Uganda Paper

Hey Ralph,

The Uganda paper is out for review at Nat. Com.

I am working with David Veesler who is interested in doing a crystal structure on the Uganda spike. He has already started working on making the trimer prior to my chatting with him at plus strand. He had remembered that we had recovered the recombinant virus at the last nidovirus meeting and wanted to know our progress.

I'd like to share the submitted manuscript, but wanted to make sure you didn't have an objection. Let me know.

Thanks

VDM

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 8/5/2019 1:24:20 PM (UTC-05:00)
Subject: SIG U19 call Thursday

Hi Everyone,
We will be having our monthly SIG U19 call on Thursday August 8 at 1:30 ET. Mark will be presenting for Project 2. Please use the calling numbers below:
Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,
Toni

To: Baric, Ralph S[rbaric@email.unc.edu]; Sims, Amy C[sims0018@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Gralinski, Lisa E[lgralins@email.unc.edu]
From: Sheahan, Timothy Patrick[sheahan@email.unc.edu]
Sent: Mon 8/12/2019 1:19:21 PM (UTC-05:00)
Subject: FYI: Characterization of cellular transcriptomic signatures induced by different respiratory viruses in human reconstituted airway epithelia.

Characterization of cellular transcriptomic signatures induced by different respiratory viruses in human reconstituted airway epithelia.

Nicolas de Lamballerie C, Pizzorno A, Dubois J, Julien T, Padey B, Bouveret M, Traversier A, Legras-Lachuer C, Lina B, Boivin G, Terrier O, Rosa-Calatrava M.

Sci Rep. 2019 Aug 7;9(1):11493. doi: 10.1038/s41598-019-48013-7.

PMID: 31391513 [PubMed - in process] **Free Article**

Similar articles

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
Cc: Hampton, Brea Kaseanna-Lanae[hamptb10@email.unc.edu]
From: Heise, Mark T[mark_heisem@med.unc.edu]
Sent: Thur 8/8/2019 10:07:46 AM (UTC-05:00)
Subject: RE: SIG U19 call Thursday
Baseline Immunity Update 8-7-19.pdf

Hi Everyone,
Here are my slides for today's SIG U19 call.
Mark

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Monday, August 5, 2019 2:24 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: SIG U19 call Thursday

Hi Everyone,
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Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

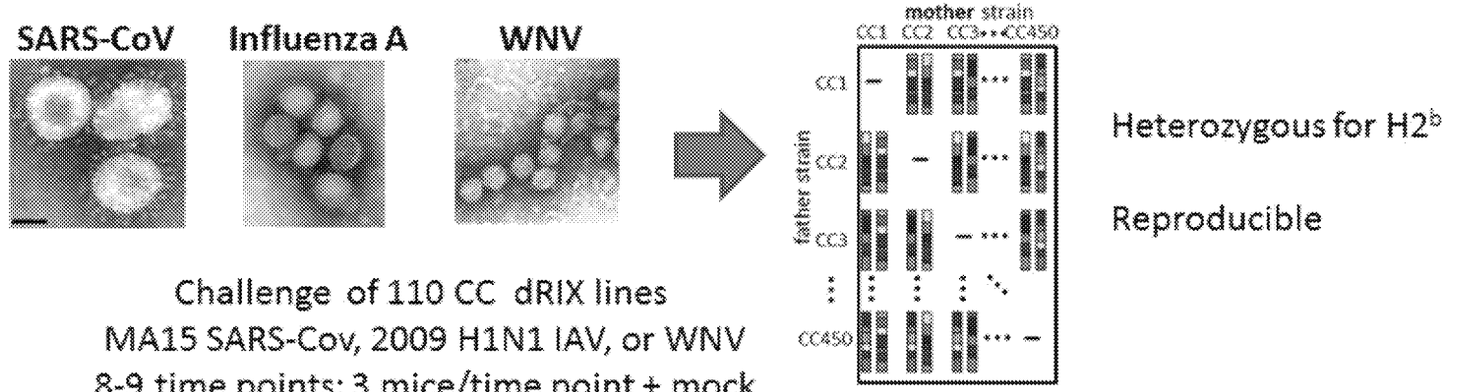
access code **552.136**

Best regards,
Toni

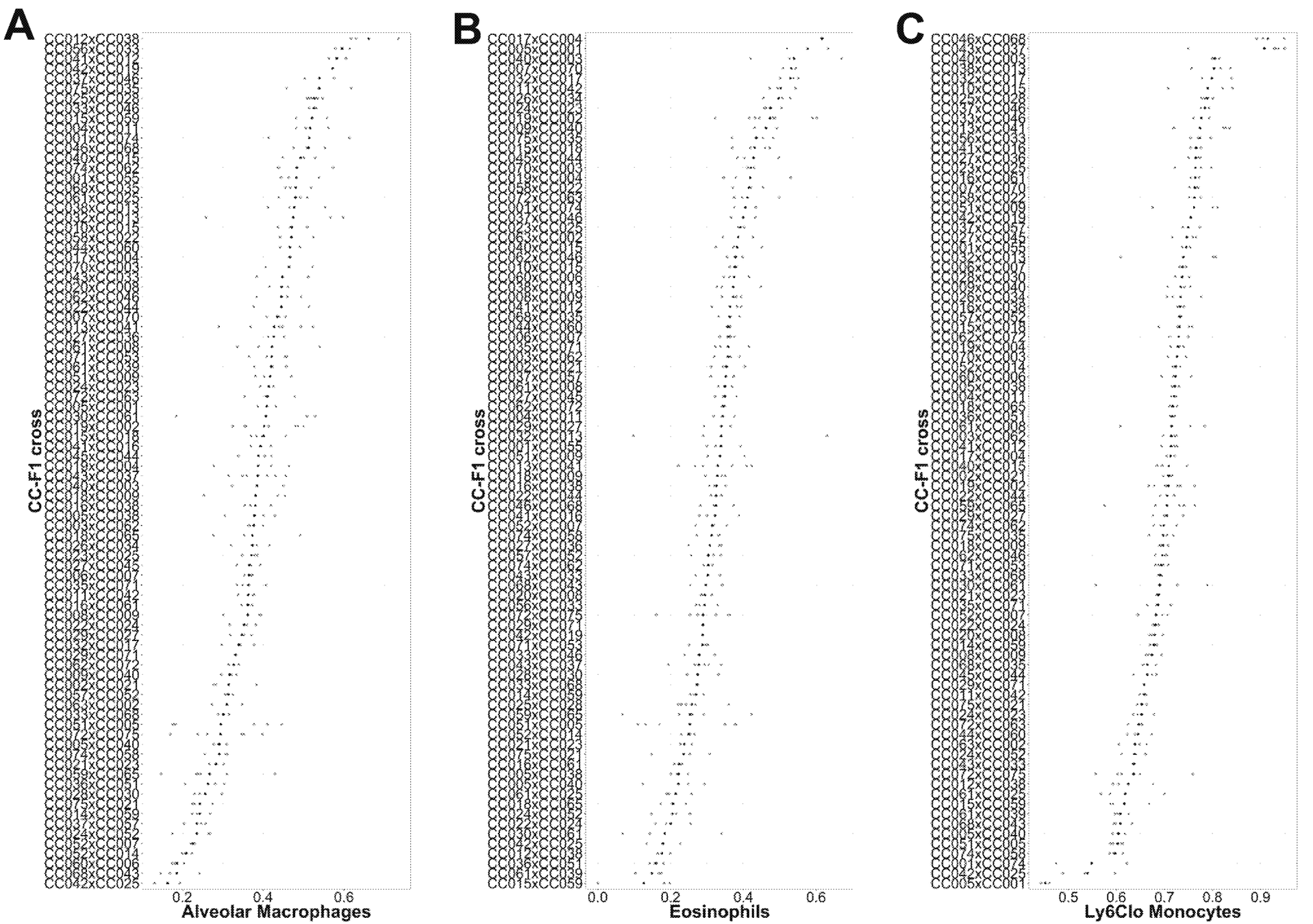
Project 2/Core B

Baseline Lung Leukocytes in the CC

Brea Hampton
Marty Ferris
Alan Whitmore
Cara Jensen



- Challenge groups of animals (n=3 mice/dRIX line/time point)
- Compare immune responses to 3 viruses across 110+ CC RIX lines
- Map QTL and identify candidate genes


A
B
C
CC-F1 cross
Alveolar Macrophages
Eosinophils
Ly6Clo Monocytes
0.2
0.4
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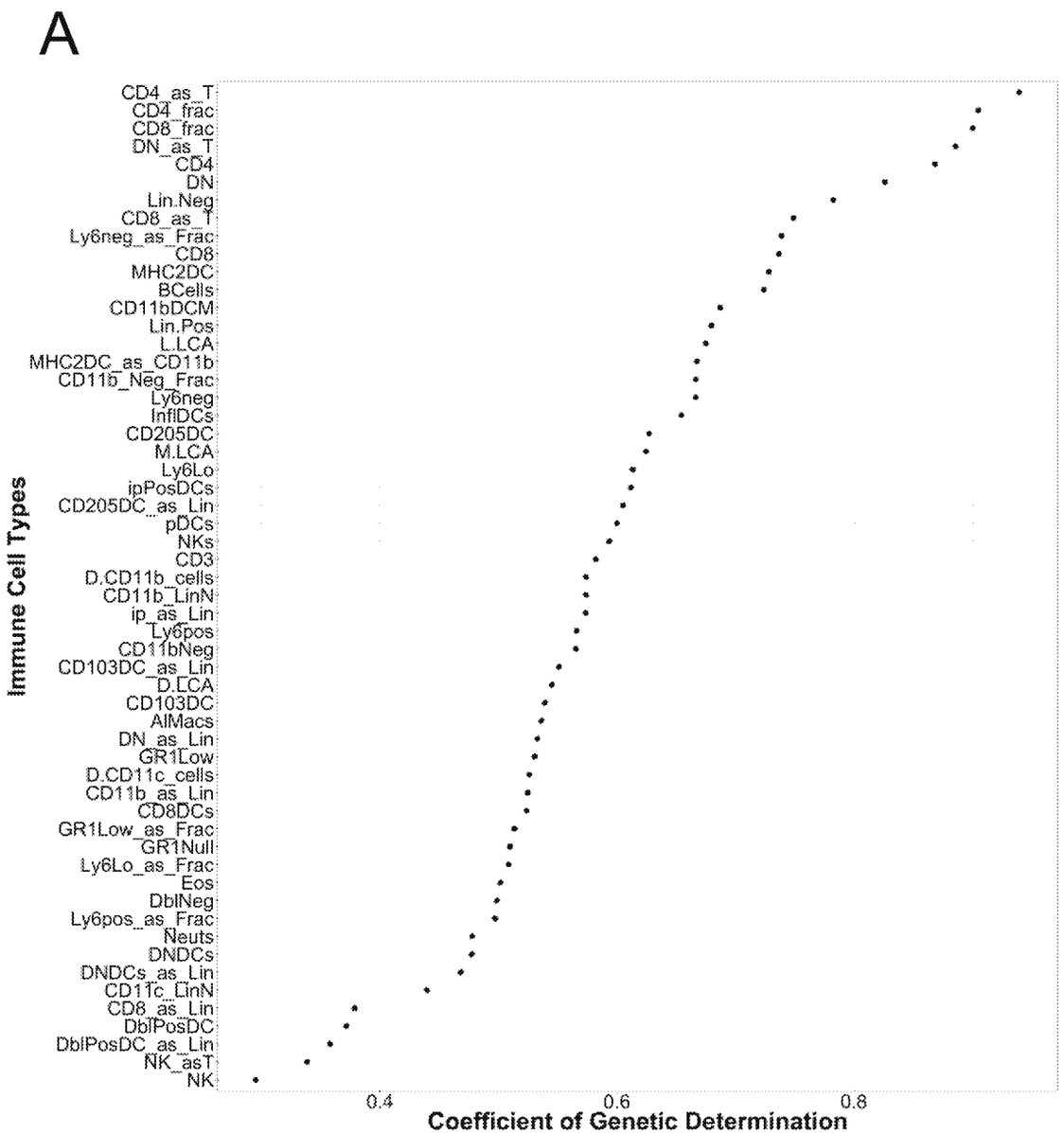
A
CD4_as_T
CD4_frac
CD8_frac
DN_as_T
CD4
DN
Lin.Neg
CD8_as_T
Ly6neg_as_Frac
CD8
MHC2DC
BCells
CD11bDCM
Lin.Pos
L.LCA
MHC2DC_as_CD11b
CD11b_Neg_Frac
Ly6neg
InflDCs
CD205DC
M.LCA
Ly6Lo
ipPosDCs
CD205DC_as_Lin
pDCs
NKs
CD3
D.CD11b_cells
CD11b_LinN
ip_as_Lin
Ly6pos
CD11bNeg
CD103DC_as_Lin
D.LCA
CD103DC
AlMacs
DN_as_Lin
GR1Low
D.CD11c_cells
CD11b_as_Lin
CD8DCs
GR1Low_as_Frac
GR1Null
Ly6Lo_as_Frac
Eos
DblNeg
Ly6pos_as_Frac
Neuts
DNDCs
DNDCs_as_Lin
CD11c_LinN
CD8_as_Lin
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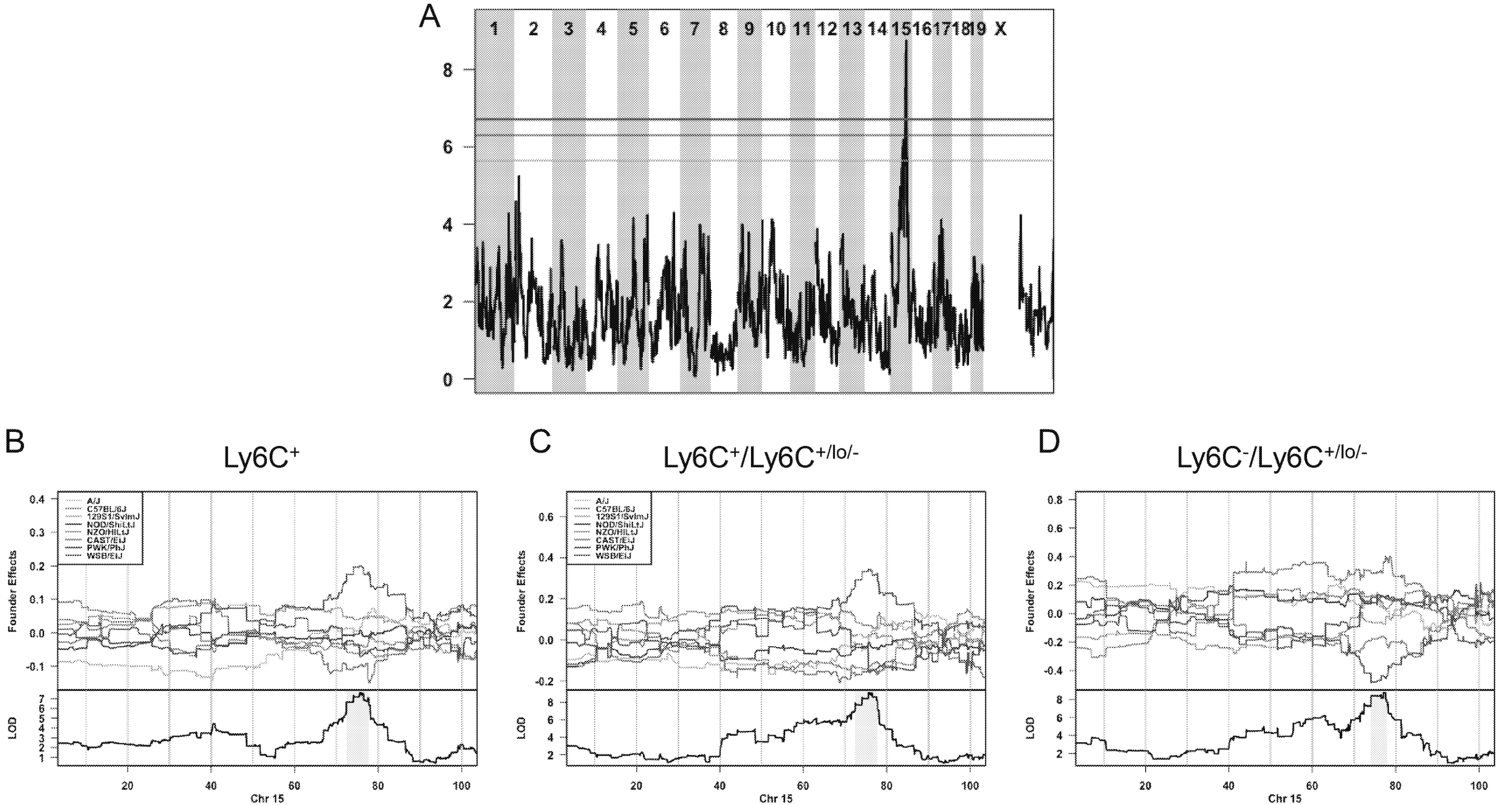
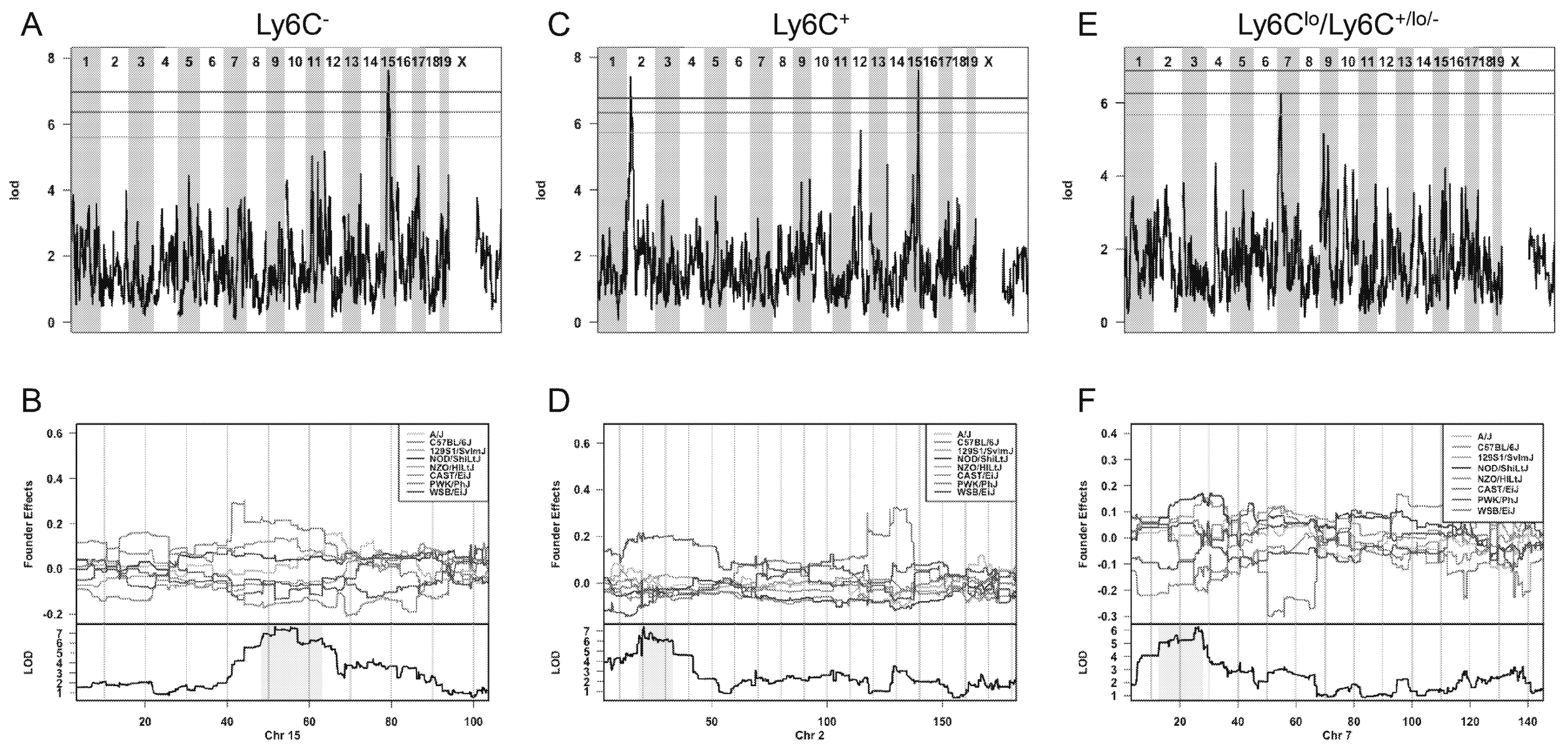
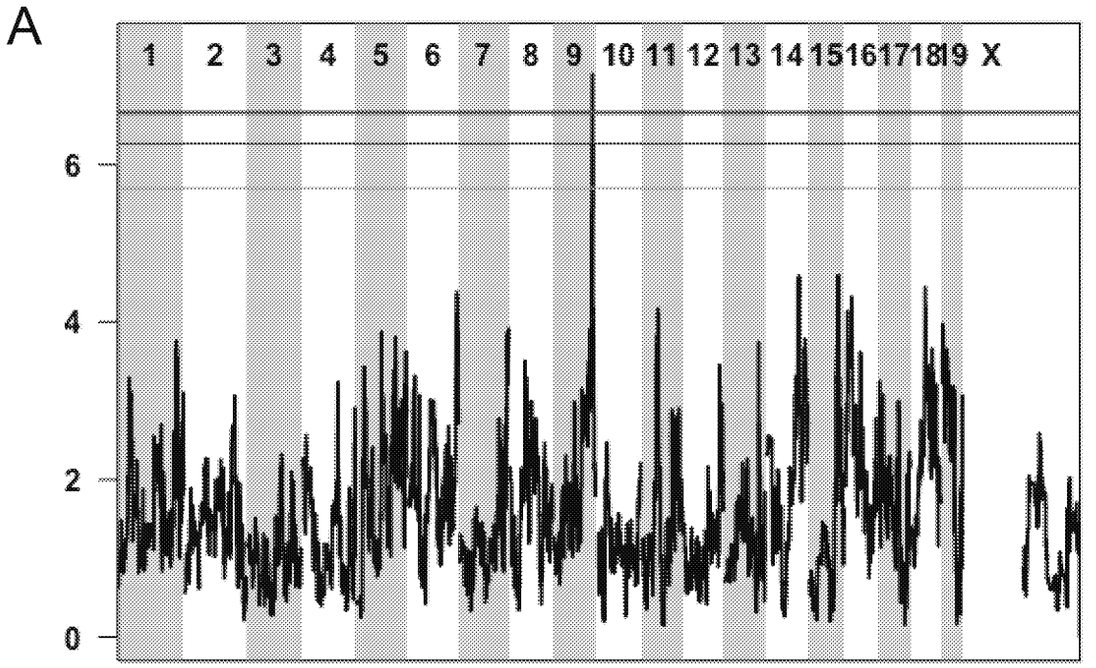
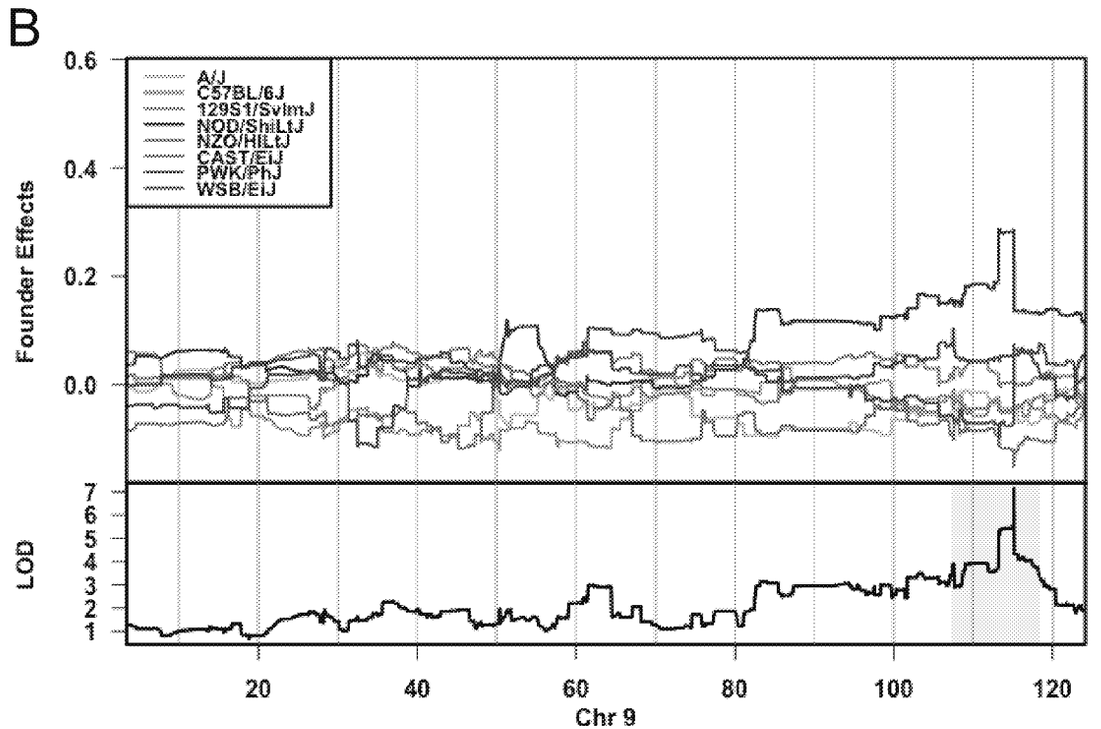
NK_asT
NK
Immune Cell Types
0.4
0.6
0.8
Coefficient of Genetic Determination
B
Lin.Pos
Ly6neg_as_Frac
Ly6neg
CD8_as_T
CD8
DN_as_T
DN
CD8_frac
BCells
ip_as_Lin
ipPosDCs
DN_as_Lin
DblNeg
D.CD11b_cells
CD11b_LinN
CD4_frac
CD4_as_T
CD4
D.LCA
M.LCA
L.LCA
CD3
CD8_as_Lin
CD8DCs
InflDCs
CD11bDCM
GR1Null
MHC2DC_as_CD11b
MHC2DC
GR1Low_as_Frac
GR1Low
Neuts
Eos
pDCs
Ly6pos_as_Frac
Ly6pos
Ly6Lo_as_Frac
NK_asT
NK
Ly6Lo
NKs
Lin.Neg
AlMacs
CD103DC_as_Lin
CD103DC
DblPosDC_as_Lin
DblPosDC
CD11b_Neg_Frac
CD205DC_as_Lin
CD205DC
DNDCs_as_Lin
DNDCs
CD11b_as_Lin
CD11bNeg
CD11c_LinN
D.CD11c_cells

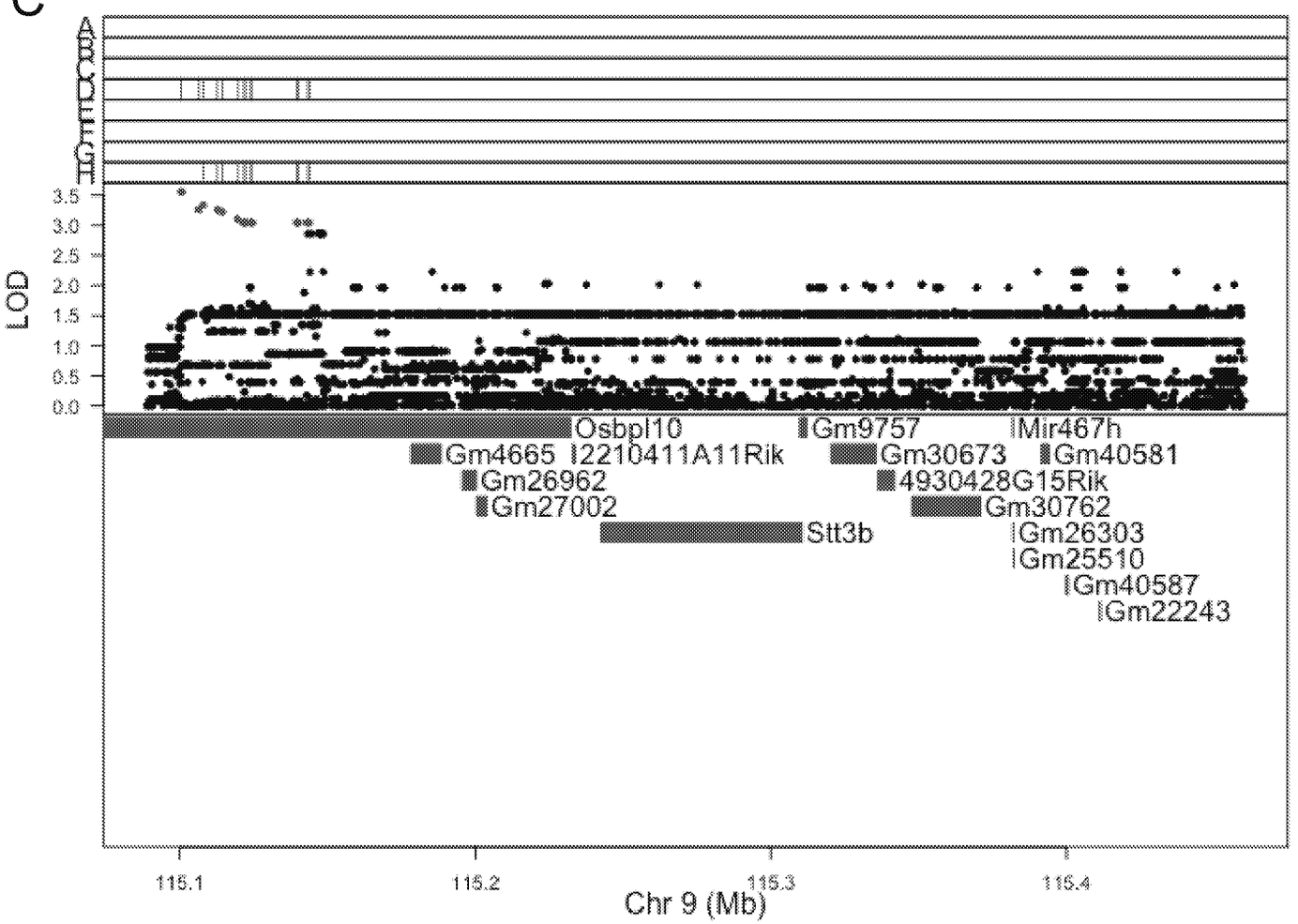




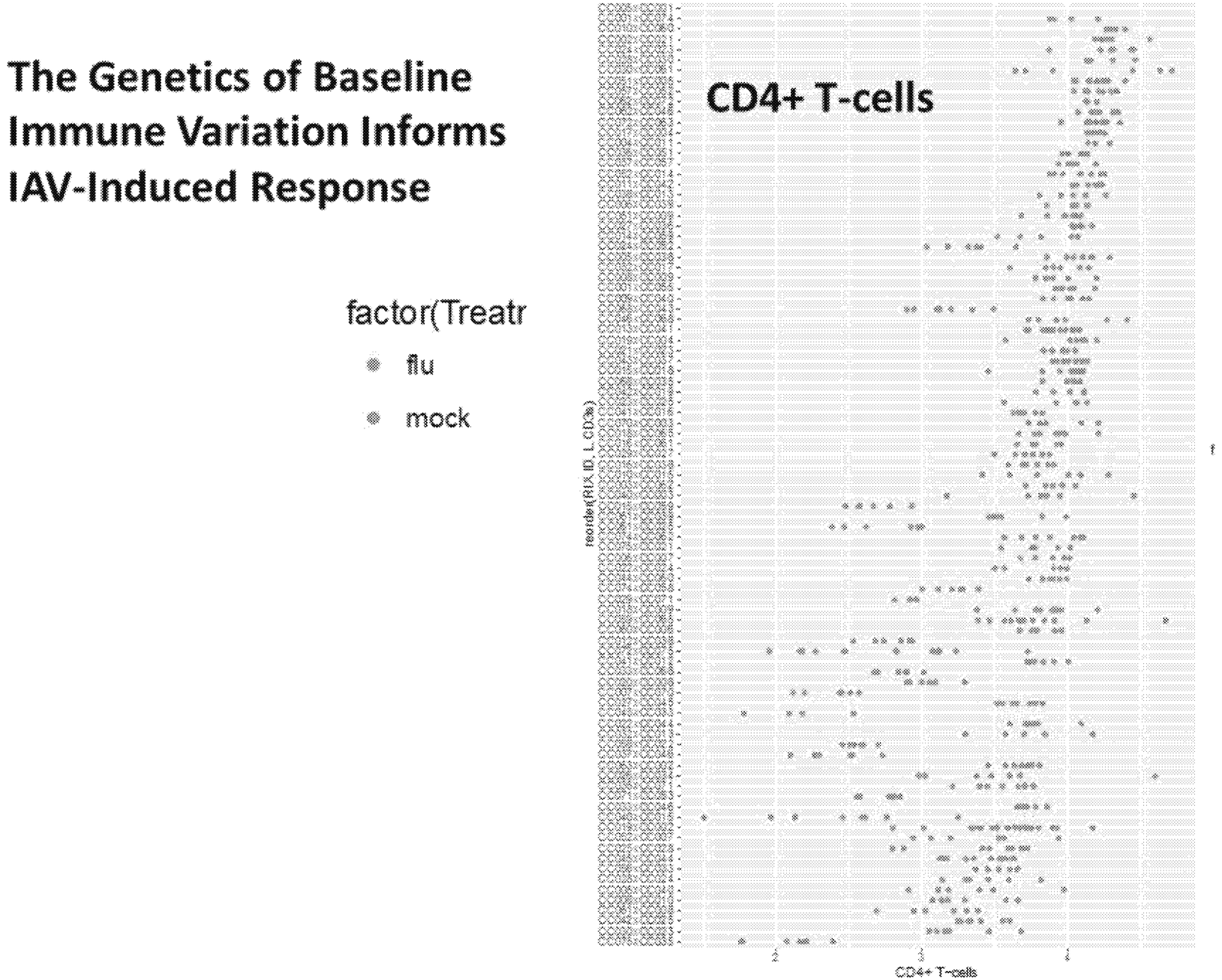
Alveolar Macrophage Frequency



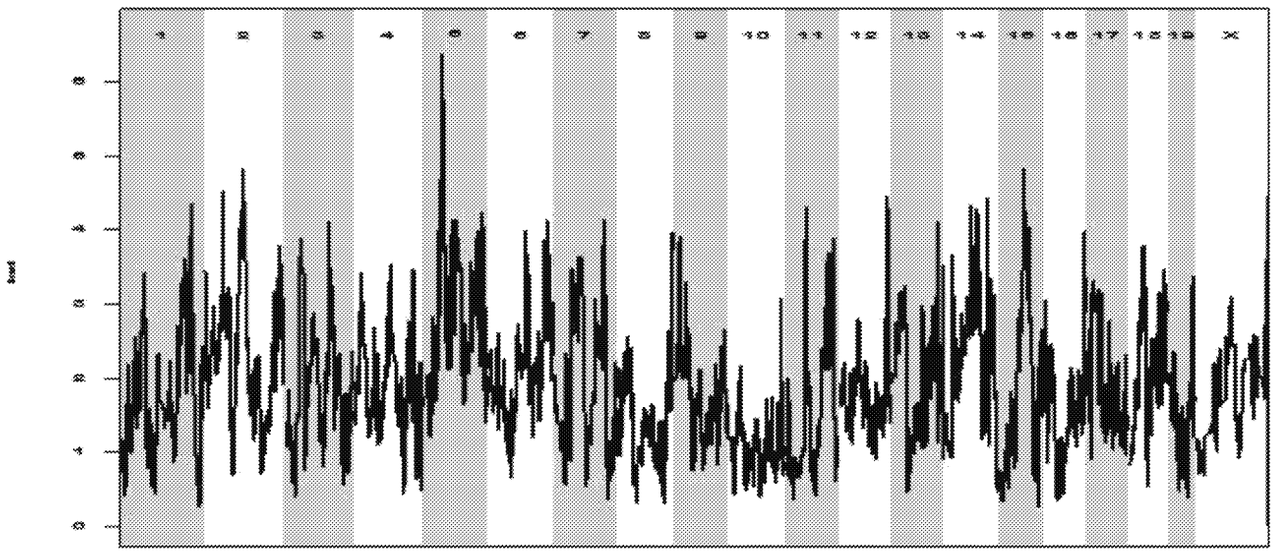


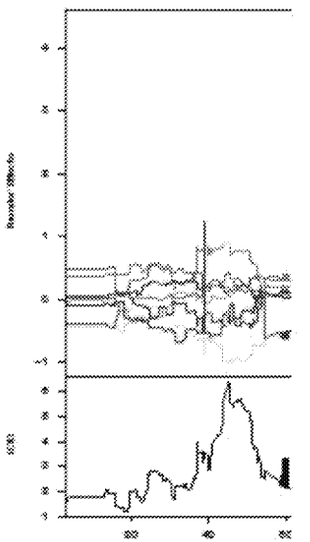


The Genetics of Baseline Immune Variation Informs IAV-Induced Response

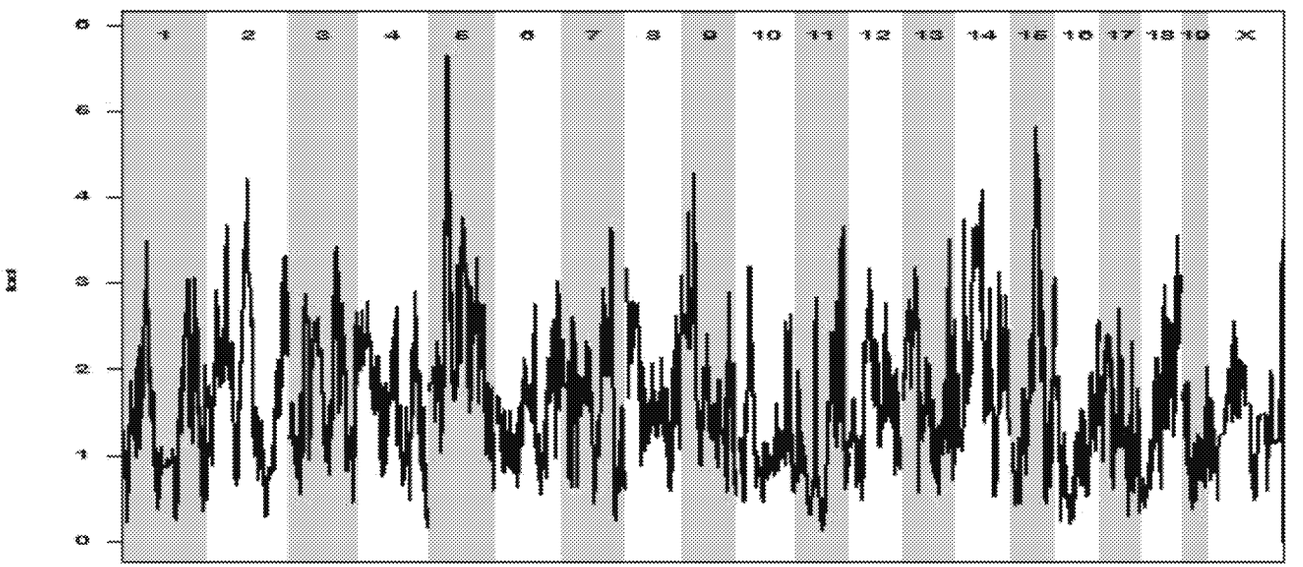


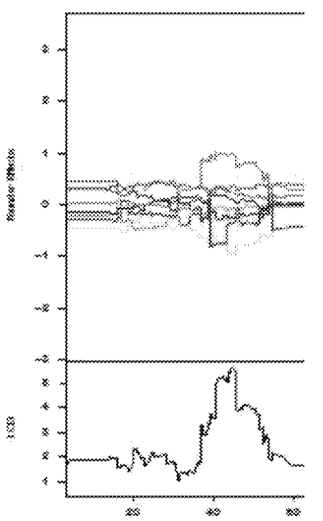
Baseline (mock)





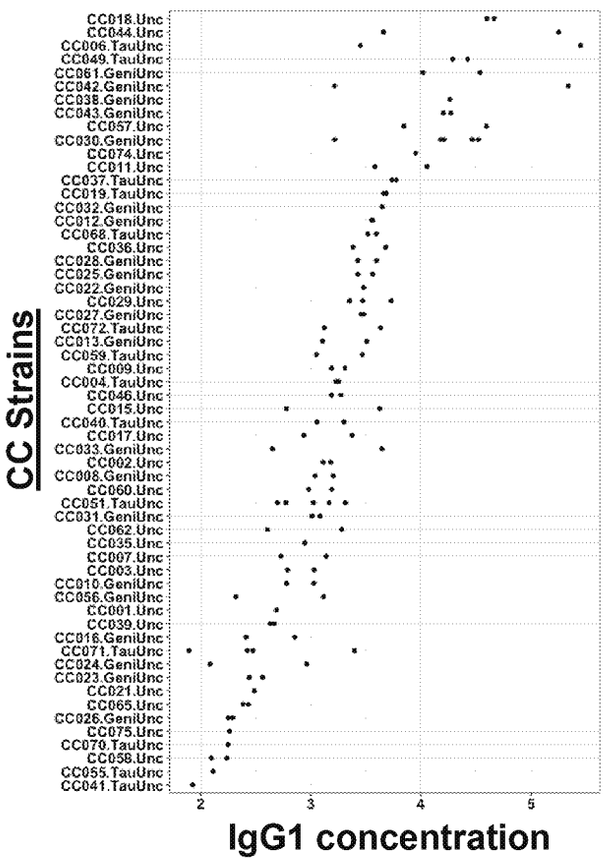
IAV (Day 4 PI)

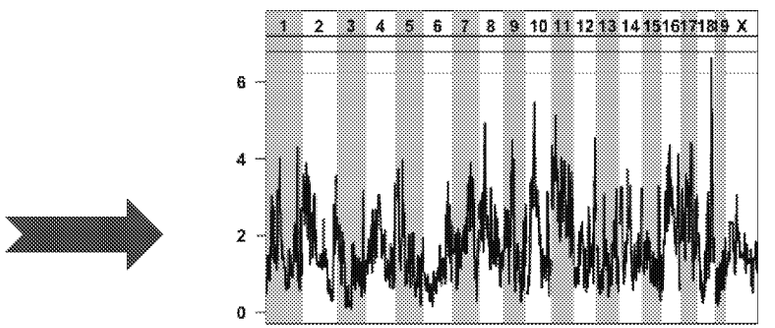


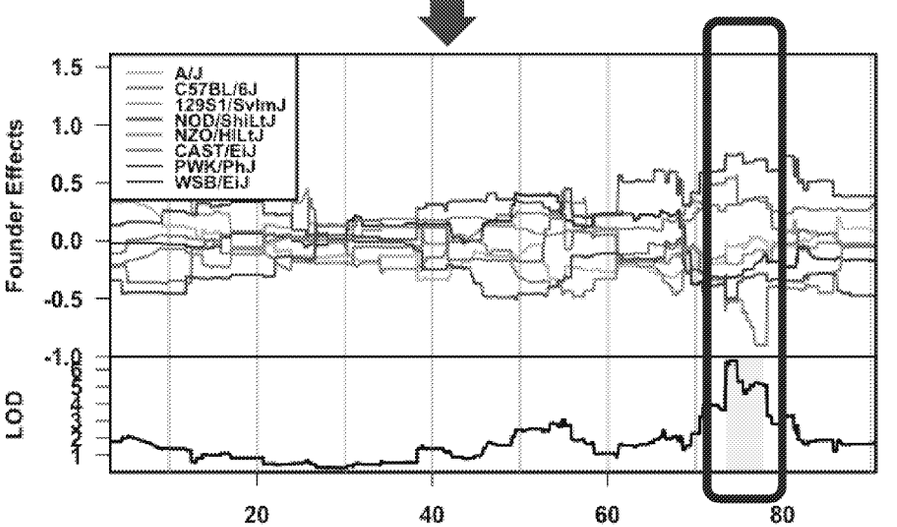


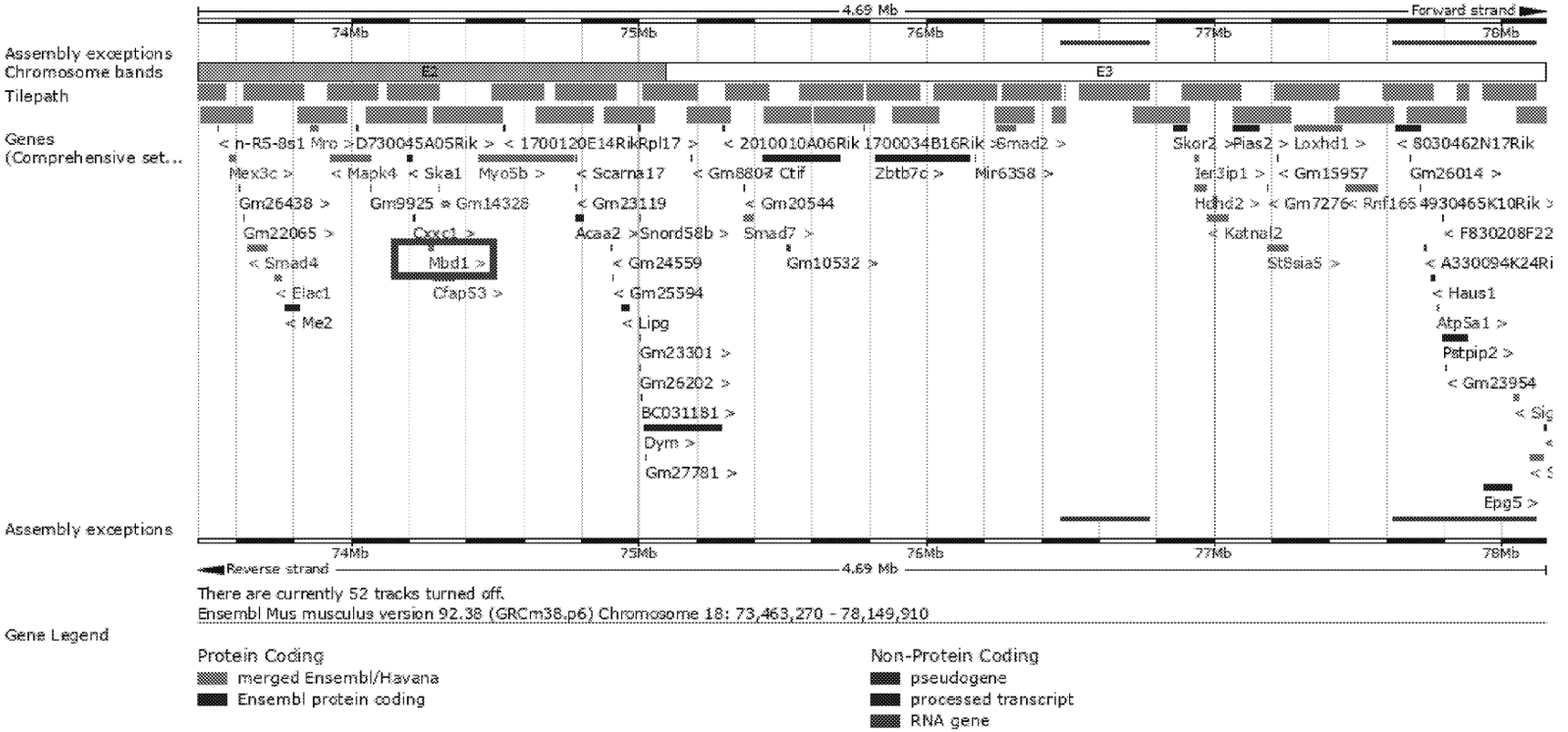
Phenotype	Phenotypic Range	Heritability Estimate	QTL	Effect size	Haplotype Effects
Alveolar Macrophages	0.1631 – 0.6610	0.536	Chr. 9: 115.0Mb – 115.2Mb	0.128	NOD/ShiLtJ – high
$CD4^+$ T cells	0.1309 – 0.8740	0.868	Chr. 5: 41.9Mb – 48.4Mb	0.240	C57BL/6J – high
$CD8^+$ T cells (as a fraction of all T cells)	0.0012 – 0.5230	0.748	Chr. 14: 46.9Mb – 58.6Mb	0.158	A/J – high NZO/SH1LtJ – low
$CD11c^+$ dendritic cells	0.1339 – 0.9032	0.526	Chr. 15: 86.8Mb – 91.4Mb	0.027	CAST/EiJ – low
$CD103^+$, $CD205^+$ dendritic cells (as a fraction of $lineage^-$ cells)	0.0003 – 0.6561	0.358	Chr. 19: 38.2Mb – 61.3Mb		NZO/SH1LtJ – low
$Lineage^-$ cells	0.3811 – 0.9971	0.782	Chr. 12: 106.3Mb – 108Mb	0.322	WSB/EiJ – low
$Ly6C^{lo}$ 'patrolling' monocytes (as a fraction of all $Ly6C^{+/lo/-}$ monocytes)	0.3164 – 0.9414	0.509	Chr. 7: 12.8Mb – 29.4Mb	0.499	C57BL/6J, WSB/EiJ – low
$Ly6C^-$ 'patrolling' monocytes (as a fraction of all $Ly6C^{+/lo/-}$ monocytes)	0.1075 – 0.9067	0.739	Chr. 15: 72.4Mb – 78.2Mb	0.515	CAST/EiJ – high WSB/EiJ – low
$Ly6C^-$ 'patrolling' monocytes	0.1708 – 0.6377	0.667	Chr. 15: 48.3Mb – 63.2Mb	0.522	CAST/EiJ – high
$Ly6C^+$ 'inflammatory' monocytes (as a fraction of all $Ly6C^{+/lo/-}$ monocytes)	0.2438 – 0.8819	0.497	Chr. 15: 72.4Mb – 77.8Mb	0.490	WSB/EiJ – high
$Ly6C^+$ 'inflammatory' monocytes	0.0838 – 0.6365	0.566	Chr. 15: 72.4Mb – 78.1Mb Chr. 2 : 18.3Mb – 33.2Mb	0.399 0.422	WSB/EiJ – high
Plasmacytoid dendritic cells	0.0529 – 0.4206	0.600	Chr. 15: 71.4Mb – 79.1Mb Chr. 14: 119.3Mb – 123.3Mb	0.422 0.051	WSB/EiJ – high WSB/EiJ – low

Variation in Baseline Antibody









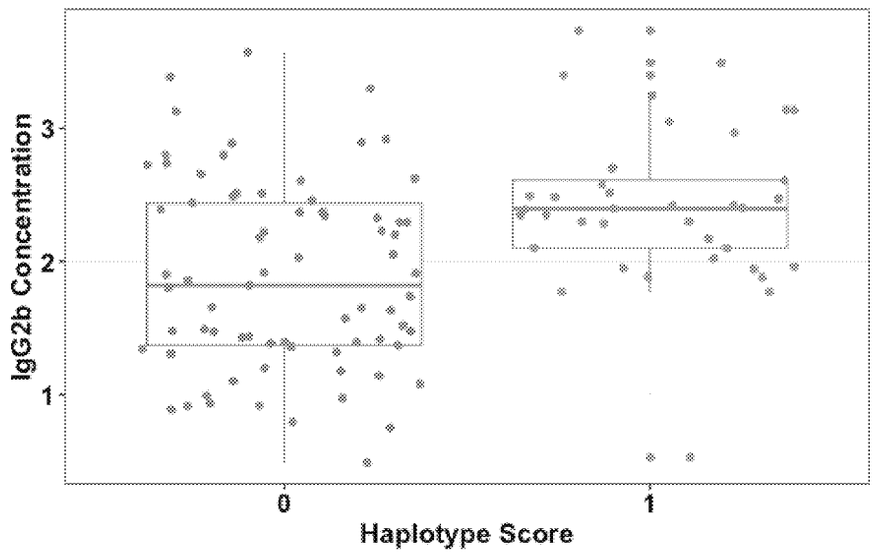
Mbd1 is the only gene that has WSB, CAST, and BL/6J private SNPs. There are no genes that have shared SNPs between the 3 high founder strains.

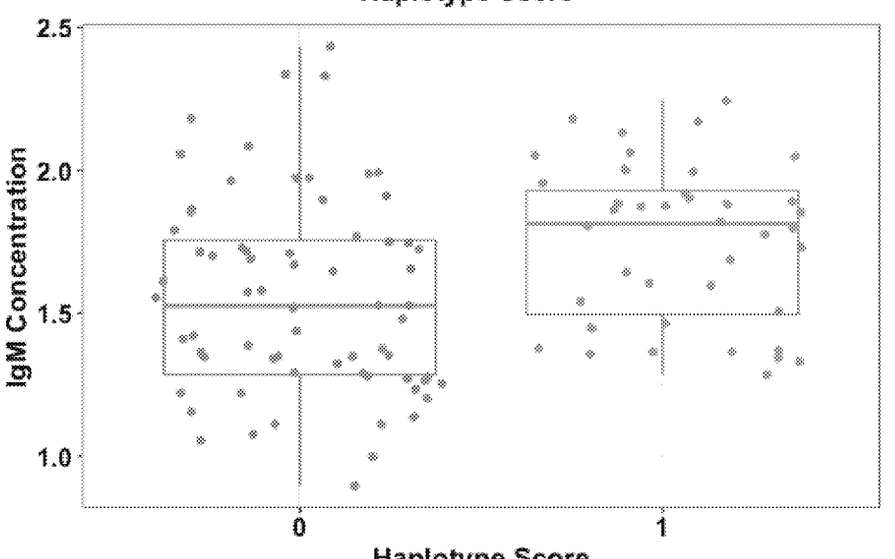
Methyl-CpG-binding domain protein 1

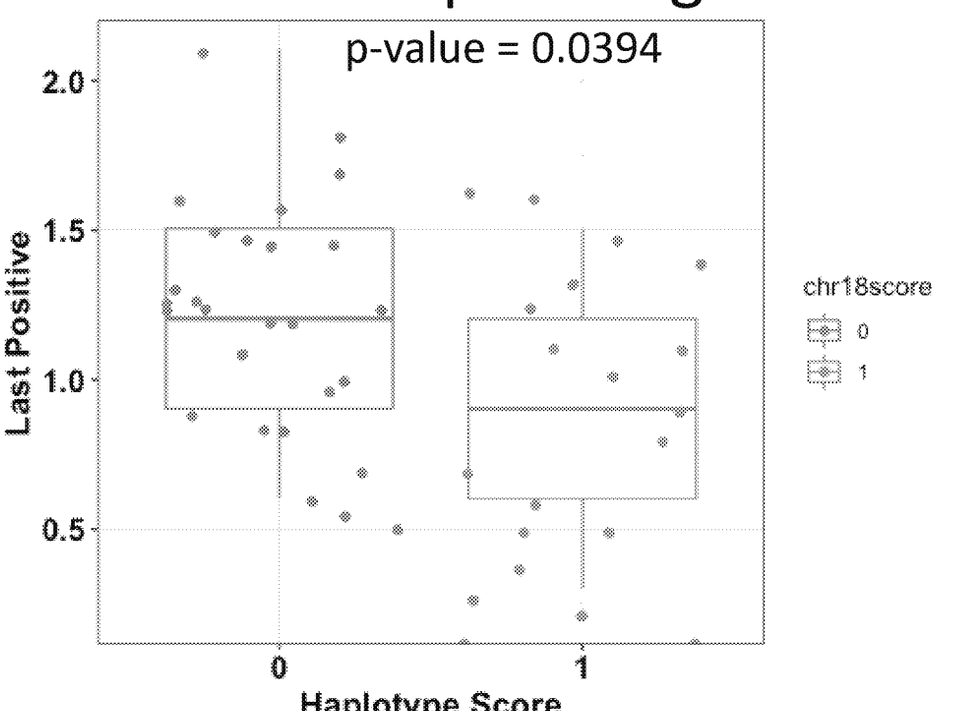
- Transcriptional Repressor
- Expression is upregulated in activated B cells
- MBD1 is involved in T cell Tolerance (Waterfield et al., 2014)

Brea Hampton

Chr. 18 QTL has broader effects on both baseline and antigen specific antibody responses







Brea Hampton

Ongoing/Next Steps

- Do baseline phenotypes or loci correlate with virus-induced disease or immune response? Analysis of existing data sets
  - Virus-induced weight loss (SARS/Flu)
  - Respiratory function (Mike M./Shannon?)
  - Virus-induced inflammatory/adaptive immune responses?
  - Relationship between immune homeostasis in the lung and periphery (Lund)?
- Do baseline immune phenotypes affect vaccine responses?
- Manuscripts!

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 9/11/2019 8:00:55 AM (UTC-05:00)
Subject: RE: SIG U19 call Thursday

Hi Everyone,
We will be having our monthly SIG U19 call on Thursday September 12 at 1:30 ET. Mike will be presenting for Core C. Please use the calling numbers below:
Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,
Toni

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 9/11/2019 11:41:31 AM (UTC-05:00)
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

We just published with Tem, Vincent is hard to read on these things. Peter would be a good choice and I've always thought Anne Moscona is a fair person. Malik may be pissed at me because I challenged some of his MERS Africa virus is highly attenuated story. Kanta might be okay. I've never been able to read Stacy.

Reviewers: Luis, Daszak, Baker and Dupree.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, September 11, 2019 12:19 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

Who do you suggest for Mbio editors

Here are the ones I have. Need to have 5

Vincent Racaniello
Mary Estes
Tem morrison
Peter Plaise
Malik Peiris
Kanta
Stacy Shultz Cherry
Anne Moscona

For reviewers, i had
Luis
Tom Gallagher
Susan Baker
Daszak
Benhur Lee
Paul Duprex

I didn't have anyone i excluded as of now.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, September 10, 2019 4:01 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

Ok. I am going to prep from Mbio and plan on getting in this week.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Tuesday, September 10, 2019 2:27 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

mBIO sounds safer to me than Cell Reports—Emily had a great experience there without all the problems you mentioned. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, September 10, 2019 12:09 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I chatted with a few people about Cell Reports, and they said it has same issues as Nat. Com. with self importance and taking a long time to decide and then asking for more and more stuff.

Think Mbio might be best bet at this point. I called this morning, but didn't get through. I can chat this afternoon if you want. Otherwise, I'll start prepping for Mbio.

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, September 9, 2019 10:52 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I'm fine if you don't want it on a preprint. As long as it gets accepted by teh Feb Review cycle.

I guess I'd lean Cell Reports at this point. I haven't had any experience there, so not sure how it goes. I would like the variety in my CV. That being said, I also don't want them to sit on it for >60 days like Nat. Com did.

I'll work on the cover letter today and get it submitted this week at Cell Reports; happy to talk about it if you think Mbio is the better spot for it.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, September 6, 2019 7:04 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

Cell reports or mbio—I'm getting to the point where it is time to move on to other things, so maybe mbio is best. Reviewer number 1 is a real ass wipe. I would like to find out who they are so that I can start reviewing their papers-sounds like one of the damn dutch. I would prefer to stay out of a preprint server at this point. However, if you feel its important for your grant submissions or in your best interest……. make the call. Be glad to chat if you want to talk about journal choices. Overall, I think Nature Communication is a shit whole of a journal. Tim's paper had also got beat to shit there by an ass reviewer with strong opinions on little issues. While I wish he would just go straight to cell reports (I think he feels the same way), we are going to send the resubmission back as he did a lot of the requested work for the second time (different set of requests both times). Personnally, I think his reviewer is just looking to kill a paper. Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, September 6, 2019 6:52 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: Decision on manuscript NCOMMS-19-23910-T

These reviews are petty and dumb.

At this point I think we should put on a preprint server.

Cell reports, plos path or mbio?

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: sonja.schmid@us.nature.com <sonja.schmid@us.nature.com>
Sent: Friday, September 6, 2019 4:23:33 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Decision on manuscript NCOMMS-19-23910-T

Dear Dr Menachery,

Your manuscript entitled "Trypsin treatment unlocks barrier for zoonotic coronavirus infection" has now been seen by 2 referees, whose comments are appended below. In the light of their advice I regret to inform you that we cannot publish your manuscript in Nature Communications.

You will see that, while the reviewers find your work of some potential interest, they raise substantive concerns that cast doubt on the advance your findings represent over earlier work and the strength of the novel conclusions that can be drawn at this stage. In particular, reviewers are not convinced that the manuscript provides a sufficient conceptual advance without additional experiments providing insights into the mechanism underlying the observations. Unfortunately, these reservations are sufficiently important to preclude publication of this study in Nature Communications.

If you opted into the journal hosting details of a preprint version of your manuscript via a link on our dedicated website (https://nature-research-under-consideration.nature.com), please note that we will now remove these details as your manuscript is no longer under consideration at Nature Communications. For more information, please refer to our FAQ page at https://nature-research-under-consideration.nature.com/posts/19641-frequently-asked-questions

I am sorry that we cannot be more positive on this occasion and thank you for the opportunity to consider your work.

Best regards,
Sonja Schmid, PhD
Senior Editor
Nature Communications
http://www.nature.com/ncomms

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

The manuscript by Menachery et al. deals with the role of trypsin-dependent protease activation on coronavirus (CoV) infections in cell cultures.
The authors used a previously generated chimeric MERS-CoV carrying the Spike gene of a MERS-CoV conspecific bat-related Coronavirus (PDF2180-CoV from Uganda) and performed cell culture experiments with and without trypsin treatment.

The finding that trypsin treatment influences cell susceptibility and probably organ tropism of MERS-related CoV is interesting, however, not overly innovative and surprising.

I have several remarks.

1. It is an intriguing but not very surprising finding that protease activation by trypsin influences CoV cell entry. Coronaviruses enter cells by receptor-mediated endocytosis using different exopeptidases (e.g. DPP4, ACE2) or by protease-mediated (HAT, TMPRSS2) direct fusion of virus particle membranes with the cellular plasma membrane. The present study shows that trypsin-treatment facilitates virus replication of bat-derived CoV but does not present a single experiment on the mechanistic details. Neither do the authors analyze the effect and mechanistic consequences of trypsin on the Spike proteins nor do they identify the proposed alternative receptor.

2. Throughout the manuscript important controls are missing.
a) The authors should confirm correct transcript sequence and expression of DPP4 in both trypsin-adapted Vero and Huh7 cell lines. These are important controls, as aberrant expression of DPP4 in immortalized cell lines may affect the conclusions.
b) The authors should show for all applied CoV that the activated protease has a direct effect on the virus (and not on a putatively new host cell receptor): the authors could e.g. "prime" virus stocks with trypsin, neutralize trypsin after incubation, then infect cells with the primed stock. Figure 5B is not sufficient and shows only HKU5-CoV infection in Vero cells co-treated with trypsin.
c) Using HAE cells the authors claim that chimeric "MERS-Uganda" does not infect the respiratory tracts of humans. How often was this experiment repeated? Were different donors tested? Again, I would expect different set-ups like virus pre-treated with trypsin, cells pre-treated with trypsin and co-treatment. The timing and the concentration of the trypsin-treatment is essential. What about other differentiated permanent cells lines like Calu-3?
d) The authors should sequence the HKU5-CoV and MERS-Uganda genomes (or at least the spike gene) after infection on trypsin-treated cells to confirm that both viruses are stable and to evaluate whether DPP4 host-adaptation (as in Letko et al., 2018) remains a contributing factor in the increased infectivity they observed.
e) The authors used an already existing MERS clone with a full-length Spike of the con-specific PDF2180-CoV. It would be important to show that the proposed recombination event led to the putative change of tropism. Different variants e.g. a MERS-CoV spike with only the S1 domain of PDF2180-CoV ,with and without the sialic acid binding domain (S1A) would be important controls.
f) What about sialic acid binding in general? Since it was shown that MERS-CoV attachment is facilitated by sialic binding I would expect that the authors show the sialic binding capacity of PDF2180-CoV to investigate how the trypsin treatment influences the attachment.
g) Another important control would be to check the susceptibility/permissiveness of bat cells (lung vs intestine) to support the hypothesis of a switch in organ tropism from bats to humans.
h) To rule out that other viral co-factors influence the entry process (and the use of DPP4) it would be beneficial to use a full-length PDF2180-CoV infectious virus.
i) Generally it would be important to titrate supernatants in order to see the influence on infectious particle production.

3. The quality of the Figures is insufficient. The immunofluorescence pictures in all of the Figures are not suitable for publication. The cells look apoptotic and there is no counterstaining to see how many cells are on the pictures. Without counterstaining the reader cannot evaluate the negative controls. There are no scale bars. I am aware that trypsin-treatment may cause these artifacts but the authors should then try to reduce trypsin concentrations or work with pretreatment of cells and /or virus stocks instead of continuous trypsin-treatment.

4. The Western blot in Fig. 3B and the fluorescence microscopy in Fig. 3A do not correspond. The WB shows a much stronger N protein band for trypsin-negative MERS-CoV infection, whereas in Fig. 3A the RFP assay the signals appear much brighter for trypsin-positive MERS-CoV infection.

5. General remark: Instead of just saying higher and lower, please indicate x-fold or percentage when discussing differences.

Reviewer #2 (Remarks to the Author):

This submission demonstrates that two potentially zoonotic coronaviruses, MERS-Uganda and MERS-like HKU5, will infect otherwise resistant cells if trypsin protease is supplied. The conclusions, therefore, are that trypsin protease "unlocks a barrier for zoonotic coronavirus infection". These results are of interest to the field because they highlight proteases as central host susceptibility factors in zoonotic coronavirus infection. As such, they move the field beyond a focus on receptors as the most relevant host susceptibility factors. Both virus receptors and proteases must now be simultaneously considered in evaluating susceptibility to zoonotic infections. Additionally, the findings in the paper are clear and convincing, and the results support the conclusions that are put forward. Finally, the paper is very well-written.

Comments for the authors:

1. Although the report has solid findings and credible interpretations of data, in some instances it does not make particularly novel insights. It is fairly well-known that some coronaviruses can be activated for cell entry by trypsin. Furthermore, the detailed architecture of the MERS spike : human DPP4 interaction is known, and it is understood that the MERS-Uganda and the MERS-like HKU5 spike proteins do not have complete hDPP4 receptor-binding motifs in their S1 domains. This latter point predicts the results shown in Fig 3, so much so that the results do not come across as especially novel. It is recommended that the authors further emphasize the novel features in this report.

2. The report could be strengthened, with potentially novel results, by further exploring the trypsin cleavage patterns of the Uganda and HKU5 spike proteins. The results shown in Fig 5B are a good start, but more could be presented. Many additional questions could be considered. What is the cleavage status of spike proteins on MERS-Uganda and HKU5 virus particles, before and after trypsin treatment? Does trypsin prime "free" virus particles for subsequent cell entry? Or does trypsin inactivate free virus particles? Put another way, do viruses have to first be attached to cells for trypsin to activate infection? Typically, there are two cleavages in the beta-coronavirus spikes that are relevant to cell entry, a priming S1/S2 cleavage and an activating S2prime cleavage. How do these substrate sites differ between MERS spikes, PDF2180/Uganda spikes and HKU5 spikes? Which of these substrate sites are cleaved by trypsin? If trypsin only cleaves at S1/S2, then what are
the proteases cleaving at S2prime? Are there Uganda spike-cleaving proteases that are present in Caco-2 cells but absent from primary HAE? To potentially elevate the novelty of the report, some or all of these questions should be addressed.

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: 9/11/2019 4:42:17 PM
To: Menachery, Vineet [vimenach@UTMB.EDU]
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

Both reviewers from ncomm wanted to see a western blot of Uganda Spike. We have anything worth putting in the paper that won't elicit more questions than answers? ralph

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, September 11, 2019 12:19 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

Who do you suggest for Mbio editors

Here are the ones I have. Need to have 5

Vincent Racaniello
Mary Estes
Tem morrison
Peter Plaise
Malik Peiris
Kanta
Stacy Shultz Cherry
Anne Moscona

For reviewers, i had
Luis
Tom Gallagher
Susan Baker
Daszak
Benhur Lee
Paul Duprex

I didn't have anyone i excluded as of now.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, September 10, 2019 4:01 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

Ok. I am going to prep from Mbio and plan on getting in this week.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Tuesday, September 10, 2019 2:27 PM

To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

mBIO sounds safer to me than Cell Reports—Emily had a great experience there without all the problems you mentioned. ralph

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, September 10, 2019 12:09 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I chatted with a few people about Cell Reports, and they said it has same issues as Nat. Com. with self importance and taking a long time to decide and then asking for more and more stuff.

Think Mbio might be best bet at this point. I called this morning, but didn't get through. I can chat this afternoon if you want. Otherwise, I'll start prepping for Mbio.

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, September 9, 2019 10:52 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Decision on manuscript NCOMMS-19-23910-T

I'm fine if you don't want it on a preprint. As long as it gets accepted by teh Feb Review cycle.

I guess I'd lean Cell Reports at this point. I haven't had any experience there, so not sure how it goes. I would like the variety in my CV. That being said, I also don't want them to sit on it for >60 days like Nat. Com did.

I'll work on the cover letter today and get it submitted this week at Cell Reports; happy to talk about it if you think Mbio is the better spot for it.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, September 6, 2019 7:04 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Decision on manuscript NCOMMS-19-23910-T

Cell reports or mbio—I'm getting to the point where it is time to move on to other things, so maybe mbio is best. Reviewer number 1 is a real ass wipe. I would like to find out who they are so that I can start reviewing their papers-sounds like one of the damn dutch. I would prefer to stay out of a preprint server at this point. However, if you feel its important for your grant submissions or in your best interest..... make the call. Be glad to chat if you want to talk about journal choices. Overall, I think Nature Communication is a shit whole of a journal. Tim's paper had also got beat to shit there by an ass reviewer with strong opinions on little issues. While I wish he would just go straight to cell reports

(I think he feels the same way), we are going to send the resubmission back as he did a lot of the requested work for the second time (different set of requests both times). Personnally, I think his reviewer is just looking to kill a paper. Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, September 6, 2019 6:52 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: Decision on manuscript NCOMMS-19-23910-T

These reviews are petty and dumb.

At this point I think we should put on a preprint server.

Cell reports, plos path or mbio?

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: sonja.schmid@us.nature.com <sonja.schmid@us.nature.com>
Sent: Friday, September 6, 2019 4:23:33 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Decision on manuscript NCOMMS-19-23910-T

Dear Dr Menachery,

Your manuscript entitled "Trypsin treatment unlocks barrier for zoonotic coronavirus infection" has now been seen by 2 referees, whose comments are appended below. In the light of their advice I regret to inform you that we cannot publish your manuscript in Nature Communications.

You will see that, while the reviewers find your work of some potential interest, they raise substantive concerns that cast doubt on the advance your findings represent over earlier work and the strength of the novel conclusions that can be drawn at this stage. In particular, reviewers are not convinced that the manuscript provides a sufficient conceptual advance without additional experiments providing insights into the mechanism underlying the observations. Unfortunately, these reservations are sufficiently important to preclude publication of this study in Nature Communications.

If you opted into the journal hosting details of a preprint version of your manuscript via a link on our dedicated website (https://nature-research-under-consideration.nature.com), please note that we will now remove these details as your manuscript is no longer under consideration at Nature Communications. For more information, please refer to our FAQ page at https://nature-research-under-consideration.nature.com/posts/19641-frequently-asked-questions

I am sorry that we cannot be more positive on this occasion and thank you for the opportunity to consider your work.

Best regards,
Sonja Schmid, PhD
Senior Editor
Nature Communications
http://www.nature.com/ncomms

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

The manuscript by Menachery et al. deals with the role of trypsin-dependent protease activation on coronavirus (CoV) infections in cell cultures.
The authors used a previously generated chimeric MERS-CoV carrying the Spike gene of a MERS-CoV conspecific bat-related Coronavirus (PDF2180-CoV from Uganda) and performed cell culture experiments with and without trypsin treatment.
The finding that trypsin treatment influences cell susceptibility and probably organ tropism of MERS-related CoV is interesting, however, not overly innovative and surprising.

I have several remarks.

1. It is an intriguing but not very surprising finding that protease activation by trypsin influences CoV cell entry. Coronaviruses enter cells by receptor-mediated endocytosis using different exopeptidases (e.g. DPP4, ACE2) or by protease-mediated (HAT, TMPRSS2) direct fusion of virus particle membranes with the cellular plasma membrane. The present study shows that trypsin-treatment facilitates virus replication of bat-derived CoV but does not present a single experiment on the mechanistic details. Neither do the authors analyze the effect and mechanistic consequences of trypsin on the Spike proteins nor do they identify the proposed alternative receptor.

2. Throughout the manuscript important controls are missing.
a) The authors should confirm correct transcript sequence and expression of DPP4 in both trypsin-adapted Vero and Huh7 cell lines. These are important controls, as aberrant expression of DPP4 in immortalized cell lines may affect the conclusions.
b) The authors should show for all applied CoV that the activated protease has a direct effect on the virus (and not on a putatively new host cell receptor): the authors could e.g. "prime" virus stocks with trypsin, neutralize trypsin after incubation, then infect cells with the primed stock. Figure 5B is not sufficient and shows only HKU5-CoV infection in Vero cells co-treated with trypsin.
c) Using HAE cells the authors claim that chimeric "MERS-Uganda" does not infect the respiratory tracts of humans. How often was this experiment repeated? Were different donors tested? Again, I would expect different set-ups like virus pre-treated with trypsin, cells pre-treated with trypsin and co-treatment. The timing and the concentration of the trypsin-treatment is essential. What about other differentiated permanent cells lines like Calu-3?
d) The authors should sequence the HKU5-CoV and MERS-Uganda genomes (or at least the spike gene) after infection on trypsin-treated cells to confirm that both viruses are stable and to evaluate whether DPP4 host-adaptation (as in Letko et al., 2018) remains a contributing factor in the increased infectivity they observed.
e) The authors used an already existing MERS clone with a full-length Spike of the con-specific PDF2180-CoV. It would be important to show that the proposed recombination event led to the putative change of tropism. Different variants e.g. a MERS-CoV spike with only the S1 domain of PDF2180-CoV ,with and without the sialic acid binding domain (S1A) would be important controls.
f) What about sialic acid binding in general? Since it was shown that MERS-CoV attachment is facilitated by sialic binding I would expect that the authors show the sialic binding capacity of PDF2180-CoV to investigate how the trypsin treatment influences the attachment.

g) Another important control would be to check the susceptibility/permissiveness of bat cells (lung vs intestine) to support the hypothesis of a switch in organ tropism from bats to humans.
h) To rule out that other viral co-factors influence the entry process (and the use of DPP4) it would be beneficial to use a full-length PDF2180-CoV infectious virus.
i) Generally it would be important to titrate supernatants in order to see the influence on infectious particle production.

3. The quality of the Figures is insufficient. The immunofluorescence pictures in all of the Figures are not suitable for publication. The cells look apoptotic and there is no counterstaining to see how many cells are on the pictures. Without counterstaining the reader cannot evaluate the negative controls. There are no scale bars. I am aware that trypsin-treatment may cause these artifacts but the authors should then try to reduce trypsin concentrations or work with pretreatment of cells and /or virus stocks instead of continuous trypsin-treatment.

4. The Western blot in Fig. 3B and the fluorescence microscopy in Fig. 3A do not correspond. The WB shows a much stronger N protein band for trypsin-negative MERS-CoV infection, whereas in Fig. 3A the RFP assay the signals appear much brighter for trypsin-positive MERS-CoV infection.

5. General remark: Instead of just saying higher and lower, please indicate x-fold or percentage when discussing differences.

Reviewer #2 (Remarks to the Author):

This submission demonstrates that two potentially zoonotic coronaviruses, MERS-Uganda and MERS-like HKU5, will infect otherwise resistant cells if trypsin protease is supplied. The conclusions, therefore, are that trypsin protease "unlocks a barrier for zoonotic coronavirus infection". These results are of interest to the field because they highlight proteases as central host susceptibility factors in zoonotic coronavirus infection. As such, they move the field beyond a focus on receptors as the most relevant host susceptibility factors. Both virus receptors and proteases must now be simultaneously considered in evaluating susceptibility to zoonotic infections. Additionally, the findings in the paper are clear and convincing, and the results support the conclusions that are put forward. Finally, the paper is very well-written.

Comments for the authors:

1. Although the report has solid findings and credible interpretations of data, in some instances it does not make particularly novel insights. It is fairly well-known that some coronaviruses can be activated for cell entry by trypsin. Furthermore, the detailed architecture of the MERS spike : human DPP4 interaction is known, and it is understood that the MERS-Uganda and the MERS-like HKU5 spike proteins do not have complete hDPP4 receptor-binding motifs in their S1 domains. This latter point predicts the results shown in Fig 3, so much so that the results do not come across as especially novel. It is recommended that the authors further emphasize the novel features in this report.

2. The report could be strengthened, with potentially novel results, by further exploring the trypsin cleavage patterns of the Uganda and HKU5 spike proteins. The results shown in Fig 5B are a good start, but more could be presented. Many additional questions could be considered. What is the cleavage status of spike proteins on MERS-Uganda and HKU5 virus particles, before and after trypsin treatment? Does trypsin prime "free" virus particles for subsequent cell entry? Or does trypsin inactivate free virus particles? Put another way, do viruses have to first be attached to cells for trypsin to activate infection? Typically, there are two cleavages in the beta-coronavirus spikes that are relevant to cell entry, a priming S1/S2 cleavage and an activating S2prime cleavage. How do these substrate sites differ between MERS spikes, PDF2180/Uganda spikes and HKU5 spikes? Which of these substrate sites are cleaved by trypsin? If trypsin only cleaves at S1/S2, then what are

the proteases cleaving at S2prime? Are there Uganda spike-cleaving proteases that are present in Caco-2 cells but absent from primary HAE? To potentially elevate the novelty of the report, some or all of these questions should be addressed.

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From: Michael J Gale[mgale@uw.edu]
Sent: Thur 9/12/2019 1:24:44 PM (UTC-05:00)
Subject: RE: SIG U19 call Thursday

Jenny and Mike M and Shannon, Slide 5 shows DDX3X as one of the genes in the interval. This is a RIG-I cofactor, so might be of interest to assess the genetics on this one.

M

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Sent: Wednesday, September 11, 2019 6:01 AM
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Subject: RE: SIG U19 call Thursday

Hi Everyone,
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Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,
Toni

To: Michael J Gale[mgale@uw.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Jackie V. Berhorst[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Renee Ireton[rireton@uw.edu]; katvoss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; Miller, Darla[darla_miller@med.unc.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Michael Mooney[mooneymi@ohsu.edu]
Sent: Thur 9/12/2019 1:32:25 PM (UTC-05:00)
Subject: RE: SIG U19 call Thursday

Thanks, Michael. I'll look more closely at the variants there.
Mike

From: Michael J Gale [mgale@uw.edu]
Sent: Thursday, September 12, 2019 11:24 AM
To: Baric, Toni C; Baric, Ralph S; Jackie V. Berhorst; D. Menachery Vineet (vimenach@utmb.edu); mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Renee Ireton; katvoss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; Miller, Darla; Michael Mooney; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
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From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 9/12/2019 3:11:03 PM (UTC-05:00)
Subject: RE: SIG U19 call Thursday

Mutations in ACTRT1 and its enhancer RNA elements lead to aberrant activation of Hedgehog signaling in inherited and sporadic basal cell carcinomas

https://www.nature.com/articles/nm.4368

Sonic hedgehog signalling in T-cell development and activation

https://www.nature.com/articles/nri2151

another interesting possibility.

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Best regards,

Toni

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Michael Mooney[mooneymi@ohsu.edu]
Sent: Thur 9/12/2019 9:46:22 AM (UTC-05:00)
Subject: RE: SIG U19 call Thursday
U19_Call_Sept_2019_CoreC.pptx

Hi all,
Slides for today's call are attached.

Mike

From: Baric, Toni C [antoinette_baric@med.unc.edu]
Sent: Wednesday, September 11, 2019 6:00 AM
To: Baric, Toni C; Baric, Ralph S; Berhorst, Jackie; D. Menachery Vineet (vimenach@utmb.edu); mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Noll, Kelsey; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Subject: RE: SIG U19 call Thursday

Hi Everyone,
We will be having our monthly SIG U19 call on Thursday September 12 at 1:30 ET. Mike will be presenting for Core C. Please use the calling numbers below:
Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,
Toni

QTL Candidate Prioritization

WNV Flow Cytometry Data

SIG U19 Call 9/12/2019
Core C

Background

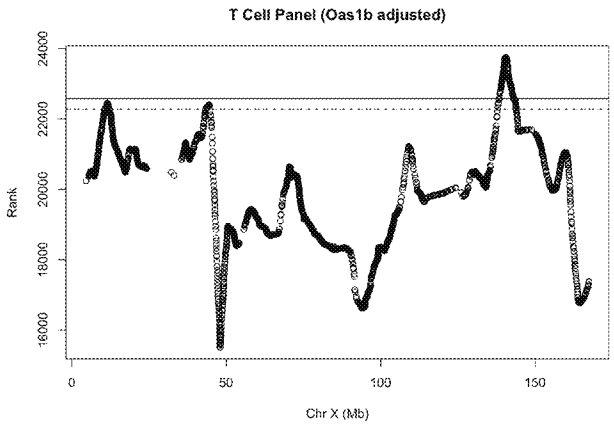
- Can we look at QTL results across phenotypes to prioritize and narrow QTL regions?
- Example Use Case: T cell measures after WNV infection
  - > 300 phenotypes
  - Many phenotypes are correlated
  - Numerous candidate QTL peaks on the X chromosome

QTL Candidate Prioritization

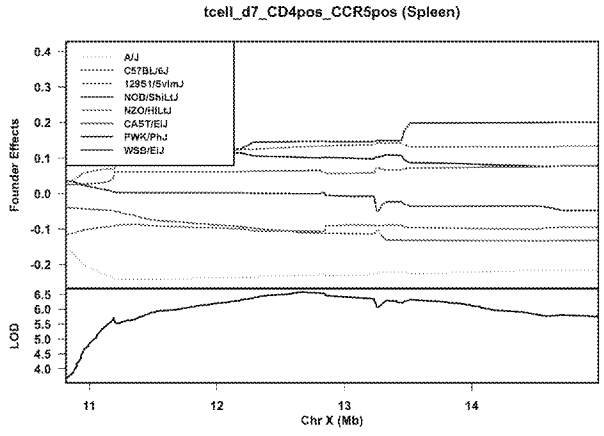
- For each phenotype, create ranks for 3Mb windows across the chromosome (based on average LOD score)
- Combine ranks across all T cell phenotypes
- Identify regions that are highly ranked across phenotypes
  - Combined ranks above 90th percentile
- Identify phenotypes that contribute most to highly-ranked regions

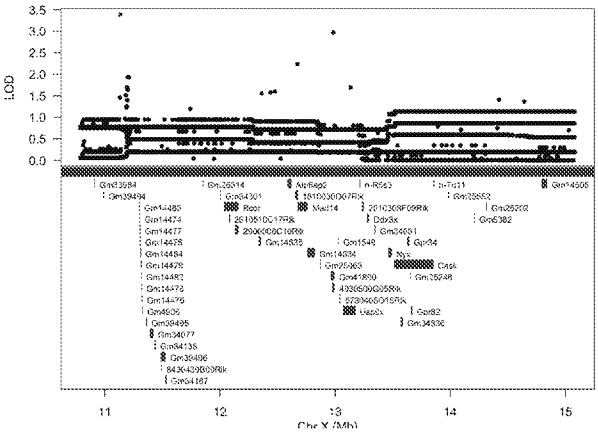
QTL Candidate Prioritization

- 3 regions prioritized:
  - ChrX: 10.79-15.08Mb
  - ChrX: 43.47-47.59Mb
  - ChrX: 137.9-143.54Mb
- Merge Analysis
  - SNP imputation and association analysis
- Variant Identification
  - Founder-specific variants



ChrX: 10.79-15.08Mb: CCR5+ CD4+ T cells

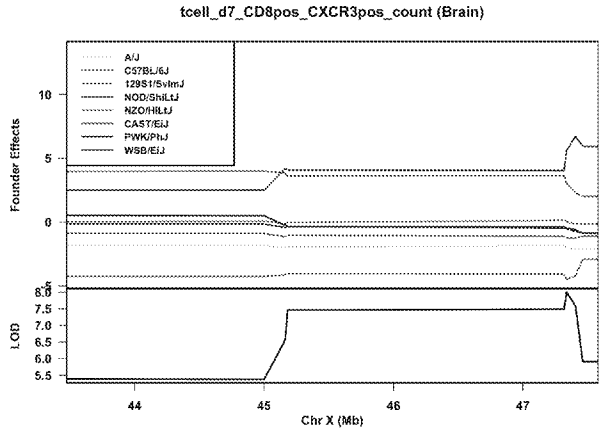


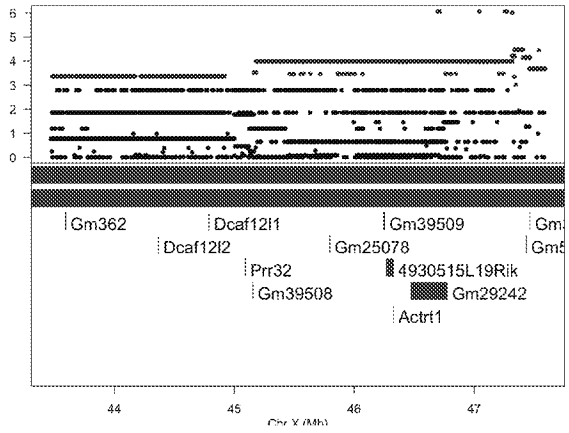


ChrX: 10.79-15.08Mb

- A/J variants:
  - Missense variant in: ***Bcor***
  - 3'UTR variant in: ***Cask***
- PWK variants:
  - Missense variants in: ***Bcor, Med14, Usp9x, Nyx, Gm14483, Gm14476, Gm14484, Gm4906, Gm5132***
  - Splice region variants in: ***Med14, Usp9x, Nyx, Cask, Gm14505***
  - 3'UTR and/or 5'UTR variants in: ***Bcor, Atp6ap2, Med14, Usp9x, Nyx, Cask, Gpr34, Gpr82, Gm5132***

ChrX: 43.47-47.59Mb: CXCR3+ CD8+ T cells



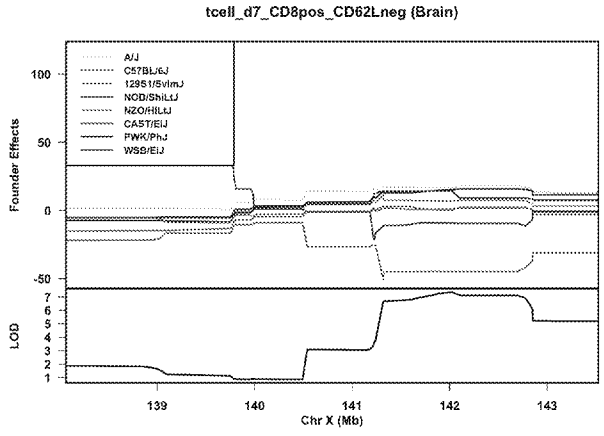


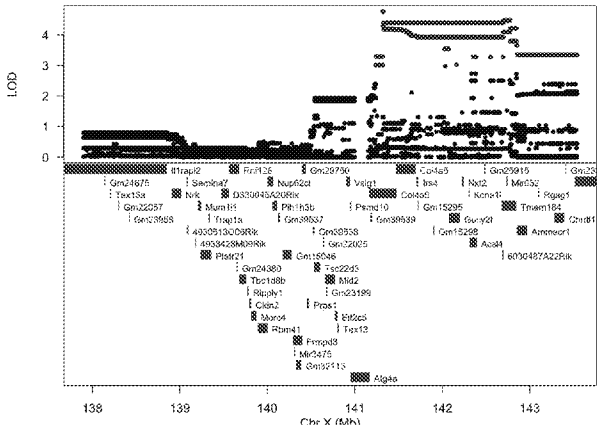
ChrX: 43.47-47.59Mb

- PWK variants:
  - Missense variant in: ***Actrt1***
  - 5' UTR variant in: ***Actrt1***
- PWK/Cast variants:
  - 3' UTR variant in: ***Dcaf12l2***
- NZO variants:
  - 3' and 5' UTR variants in: ***Dcaf12l2***
  - Synonymous variant in: ***Dcaf12l2***

* Those genes highlighted in Red contain variants with LOD > 3 in the merge analysis

ChrX: 137.9-143.54Mb
CD8+ CD62L- T Cells





ChrX: 137.9-143.54Mb

- Cast variants:
  - Missense variants in: ***Tex13a, Nrk, Rnf128, Tbc1d8b, Tsc22d3, Mid2, Vsig1, Col4a6, Col4a5, Gucy2f, Rgag1, Gm15013***
- PWK/Cast variants:
  - Missense variants in: ***Tex13a, Mum1l1, Rnf128, Tbc1d8b, Ripply1, Cldn2, Morc4, Tsc22d3, Col4a6, Ammecr1, Rgag1, Chrdl1, Gm15294***

* Those genes highlighted in Red contain variants with LOD > 3 in the merge analysis

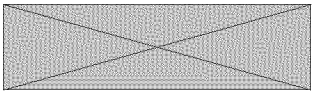
Next Steps

- Perform merge analyses on additional T cell phenotypes to determine if the same variants are associated with multiple traits
- Apply method to other flow panels and possibly other data types with correlated measures
- Further prioritize candidates by integrating with other data:
  - Gene functions/pathways
  - Differentially expressed gene lists

To: Baric, Ralph S[rbaric@email.unc.edu]; Michael J Gale[mgale@uw.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Jackie V. Berhorst[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica B[jgraham@fredhutch.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Renee Ireton[rireton@uw.edu]; katvoss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; McWeeney, Shannon [mcweeney@ohsu.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica L[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Lund, Jennifer[jlund@fredhutch.org]
Sent: Thur 9/12/2019 3:21:48 PM (UTC-05:00)
Subject: Re: SIG U19 call Thursday

In that case, I think this is one of the intervals we should focus on, and I look forward to seeing how many & which phenotypes are linked to this locus. Maybe we can do some experiments using PWK mice to see if there are T cell defects even at steady state? Actually, are any of the steady-state/mock phenotypes linked to this locus?

Jennifer M. Lund
Associate Member
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org



Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Thursday, September 12, 2019 at 1:11 PM
To: Michael J Gale <mgale@uw.edu>, "Baric, Toni C" <antoinette_baric@med.unc.edu>, "Jackie V. Berhorst" <jdao@uw.edu>, "D. Menachery Vineet (vimenach@utmb.edu)" <vimenach@utmb.edu>, mtferris <mtferris@email.unc.edu>, "Fischer, William A. II" <william_fischer@med.unc.edu>, "Graham, Jessica B" <jgraham@fredhutch.org>, "Graham, Rachel" <rlgraham@email.unc.edu>, Lisa Gralinski <lgralins@email.unc.edu>, "Heise, Mark T" <mark_heisem@med.unc.edu>, Renee Ireton <rireton@uw.edu>, katvoss <katvoss@uw.edu>, "Klaus Schughart (kschugha@uthsc.edu)" <kschugha@uthsc.edu>, "Leist, Sarah Rebecca" <leist@email.unc.edu>, "Linnertz, Colton" <colton_linnertz@med.unc.edu>, "Lund, Jennifer" <jlund@fredhutch.org>, "McWeeney, Shannon" <mcweeney@ohsu.edu>, "Miller, Darla" <darla_miller@med.unc.edu>, "Mooney, Michael" <mooneymi@ohsu.edu>, "Noll, Kelsey" <kenoll@email.unc.edu>, "Pardo Manuel de Villena, Fernando" <fernando_pardo-manuel@med.unc.edu>, "Schaefer, Alexandra" <aschaefe@email.unc.edu>, "Schughart, Klaus" <Klaus.Schughart@helmholtz-hzi.de>, "Shaw, Ginger" <ginger_shaw@med.unc.edu>, "Sheahan, Timothy Patrick" <sheahan@email.unc.edu>, "Suthar, Mehul S. (mehul.s.suthar@emory.edu)" <mehul.s.suthar@emory.edu>, "Swarts, Jessica L" <jswarts@fredhutch.org>, "West, Ande" <westande@email.unc.edu>
Subject: RE: SIG U19 call Thursday

Mutations in ACTRT1 and its enhancer RNA elements lead to aberrant activation of Hedgehog signaling in inherited and sporadic basal cell carcinomas

https://www.nature.com/articles/nm.4368

Sonic hedgehog signalling in T-cell development and activation

https://www.nature.com/articles/nri2151

another interesting possibility.

From: Michael J Gale <mgale@uw.edu>
Sent: Thursday, September 12, 2019 2:25 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Jackie V. Berhorst <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Renee Ireton <rireton@uw.edu>; katvoss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: RE: SIG U19 call Thursday

Jenny and Mike M and Shannon, Slide 5 shows DDX3X as one of the genes in the interval. This is a RIG-I cofactor, so might be of interest to assess the genetics on this one.

M

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, September 11, 2019 6:01 AM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Jackie V. Berhorst <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Renee Ireton <rireton@uw.edu>; katvoss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; Michael J Gale <mgale@uw.edu>; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: RE: SIG U19 call Thursday

Hi Everyone,
We will be having our monthly SIG U19 call on Thursday September 12 at 1:30 ET. Mike will be presenting for Core C. Please use the calling numbers below:
Phone: 1-800-747-5150
Passcode: 552.136
Germany, calling number below:
08001014525

access code 552.136

Best regards,
Toni

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 9/19/2019 8:21:04 AM (UTC-05:00)
Subject: FW: Systems Immunology U19 program's accomplishment and next Annual meeting

Hi Everyone,

Please see below for the information requested from program. I am so sorry for the short notice, but we just received this request minutes ago. Please return the information requested to Mark by close of business on Tuesday Sept 24.

Thank you
Toni

From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Thursday, September 19, 2019 9:04 AM
To: Arlene Sharpe <arlene_sharpe@hms.harvard.edu>; Ulevitch, Richard <Ulevitch@scripps.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Patricia Rutledge <pattyr@scripps.edu>; Hillman, Sarah Ellen <Sarah_Hillman@hms.harvard.edu>
Subject: RE: Systems Immunology U19 program's accomplishment and next Annual meeting
Importance: High

Dear All,

I hope that you have had a great summer.

Thinking about the future of the Systems Approach to Immunity and Inflammation (U19) program, **could you provide me the accomplishment of your current program? For Richard and Ralph, could you please also separately provide me all the accomplishment since you had the program?** The accomplishment may include:

1. How many novel genes and pathways you have identified.
2. How many genes and pathways you have validated.
3. How many mutant or genetically modified mouse strains you have obtained and shared.
4. How many papers you have published.
5. How many collaboration you have established.
6. How many Ph.D. students and postdoctoral fellows you have trained (how many they have become independent).
7. How many new technologies you have generated.
8. How many new analytical tools you have created.
9. Any other information you think worth to include.

It would be greatly appreciated if you could send the information to me by next Wednesday (Sept. 25th).

Now we need to plan our next annual meeting. Because the big conference room in our building will start renovation in June next year, every branch is competing for space. We need to decide a date for reserving the room ASAP. **I will send out a doodle poll soon for our next annual meeting, so would you please respond it as early as possible?** Will April 2010 work for you? I think our last one-day meeting worked great, so I would assume we would have a one-day meeting again for next year. Please let me know if you don't like the idea.

Also, it is the time to set up a Steering Committee Meeting. Arlene had proposed the agenda. Again, **I will send another doodle poll for this Steering Committee meeting. Please respond quickly**. We will discuss following topics in our next meeting:

1. Collaborations between U19 programs
2. Webinar – need to discuss how this will work, and what topics it will cover.
3. Data deposition on ImmPort.

Please let me know if you have anything else to discuss.

Best regards,
Joy

Qian"Joy" Liu, MD, MSc
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases
5601 Fishers Lane, Rm 7B54, Rockville, MD 20852
(E) liujoy@mail.nih.gov| (P) 301-761-6621

To: Menachery, Vineet[vimenach@UTMB.EDU]; Baric, Toni C[antoinette_baric@med.unc.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Mon 10/7/2019 5:08:22 PM (UTC-05:00)
Subject: RE: Pew Scholar Nomination

Hi Vineet, I'll be delighted to do these things. I'll get the pew letter out in a couple of days as I head to Sydney on Thursday for 2 weeks. Hope your doing well. Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, October 7, 2019 12:19 PM
To: Baric, Ralph S <rbaric@email.unc.edu>; Baric, Toni C <antoinette_baric@med.unc.edu>
Subject: Re: Pew Scholar Nomination

Hey Ralph,

The Pew Letter is due in 10-days or so. I've attached my most recent CV and my last biosketch from my R01. Let me know if you have any questions about the Pew Award.

I would also appreciate it if you'd be willing to nominate me for the ASV Young Investigator Award. I have spoken to some people about the award and I can have only one nominator/letter of nomination. However, I was informed that previous winners have had multiple people sign the nomination letter with one person coordinating that. With that in mind, I imagine you could ask a number of people to also endorse my nomination either in the CoV field (Perlman, Weiss, Baker, Enjuanes) or more broadly (Diamond, Gale, Pei Yong Shi, Heise, Yoshi).

The ASV award nomination is due November 15th and I need to provide a ASV specific biosketch, (assuming you are willing). If you are unable or unwilling, let me know and I can also have my chair nominate me.

Thanks

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, September 4, 2019 8:53 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Pew Scholar Nomination

You didn't reply, but should be getting reminders from Pew each week.

I haven't heard about the paper. Got sent out July 26th according to the status. I will email Monday if I don't hear from them.

I'll send you an updated CV this week; our first paper got accepted in JVI paper and is online now.
https://www.ncbi.nlm.nih.gov/pubmed/31462558

I just sent in the CC R21 yesterday and working on an R01 for October. I am also losing my post-doc, he took a great job in industry. I assume you all are hiring post-docs? If you have anybody you can't take and good, feel free to send them along my way.

Also, chatted with Amy about her job at PNNL. Hopefully it will work out well for her.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Tuesday, September 3, 2019 12:49 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Pew Scholar Nomination

Hi Vineet, nice to hear from you and congrats on the nomination. I'll be delighted to write a letter. Pass along the pertinent info (updated cv, short project description). Nothing was attached. Or have I already answered and am currently in Oz. Hope things are going well. Any news on the paper? Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, August 20, 2019 4:13 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Pew Scholar Nomination

Ralph,

I have been nominated by UTMB to submit an application for the Pew Scholars Program: https://www.pewtrusts.org/en/projects/pew-biomedical-scholars

Pew Biomedical Scholars
Pew has a decades-long commitment to support groundbreaking research by promising early-career biomedical scientists in the United States and Latin America. Our multiyear grants encourage informed risk-taking and collaboration among researchers.
www.pewtrusts.org

I am hoping you would be willing to provide a letter of reference for the award. They require a letter from my post-doctoral advisor and are interested in my work in your lab and as a graduate student overall.

The letters are due by October 17, 2019, but can be submitted prior to that date. They will send a weekly prompt as a reminder.

If you need to update a previous letter, I have attached a CV with recent accomplishments and manuscripts. The project I am writing for the Pew project explores transmission and super spreading in the context of coronavirus infection.

Thanks for your consideration and I have already added your name to the roster and you should hear from them in the next week or so.

Thanks

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Tue 10/15/2019 11:02:54 PM (UTC-05:00)
Subject: RE: mBio02431-19 Decision Letter

552.117

Hi Vineet, looks good. Please proceed. Hope you survive jury duty and things are well with you and [redacted] ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, October 15, 2019 2:17 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: mBio02431-19 Decision Letter

I have it all ready to submit to JVI. I will do it by the end of my day today, unless you want to modify it and let me know.

Thanks

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, October 14, 2019 4:33 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: mBio02431-19 Decision Letter

Hey Ralph,

Hope you are enjoying the meeting.

I made a few changes based on the 2nd reviewer. The changes are tracked here, but its only about 4-5 lines differences. I emphasize this is novel for bat CoVs and make sure to cite paper from 1988 on PEDV. I also added bat CoV (vs zoonotic) to the title and other relevant places.

I am at jury duty this week, but otherwise I think this is ready to go. I didn't make any modifications based on Rev. 1 who doesn't think this is a MERS-like virus and wants an entirely different paper.

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Saturday, October 12, 2019 8:24 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: mBio02431-19 Decision Letter

Jvi or plos path. I'd say jvi at this point. I'll work on getting it in next week.

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, October 11, 2019 5:18:09 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: mBio02431-19 Decision Letter

Well this blows. I think we should just go to JVI and move on. Thoughts? Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, October 11, 2019 1:26 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Fw: mBio02431-19 Decision Letter

From: mbio@asmusa.org <mbio@asmusa.org>
Sent: Friday, October 11, 2019 12:17 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: mBio02431-19 Decision Letter

October 11, 2019

Dr. Vineet D. Menachery
University of Texas Medical Branch at Galveston
301 University Boulevard
Galveston, TEXAS 77555-1070

Re: mBio02431-19 (Trypsin treatment unlocks barrier for zoonotic coronaviruses infection.)

Dear Dr. Menachery:

We have completed our review of your manuscript, and I regret to inform you that we will not be able to accept it for publication in mBio. This decision reflects the priorities of mBio and the disposition of this particular review; it is not meant to imply that the manuscript is unsuitable for publication elsewhere.

While this manuscript may not be a good fit for mBio, the editor felt that the work had merit and would like to offer you the opportunity to transfer to the following journal:

Journal of Virology (JVI): Publishes important new discoveries covering the viruses of animals, plants, bacteria, fungi, and protozoa. Key issues investigated are virus structure and assembly, viral genome replication and regulation of viral gene expression, viral genetic diversity and evolution, virus-cell interactions, cellular responses to viral infection, transformation and oncogenesis, gene delivery, viral pathogenesis and immunity, and vaccines and antiviral agents. JVI offers the option of immediate open access with payment of an Article Processing Charge (APC) in lieu of page charges.

With your consent, we will transfer your manuscript files and data. Please let us know if you would like to:

(1) Transfer the manuscript and the mBio reviews.
(2) Resubmit on your own to another ASM journal. (Use this option if you wish to send your manuscript to another ASM journal without the mBio reviews.)

Please note that each ASM journal is editorially independent; transferring your manuscript constitutes a new submission.

Your manuscript will be subject to the editorial decisions of the receiving journal. You may be asked to revise your manuscript and your manuscript may be sent out for additional review.

Enclosed are the comments generated during the review. I hope they will be useful to you.

Thank you for your interest in mBio.

Sincerely,

Arturo Casadevall
Editor in Chief, mBio
mBioEditorInChief@asmusa.org
(Signing for the editors)

Editor comments:

The reviewers pointed out that trypsin dependence of coronaviruses is not new, that more mechanistic insight is needed and that the paper is more suitable for a specialised virology journal.

Reviewer #1 (Comments for the Author):

This MS describes mainly technical observations regarding the spike protein of a bat-derived coronavirus (CoV) with implications on growth in cell culture. The subject is a virus sequence termed PDF-2180 (PDF) whose majority of genes cluster with MERS-CoV close enough for both viruses to fall into the same viral species. Also the spike protein of another bat-derived CoV is investigated, one that does not belong to the same species but is still part of the wider phylogenetic group (group 2C) to which the MERS virus belongs. The technical observation is that addition of trypsin to culture medium enhances replication of MERS-CoV and permits replication of a chimeric MERS-CoV whose spike protein is exchanged against that of PDF. This permissiveness includes Vero cells, HuH7 cells, as well as CaCo-2 cells.

I find the technical insight to be useful for those (few) laboratories working on CoVs. However, I cannot support most of the generalizations made with regard to the insight from these findings for the wider field of pandemic preparedness research (which is the rationale behind presenting the work to a wider audience in the target journal). I believe the finding should be presented as an interesting technical observation to a specialized journal. It could also be developed into a full paper for a discipline-specific journal, but would then need more experimental work in terms of controls and mechanistic insight.

My general concerns are: the phylogeny of PDF (as well as the related Neo-CoV) in Anthony et al (Ref 18) shows that the spike S1 domain does not group with MERS-CoV. Considering the sister relationship of MERS and PDF in the other genes, this suggests either a long-term differentiating pressure or more recent recombination (the latter is more likely). In any case, the spike protein S1 domain cannot be regarded as representative of MERS-CoV. This maybe a weakness of Anthony et al. rather than the present work, but clearly the here-presented data do not represent the evolution of receptor tropism of MERS-CoV. This virus as well as the HKU-5 virus that belongs to another species should not be referred to as "MERS-like". What we are looking at are spike proteins that have adapted to an environment with presence of trypsin (gut). The requirement of a different receptor is not sufficiently addressed because the whole phenomenon of sialic acid binding via the N-terminal spike domain (missing in MERS-CoV but present in HKU5 and other 2C viruses) is omitted. Also, the use of CaCo-2 cells as a model for the human gut is insufficient as these cells are known to constitutively express TMPRSS2, a transmembrane protease rarely found on the surface of most other permanent cell lines. It is known that CaCo-2 cells are much more permissive for MERS-CoV than other cells, so that we need some mechanistic insight into the observed effects. Telling a story ("new paradigm") about adaptive trajectories makes little sense in this light. The whole work may just describe another two CoV spike proteins that need trypsin in cell culture. This is not novel, as several other CoVs do (which is correctly mentioned in the manuscript).

Some details

-Trypsin is inactivated by serum proteins such as alpha 1 - antitrypsin. Normally, trypsin application in flu culture requires serum-free medium. The methods section is not explicit about this.
-When applying typsin to ALI cultures, are the conditions based on preliminary experience? Can a control virus be included whose growth improves upon addition of trypsin?
-DPP4 expression in all cell lines should be checked.
-Mode of action of trypsin should be studied: can virus be activated by trypsin pretreatment? Does trypsin remain active in TMPRSS2-positive cells with the clathrin pathway chemically inactivated?
-The N terminus as well as the whole aspect of sialic acid binding should be addressed experimentally
-All figures must be improved but I assume this is an issue with PDF creation. Cell nuclei should be stained.

Reviewer #2 (Comments for the Author):

This manuscript describes the results of the use of trypsin to facilitate the recovery of MERS-like bat coronaviruses, PDF2180 and HKU5. Interestingly, trypsin treatment of PDF2180 facilitates the infection of human gut tissue, but not human lung cells. They also found that blocking DPP4 was ineffective in blocking PDF2180 infection, indicating that DPP4-independent entry mechanism was used in this cell culture model. The authors confirm and extend the previously well-established finding that the presence of exogenous trypsin facilitates the recovery of coronaviruses in cell culture. The results of this study do make an important contribution to the field by evaluating gut and lung tropism and revealing that a MERS-like bat coronavirus infection is not blocked by the addition of antibodies to DPP4.
Comments for the authors' consideration:
1. The introduction section should have a paragraph about the extensively documented use of trypsin in the recovery of coronaviruses. For example, citing Hofmann and Wyler, 1988 on the propagation of PEDV in cell culture; and Wicht et al, 2014 J. Virology and the references within this paper. This paragraph should be added at line 50 of the introduction and would provide excellent rationale for the experiments described in the current study. References 18, 34, 35 and 36 should be cited in the introduction, not only in the discussion section.
2. Modify the sentences about the addition of trypsin or the activation of spike as a new paradigm (line 225) or a new strategy (line 289), or a new framework (line 298) for the recovery of emerging coronaviruses. As indicated in Wyler et al., 1988, Wicht et al., 2014, and others and cited references 18, 34, 35, and 36, this is an established strategy. The strategy was also proposed by others for the recovery of clinical samples for FIPV (Mettelman et al., 2019 Virology). The current work does provide evidence of the utility of the approach, so the results presented are important and timely for the study of emerging coronaviruses.
3. Figure 1. Remove A and B as the structural information is not needed here.
4. Figure 6. This schematic diagram could be improved to better illustrate the results of this study. Consider altering the diagram to more clearly depict how a virus that binds to a cell using a lower affinity interaction at the plasma membrane could be activated for fusion by the addition of an exogenous protease (like trypsin). What do you mean by protease incompatibility? Does this paper address anything about the use of cathepsins?

To: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][jjohnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]
From: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Sent: Mon 4/27/2020 2:48:52 PM (UTC-05:00)
Subject: COVID-19 Weekly Investigator Call April 28th

Hi Everyone,
On this week's call we'll have highlights from Sue Gerber from CDC and Yoshi Kawaoka from the Univ of Wisconsin. Please see below for last week's attendees. As usual, if you just dialed in via phone the system recorded you as Caller X, so please let me and Rebecca Lampley know if your name should be added.

Please also let us know if you would like to present on May 12th or 19th.
Erik

Attendees 4/21
Erik Stemmy

Marciela DeGrace

Rebecca Lampley

Adolfo Garcia-Sastre

Alan Embry

Ali Ellebedy

Andrea Sant

Andrew Pekosz

Annice Lowen

Brooke Bozick

Charles Russell

Chris Roberts

Connie

David Topham

David Wentworth

Diane Post

Donna Neu

Eunchung Park

Florian Krammer

Gabriele Neumann

Ghazi Kayali

Harm van Bakel

Ian Crozier

James Kobie

Jim Chappell

Juergen Richt

Kanta Subbarao

Katy Shaw-Saliba

Kimberly Stemple

Larry Anderson

Lisa Hensley

Mark Denison

Mark Sangster

Marlene Espinoza

Masato Hatta (UW)

Matt Frieman

Maureen McGargill

Melissa Uccellini

Pamela McKenzie

Paul Thomas

Peter Daszak

Peter Palese

Punam Mathur

Ralph Baric

Reed Johnson

Richard Rothman

Ron Fouchier

Sander Herfst

Simon Anthony

Stacey Schultz-Cherry

Stanley Perlman

Stephen Tompkins

Susan Gerber

Susan Weiss

Troy Sutton

Tom Fabrizio

Vineet Menachery

Vivanna

Walt Orenstein

Weina Sun

Yoshihiro Kawaoka

UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL

DEPARTMENT OF EPIDEMIOLOGY F 919.966.2089
McGAVRAN-GREENBERG HALL
CAMPUS BOX 7435
CHAPEL HILL, NC 27599-7435

November 25, 2019

To the Editors,

Please find our revised manuscript, "Trypsin treatment unlocks barrier for zoonotic bat coronaviruses infection" by Menachery, Dinnon, et al.

We take this opportunity to thank the reviewer for the comments and suggestions. We have included new requested data and responded to all the comments of the reviewer. We thank the reviewers for the helpful comments and feel that the improved manuscript is now appropriate for publication. Detailed modifications have been highlighted in the manuscript, and the significant changes are described in the response to reviewers.

Both reviewers recognized the significance and importance of our findings. However, both reviewers asked for clarification and elaboration on specific points and additional experiments to support our conclusions. Specifically, Reviewer 1 requested modification of the text and expansion on several points of interest. In addition, we revised our description of the HAE infections to more clearly describe the experiments. Reviewer 2 requested documentation of spike cleavage and examination of the proteolytic cleavage site sequences. Each has been added to the manuscript and figures have been modified as outlined in the response to reviews.

Overall, we believe that these responses have improved the quality of the manuscript and made it more appropriate for publication in Journal of Virology. Thank you for your consideration of this revised manuscript..

Sincerely,

Ralph S. Baric, PhD
Professor
University of North Carolina at Chapel Hill
Chapel Hill, North Carolina
[HYPERLINK "mailto:rbaric@email.unc.edu"]

Vineet D. Menachery, Ph.D.
Assistant Professor
University of Texas Medical Branch
Galveston, Texas
[HYPERLINK "mailto:vimenach@utmb.edu"]

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 12/11/2019 1:00:43 PM (UTC-06:00)
Subject: December Conference call

Hi Everyone,
We are planning on having a very short call tomorrow for SIG U19.

Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 11/13/2019 12:07:21 PM (UTC-06:00)
Subject: November conference call cancelled for SIG U19

Hi All,
Mark and Ralph are out of town, so no conference call this month.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 12/11/2019 2:52:46 PM (UTC-06:00)
Subject: RE: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Hilarious!

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, December 11, 2019 3:52 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

https://www.youtube.com/watch?v=zBY0UQpUNdA

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Wednesday, December 11, 2019 2:50 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Seriously, that really is nice.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, December 11, 2019 3:08 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Fw: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

guess somebody thought it was interesting.

I"ll work on this and send you a draft by Friday.

VDM

From: Dutch, Rebecca <rebecca.dutch@uky.edu>
Sent: Wednesday, December 11, 2019 12:44 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Dear Vineet,

Congratulations! Your article, "Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection " (JVI01774-19) has been selected by the editors of the Journal of Virology for inclusion in "Spotlight," a feature in the Journal that highlights research articles of significant interest from the current issue. This section follows the table of contents and includes short descriptions of five especially meritorious articles.

If you wish your article to be included in this section, please draft a short, declarative title and a brief summary of your manuscript (between 50-100 words) and forward these to me. The summary should be

composed in general terms, highlighting the broad biological significance of the work. Also, please select a panel of one figure from your paper to display alongside the text in the Spotlight section. Please crop the figure file so that it includes only the portion of the figure to be published in the Spotlight, and send the resulting high-resolution (300dpi) TIF (preferred), EPS, or PPT file to me. The figure can convey the most important experimental result of your study or an interesting image. Do not send a multi-panel figure. We only have space for a single panel. Please include a short descriptive title for the figure. The title used in the legend for the chosen figure may suffice. You will find an example of what we are aiming for in this section, attached.

As our printing deadlines are very tight, we must receive your material – the headline, paragraph of text, cropped figure file, and brief figure legend by 5 pm (Eastern Standard Time) on Tuesday the 17th of December. Please let me know if I can help you with any questions. Thank you for contributing to the Journal of Virology Spotlight.

Sincerely,
Becky Dutch
Editor, Journal of Virology

Rebecca Dutch
Professor and Chair, Molecular and Cellular Biochemistry
University of Kentucky College of Medicine
143 BBSRB
741 S. Limestone St.
Lexington, KY 40536-0509

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]
Sent: Wed 12/11/2019 7:06:30 PM (UTC-06:00)
Subject: Re: December Conference call

Will call in.

Fernando

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, December 11, 2019 2:00 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: December Conference call

Hi Everyone,
We are planning on having a very short call tomorrow for SIG U19.

Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 12/11/2019 2:46:34 PM (UTC-06:00)
Subject: RE: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Awesome! They do love us…..they really do love us! (The Mask)

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, December 11, 2019 3:08 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Fw: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

guess somebody thought it was interesting.

I"ll work on this and send you a draft by Friday.

VDM

From: Dutch, Rebecca <rebecca.dutch@uky.edu>
Sent: Wednesday, December 11, 2019 12:44 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Dear Vineet,

Congratulations! Your article, "Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection " (JVI01774-19) has been selected by the editors of the Journal of Virology for inclusion in "Spotlight," a feature in the Journal that highlights research articles of significant interest from the current issue. This section follows the table of contents and includes short descriptions of five especially meritorious articles.

If you wish your article to be included in this section, please draft a short, declarative title and a brief summary of your manuscript (between 50-100 words) and forward these to me. The summary should be composed in general terms, highlighting the broad biological significance of the work. Also, please select a panel of one figure from your paper to display alongside the text in the Spotlight section. Please crop the figure file so that it includes only the portion of the figure to be published in the Spotlight, and send the resulting high-resolution (300dpi) TIF (preferred), EPS, or PPT file to me. The figure can convey the most important experimental result of your study or an interesting image. Do not send a multi-panel figure. We only have space for a single panel. Please include a short descriptive title for the figure. The title used in the legend for the chosen figure may suffice. You will find an example of what we are aiming for in this section, attached.

As our printing deadlines are very tight, we must receive your material – the headline, paragraph of text, cropped figure file, and brief figure legend by 5 pm (Eastern Standard Time) on Tuesday the 17th of December. Please let me know if I can help you with any questions. Thank you for contributing to the Journal of Virology Spotlight.

Sincerely,
Becky Dutch
Editor, Journal of Virology

Rebecca Dutch
Professor and Chair, Molecular and Cellular Biochemistry
University of Kentucky College of Medicine
143 BBSRB
741 S. Limestone St.
Lexington, KY 40536-0509

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Mike[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney (mcweeney@ohsu.edu)[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 12/19/2019 11:59:08 AM (UTC-06:00)
Subject: SIG U19 face to face

Good afternoon everyone!

We have selected the date for the face to face meeting in Chapel Hill. There was not a date that worked for everyone, so we needed to pick a date that worked for most. The meeting will be March 10-12. The tentative timeline is as follows:

March 10- group dinner
March 11 meeting all day, group dinner
March 12 ½ day meeting so West Coast folks can catch the afternoon flight out.

Happy holidays to all.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 5/11/2020 11:57:12 AM (UTC-05:00)
Subject: SIGU19 monthly call cancelled

Hi Everyone,
The SIG U19 conference call will be cancelled for the month of May. Please remember to send me next year's budgets and your progress reports.

Best regards,

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 12/20/2019 8:02:07 AM (UTC-06:00)
Subject: RE: B-Cell paper

Ok, have a great trip to India. I'll get it to you over the next couple of hrs. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, December 20, 2019 8:35 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: B-Cell paper

Ok. You can send it to me if you'd like. We are going to India over the break and am collecting stuff to do if I feel like it.

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, December 20, 2019 6:04:17 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: B-Cell paper

Yes, haven't had a chance to deal with it yet. ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, December 19, 2019 3:59 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: B-Cell paper

Hey Ralph,

I am going through my list of things and saw Anne's B-cell paper. She said she was going to send it to you; did you ever get a draft from her for resubmission?

VDM

To: Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]
From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]
Sent: Fri 5/15/2020 10:10:59 AM (UTC-05:00)
Subject: RE: nCoV weekly investigators meeting

Hi everyone,

We will be switching from GoToMeeting to Zoom for these meetings, so I will be cancelling this meeting invitation. Please look out for a new invitation from Rebecca Lampley so that you have the most up to date link for next week's discussion.

Thanks!

Marciela

-----Original Appointment-----
From: Degrace, Marciela (NIH/NIAID) [E]
Sent: Friday, January 24, 2020 8:08 AM
To: Degrace, Marciela (NIH/NIAID) [E]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier;

yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott
Cc: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved
Subject: nCoV weekly investigators meeting
When: Tuesday, May 19, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: GoToWebinar

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join/ **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code: **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Location: GoToWebinar

Importance: Normal

Subject: Canceled: nCoV weekly investigators meeting

Start Time: Tue 1/28/2020 9:00:00 AM (UTC-05:00)

End Time: Tue 1/28/2020 10:00:00 AM (UTC-05:00)

Required Attendees: Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott

Optional Attendees: Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Stemmy, Erik (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved

Hi everyone,

Please see updated webinar links below. Hopefully this resolves any issues people had last time with sound.

Hello everyone,

Below please find the registration link for our weekly investigators meeting regarding the nCoV. **Please do not forward**. If you would like anyone else to be added to the invitation, please let me (Marciela.degrace@nih.gov) or Erik (erik.stemmy@nih.gov) know.

Our tentative agendas will be:

- Epi Updates
- NIAID Updates
- Other HHS partner Updates, if applicable
- Investigator research updates
- Discussion and Action Items
-

updated webinar link
https://global.gotomeeting.com/join **552.136**

You can also dial in using your phone.
United States: +1 (571) 317-3129

Access Code: **552.136**

Thank you,

Marciela DeGrace, Ph.D.
Project Officer, CEIRS
NIH/NIAID/DMID/RDB

To: Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/OD) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 5/15/2020 12:57:32 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - May 12, 2020

Hi!

Thank you Dr. Baric for your presentation on May 12th. Hopefully the discussion was helpful for everyone who dialed in.

Next week, Dr. Gavin Smith will be presenting preliminary sequencing results from recruited patients along with the detections and genomic characterization of a deletion variant.

Here is the attendance from last week. If your name is not listed and you attended the call, please let me know.

Erik Stemmy

Marciela DeGrace

Rebecca Lampley

Adolfo Garcia-Sastre

Alan Embry

Ali Ellebedy

Alison Augustine

Amy Krafft

Andrea Sant

Andrew Pekosz

Aneesh Mehta

Ann Eakin

Annice Lowen

Atsuo Kuki

Aubree Gordon

Brooke Bozick

Catherine Luke

Charles Russell

Chelsea Lane

Chris Roberts

Conrad Mallia

Colleen Jonsson

Connie

Daved Fremont

David Renner (Susan Weiss lab)

David Topham

David Wentworth

Diane Post

Don Milton

Donna Neu

Elizabeth Fitzpatrick

Erica Raterman

Eunchung Park

Florian Krammer

Gabriele Neumann

Ghazi Kayali

Greg Deye

Hana Golding

Harm van Bakel

Ian Crozier

Jae Jung

James Kobie

Jean Patterson

Jonathan Runstadler

Judy Hewitt

Juergen Richt

Kanta Subbarao

Kimberly Stemple

Kristina Lu

Larry Anderson

Lisa Hensley

Mark Challberg

Mark Denison

Mark Sangster

Masato Hatta (UW)

Matt Frieman

Maureen McGargill

Melissa Uccellini

Mindy Davis

Pamela McKenzie

Patrice Becker

Paul Thomas

Peter Daszak

Peter Palese

Punam Mathur

Ralph Baric

Randall Tressler

Reed Johnson

Richard Sciotti

Richard Webby

Ryan Langlois

Sander Herfst

Sara Cherry

Scott Strome

Seema Lakdawala

Stacey Schultz-Cherry

Stephen Tompkins

Steve Smiley

Surender Khurana

Susan Weiss

Troy Sutton

Vineet Menachery

W Leitner

Walt Orenstein

Yoshihiro Kawaoka

Thank you,
Rebecca

Rebecca M. Lampley M.S. [C]

Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Jacob Kocher[jake.kocher22@gmail.com]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 1/2/2020 12:15:04 PM (UTC-06:00)
B cell paper figures 10062019.docx
B cell paper together 10062019.docx

Hi Jacob and Vineet, Here is the version of Anne's B cell paper with her final comments. Jake, can you take a look to make sure the new data you generated is appropriately presented. Vineet, I appreciate your comments. I'd also like your thoughts on where to submit this. Its been a year plus since it was reviewed at JV-should we go back or chase a sure thing. Jake, congrats on the new baby! Hope you both had a Happy Holiday and New Year. Ralph

FIGURES

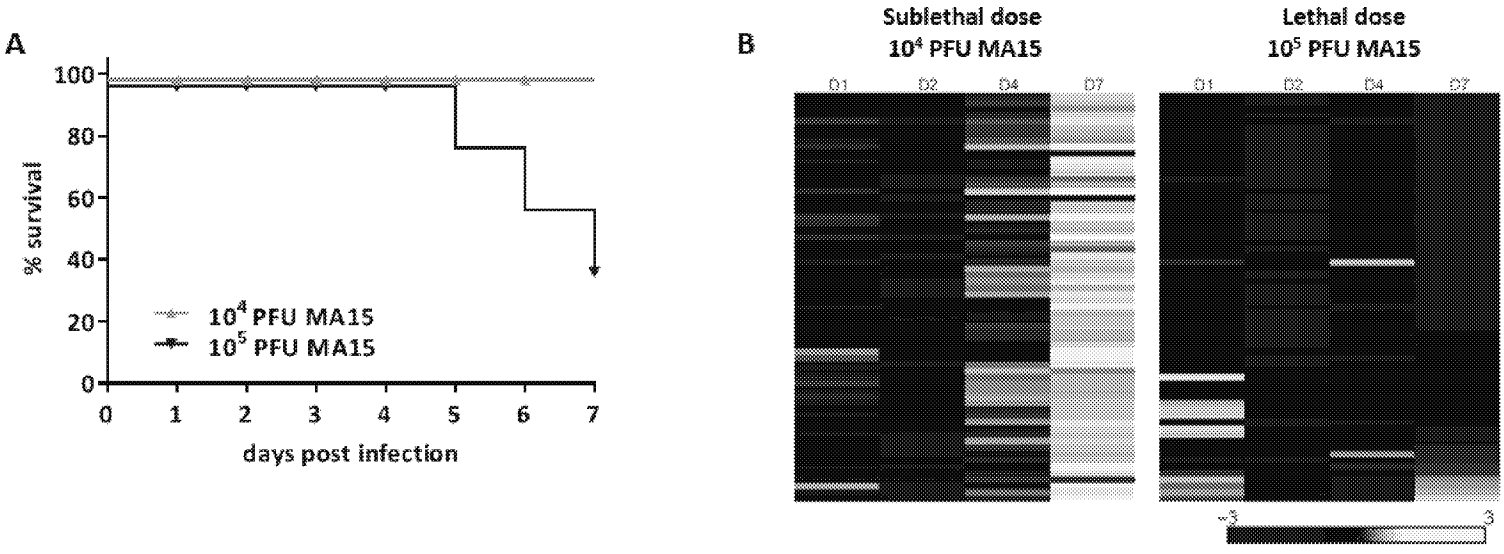
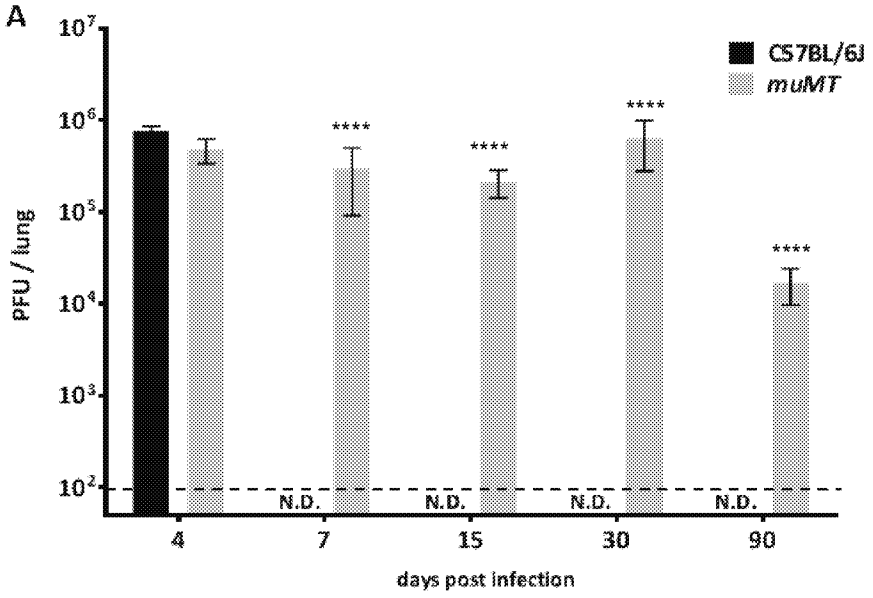
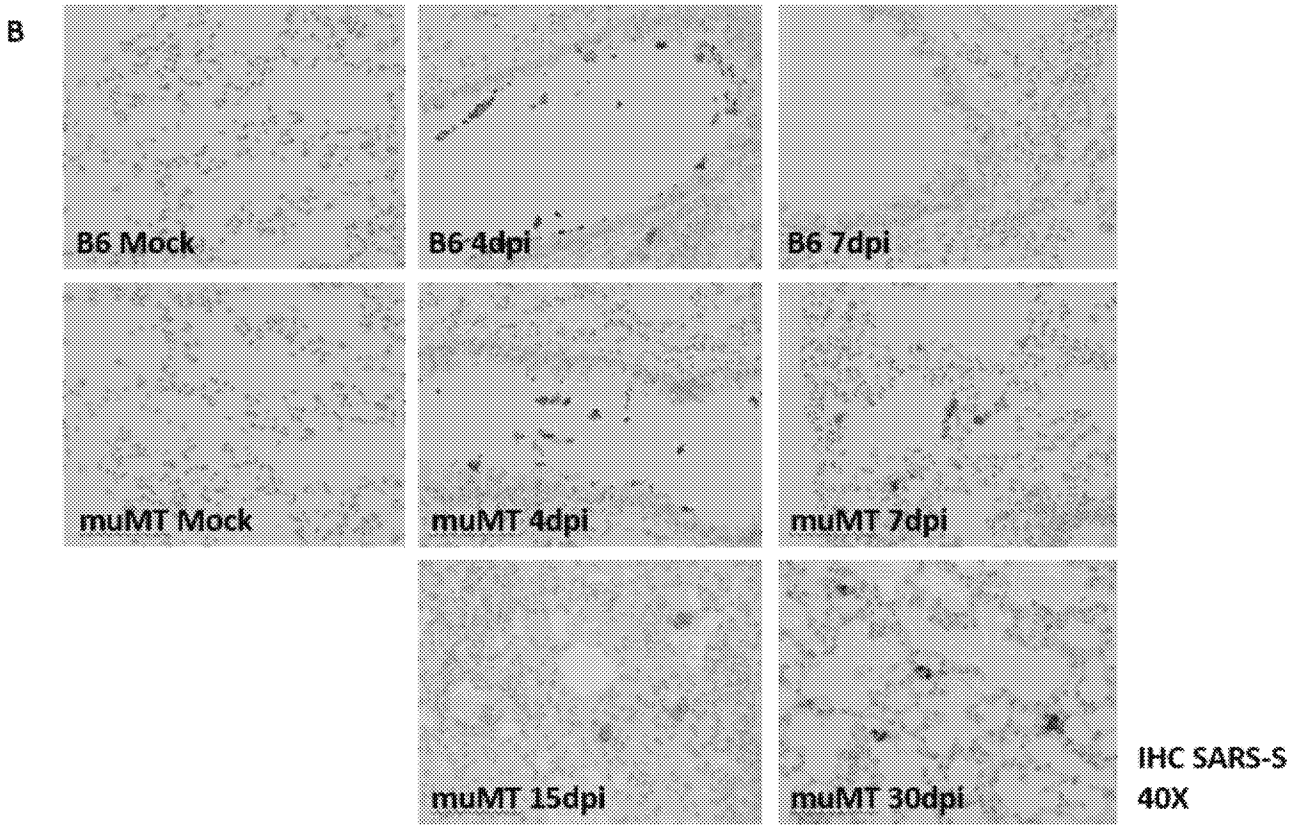
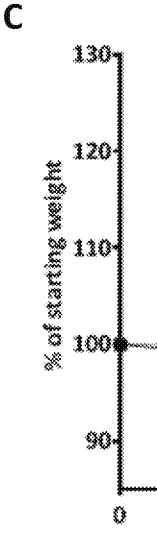
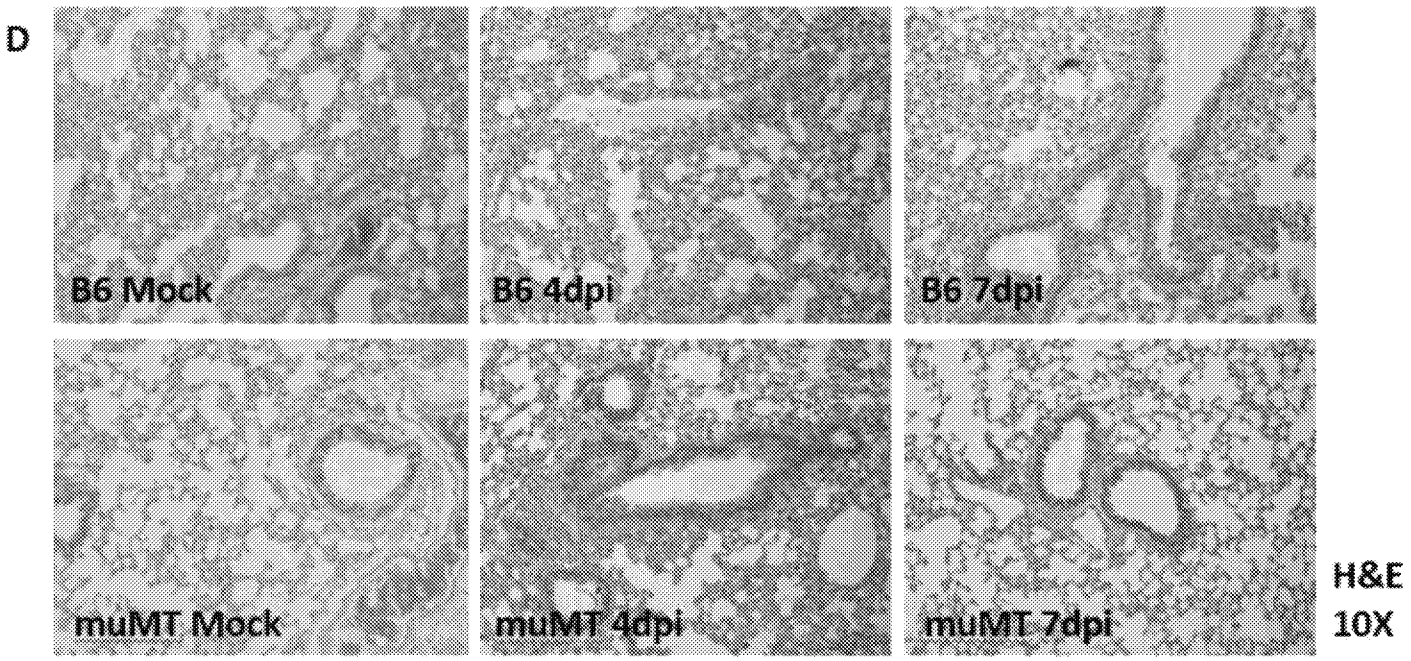


Fig 1. Bioinformatics points to an important role for B cells. 20 week old C57BL/6J mice were infected intranasally with a 50uL sublethal (10^4 PFU/mouse) or lethal (10^5 PFU/mouse) dose of MA15 SARS-CoV diluted in PBS. (A) Survival curves for infected mice. Mice dropping below 70% weight loss were humanely sacrificed and counted as succumbing to disease for the purposes of the experiment. All mice were sacrificed at 7 dpi. n=5 per group. (B) Log_2 fold change ratio of immunoglobulin family-related gene expression from the lungs of MA15 SARS-CoV-infected C57BL/6J mice after infection compared to mock infected mice. Yellow indicates increased gene expression compared to mock. Blue indicates decreased expression compared to mock. Probe and gene descriptions provided in Fig S1.


A
C57BL/6J
muMT
PFU / lung
10^7
10^6
10^5
10^4
10^3
10^2
****
****
****
****
N.D.
N.D.
N.D.
N.D.
4
7
15
30
90
days post infection


B
B6 Mock
B6 4dpi
B6 7dpi
muMT Mock
muMT 4dpi
muMT 7dpi
muMT 15dpi
muMT 30dpi
IHC SARS-S
40X


C
% of starting weight
130
120
110
100
90
0



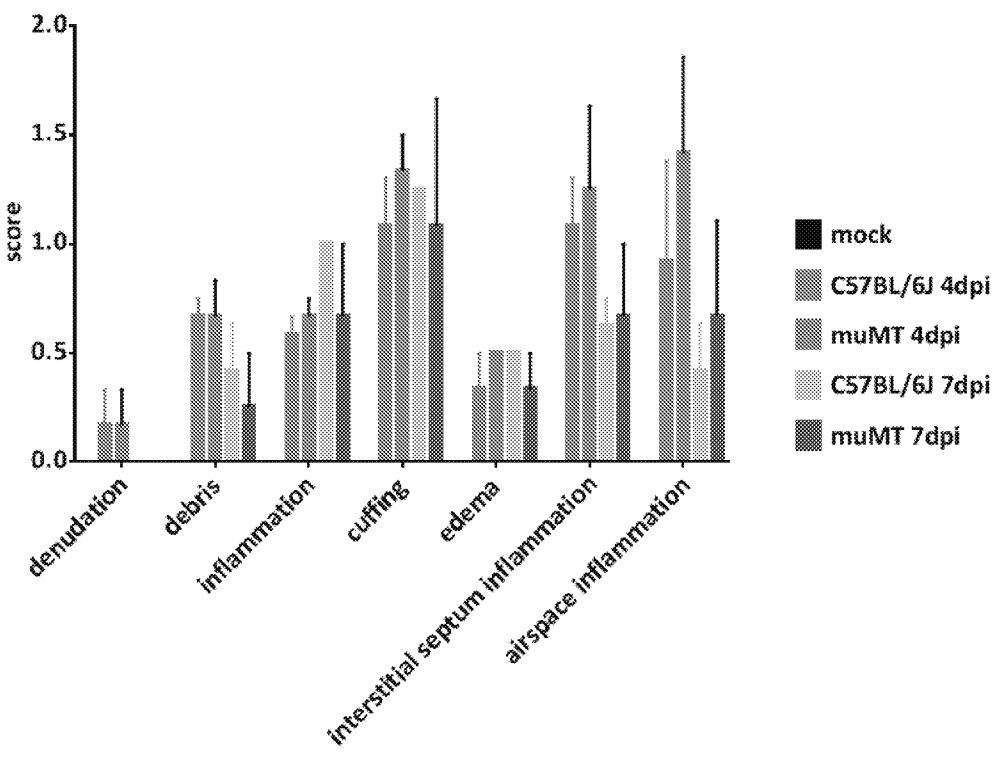
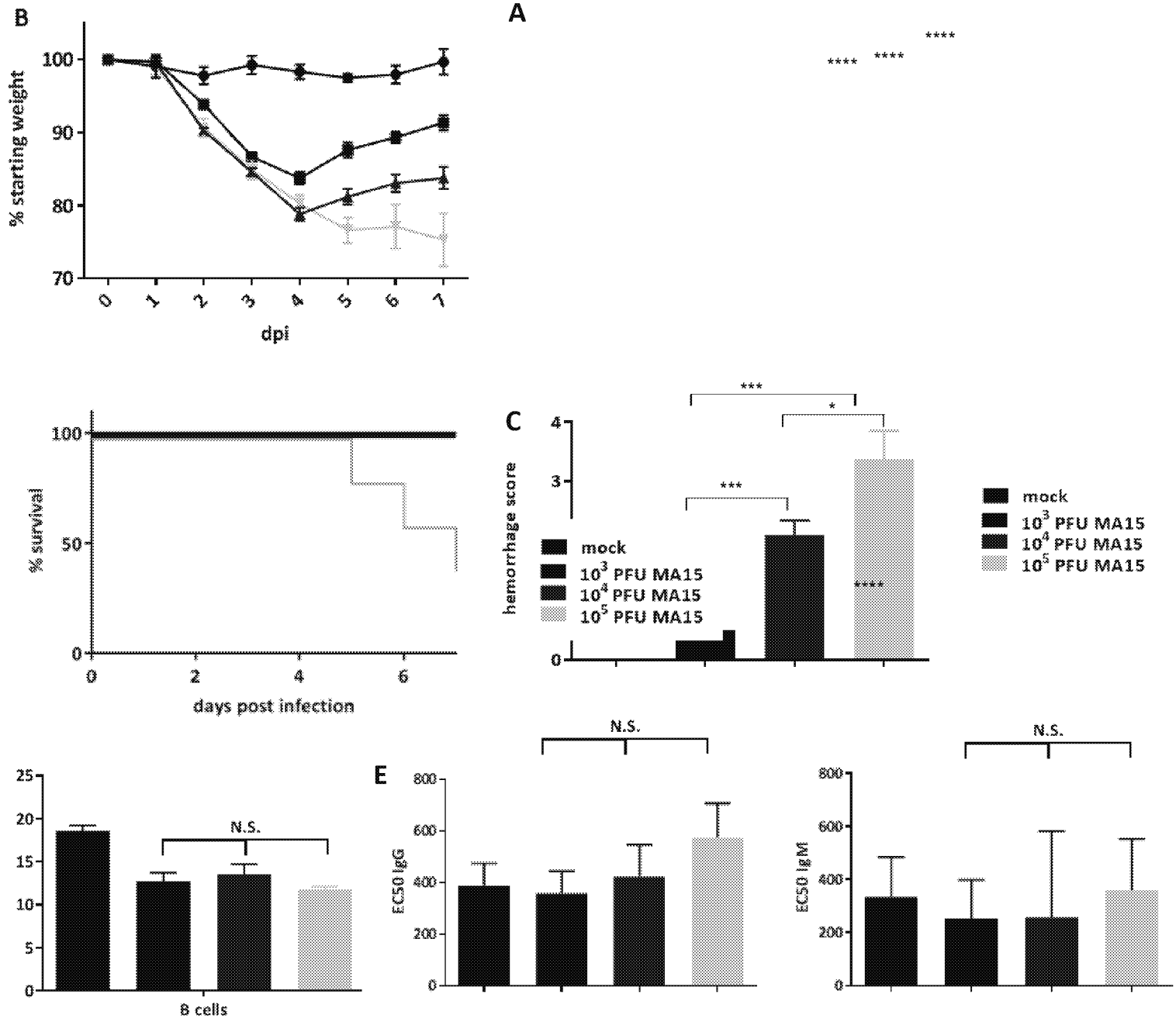


Fig 2. B cells are required to clear SARS-CoV. 10 week old C57BL/6J or muMT B cell deficient mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. (A) Lung mean virus load was quantitated by plaque

assay. Statistical significance determined using ANOVA analysis, with **** signifying $p<0.0001$. (B) Representative images of lung sections at indicated timepoints post-infection. SARS-CoV staining was performed via immunohistochemistry using anti-SARS-N and is shown in brown. (C) Mean weight loss per group is represented as a percent of starting weight for each mouse. Mice were weighed daily. (D) Representative images of lung sections at indicated timepoints post-infection. H&E staining is shown. (E) Lung injury scores from mice at indicated times. None show significant differences between C57BL/6J and *muMT* mice at matched timepoints.


B
% starting weight
100
90
80
70
0
1
2
3
4
5
6
7
dpi
A
****
****
****
B
% survival
100
50
0
0
2
4
6
days post infection
C
hemorrhage score
4
3
0
***
***
*
****
mock
10^3 PFU MA15
10^4 PFU MA15
10^5 PFU MA15
mock
10^3 PFU MA15
10^4 PFU MA15
10^5 PFU MA15
D
% of LCA+
25
20
15
10
5
0
N.S.
B cells
E
EC50 IgG
800
600
400
200
0
N.S.
EC50 IgM
800
600
400
200
0
N.S.

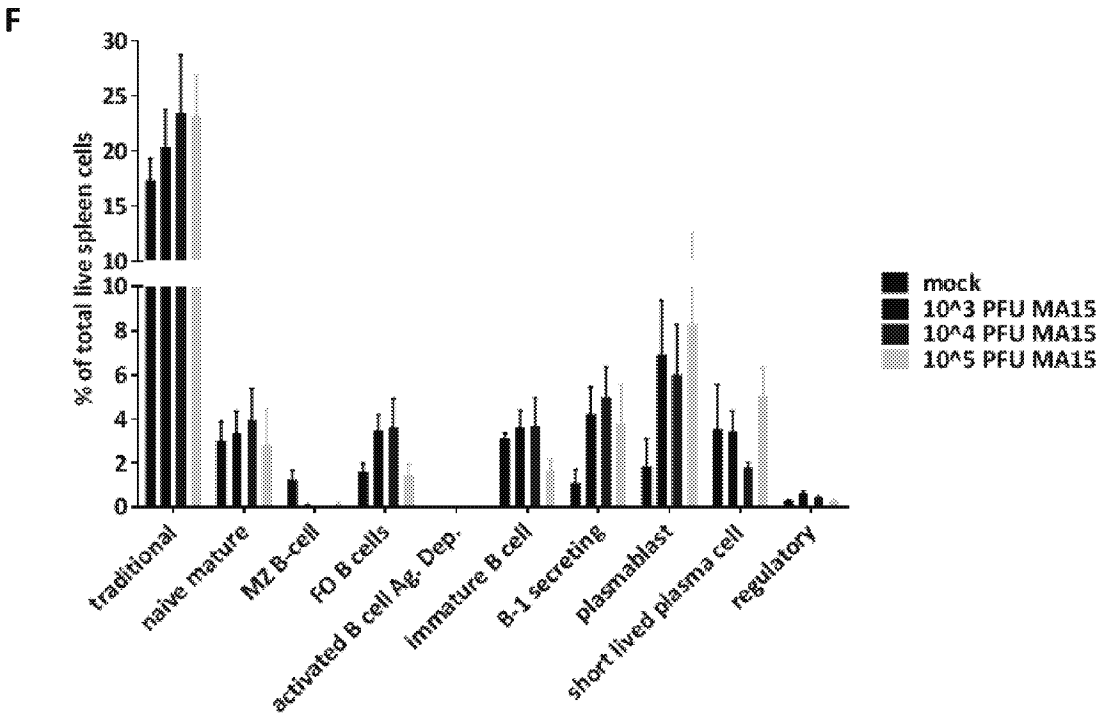


Fig 3. B cell and antibody responses do not correlate with pathogenesis. 20 week old mice were infected intranasally with a lethal (10^5 PFU/mouse) or sublethal (10^3 or 10^4 PFU/mouse) dose of MA15 SARS-CoV. n=5/group. (A) Mean weight loss per group is represented as a percent of starting weight for each mouse. Weights at each dose significantly differed from each other group at 5, 6, and 7 dpi. (B) Survival curves of infected mice. (C) Mean hemorrhage score of mouse lungs taken during 7 dpi harvest. (E) Mean total B cells as a percent of LCA+ cells. B cells are defined as B220+ and CD20+. (E) Mean SARS-S reactive immunoglobulin levels represented as EC50. (F) Splenic B cell populations after MA15 SARS-CoV infection at mock, sub-lethal, and lethal infection doses in 10 week old C57BL/6J mice – no significant differences were seen in B cell populations. All statistics performed by t test. * $p<0.01$. *** $p<0.0001$. ****$p<0.00001$.

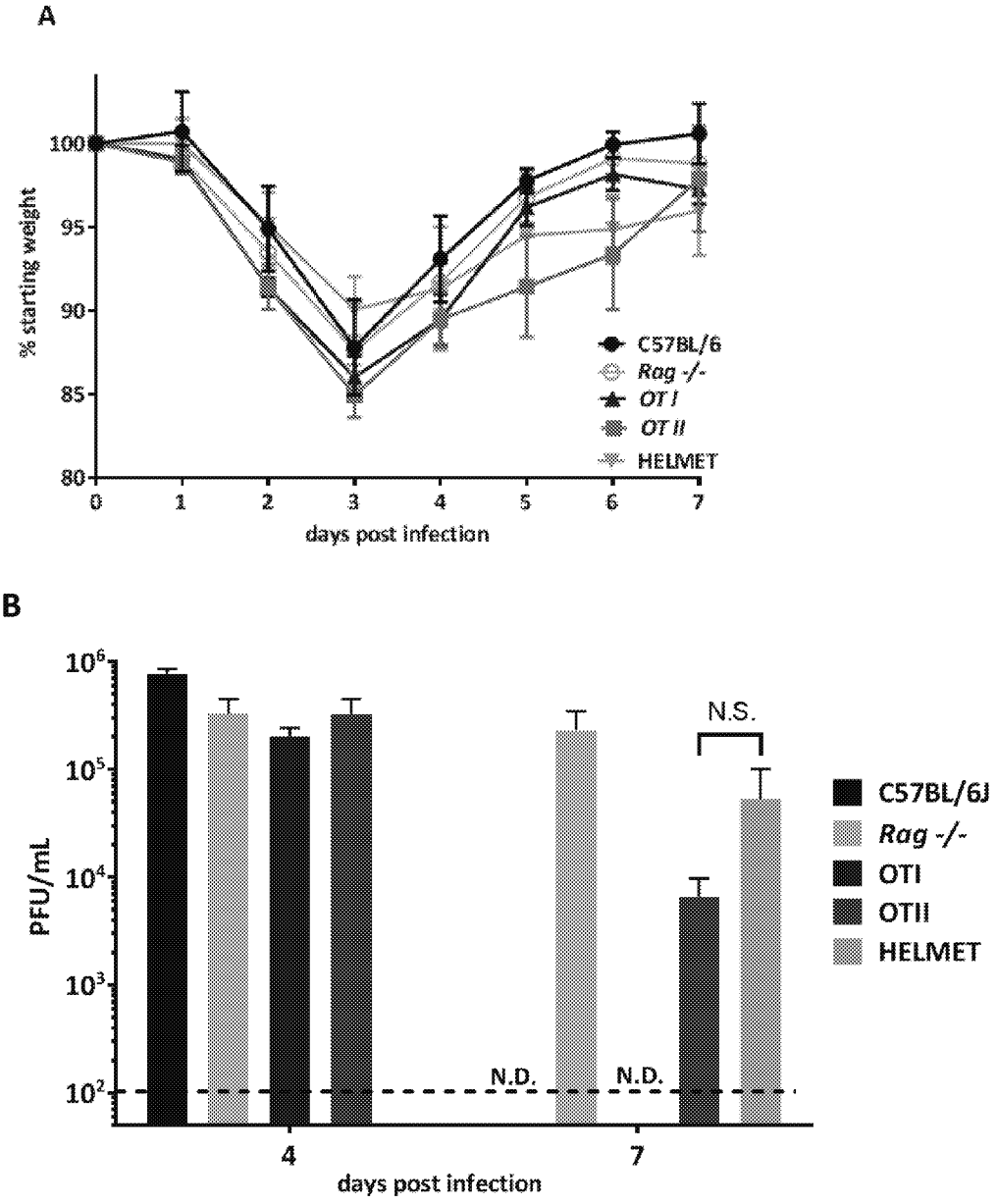


Fig 4. Lack of antigen-specific CD4+T cell responses results in delayed SARS-CoV clearance. 10 week old mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group at 4 and 7 dpi. n=3/group at 15 dpi. (A) Mean weight loss per group is represented as a percent of starting weight for each mouse. Mice were weighed daily. No significant difference between weight groups. (B) Lung mean virus load was quantitated by plaque assay. All statistics performed by t test.

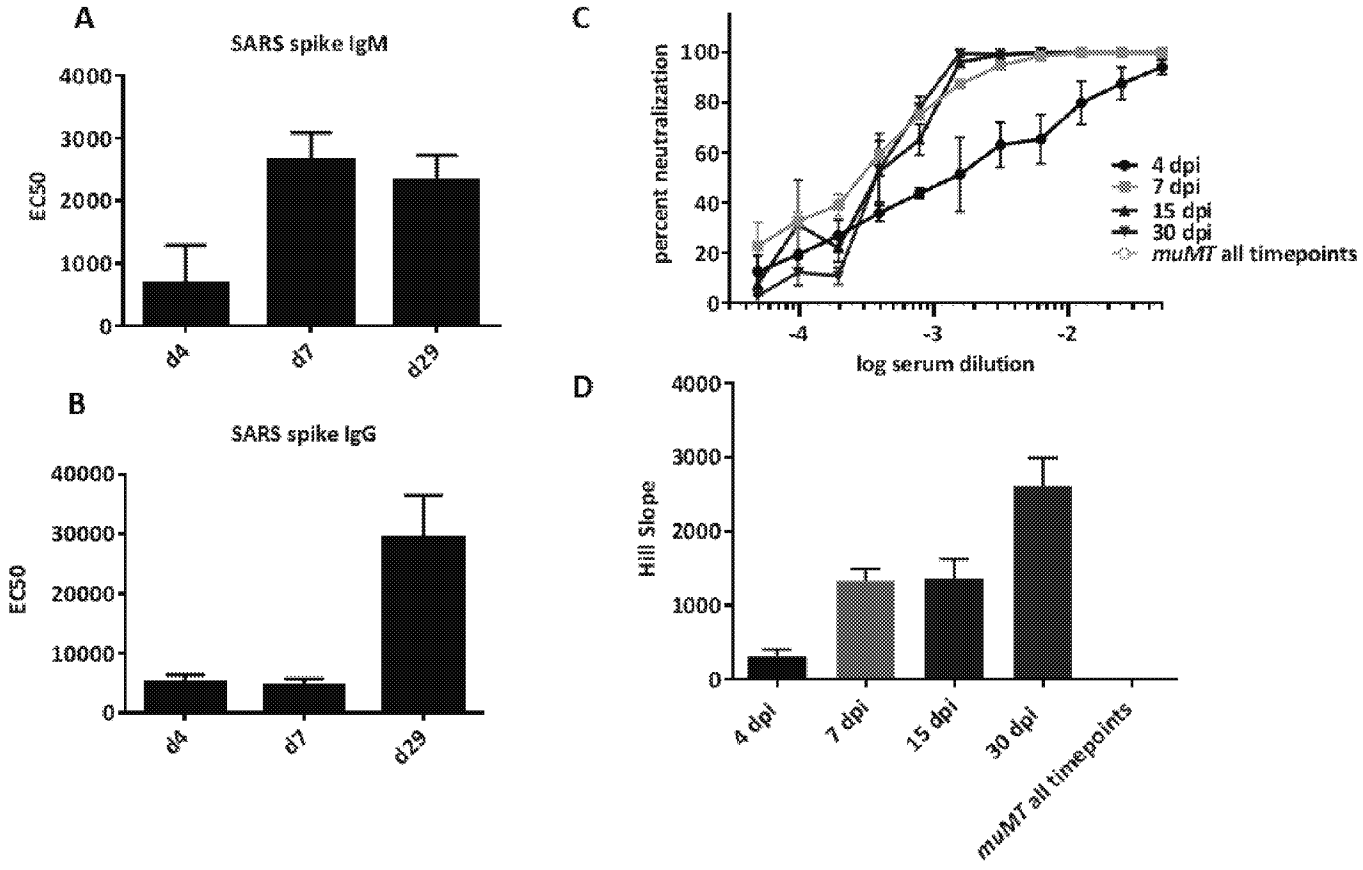


Fig 5. Serum antibodies at 7 days post infection can efficiently neutralize SARS-CoV *in vitro*. 10 week old mice were infected intranasally with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. (A-B) Mean serum IgM (A) and IgG (B) EC50 against SARS-CoV spike protein. n=5 mice/group. (C) SARS-CoV plaque neutralization and (D) hill slopes of neutralization curves were determined by plaque assay using serum taken from MA15 SARS-infected mice at the indicated timepoints.

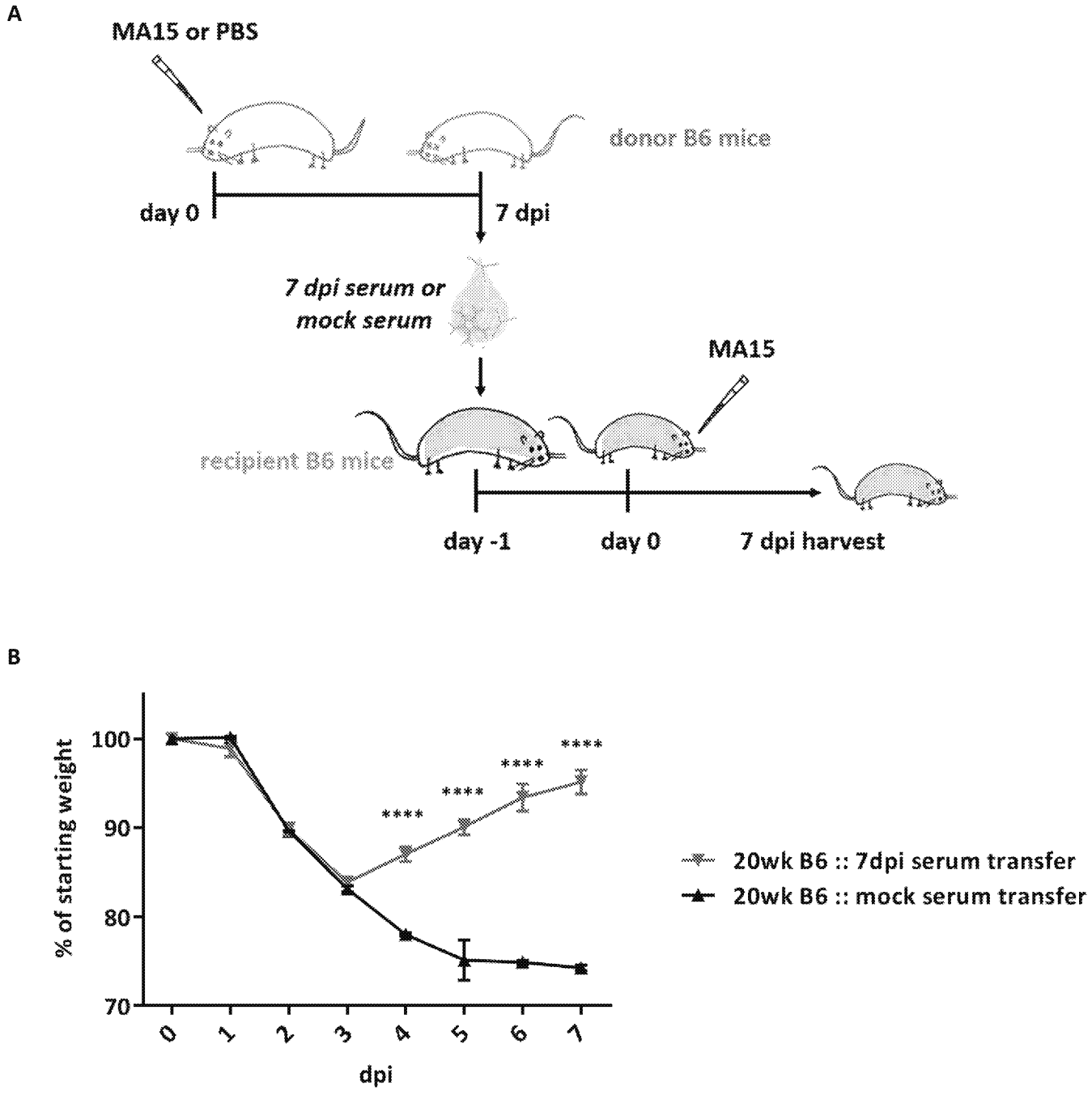


Fig 6. Prophylactic transfer of early antibody prevents mortality during lethal SARS-CoV infection through viral neutralization *in vivo*. Experimental set up of serum transfer experiments. C57BL/6J mice were infected with SARS-CoV at a sublethal dose and serum was harvested at the indicated time point after infection. Serum was transferred at a 1:1 ratio i.p. to the experimental mouse, which was infected with a lethal dose of SARS-CoV 24 hours later. Mice were weighed daily and harvested 7dpi. (A) Mean weight loss of mock serum of 7dpi serum transfer to 12 week or 20 week old C57Bl/6J mice. (B) :: shorthand for received. Statistical significance determined using ANOVA analysis, with **** signifying $p<0.0001$.

SUPPLEMENTARY FIGURES

SUPPLEMENT 1. Heat map genes in order of display in Figure 1.

Probe	Gene	Description
A_51_P103364	ENSMUST00000103552	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S12] [ENSMUST00000103552]
A_51_P104768	ENSMUST00000103498	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S55] [ENSMUST00000103498]
A_51_P128248	Igh	Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody [M20831]
A_51_P150705	Igj	Mus musculus immunoglobulin joining chain (Igj), mRNA [NM_152839]
A_51_P150710	Igj	Mus musculus immunoglobulin joining chain (Igj), mRNA [NM_152839]
A_51_P183581	Pou2af1	Mus musculus POU domain, class 2, associating factor 1 (Pou2af1), mRNA [NM_011136]
A_51_P203148	AB017433	Mus musculus mRNA for anti-IL-18 IgG heavy chain, clone 125-2H, partial cds. [AB017433]
A_51_P230716	Igh-VJ558	K0727F04-5N NIA Mouse Hematopoietic Stem Cell (Lin-[CA578712]
A_51_P270807	Tnfrsf17	Mus musculus tumor necrosis factor receptor superfamily, member 17 (Tnfrsf17), mRNA [NM_011608]
A_51_P272341	EG211331	BY724721 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530011I23 5'. [BY724721]
A_51_P288295	ENSMUST00000103496	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-7] [ENSMUST00000103496]
A_51_P298802	Bfsp2	Mus musculus beaded filament structural protein 2, phakinin (Bfsp2), mRNA [NM_001002896]
A_51_P328275	ENSMUST00000103505	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S45] [ENSMUST00000103505]
A_51_P346681	AY090902	Mus musculus clone GN-2-M1 monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial cds [AY090902]
A_51_P405638	LOC544905	601217727F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586566 5'. [BE371942]
A_51_P442889	LOC639988	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC639988), mRNA [XM_916675]
A_51_P452153	2010001M09Rik	Mus musculus RIKEN cDNA 2010001M09 gene (2010001M09Rik), mRNA [NM_027222]
A_51_P461902	L22886	Mus musculus rearranged IgH mRNA, V-region, cell line Cyd-1. [L22886]
A_51_P476757	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_51_P503757	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010004G10 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008094]
A_51_P513770	ENSMUST00000103535	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S5] [ENSMUST00000103535]
A_51_P515985	U55685	Mus musculus anti-DNA immunoglobulin light chain IgG, antibody 452s.36, partial cds. [U55685]
A_52_P1054013	AK041235	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530093J23 product:immunoglobulin heavy chain 4 (serum IgG1), full insert sequence. [AK041235]
A_52_P139027	Igh-VJ558	Mus musculus J558+ IgM heavy chain mRNA, hybridoma clone ME2B7, partial cds. [U39781]
A_52_P14626	Igk-V33	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830304C16 product:Ig kappa chain V-VI region XRPC 44 homolog

		[Mus musculus], full insert sequence [AK157689]
A_52_P149235	Mel13	Mouse anti-idiotype antibody-resistant variant IgK (Vk-Ox1 gene family) mRNA, VJ5 region [M57586]
A_52_P151887	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_52_P174000	AB070542	Mus musculus VH186.2-D-J-IgG1 mRNA, partial cds, sequence:kec-5. [AB070542]
A_52_P213483	Ighv1-77	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC619994), mRNA [XM_138377]
A_52_P214437	EG668544	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC668544), mRNA [XM_001002167]
A_52_P225158	NAP113251-1	Unknown
A_52_P238230	AF152371	Mus musculus kappa light chain of Mab7 mRNA, partial cds. [AF152371]
A_52_P246248	AF240166	Mus musculus MRP3 mRNA, complete cds. [AF240166]
A_52_P259779	LOC631531	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S4] [ENSMUST00000103523]
A_52_P30641	Gm459	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE_DB;Acc:IGKV4-86] [ENSMUST00000103337]
A_52_P358406	ENSMUST00000103518	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-47] [ENSMUST00000103518]
A_52_P383114	Igl-V1	Mus musculus anti-deoxynivalenol scFv lambda light chain variable region mRNA, partial cds. [AY151141]
A_52_P385767	BC055911	Mus musculus cDNA clone MGC:68301 IMAGE:3662102, complete cds. [BC055911]
A_52_P449214	Gm1418	PREDICTED: Mus musculus gene model 1418, (NCBI) (Gm1418), mRNA [XM_357683]
A_52_P450276	Igl-V1	Mus musculus immunoglobulin lambda chain (IgL) mRNA, complete cds. [M94350]
A_52_P463637	AY895789	Mus musculus clone RLS1478F immunoglobulin heavy chain (Igh) mRNA, partial cds. [AY895789]
A_52_P469009	AY182513	Mus musculus clone BaFL-P40 immunoglobulin heavy chain variable region mRNA, partial cds. [AY182513]
A_52_P476989	AF210281	Mus musculus isolate B880 immunoglobulin heavy chain variable region mRNA, partial cds. [AF210281]
A_52_P47786	AB069910	Mus musculus V303-D-J-C mu mRNA, partial cds, sequence:R2-10. [AB069910]
A_52_P479163	NAP106724-1	Unknown
A_52_P480019	L48666	Mus musculus (cell line C3H/F2-15) chromosome 12 anti-DNA antibody heavy chain mRNA. [L48666]
A_52_P490470	NP614311	GB|AF459850.1|AAO59848.1 immunoglobulin heavy chain VDJ region [Mus musculus] [NP614311]
A_52_P492532	Gm189	Mus musculus single chain Fv antibody (E4(Fv)) mRNA, partial cds [AF025535]
A_52_P532769	Igh	Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody [M20831]
A_52_P544090	AF218659	Mus musculus clone nMeV21 immunoglobulin heavy chain variable region mRNA, partial cds. [AF218659]
A_52_P559566	ENSMUST00000103527	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-56] [ENSMUST00000103527]
A_52_P565106	NAP107273-1	Unknown

A_52_P565636	AY172876	Mus musculus clone BApecB1a-P3 immunoglobulin heavy chain variable region mRNA, partial cds. [AY172876]
A_52_P578436	Gm1418	PREDICTED: Mus musculus gene model 1418, (NCBI) (Gm1418), mRNA [XM_357683]
A_52_P582068	ENSMUST00000103351	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE_DB;Acc:IGKV4-63] [ENSMUST00000103351]
A_52_P58543	Gm1524	AGENCOURT_10055965 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6479347 5', mRNA sequence [BQ937284]
A_52_P614207	BC080787	Mus musculus immunoglobulin kappa chain complex, mRNA (cDNA clone MGC:91220 IMAGE:4206216), complete cds. [BC080787]
A_52_P622355	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]
A_52_P638100	AB070552	Mus musculus V102-D-J-IgG1 mRNA, partial cds, sequence:lec-8. [AB070552]
A_52_P648824	X12388	Mouse hybridoma 10B10S mRNA for IgM(b) heavy chain variable region V(H)-J(H)2. [X12388]
A_52_P672903	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]
A_52_P686392	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_52_P829408	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]

1 **Humoral immunity is required for Clearance of SARS-CoV Infection**

2 Beall, A.; Kocher, J.; Leist, S.; Menachery, V.; Baric, R.

3 B cells, MERS-CoV, clearance

4 Corresponding Author: Ralph S. Baric

5 Address: University of North Carolina at Chapel Hill, 2107 McGavran-Greenberg Hall CB 7435,

6 Chapel Hill, NC 27599-7435

7 Telephone: 919-966-7991 Fax: 919-966-0584

8 Email: [HYPERLINK "mailto:Rbaric@email.unc.edu"]

9

ABSTRACT

Severe acute respiratory syndrome (SARS) is a highly lethal human respiratory disease caused by a coronavirus, a virus family marked by increasingly frequent outbreaks, pre-emergent zoonotic viruses, and high mortality rates. Understanding the roles of innate, cellular, and humoral immunity in viral pathogenesis and clearance *in vivo* have the potential to illustrate novel treatments for these highly pathogenic viruses. Numerous studies have implicated innate immune cells and T cells as critical mediators of SARS-CoV pathogenesis and clearance *in vivo*. However, the role of B cells and antibodies in early SARS-CoV virus clearance and disease control has not been rigorously studied. Previous studies have demonstrated robust antibody production in late-stage convalescent patients as well as a role for SARS-CoV-specific monoclonal antibodies in prophylactic protection against viral infection and disease. In support of these findings, we show that eigengene module analyses has indicated a strong decrease in B cell and antibody-related gene expression during lethal infection as compared to sublethal infection. Using mouse strains deficient in multiple arms of adaptive immunity, we show that B cell-deficient mice become persistently infected with SARS-CoV and that early B cell and serum immune responses can mediate virus clearance during infection. Interestingly, convalescent sera from as early as 7 days post infection can be used as a prophylactic treatment to prevent lethality during a primary SARS-CoV infection. These findings demonstrate an important role for antibody and antigen non-specific B-cell help in SARS-CoV clearance, and supports a potential clinical role for early serum transfer and antibody treatment during future coronavirus outbreaks.

INTRODUCTION

Severe acute respiratory syndrome (SARS), caused by a novel coronavirus (SARS-CoV), resulted in over 8,000 cases of respiratory disease with high mortality in 2002 and 2003 [ADDIN EN.CITE <EndNote><Cite><RecNum>67</RecNum><DisplayText>(1)</DisplayText><record><rec-number>67</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501042421">67</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>World Health Organization</author></authors></contributors><titles><title>WHO | Update 49 - SARS case fatality ratio, incubation period</title><secondary-title>WHO</secondary-title></titles><dates></dates><urls></urls><access-date>2017-07-26 04:13:05</access-date></record></Cite></EndNote>]. Patients with severe pathology developed acute lung injury associated with neutrophilia, lymphopenia, and prolonged proinflammatory cytokine expression [ADDIN EN.CITE ADDIN EN.CITE.DATA]. In surviving patients, infectious virus was cleared between 1 and 3 weeks after infection [ADDIN EN.CITE <EndNote><Cite><Author>Chan</Author><Year>2004</Year><RecNum>88</RecNum><DisplayText>(3)</DisplayText><record><rec-number>88</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501082298">88</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Chan, K. H.</author><author>Poon, L. L.</author><author>Cheng, V. C.</author><author>Guan, Y.</author><author>Hung, I. F.</author><author>Kong, J.</author><author>Yam, L. Y.</author><author>Seto, W.

H.</author><author>Yuen, K. Y.</author><author>Peiris, J. S.</author></authors></contributors><auth-address>Queen Mary Hospital, Hong Kong Special Administrative Region, People's Republic of China.</auth-address><titles><title>Detection of SARS coronavirus in patients with suspected SARS</title><secondary-title>Emerg Infect Dis</secondary-title></titles><periodical><full-title>Emerging Infectious Diseases</full-title><abbr-1>Emerg Infect Dis</abbr-1></periodical><pages>294-9</pages><volume>10</volume><number>2</number><keywords><keyword>Antibodies, Viral/blood</keyword><keyword>Humans</keyword><keyword>RNA, Viral/genetics/isolation & purification</keyword><keyword>Reverse Transcriptase Polymerase Chain Reaction</keyword><keyword>SARS Virus/genetics/*isolation & purification</keyword><keyword>Severe Acute Respiratory Syndrome/*diagnosis/immunology/*virology</keyword><keyword>Time Factors</keyword></keywords><dates><year>2004</year><pub-dates><date>Feb</date></pub-dates></dates><isbn>1080-6040 (Print)
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Because human isolates of SARS-CoV replicate, but do not produce severe disease in mice, *in vivo* pathogenesis studies have focused on a mouse-adapted SARS-CoV strain designated MA15 to reveal fundamental insights into pathogenesis and immunity [ADDIN EN.CITE <EndNote><Cite><Author>Roberts</Author><Year>2007</Year><RecNum>82</RecNum><

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84 R.</author><author>Baric, R.</author><author>Subbarao,
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102 Several studies have demonstrated the critical importance of innate immune responses and
103 wound repair pathways in regulating SARS-CoV pathogenesis [ADDIN EN.CITE ADDIN
104 EN.CITE.DATA]; additionally, T cell responses have been found to be critical for virus
105 clearance and protection from clinical disease in mice infected with SARS-CoV. Survival has
106 been associated with robust SARS-CoV specific CD4+ and CD8+ T cell responses during
107 infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Findings to date have shown
108 critical roles for both innate and T cell-mediated immune functions in virus clearance, however,
109 the role of B cells in primary infection and viral clearance have not yet been characterized.
110 Serum analysis of SARS-CoV-infected patients and in SARS-CoV mouse models have
111 primarily focused on the development of protective neutralizing IgG antibody responses in the
112 weeks and months after infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The
113 SARS nucleocapsid is an immunodominant antigen during infection and the vast majority of
114 SARS-CoV reactive antibodies (80-90%) in patients bind to the nucleocapsid protein (N) [
115 ADDIN EN.CITE
116 <EndNote><Cite><Author>Leung</Author><Year>2004</Year><RecNum>12</RecNum><Di
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137 provider><access-date>2017/04/18/00:36:22</access-date></record></Cite></EndNote>].
138 During the SARS-CoV outbreak, IgG titers against the N protein as well as the spike
139 glycoprotein (S) were initially detected in patients at ~2 weeks post-infection. These IgG titers
140 peaked at approximately 4 weeks post-infection [ADDIN EN.CITE ADDIN EN.CITE.DATA
141]. Though anti-SARS-CoV IgG titers were detectable through one year post-infection, IgG
142 antibody titers declined over this period and subsequently became undetectable in many patients
143 six years after infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. At approximately
144 two weeks post-infection in human patients, antibody titers skew towards a higher IgG to IgM
145 ratio, suggesting that CD4+ T cells are highly activated after initial infection [ADDIN EN.CITE

146 <EndNote><Cite><Author>Xie</Author><Year>2005</Year><RecNum>9</RecNum><Displa
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175 provider><language>eng</language></record></Cite></EndNote>]. Taken together, these
176 previous reports indicate that antigen-specific antibody responses are robust in patients that clear
177 virus infection and survive infection.
178 Passive transfer of SARS-specific monoclonal and polyclonal sera has been shown to be
179 protective in both young and aged mouse models of human disease, as well as in humans during
180 the SARS-CoV outbreak [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Prophylactic
181 treatment with monoclonal anti-SARS-CoV antibodies reduces viral load in the mouse lung and
182 eases disease burden in mouse models of human coronavirus (CoV) infection [ADDIN
183 EN.CITE ADDIN EN.CITE.DATA]. During the SARS-CoV outbreak, antibodies from
184 convalescent sera of recovered patients were passively transferred to symptomatic SARS patients
185 who had not responded to other forms of treatment. Patients receiving convalescent sera
186 recovered from infection and rapidly cleared virus [ADDIN EN.CITE
187 <EndNote><Cite><Author>Yeh</Author><Year>2005</Year><RecNum>8</RecNum><Displ
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210 database-provider>academic.oup.com</remote-database-provider><access-
211 date>2017/04/10/05:48:12</access-date></record></Cite></EndNote>]. Coupled with the
212 above studies of anti-SARS-CoV antibody responses, these results suggest the importance of
213 humoral immunity in virus clearance and convalescent sera transfer as a possible treatment for

CoV infection. However, the exact role of B cells and antibodies in the control of primary infection has not yet been critically examined.

In this study, we focus on B cell and antibody responses to MA15 during the first two weeks of infection. Previous studies have shown that *Rag*$^{-/-}$ and SCID mice, both without functional adaptive immune cells, are unable to clear MA15, whereas immunocompetent mice clear virus within 7-10 days post infection (dpi) [ADDIN EN.CITE ADDIN EN.CITE.DATA]. To investigate the role of lymphocytes and humoral immunity in virus clearance, we infected B cell-deficient (*muMT*$^{-/-}$), CD4 T cell receptor (TCR) fixed (OTII), and CD8 TCR fixed (OTI) mouse strains with MA15. While both TCR-fixed mouse strains cleared virus by 15 dpi, the *muMT*$^{-/-}$ mice were unable to clear virus from the lung, and maintained high viral titers well past 15 dpi. Because T cells have primarily been implicated as responsible for MA15 clearance, the inability to clear virus in T cell competent, B cell deficient mice was surprising. Furthermore, we show that 7 dpi convalescent serum is capable of neutralizing MA15 *in vitro*. *In vivo*, prophylactically transferred 7 dpi convalescent sera prevented mortality in 12- and 20-week old mice challenged with a lethal dose of MA15. Together, these data indicate a major role for humoral immunity in control of primary SARS-CoV infection and signal a possible new treatment avenue for CoV-mediated disease in the context of a future outbreaks.

RESULTS

Activation of antibody-related networks is decreased during lethal SARS-CoV infection.

Using existing systems biology datasets for SARS-CoV infection [ADDIN EN.CITE ADDIN EN.CITE.DATA], network analysis comparing lethal and sublethal MA15 challenge

revealed a module eigengene (dark-red), a cluster of coordinately expressed genes regulating immunoglobulin, antibody heavy, and antibody light chain transcript expression [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Expression of this eigengene cluster was significantly diminished at 4 and 7 dpi in the lethal model as compared to the sublethal model of MA15 infection (Fig. 1, S. Table 1). Consistent with reports from human studies [ADDIN EN.CITE ADDIN EN.CITE.DATA], these data suggest a role for B cell and antibody responses in regulating disease progression following MA15 infection. The role of early humoral immune response to MA15 infection in viral clearance and pathogenesis has yet to be systematically evaluated. Based on these factors, we decided to explore the role of B cells and antibodies within the first 7 dpi of MA15 infection.

B cell-deficient mice are not able to clear MA15.

To determine the role of B cells and antibody in viral clearance, we infected 10-week old B cell-deficient (*muMT*$^{-/-}$) [ADDIN EN.CITE <EndNote><Cite><Author>Kitamura</Author><Year>1991</Year><RecNum>83</RecNum><DisplayText>(31)</DisplayText><record><rec-number>83</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501076080">83</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Kitamura, D.</author><author>Roes, J.</author><author>Kuhn, R.</author><author>Rajewsky, K.</author></authors></contributors><auth-address>Institute for Genetics, University of Cologne, Germany.</auth-address><titles><title>A B cell-deficient mouse by targeted disruption of the membrane exon of the immunoglobulin mu chain gene</title><secondary-

title>Nature</secondary-title></titles><periodical><full-title>Nature</full-title></periodical><pages>423-6</pages><volume>350</volume><number>6317</number><keywords><keyword>Animals</keyword><keyword>Antigens, Differentiation, B-Lymphocyte/analysis</keyword><keyword>B-Lymphocytes/*physiology</keyword><keyword>Blotting, Southern</keyword><keyword>DNA Mutational Analysis</keyword><keyword>Flow Cytometry</keyword><keyword>*Genes, Immunoglobulin</keyword><keyword>Hematopoiesis</keyword><keyword>Immunoglobulin Light Chains</keyword><keyword>Immunoglobulin Light Chains, Surrogate</keyword><keyword>Immunoglobulin mu-Chains/*genetics</keyword><keyword>Immunologic Deficiency Syndromes/*genetics</keyword><keyword>Membrane Glycoproteins/genetics</keyword><keyword>Mice</keyword><keyword>Receptors, Antigen, B-Cell/*genetics</keyword></keywords><dates><year>1991</year><pub-dates><date>Apr 04</date></pub-dates></dates><isbn>0028-0836 (Print)
0028-0836 (Linking)</isbn><accession-num>1901381</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/1901381</url></related-urls></urls><electronic-resource-num>10.1038/350423a0</electronic-resource-num></record></Cite></EndNote>] and immune intact C57BL/6J (B6) control mice with a sublethal dose of MA15, weighed and monitored mice daily, and harvested lung for titer and histology at timepoints between 4 and 90 dpi (Fig 2) [ADDIN EN.CITE <EndNote><Cite><Author>Roberts</Author><Year>2007</Year><RecNum>82</RecNum><

DisplayText>(4)</DisplayText><record><rec-number>82</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501075746">82</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Roberts, A.</author><author>Deming, D.</author><author>Paddock, C. D.</author><author>Cheng, A.</author><author>Yount, B.</author><author>Vogel, L.</author><author>Herman, B. D.</author><author>Sheahan, T.</author><author>Heise, M.</author><author>Genrich, G. L.</author><author>Zaki, S. R.</author><author>Baric, R.</author><author>Subbarao, K.</author></authors></contributors><auth-address>Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, United States of America.</auth-address><titles><title>A mouse-adapted SARS-coronavirus causes disease and mortality in BALB/c mice</title><secondary-title>PLoS Pathog</secondary-title></titles><periodical><full-title>PLoS Pathog</full-title></periodical><pages>e5</pages><volume>3</volume><number>1</number><keywords><keyword>Animals</keyword><keyword>Disease Models, Animal</keyword><keyword>Humans</keyword><keyword>Mice</keyword><keyword>Mice, Inbred BALB C</keyword><keyword>Molecular Sequence Data</keyword><keyword>RNA Virus Infections</keyword><keyword>SARS Virus/*isolation & purification/*pathogenicity</keyword><keyword>Severe Acute Respiratory Syndrome/mortality/*virology</keyword></keywords><dates><year>2007</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>1553-7374 (Electronic)
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urls></urls><custom2>PMC1769406</custom2><electronic-resource-num>10.1371/journal.ppat.0030005</electronic-resource-num></record></Cite></EndNote>].

As expected, control mice retained virus at high titer in the lung through 4 dpi, followed by rapid virus clearance to below the limit of detection by 7 dpi. Surprisingly, *muMT*$^{-/-}$ mice retained high viral titers in the lung through 90 dpi despite the presence of an otherwise intact immune system. We stained lung histology sections from later timepoints for SARS N protein. In control animals, we detected no viral antigen, but SARS N antigen staining was clearly evident at late time points in the *muMT*$^{-/-}$ model, consistent with our lung titer data (Fig 2B). Both B6 and *muMT*$^{-/-}$ mice demonstrated equivalent weight loss and recovery, despite *muMT*$^{-/-}$ mice retaining high virus titer in the lungs at later timepoints (Fig. 2C). Additionally, pathology scoring on histological slides showed no significant difference in lung injury or recovery between B6 and *muMT*$^{-/-}$ mice (Fig 2D-E), suggesting that total viral clearance is not required for recovery from SARS disease, consistent with previous findings [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These data support the hypothesis that B cells are directly or indirectly required for clearance of MA15 infection following primary challenge.

To determine whether B cell or antibody responses to SARS-CoV infection were differential between lethal and sublethal infections, we infected 20 week old B6 mice with a mock, low, sublethal, or lethal dose of MA15 (Fig. 3). We monitored mice and weight daily through 7 dpi (Fig. 3A-B), then harvested mice for lung hemorrhage scoring, flow cytometry analysis of the lung and spleen, and serum antibody titer (Fig. 3C-F). Serum antibody was analyzed by ELISA against purified SARS-S protein for anti-SARS-CoV IgG and IgM. We observed no significant differences in splenic B cell numbers, B cell activation, or serum antibody titer between infectious doses (Fig. 3F). These data together suggest that though B cell

329 and antibody responses impact viral clearance in the lung, the lack of these responses do not
330 impact weight loss and recovery from lung injury in the MA15 model under these treatment
331 conditions.
332
333 **Lack of antigen-specific CD4+ T cell responses results in delayed MA15 clearance.**
334 To further characterize interactions that may explain the critical role for B cells, we
335 sought to evaluate the role of T lymphocytes in MA15 clearance by infecting OTI and OTII
336 (fixed CD8 or CD4 TCR, respectively) mice with a sublethal dose of MA15 (Fig. 4) [ADDIN
337 EN.CITE ADDIN EN.CITE.DATA]. Wild-type B6 mice were used as an
338 immunocompetent control and *Rag*$^{-/-}$ mice were used an immunodeficient control. All mice
339 displayed similar weight loss and recovery phenotypes during infection, suggesting that neither
340 CD4+T nor CD8+T MA15-specific responses are individually required for recovery from
341 disease (Fig. 4A). At 4 dpi, B6, OTI, OTII, and *Rag*$^{-/-}$ mice retained high titers of MA15 in the
342 lung. However, by 7 dpi, B6 and OTI mice had cleared virus in the lung, suggesting that MA15-
343 specific CD8+T cells are not required for clearance in this model (Fig 3B). However, viral
344 clearance in OTII mice was delayed until 15 dpi. These data suggest that a CD4+T cell response
345 to MA15 infection contributes to, but is not essential for, viral clearance. Because of the
346 importance of CD4+T cell help in B cell activation in response to viral infection [ADDIN
347 EN.CITE
348 <EndNote><Cite><Author>Crotty</Author><Year>2015</Year><RecNum>123</RecNum><
349 DisplayText>(35)</DisplayText><record><rec-number>123</rec-number><foreign-keys><key
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352 Article">17</ref-type><contributors><authors><author>Crotty,
353 S.</author></authors></contributors><auth-address>Division of Vaccine Discovery, La Jolla
354 Institute for Allergy and Immunology, 9420 Athena Circle, San Diego, California 92037,
355 USA.</auth-address><titles><title>A brief history of T cell help to B cells</title><secondary-
356 title>Nat Rev Immunol</secondary-title></titles><periodical><full-title>Nat Rev
357 Immunol</full-title></periodical><pages>185-
358 9</pages><volume>15</volume><number>3</number><keywords><keyword>Allergy and
359 Immunology/*history</keyword><keyword>B-
360 Lymphocytes/*immunology</keyword><keyword>History, 20th
361 Century</keyword><keyword>History, 21st
362 Century</keyword><keyword>Humans</keyword><keyword>T-Lymphocytes, Helper-
363 Inducer/*immunology</keyword></keywords><dates><year>2015</year><pub-
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365 (Linking)</isbn><accession-num>25677493</accession-num><urls><related-
366 urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25677493</url></related-
367 urls></urls><custom2>PMC4414089</custom2><electronic-resource-
368 num>10.1038/nri3803</electronic-resource-num></record></Cite></EndNote>], this delay in
369 clearance in the OTII model points to a role for CD4+T cell activation of B cells in viral
370 clearance during the first week of infection. Together, these data further support a role for B cell
371 and antibody responses in MA15 clearance early in infection [ADDIN EN.CITE ADDIN
372 EN.CITE.DATA].
373
374 **Antigen-specific B cells are not required for SARS-CoV clearance.**

We next investigated B cell function and antigen specificity and its impact on virus control and clearance. For these purposes, we used the HELMET mouse strain, wherein B cells are present in normal levels carry B cell receptors only reactive to HEL, the hen egg lysozyme, rendering them unable to create viral antigen-specific antibodies [ADDIN EN.CITE ADDIN EN.CITE.DATA]. HELMET mice were infected with a sublethal dose of MA15, as above, and were monitored and weighed daily. HELMET mice showed similar weight loss and recovery to other mouse strains (OTI, OTII, *Rag*$^{-/-}$, B6), suggesting that a fixed BCR did not result in increased pathology during infection (Fig. 4A). However, MA15-infected HELMET mice maintained high virus titers in the lung through 7 dpi, but, eventually cleared virus infection by 15 dpi (Fig 4B). These data suggest an important role for antigen-specific B cells in early viral clearance in the lung, but are also consistent with previous findings outlining the capability of virus-specific T cells to clear virus from the lungs [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Importantly, the results suggest that B cells or antibody are needed in an antigen-independent capacity to help prime T cell-mediated clearance. Together, the data indicate an overlapping and complementary role for virus-specific B and T cells in MA15 clearance in the lung.

Convalescent serum at 7 days post infection can efficiently neutralize MA15 *in vitro*.

In order to analyze serum antibody responses to MA15 infection over time, we infected B6 mice with a sublethal dose of MA15 and harvested sera at 4, 7, and 29 dpi (Fig. 5). We analyzed sera for IgG and IgM antibody concentration against purified SARS-S glycoprotein. During infection, IgM responses against MA15 were established within the first week, peaked early and remained high through 29dpi (Fig. 5A). IgG responses were evident early infection, but

peak titers were evident at 29dpi, which is a common antibody kinetic response to acute viral infection [ADDIN EN.CITE <EndNote><Cite><Author>Prince</Author><Year>2014</Year><RecNum>124</RecNum><DisplayText>(39)</DisplayText><record><rec-number>124</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1570411486">124</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Prince, H. E.</author><author>Lape-Nixon, M.</author></authors></contributors><auth-address>Focus Diagnostics Reference Laboratory, Cypress, California, USA hprince@focusdx.com.
Focus Diagnostics Reference Laboratory, Cypress, California, USA.</auth-address><titles><title>Role of cytomegalovirus (CMV) IgG avidity testing in diagnosing primary CMV infection during pregnancy</title><secondary-title>Clin Vaccine Immunol</secondary-title></titles><periodical><full-title>Clin Vaccine Immunol</full-title></periodical><pages>1377-84</pages><volume>21</volume><number>10</number><keywords><keyword>Antibodies, Viral/*blood</keyword><keyword>*Antibody Affinity</keyword><keyword>Cytomegalovirus/*immunology</keyword><keyword>Cytomegalovirus Infections/*diagnosis</keyword><keyword>Female</keyword><keyword>Humans</keyword><keyword>Immunoglobulin G/*blood</keyword><keyword>Pregnancy</keyword><keyword>Pregnancy Complications, Infectious/*diagnosis</keyword><keyword>Time Factors</keyword></keywords><dates><year>2014</year><pub-

421 dates><date>Oct</date></pub-dates></dates><isbn>1556-679X (Electronic)
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422 (Linking)</isbn><accession-num>25165026</accession-num><urls><related-
423 urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25165026</url></related-
424 urls></urls><custom2>PMC4266349</custom2><electronic-resource-
425 num>10.1128/CVI.00487-14</electronic-resource-num></record></Cite></EndNote>] (Fig.
426 5B). Sera neutralization titers were determined using Vero cell neutralization assays against
427 MA15, with neutralization reported as the 50% effective concentration of antibody (EC_{50}).
428 Serum antibodies at all timepoints showed a time-dependent neutralization of MA15 (Fig 5C-D).
429 Surprisingly, as early as 7 dpi, convalescent sera was able to efficiently neutralize virus *in vitro*
430 and displayed similar neutralization efficiency to 15 dpi convalescent sera. This early
431 neutralization response may explain the requirement for B cells in MA15 clearance during early
432 MA15 infection.
433
434 **Prophylactic transfer of early antibody protects from MA15 pathogenicity.**
435 In order to determine whether inoculation with 7 dpi convalescent sera can protect
436 against lethal MA15 infection, we again purified sera from MA15-infected B6 mice at 7 dpi.
437 Sera from infected mice was pooled then used to intraperitoneally inoculate 20 week old B6
438 mice prior to receiving a lethal inoculation of MA15 24 hours later (Fig. 6A). We monitored
439 mice for weight loss daily then harvested at 7 dpi or when moribund. Passive transfer of
440 convalescent sera from 7 dpi protected mice following lethal MA15 challenge from severe
441 disease and weight loss (Fig. 6B). These data suggest that early convalescent sera could be used
442 prophylactically to neutralize virus and prevent mortality in coronavirus infection.
443

DISCUSSION

Lethal SARS-CoV infection causes an immune-mediated disease marked by dysregulated innate immune responses, cytokine levels, and T cell responses, which contribute to severe disease and death [ADDIN EN.CITE <EndNote><Cite><Author>Channappanavar</Author><Year>2014</Year><RecNum>30</RecNum><DisplayText>(16)</DisplayText><record><rec-number>30</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501036947">30</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Channappanavar, Rudragouda</author><author>Zhao, Jincun</author><author>Perlman, Stanley</author></authors></contributors><titles><title>T-cell-mediated immune response to respiratory coronaviruses</title><secondary-title>Immunologic research</secondary-title><alt-title>Immunol Res</alt-title></titles><periodical><full-title>Immunologic research</full-title><abbr-1>Immunol Res</abbr-1></periodical><alt-periodical><full-title>Immunologic research</full-title><abbr-1>Immunol Res</abbr-1></alt-periodical><pages>118-128</pages><volume>59</volume><number>0</number><dates><year>2014</year><pub-dates><date>2014/08//</date></pub-dates></dates><isbn>0257-277X</isbn><urls><related-urls><url>http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4125530/</url></related-urls><pdf-urls><url>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4125530/pdf/nihms597563.pdf</url></pdf-urls></urls><electronic-resource-num>10.1007/s12026-014-8534-z</electronic-resource-num><remote-database-provider>PubMed Central</remote-database-provider><access-date>2017/05/07/21:20:57</access-date></record></Cite></EndNote>]. Conversely, survival is associated with activation of virus-specific T cells which contribute to early virus clearance and

diminish clinical disease [ADDIN EN.CITE ADDIN EN.CITE.DATA]. In this study, we extend these studies to show that B cell and antibody responses also play a critical role in disease control and virus clearance during MA15 infection in lethal B6 mouse models. Using a systems based approach, we utilized eigengene modules to predict an important role for B cell responses in protection from lethal disease outcomes, then used a panel of genetically immunodeficient mice and convalescent serum transfer experiments to support the hypothesis that early B cell and antibody responses also play an important role in protection from severe MA15 infection and by contributing to virus clearance.

Our systems biology approach applies robust statistical modeling to large expression datasets in order to discover coordinated expression patterns associated with lethal and sublethal viral infections. This has led to the discovery of key signaling and expression pathways in SARS-CoV pathogenesis and disease [ADDIN EN.CITE ADDIN EN.CITE.DATA]. As in human infections [ADDIN EN.CITE ADDIN EN.CITE.DATA], transcriptomic analysis comparing lethal and non-lethal MA15 infection of the mouse lung revealed that B cell activation and antibody production was impaired in lethal, but not sublethal, infection, suggesting a role for humoral immunity in SARS-CoV pathogenesis and clearance. Additionally, previous studies have shown that while MA15 was cleared from the lungs of wild-type mice within 7 dpi, immunodeficient SCID and *Rag*$^{-/-}$ mice retained high titers of virus in the lung up to three weeks after infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Because SCID and *Rag*$^{-/-}$ mice lack functional lymphocytes, these findings pointed to a critical role for lymphocytes in viral clearance within the first week of infection.

During primary infection, SARS-CoV infects the lung epithelium where dendritic cells are able to sequester viral antigen and migrate to the lymph node in order to activate

lymphocytes through direct antigen presentation, MHC activation, and secondary activation signals [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Consequently, virus-specific T cells act as effectors that activate and recruit subsequent immune cell populations [ADDIN EN.CITE <EndNote><Cite><Author>Channappanavar</Author><Year>2014</Year><RecNum>30</RecNum><DisplayText>(16)</DisplayText><record><rec-number>30</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501036947">30</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Channappanavar, Rudragouda</author><author>Zhao, Jincun</author><author>Perlman, Stanley</author></authors></contributors><titles><title>T-cell-mediated immune response to respiratory coronaviruses</title><secondary-title>Immunologic research</secondary-title><alt-title>Immunol Res</alt-title></titles><periodical><full-title>Immunologic research</full-title><abbr-1>Immunol Res</abbr-1></periodical><alt-periodical><full-title>Immunologic research</full-title><abbr-1>Immunol Res</abbr-1></alt-periodical><pages>118-128</pages><volume>59</volume><number>0</number><dates><year>2014</year><pub-dates><date>2014/08//</date></pub-dates></dates><isbn>0257-277X</isbn><urls><related-urls><url>http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4125530/</url></related-urls><pdf-urls><url>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4125530/pdf/nihms597563.pdf</url></pdf-urls></urls><electronic-resource-num>10.1007/s12026-014-8534-z</electronic-resource-num><remote-database-provider>PubMed Central</remote-database-provider><access-date>2017/05/07/21:20:57</access-date></record></Cite></EndNote>]. Additionally, virus-specific T cells migrate to the site of infection and secrete antiviral cytokines, chemokines, and cytotoxic molecules which lead to inflammation, increased antigen presentation, inhibition of

513 viral replication, and direct killing of virus-infected cells [ADDIN EN.CITE ADDIN
514 EN.CITE.DATA]. Based on current studies, SARS-CoV clearance early after infection is
515 thought to be heavily regulated by T cell activities, as opposed to B cell or antibody-mediated
516 processes. However, Chen et al. determined that depletion of CD4+T cells, but not CD8+T cells,
517 delayed viral clearance and led to a poor virus-specific antibody response in aged Balb/c mice in
518 response to SARS-CoV Urbani infection, suggesting a role for helper T cell activation of B cells
519 and subsequent antibody-aided viral clearance [ADDIN EN.CITE ADDIN EN.CITE.DATA
520].

521 Studies with similar viruses have addressed the question of the role of humoral immunity
522 in viral clearance. Immunocompromised *Rag*$^{-/-}$ mice fail to clear another coronavirus, murine
523 hepatitis virus (MHV-1), instead maintaining high viral titers within the lung for weeks
524 following primary infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Additionally,
525 Chachu et al. determined that *muMT*$^{-/-}$ and HELMET mice did not clear murine norovirus as
526 efficiently as immunocompetent mice due to a lack of virus-specific antibody responses [
527 ADDIN EN.CITE
528 <EndNote><Cite><Author>Chachu</Author><Year>2008</Year><RecNum>100</RecNum><
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532 Article">17</ref-type><contributors><authors><author>Chachu, K.
533 A.</author><author>Strong, D. W.</author><author>LoBue, A. D.</author><author>Wobus,
534 C. E.</author><author>Baric, R. S.</author><author>Virgin, H. W.
535 th</author></authors></contributors><auth-address>Department of Pathology and Immunology,

Washington University School of Medicine, 660 S. Euclid Avenue, St. Louis, MO 63110, USA.</auth-address><titles><title>Antibody is critical for the clearance of murine norovirus infection</title><secondary-title>J Virol</secondary-title></titles><periodical><full-title>J Virol</full-title></periodical><pages>6610-7</pages><volume>82</volume><number>13</number><keywords><keyword>Adoptive Transfer</keyword><keyword>Animals</keyword><keyword>Antibodies, Viral/*immunology</keyword><keyword>B-Lymphocytes/*immunology</keyword><keyword>Caliciviridae Infections/*immunology</keyword><keyword>Cell Line</keyword><keyword>Enzyme-Linked Immunosorbent Assay</keyword><keyword>Gastroenteritis/*immunology/virology</keyword><keyword>Homeodomain Proteins/genetics</keyword><keyword>Mice</keyword><keyword>Mice, Knockout</keyword><keyword>*Norovirus</keyword><keyword>Statistics, Nonparametric</keyword></keywords><dates><year>2008</year><pub-dates><date>Jul</date></pub-dates></dates><isbn>1098-5514 (Electronic)
0022-538X (Linking)</isbn><accession-num>18417579</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/18417579</url></related-urls></urls><custom2>PMC2447077</custom2><electronic-resource-num>10.1128/JVI.00141-08</electronic-resource-num></record></Cite></EndNote>]. Consonant with our findings reported with SARS-CoV, adoptive transfer of polyclonal or monoclonal antibodies against murine norovirus led to viral clearance, suggesting a distinct role for antibody in virus clearance [ADDIN EN.CITE ADDIN EN.CITE.DATA]. In the case of adoptive transfer of virus-neutralizing antibody, various SARS-CoV studies have used exogenous monoclonal SARS-

559 specific IgG to induce sterilizing immunity to primary infection but also to drive virus clearance
560 [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These data demonstrate that virus-specific
561 antibody will protect animals from lethal disease and clear virus after infection
562 Based on a number of elegant studies [ADDIN EN.CITE ADDIN EN.CITE.DATA
563], it is clear that T cell responses play a significant role in SARS-CoV clearance and the control
564 of severe disease outcomes [ADDIN EN.CITE ADDIN EN.CITE.DATA]. In our study,
565 *muMT*$^{-/-}$ mice, lacking mature B cells and membrane-bound IgM, were not able to clear MA15
566 virus. Our *muMT*$^{-/-}$ findings are novel to the current dogma of the field and support a significant
567 role for B cells in MA15 clearance. Consonant with our findings, influenza, a respiratory (-
568)ssRNA virus, is not efficiently cleared from the lungs of *muMT*$^{-/-}$ mice [ADDIN EN.CITE
569 <EndNote><Cite><Author>Topham</Author><Year>1998</Year><RecNum>101</RecNum>
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573 Article">17</ref-type><contributors><authors><author>Topham, D.
574 J.</author><author>Doherty, P. C.</author></authors></contributors><auth-
575 address>Department of Immunology, St. Jude Children's Research Hospital, Memphis,
576 Tennessee 38101-0318, USA.</auth-address><titles><title>Clearance of an influenza A virus by
577 CD4+ T cells is inefficient in the absence of B cells</title><secondary-title>J Virol</secondary-
578 title></titles><periodical><full-title>J Virol</full-title></periodical><pages>882-
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588 dates><date>Jan</date></pub-dates></dates><isbn>0022-538X (Print)
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589 (Linking)</isbn><accession-num>9420305</accession-num><urls><related-
590 urls><url>https://www.ncbi.nlm.nih.gov/pubmed/9420305</url></related-
591 urls></urls><custom2>PMC109454</custom2></record></Cite></EndNote>]. However, MA15
592 failed to be effectively cleared even after 90 dpi, when high viral titers were still present in the
593 lung. These data support the hypothesis that B cell and/or antibody responses are required for
594 MA15 clearance during primary infection. While *muMT*$^{-/-}$ mice lack mature B cells in the B6, but
595 not BALB/c [ADDIN EN.CITE ADDIN EN.CITE.DATA] mouse model, we note that
596 *muMT*$^{-/-}$ mice can also use a different pathway to produce some CD19+/CD0+/IgD+ B1 cells and
597 to produce non-specific IgE and IgG antibodies [ADDIN EN.CITE ADDIN EN.CITE.DATA
598]. However, our data suggest that these cells and activities do not appear to function in MA15
599 clearance.

600 To address the role of T lymphocytes in our MA15 clearance model, we investigated
601 whether mice deficient in virus-specific CD4+T cells (OTII) or CD8+T cells (OTI) showed the
602 same inability to clear virus that was seen in *Rag*$^{-/-}$, SCID, and *muMT*$^{-/-}$ mice. OTI mice, which
603 lack a virus-specific CD8+T cell response, were able to clear virus on the same timescale as B6
604 mice, while OTII mice, which lack a virus-specific CD4+T cell response, demonstrated delayed

viral clearance in the lung. These data corroborate previous findings in which depletions of CD4+T cells and CD8+T cells in senescent Balb/c demonstrated delayed MA15 clearance after infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. One of the primary roles of CD4+T cells during a respiratory viral infection is to help in B cell activation [ADDIN EN.CITE

<EndNote><Cite><Author>Crotty</Author><Year>2015</Year><RecNum>123</RecNum><DisplayText>(35)</DisplayText><record><rec-number>123</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1570409285">123</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Crotty, S.</author></authors></contributors><auth-address>Division of Vaccine Discovery, La Jolla Institute for Allergy and Immunology, 9420 Athena Circle, San Diego, California 92037, USA.</auth-address><titles><title>A brief history of T cell help to B cells</title><secondary-title>Nat Rev Immunol</secondary-title></titles><periodical><full-title>Nat Rev Immunol</full-title></periodical><pages>185-9</pages><volume>15</volume><number>3</number><keywords><keyword>Allergy and Immunology/*history</keyword><keyword>B-Lymphocytes/*immunology</keyword><keyword>History, 20th Century</keyword><keyword>History, 21st Century</keyword><keyword>Humans</keyword><keyword>T-Lymphocytes, Helper-Inducer/*immunology</keyword></keywords><dates><year>2015</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1474-1741 (Electronic)
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urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25677493</url></related-urls></urls><custom2>PMC4414089</custom2><electronic-resource-num>10.1038/nri3803</electronic-resource-num></record></Cite></EndNote>]. After infection, B cells are primed by viral antigen binding the B cell receptor, then activated by CD4+T cells via CD40/CD40L and cytokine signaling [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Activated B cell can then divide and produce antigen-specific antibodies [ADDIN EN.CITE <EndNote><Cite><Author>Nutt</Author><Year>2015</Year><RecNum>127</RecNum><DisplayText>(52)</DisplayText><record><rec-number>127</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1570417570">127</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Nutt, S. L.</author><author>Hodgkin, P. D.</author><author>Tarlinton, D. M.</author><author>Corcoran, L. M.</author></authors></contributors><auth-address>The Walter and Eliza Hall Institute of Medical Research, 1G Royal Parade, Melbourne, Victoria 3052, Australia, and the Department of Medical Biology, University of Melbourne, Victoria 3010, Australia.</auth-address><titles><title>The generation of antibody-secreting plasma cells</title><secondary-title>Nat Rev Immunol</secondary-title></titles><periodical><full-title>Nat Rev Immunol</full-title></periodical><pages>160-71</pages><volume>15</volume><number>3</number><keywords><keyword>Antibodies/*immunology</keyword><keyword>Antibody Formation/immunology</keyword><keyword>B-Lymphocytes/*immunology</keyword><keyword>Cell Differentiation/*immunology</keyword><keyword>Humans</keyword><keyword>Plasma

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655 urls></urls><electronic-resource-num>10.1038/nri3795</electronic-resource-
656 num></record></Cite></EndNote>]. While other cell types are capable of activating B cells,
657 CD4+T cells are primarily responsible for robust B cell activation during the first days of viral
658 infection [ADDIN EN.CITE
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664 S.</author></authors></contributors><auth-address>Division of Vaccine Discovery, La Jolla
665 Institute for Allergy and Immunology, 9420 Athena Circle, San Diego, California 92037,
666 USA.</auth-address><titles><title>A brief history of T cell help to B cells</title><secondary-
667 title>Nat Rev Immunol</secondary-title></titles><periodical><full-title>Nat Rev
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671 Lymphocytes/*immunology</keyword><keyword>History, 20th
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678 urls></urls><custom2>PMC4414089</custom2><electronic-resource-
679 num>10.1038/nri3803</electronic-resource-num></record></Cite></EndNote>]. It is likely that
680 the observed delay of MA15 viral clearance in OTII mice, or CD4+ T cell depleted mice in Chen
681 et. al. [ADDIN EN.CITE ADDIN EN.CITE.DATA], is likely due to impaired B cell
682 activation and therefore delayed or weakened antibody responses. Because HELMET mice
683 eventually clear virus, the data also support the idea that antigen non-specific B cells may play a
684 key role in T cell priming/help and T cell-mediated clearance.

685 Passive immunotherapy approaches are being developed to prevent and treat several
686 human medical conditions where alternative therapeutic options are absent, including MERS-
687 CoV infection [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Our data support previous
688 passive transfer experiments in humans, which have appeared to enhance protection from lethal
689 disease after SARS-CoV infection [ADDIN EN.CITE
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696 Paul K. S.</author><author>Peng, Ming-Yieh</author><author>Wan, Hsiang-

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713 database-provider>academic.oup.com</remote-database-provider><access-
714 date>2017/04/10/05:48:12</access-date></record></Cite></EndNote>]. In support of these
715 findings, we showed that 7 dpi convalescent mouse sera was able to efficiently neutralize MA15
716 in in vitro neutralization assays. Moreover, prophylactic transfer of 7 dpi convalescent sera
717 significantly protected mice in a lethal MA15 challenge. While sera was chosen from patients
718 late after infection and with high antiviral IgG and IgM titers (26), our data suggests that
719 neutralizing sera isolated from convalescent patients much earlier after infection could neutralize

virus in patients, possibly protecting from severe disease and mortality. The ongoing MERS-CoV outbreak and discovery of SARS-like CoVs circulating in bats and other wild animals suggest that recurrence of another coronavirus-mediated disease remains a possibility [ADDIN EN.CITE ADDIN EN.CITE.DATA] and that passive immunotherapy might serve as a rapid response treatment option [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Thus, rapid treatment using sera transfer could be an important factor in suppressing viral replication and mortality in the early days of an outbreak.

Our systems based studies clearly demonstrated significant differences in B cell immunoglobulin gene expression responses following lethal infection in mice. In humans, patients with poor outcomes had poor ISG and immunoglobulin gene expression levels, persistent chemokine levels, and deficient anti-SARS spike antibody production as well [ADDIN EN.CITE ADDIN EN.CITE.DATA], demonstrating concordant outcomes in mouse and human models. SARS-CoV clearance is a complex phenotype both in humans and in mice and appears to be heavily regulated by both T cell function and early induction of neutralizing antibodies. Future studies focusing of the role of B cell activation and antibody secretion in the initial days of viral infection may provide critical new insights into pathogenic mechanisms of emerging coronaviruses, leading to new therapeutic regiments for disease control and public health preparedness.

METHODS

ETHICS STATEMENT AND BIOSAFETY

Mouse studies were carried out in accordance with the recommendations for the care and use of animals by the Office of Laboratory Animal Welfare at the NIH. IACUC at UNC-CH approved the animal studies performed under IACUC protocol 15-155. All virus work was performed in a certified biosafety level 3 (BSL3) laboratory containing redundant exhaust fans while wearing personal protective equipment including HEPA-filtered powered air purifying respirators, Tyvek suits, hoods, and boots; work was additionally confined to a class II biological safety cabinet.

CELL CULTURE AND VIRUS

Recombinant mouse-adapted SARS-CoV (MA15) was generated, passaged once, and titered on Vero E6 cells. For viral titering, the right bottom lobe of each mouse was homogenized then serially diluted to assess plaque forming units (PFU) in Vero E6 cells, with a detection limit of 100 PFU, as previously described by our group [ADDIN EN.CITE <EndNote><Cite><Author>Frieman</Author><Year>2008</Year><RecNum>92</RecNum><DisplayText>(5)</DisplayText><record><rec-number>92</rec-number><foreign-keys><key app="EN" db-id="rd00vaprasew0ce99v5vzr2y050rewr92tzz" timestamp="1501082558">92</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Frieman, M.</author><author>Baric, R.</author></authors></contributors><auth-address>University of North Carolina, 210 McGaveran-Greenberg Hall, CB 7435, Chapel Hill, NC 27599, USA.</auth-address><titles><title>Mechanisms of severe acute respiratory syndrome pathogenesis and

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777 num>10.1128/MMBR.00015-08</electronic-resource-num></record></Cite></EndNote>].
778
779 **ANIMALS AND INFECTIONS**
780 Mice were obtained from the Jackson labs (Bar Harbor, ME), housed and bred in pathogen-free
781 conditions in accordance with guidelines established by the Department of Comparative
782 Medicine at UNC-CH. Strains used include C57BL/6J (B6), *muMT*$^{-/-}$, HELMET (HELMET),
783 *Rag*$^{-/-}$, OTI, and OTII mice. All mice were female. During infection, mice were maintained in
784 SealSafe ventilated caging system in a BSL3 laboratory, equipped with redundant fans as

785 previously described by our group (5). Before viral infection, mice were anesthetized by
786 administering 50 µl ketamine/xylazine mixture intraperitoneally and then infected intranasally
787 with 50 µl virus solution or control PBS. 10-week old mice were used in sublethal models or 20-
788 week old mice in lethal models. Twenty week aged mice were infected with 10^4 PFU MA15, a
789 lethal dose and 10-12-week old mice were infected with 10^5 PFU MA15, a sublethal dose [
790 ADDIN EN.CITE ADDIN EN.CITE.DATA]. Following sedation and infection, mice were
791 monitored daily for weight loss and survival, as well as for signs that the animals were moribund
792 (including labored breathing, lack of movement and lack of grooming). Mice that reached 20%
793 weight loss were placed under exception and monitored at least twice daily. Mice deemed
794 moribund or near 30% weight loss were euthanized at the discretion of the researcher. Mice were
795 euthanized with an isoflurane overdose followed by major organ removal, at various time points,
796 to collect lung tissues. Cervical dislocation was used as a secondary euthanasia method. All are
797 approved methods of the Institutional Animal Care and Use Committee (IACUC) at the UNC-
798 CH.
799
800 **ELISA AND NEUTRALIZATION ASSAYS**
801 ELISA plates were coated in carbonate buffer (0.8ug/mL of SARS-S antigen) overnight and
802 blocked at 4°C, before serum was serially diluted 2-fold 10 times with 3 replicates per sample
803 and added to a 96-well plate. HRP conjugated secondary was used at 1:2000 for 1 hour, then
804 developed in Thermo Scientific Pierce 1-Step Ultra TMB ELISA Substrate then stopped in 0.1M
805 sodium fluoride, and read by plate reader at 450nm.
806

To perform plaque reduction neutralization assays ($PRNT_{50}$) serum was serially diluted 2-fold and incubated with 100 PFU of the MA15 for 1 hour at 37°C. The virus and antibodies were then added to a 6-well plate with 1 $\times 10^5$ Vero E6 cells/well with n=2 replicates per sample. After 1 hour incubation, cells were overlaid with 0.8% agarose in media. Plates were incubated for 48 hours then stained with neutral red for 3 hours, and plaques were counted. The percentage of plaque reduction was calculated as [1 − (no. of plaques with antibody/no. of plaques without antibody)] × 100.

HISTOLOGICAL ANALYSIS AND LUNG SCORING

Lung samples were fixed in 10% phosphate-buffered formalin for >7 days, then moved to new formalin solution at 4°C before removal from BSL3. Fixed samples were them placed in cassettes, rehydrated, and moved to ethanol solution prior to submission to the Lineberger Comprehensive Cancer Center Animal Histopathology Core for processing and sectioning. Histopathology tissue sections were boiled in Tris-EDTA buffer for antigen retrieval, then stained using anti-SARS-S antibody and HRP-conjugated secondary antibody. HRP was developed using DAB (Thermo Scientific Metal Enhanced DAB Substrate Kit), then counterstained. Histopathology was scored, blinded to infection and animal status, for airway disease, vascular disease, parenchymal pneumonia, diffuse alveolar damage, eosinophils and immunohistochemistry on a scale of 0–3 (0, none; 1, mild; 2, moderate; 3, severe). Gross hemorrhage of lung tissue was observed during harvest and scored on a scale of 0 (no hemorrhage in any lobe) to 4 (extreme and complete hemorrhage in all lobes of the lung).

FLOW CYTOMETRY

The left lung of each mouse was used for flow cytometric staining of inflammatory cells. Mouse lungs were perfused with PBS before harvest. Tissue was dissected and digested in RPMI (Gibco) supplemented with DNAse and Collagenase (Roche) in an incubated shaker. Samples were strained using a 70 micron filter (BD) and any residual red blood cells were lysed using ACK lysis buffer, stained, then fixed in 2% formalin solution. Cells were stained in three separate panels using: (1) FITC anti-Ly-6C clone AL21 (BD), PE anti-SigLecF clone E50-2440 (BD), PETR anti-CD11c clone N418 (MP), PerCP anti-B220 clone RA3-6B2 (MP), PE-Cy7 anti-Gr–1 clone RB6-8C5 (eBio), eF450 anti-CD11b clone M1/70 (eBio), APC anti-LCA clone 30-F11 (eBio), APC-eF780 anti-MHC class II clone M5/114 (eBio) or (2) FITC anti-CD94 clone 18d3 (eBio), PE anti-CD3Ɛ clone 145-2C11 (eBio), PETR anti-CD4 clone RM4-5 (MP), PerCP anti-CD8 clone 53–6.7 (BD), PE-Cy7 anti-CD49b clone DX5 (eBio), eF450 anti-LCA clone 30-F11 (eBio), AF647 anti-CD19 clone 6D5 (Biolegend), APC-eF780 anti-B220 clone RA3-6B2 (eBio), (3) BB515 anti-CD19 (BD), APC-R700 CD45R (BD), BV606 anti-IgD (BD), BV421 anti-IgM (BD), PE anti-CD21 (BD), APC anti-CD138 (BD), BV737 anti-CD80 (BD), BV786 anti-CD5 (BD), APC-Cy7 anti-MHCII (BD). Samples were run in the UNC Flow Cytometry Core Facility on a Beckton Dickinson LSR II and analyzed in FlowJo, as previously described by our group [ADDIN EN.CITE ADDIN EN.CITE.DATA].

ADOPTIVE SERUM TRANSFER

Whole blood was harvested from sublethally infected or mock-infected animals at various timepoints after infection and moved to EDTA serum tubes and spun down. Serum was collected, measured for volume, and pooled by harvest date and stored at -80°C. A 1:1 volume

(500uL) of serum was transferred to uninfected mice intraperitoneally one day prior to intranasal infection. Infection and subsequent mouse handling was performed as described above.

GENE ANALYSIS AND NETWORK MODULES

All infection response networks, network modules, and heat maps were generated and analyzed within our previous publication (28).

ACKNOWLEDGMENTS

This work was supported by funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, research grants AI106772 and AI00625 (RSB) and T32 PHS GRANT 5 T32 AI 7419-22. AB is a recipient from NIH training grant T32 AI007419. The UNC Flow Cytometry Core Facility is supported in part by P30 CA016086 Cancer Center Core Support Grant to the UNC Lineberger Comprehensive Cancer Center. Animal histopathology was performed by the Animal Histopathology & Laboratory Medicine Core at the University of North Carolina, which is supported in part by an NCI Center Core Support Grant (5P30CA016086-41) to the UNC Lineberger Comprehensive Cancer Center.

REFERENCES

[ADDIN EN.REFLIST]

873 **FIGURE LEGENDS**

874 **Fig 1. Fig 1. Bioinformatics points to an important role for B cells.** 20 week old C57BL/6J
875 mice were infected intranasally with a 50uL sublethal (10^4 PFU/mouse) or lethal (10^5
876 PFU/mouse) dose of MA15 SARS-CoV diluted in PBS. (A) Survival curves for infected mice.
877 Mice dropping below 70% weight loss were humanely sacrificed and counted as succumbing to
878 disease for the purposes of the experiment. All mice were sacrificed at 7 dpi. n=5 per group. (B)
879 Log_2 fold change ratio of immunoglobulin family-related gene expression from the lungs of
880 MA15 SARS-CoV-infected C57BL/6J mice after infection compared to mock infected mice.
881 Yellow indicates increased gene expression compared to mock. Blue indicates decreased
882 expression compared to mock. Probe and gene descriptions provided in Fig S1.

883 **Fig 2. B cells are required to clear SARS-CoV.** 10 week old C57BL/6J or muMT B cell
884 deficient mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse).
885 n=5/group. (A) Lung mean virus load was quantitated by plaque assay. Statistical significance
886 determined using ANOVA analysis, with **** signifying $p<0.0001$. (B) Representative images
887 of lung sections at indicated timepoints post-infection. SARS-CoV staining was performed via
888 immunohistochemistry using anti-SARS-N and is shown in brown. (C) Mean weight loss per
889 group is represented as a percent of starting weight for each mouse. Mice were weighed daily.
890 (D) Representative images of lung sections at indicated timepoints post-infection. H&E staining
891 is shown. (E) Lung injury scores from mice at indicated times. None show significant differences
892 between C57BL/6J and *muMT* mice at matched timepoints.

893 **Fig 3. B cell and antibody responses do not correlate with pathogenesis.** 20 week old mice
894 were infected intranasally with a lethal (10^5 PFU/mouse) or sublethal (10^3 or 10^4 PFU/mouse)
895 dose of MA15 SARS-CoV. n=5/group. (A) Mean weight loss per group is represented as a

percent of starting weight for each mouse. Weights at each dose significantly differed from each other group at 5, 6, and 7 dpi. (B) Survival curves of infected mice. (C) Mean hemorrhage score of mouse lungs taken during 7 dpi harvest. (E) Mean total B cells as a percent of LCA+ cells. B cells are defined as B220+ and CD20+. (E) Mean SARS-S reactive immunoglobulin levels represented as EC50. (F) Splenic B cell populations after MA15 SARS-CoV infection at mock, sub-lethal, and lethal infection doses in 10 week old C57BL/6J mice – no significant differences were seen in B cell populations. All statistics performed by t test. * $p<0.01$. *** $p<0.0001$. ****$p<0.00001$.

Fig 4. Lack of antigen-specific CD4+T cell responses results in delayed SARS-CoV clearance. 10 week old mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group at 4 and 7 dpi. n=3/group at 15 dpi. (A) Mean weight loss per group is represented as a percent of starting weight for each mouse. Mice were weighed daily. No significant difference between weight groups. (B) Lung mean virus load was quantitated by plaque assay. All statistics performed by t test.

Fig 5. Serum antibodies at 7 days post infection can efficiently neutralize SARS-CoV *in vitro*. 10 week old mice were infected intranasally with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. (A-B) Mean serum IgM (A) and IgG (B) EC50 against SARS-CoV spike protein. n=5 mice/group. (C) SARS-CoV plaque neutralization and (D) hill slopes of neutralization curves were determined by plaque assay using serum taken from MA15 SARS-infected mice at the indicated timepoints.

Fig 6. Prophylactic transfer of early antibody prevents mortality during lethal SARS-CoV infection through viral neutralization *in vivo*. Experimental set up of serum transfer experiments. C57BL/6J mice were infected with SARS-CoV at a sublethal dose and serum was

harvested at the indicated time point after infection. Serum was transferred at a 1:1 ratio i.p. to the experimental mouse, which was infected with a lethal dose of SARS-CoV 24 hours later. Mice were weighed daily and harvested 7dpi. (A) Mean weight loss of mock serum of 7dpi serum transfer to 12 week or 20 week old C57Bl/6J mice. (B) :: shorthand for received. Statistical **significance determined using ANOVA analysis, with **** signifying p<0.0001.**

[ADDIN]

To: Efrem Lim[Efrem.Lim@asu.edu]; Brenda Hogue[bhogue@asu.edu]; Alexandra Lucas[arlucas5@asu.edu]; Matthew Frieman[mfrieman@som.umaryland.edu]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; Ralph Baric[rbaric@email.unc.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]; Mark Denison[mark.denison@vanderbilt.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Kanta Subbarao[Kanta.Subbarao@mh.org.au]; Gallagher, Thomas[tgallag@luc.edu]; Paul S Keim[Paul.Keim@nau.edu]; Janko Nikolich[jnikolich@medadmin.arizona.edu]; Janko Nikolich-Zugich[nikolich@email.arizona.edu]
Cc: Ian Hogue[ihogue@asu.edu]; Erika Arch[earch@asu.edu]; Kathy Spindler[krspin@umich.edu]
From: Grant McFadden[grantmcf@asu.edu]
Sent: Mon 6/1/2020 2:58:50 PM (UTC-05:00)
Subject: FW: COVID seminar series
Viroholics Seminar Series Spring Summer 2020 Friday Revised V11.docx

To all the Speakers in the 2020 ASU Viroholics (COVID-edition) seminar series:

Everyone, I am happy to report that we have come to terms in principle with the American Society for Virology (ASV) for their web site to host the recorded seminars for our COVID-19 seminar series once we are finished our schedule at the end of June.

For those of you who have agreed to have your talks recorded, there is nothing you need do, unless you have any issues with this plan to archive the talks at the ASV.

Other than that, please join us this Friday at 12 noon PT/3pm EST: our speaker will be Kanta Subbarao (Australia), who will need to get up at an ungodly hour in order to present to us at our much-more-godlier hour here in North America.

Grant

Grant McFadden
Director, Center for Immunotherapy, Vaccines, and Virotherapy (B-CIVV)
Biodesign Institute
727 E Tyler Street, Room A330E
Arizona State University
Tempe, AZ, 85287

Ph: 480-727-3388
FAX: 480-965-1844
Cell: 352-672-2263
Email: grantmcf@asu.edu
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From: "krspin@umich.edu" <krspin@umich.edu>
Date: Saturday, May 30, 2020 at 4:57 PM
To: "grantmcf@asu.edu" <grantmcf@asu.edu>
Cc: Erika Arch <earch@asu.edu>, Ian Hogue <ihogue@asu.edu>, American for Virology <asv@asv.org>
Subject: Re: COVID seminar series

Hi Grant,
ASV Exec Committee is fine with this, so we'll just need to work out the details. Will we be actually hosting the videos on our site, or providing a link to them elsewhere (YouTube, etc.)?

Just let us know when you're ready. I've cc'd Andréa (asv@asv.org) too.

Cheers,
Kathy

On May 29, 2020, at 5:40 PM, Grant McFadden <grantmcf@asu.edu> wrote:

Kathy:

Great, I already have written permission from all the speakers (except Ralph), but I would still let them all know we are contemplating this use of their talks if ASV agrees, to make sure there is no miscommunication!

Grant

Grant McFadden
Director, Center for Immunotherapy, Vaccines, and Virotherapy (B-CIVV)
Biodesign Institute
727 E Tyler Street, Room A330E
Arizona State University
Tempe, AZ, 85287

Ph: 480-727-3388
FAX: 480-965-1844
Cell: 352-672-2263
Email: grantmcf@asu.edu
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From: "krspin@umich.edu" <krspin@umich.edu>
Date: Friday, May 29, 2020 at 2:38 PM
To: "grantmcf@asu.edu" <grantmcf@asu.edu>
Cc: Erika Arch <earch@asu.edu>, Ian Hogue <ihogue@asu.edu>
Subject: Re: COVID seminar series

Hi Grant,
It sounds terrific. Let me run it by the Exec committee and see if they agree.

We have a beta version of a new website, which we hope to get up soon - we have to choose the images from those being submitted, and give it one more look, then we're good to go. So we could just design a place for this right from the start.

Do you think you need to get permission from the speakers for us to have it on the website? (Maybe you already did…)

Have a great weekend!
Kathy

> On May 29, 2020, at 4:59 PM, Grant McFadden <grantmcf@asu.edu> wrote:
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> Hi Kathy!
>
> We are heading into the final month of our Viroholics (COVID-19 edition) seminar series featuring some of the top coronavirus experts (see appended list), and I am looking for a public venue to make the series more widely available.
>
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>
> So, my question is this: would ASV be interested in posting this seminar series talks on it's web site, once

we are finished at the end of June?

Not sure if you need President's/Council approval, but I thought I would start by asking you first!

Grant

Grant McFadden
Director, Center for Immunotherapy, Vaccines, and Virotherapy (B-CIVV)
Biodesign Institute
727 E Tyler Street, Room A330E
Arizona State University
Tempe, AZ, 85287

Ph: 480-727-3388
FAX: 480-965-1844
Cell: 352-672-2263
Email: grantmcf@asu.edu
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<Viroholics Seminar Series Spring Summer 2020 Friday Revised V11.docx>

ASU BIODESIGN INSTITUTE
ARIZONA STATE UNIVERSITY

Viroholics 2020 Friday Seminars (COVID19-Edition)

12 noon – 1:00 pm Fridays (Pacific Daylight Time)

Join via Zoom from PC, Mac, Linux, iOS or Android: [HYPERLINK "https://asu.zoom.us/j/244676617"]

March 20 **Efrem Lim PhD**, Assistant Professor, Bodesign Center for Fundamental and Applied Microbiomics; School of Life Sciences at Arizona State University – Title: **"SARS-CoV-2 surveillance at ASU and Arizona"**

27 **Brenda Hogue PhD**, Professor, Biodesign Center for Immunotherapy, Vaccines and Virotherapy; School of Life Sciences at Arizona State University – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/2018lxqsjn20rp1/Brenda%20Hogue%203_27_2020_ASU_Viroholics_COVID19_Edition.mp4?dl=0"]

April 3 **Alexandra Lucas MD**, Professor, Biodesign Virginia D. Piper Center for Personalized Diagnostics at Arizona State University – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/25y4c1z2emymuui/Alexandra%20Lucas%204_3_2020_ASU_Viroholics_COVID19_Edition.mp4?dl=0"]

10 **Matthew Frieman PhD**, Associate Professor, Department of Microbiology and Immunology, University of Maryland School of Medicine – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/ryjrlrs16h17voq/Matthew%20Frieman%204_10_2020_ASU_Viroholi

17 **Darryl Falzarano PhD**, Research Scientist II & Adjunct Professor, Vaccine and Infectious Disease Organization - International Vaccine Centre (VIDO-InterVac), University of Saskatchewan – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/i6vt1mnt0rftozk/Darryl%20Falzarano%204_17_2020_ASU_Viroholi

24 **Vineet Menachery PhD**, Assistant Professor, Department of Microbiology and Immunology, UTMB Health – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/xx6ndiw6v48ifc/Vineet%20Menachery%204_24_2020_ASU_Viroholi

May 1 **Marion Koopmans DVM, PhD,** Head of the Department of Viroscience, Erasmus MC - The Netherlands – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/61chr4d19t3bu0p/Marion%20Koopmans%205_1_2020_ASU_Viroholics_COVID19_Edition.mp4?dl=0"]

8 **Adolfo Garcia-Sastre PhD**, Professor, Department of Microbiology and Director, [HYPERLINK "http://icahn.mssm.edu/research/global-health"] of Icahn School of Medicine at Mount Sinai, New York – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/u5ah8ou9ss0fcgv/Adolfo%20Garcia-

15 **Ralph Baric MD, PhD**, William R. Kenan, Jr. Distinguished Professor, Department of Epidemiology; Professor, Department of Microbiology and Immunology, University of North Carolina, Chapel Hill – Title: **"Epidemic and Pandemic Coronaviruses"** (not recorded)

22 **Stanley Perlman MD, PhD**, Professor of Microbiology and Immunology; Professor of Pediatrics, University of Iowa Health Care, Carver College of Medicine – Link to Presentation: [HYPERLINK "https://www.dropbox.com/s/eiqv21q7hkt1nj5/Stanley%20Perlman%205_22_2020_ASU_Viroholics_COVID19_Edition.mp4?dl=0"]

29 **Mark Denison MD**, Director, Division of Pediatric Infectious Diseases, Department of Pediatrics, Vanderbilt University Medical Center – Title: **"COVID-19: Emergence, Evolution, and Targets for antivirals"**

Biodesign Center for
Immunotherapy, Vaccines and Virotherapy
727 E. Tyler St.
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Password: 7277 (starting June 5, 2020)

June 5 **Kanta Subbarao MBBS, MPH**, Director of the WHO Collaborating Centre for Reference and Research on Influenza, Doherty Institute – Title: **"Vaccines and Immunotherapy for COVID-19: lessons from SARS and other respiratory viruses"**

12 **Tom Gallagher PhD**, Professor of Microbiology and Immunology, Department of Microbiology and Immunology, Loyola University Chicago – Title: TBA

19 **Arizona COVID-19 Genomics Consortium:** Paul Keim PhD (NAU), Jason Ladner PhD (NAU), Brendan Larsen (UA), Crystal Hepp PhD (NAU), and Jolene Bower PhD (TGen) – Title: **"Defining the Pandemic at the State Level: Sequence-Based Epidemiology of the SARS-CoV-2 virus by the Arizona COVID-19 Genomics Union (ACGU)"**

26 **Janko Nikolich-Zugich MD, PhD**, Bowman Professor and Head, Department of Immunology; Co-Director, University of Arizona Center on Aging, University of Arizona College of Medicine, Tucson – Title: TBA

Biodesign Center for
Immunotherapy, Vaccines and Virotherapy
727 E. Tyler St.
PO Box 875401
Tempe, AZ 85287-5401
Ph: 480.727.8322
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biodesign.asu.edu

To: Grant McFadden[grantmcf@asu.edu]; Efrem Lim[Efrem.Lim@asu.edu]; Brenda Hogue[bhogue@asu.edu]; Alexandra Lucas[arlucas5@asu.edu]; Matthew Frieman[mfrieman@som.umaryland.edu]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; Ralph Baric[rbaric@email.unc.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]; Mark Denison[mark.denison@vanderbilt.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Kanta Subbarao[Kanta.Subbarao@mh.org.au]; Gallagher, Thomas[tgallag@luc.edu]; Paul S Keim[Paul.Keim@nau.edu]; Janko Nikolich[jnikolich@medadmin.arizona.edu]; Janko Nikolich-Zugich[nikolich@email.arizona.edu]
Cc: Ian Hogue[ihogue@asu.edu]; Erika Arch[earch@asu.edu]; Kathy Spindler[krspin@umich.edu]
From: M.P.G. Koopmans[m.koopmans@erasmusmc.nl]
Sent: Mon 6/1/2020 3:01:15 PM (UTC-05:00)
Subject: Re: COVID seminar series

Thanks!

From: Grant McFadden <grantmcf@asu.edu>
Sent: Monday, June 1, 2020 9:58:50 PM
To: Efrem Lim <Efrem.Lim@asu.edu>; Brenda Hogue <bhogue@asu.edu>; Alexandra Lucas <arlucas5@asu.edu>; Matthew Frieman <mfrieman@som.umaryland.edu>; Falzarano, Darryl <darryl.falzarano@usask.ca>; Menachery, Vineet <vimenach@utmb.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Adolfo Garcia-Sastre <Adolfo.Garcia-Sastre@mssm.edu>; Ralph Baric <rbaric@email.unc.edu>; Stanley Perlman <stanley-perlman@uiowa.edu>; Mark Denison <mark.denison@vanderbilt.edu>; Subbarao, Kanta <kanta.subbarao@influenzacentre.org>; Kanta Subbarao <Kanta.Subbarao@mh.org.au>; Gallagher, Thomas <tgallag@luc.edu>; Paul S Keim <Paul.Keim@nau.edu>; Janko Nikolich <jnikolich@medadmin.arizona.edu>; Janko Nikolich-Zugich <nikolich@email.arizona.edu>
Cc: Ian Hogue <ihogue@asu.edu>; Erika Arch <earch@asu.edu>; Kathy Spindler <krspin@umich.edu>
Subject: FW: COVID seminar series

To all the Speakers in the 2020 ASU Viroholics (COVID-edition) seminar series:

Everyone, I am happy to report that we have come to terms in principle with the American Society for Virology (ASV) for their web site to host the recorded seminars for our COVID-19 seminar series once we are finished our schedule at the end of June.

For those of you who have agreed to have your talks recorded, there is nothing you need do, unless you have any issues with this plan to archive the talks at the ASV.

Other than that, please join us this Friday at 12 noon PT/3pm EST: our speaker will be Kanta Subbarao (Australia), who will need to get up at an ungodly hour in order to present to us at our much-more-godlier hour here in North America.

Grant

Grant McFadden
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--

From: "krspin@umich.edu" <krspin@umich.edu>
Date: Saturday, May 30, 2020 at 4:57 PM

To: "grantmcf@asu.edu" <grantmcf@asu.edu>
Cc: Erika Arch <earch@asu.edu>, Ian Hogue <ihogue@asu.edu>, American for Virology <asv@asv.org>
Subject: Re: COVID seminar series

Hi Grant,
ASV Exec Committee is fine with this, so we'll just need to work out the details. Will we be actually hosting the videos on our site, or providing a link to them elsewhere (YouTube, etc.)?

Just let us know when you're ready. I've cc'd Andréa (asv@asv.org) too.

Cheers,
Kathy

> On May 29, 2020, at 5:40 PM, Grant McFadden <grantmcf@asu.edu> wrote:
>
> Kathy:
>
> Great, I already have written permission from all the speakers (except Ralph), but I would still let them all know we are contemplating this use of their talks if ASV agrees, to make sure there is no miscommunication!
>
> Grant
>
> Grant McFadden
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> --

From: "krspin@umich.edu" <krspin@umich.edu>
Date: Friday, May 29, 2020 at 2:38 PM
To: "grantmcf@asu.edu" <grantmcf@asu.edu>
Cc: Erika Arch <earch@asu.edu>, Ian Hogue <ihogue@asu.edu>
Subject: Re: COVID seminar series

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<Viroholics Seminar Series Spring Summer 2020 Friday Revised V11.docx>

To: paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Brooke, Christopher Byron[cbrooke@illinois.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Tue 6/2/2020 9:29:00 AM (UTC-05:00)
Subject: RE: SARS-CoV-2 Weekly Investigators Meeting
nCoV PI call attendee list.xlsx

Hi All!

Thank you Dr. Richt for a wonderful presentation and to those who called in. I have attached my attendance tracker for your awareness.

Next week, Drs. Gaur and Hoffman will be presenting their research on testing asymptomatic healthcare workers.

Please reach out to me if you'd like to present during a future call.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

-----Original Appointment-----
From: Lampley, Rebecca (NIH/NIAID) [C]
Sent: Friday, May 15, 2020 11:52 AM
To: paul-mccray@uiowa.edu; Lampley, Rebecca (NIH/NIAID) [C]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Juergen Richt; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana
Cc: Hendricks, Tanya J; Hoffman, James; Brooke, Christopher Byron
Subject: SARS-CoV-2 Weekly Investigators Meeting
When: Tuesday, June 2, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Hi Everyone,

Below you will find the updated meeting link for our weekly investigators call regarding COVID-19.

Our tentative agendas will be:

- COVID-19 research presentation given by PI
- Animal Model updates
- Assay discussion
- Other Needs/Issues
- Call for presenters

ZoomGov Meeting:
https://www.zoomgov.com/j/1609711373?pwd= **552.136**

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Find your local number: https://www.zoomgov.com/u/abZFb1stu0

If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Brooke Bozick	x		x	x	x	x	
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Diana Finzi						x	
Diane Post	x	x	x	x	x	x	
Don Milton						x	
Donna Neu		x	x	x	x	x	
Elizabeth Fitzpatrick						x	
Erica Raterman							
Eunchung Park				x	x	x	
Florian Krammer	x	x	x	x	x	x	

Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabele Phan						
Jae Jung						x
James Kobie		x	x		x	x
Jean Patterson						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Marlene Espinoza		x	x	x	x	x
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter Palese	x	x	x	x	x	x
Punam Mathur	x	x	x	x	x	x

Ralph Baric		x			x	
Randall Tressler						
Reed Johnson	x	x	x	x	x	x
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Ron Fouchier		x		x	x	
Ryan Langlois						x
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Strome						x
Seema Lakdawala						x
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun
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To: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Brooke, Christopher Byron[cbrooke@illinois.edu]
From: Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]
Sent: Wed 6/3/2020 7:24:51 AM (UTC-05:00)
Subject: RE: SARS-CoV-2 Weekly Investigators Meeting
Top 40 Industrial Distributors - USA - CEO and SVP of Sales con.. _.xlsx

Hi Everyone,
Following up from our call yesterday, attached is the list of potential vendors for ordering supplies.

Erik

From: Lampley, Rebecca (NIH/NIAID) [C] <rebecca.lampley@nih.gov>
Sent: Tuesday, June 2, 2020 10:29 AM
To: paul-mccray@uiowa.edu; Leo Poon <llmpoon@hku.hk>; Webby, Richard <Richard.Webby@STJUDE.ORG>; malik

<malik@hku.hk>; Ghazi Kayali <ghazi@human-link.org>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@STJUDE.ORG>; 'david_topham@urmc.rochester.edu'; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>; Baric, Ralph <rbaric@email.unc.edu>; 'Perlman, Stanley' <stanley-perlman@uiowa.edu>; daszak@ecohealthalliance.org; zhu huachen <zhuhch@hku.hk>; Aubree Gordon <gordonal@umich.edu>; Munster, Vincent (NIH/NIAID) [E] <vincent.munster@nih.gov>; PETERPALESE <peter.palese@mssm.edu>; 'Krammer, Florian' <florian.krammer@mssm.edu>; Ben Cowling <bcowling@hku.hk>; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C <antoinette_baric@med.unc.edu>; MASATO HATTA <masato.hatta@wisc.edu>; Gabriele Neumann (gabriele.neumann@wisc.edu) <gabriele.neumann@wisc.edu>; Subbarao, Kanta <kanta.subbarao@influenzacentre.org>; Mathur, Punam (NIH/NIAID) [E] <mathurpu@niaid.nih.gov>; jmclellan@austin.utexas.edu; Mark Denison <mark.denison@vumc.org>; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E] <johnsonreed@niaid.nih.gov>; Hensley, Lisa (NIH/NIAID) [E] <lisa.hensley@nih.gov>; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E] <kstemple@niaid.nih.gov>; Sutton, Troy Clavell <tcs38@psu.edu>; marlene.espinozamoraga@mssm.edu; Simon, Viviana <viviana.simon@mssm.edu>; Van bakel, Harm <harm.vanbakel@mssm.edu>; McKenzie, Pamela <Pamela.McKenzie@STJUDE.ORG>; Deckhut, Alison (NIH/NIAID) [E] <augustine@niaid.nih.gov>; Donald K. Milton <dmilton@umd.edu>; Hensley, Scott <hensley@pennmedicine.upenn.edu>; Degrace, Marciela (NIH/NIAID) [E] <marciela.degrace@nih.gov>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Fry, Alicia (CDC/DDID/NCIRD/ID) <agf1@CDC.GOV>; Pallansch, Mark A. (CDC/DDID/NCIRD/OD) <map1@CDC.GOV>; Hall, Aron (CDC/DDID/NCIRD/DVD) <esg3@CDC.GOV>; Post, Diane (NIH/NIAID) [E] <postd@niaid.nih.gov>; Embry, Alan (NIH/NIAID) [E] <embrya@niaid.nih.gov>; Andy Pekosz <apekosz1@jhu.edu>; Topham, David <David_Topham@URMC.Rochester.edu>; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED) <bhx1@cdc.gov>; zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E] <brooke.bozick@nih.gov>; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E] <connie.schmaljohn@nih.gov>; Wentworth, David E. (CDC/DDID/NCIRD/ID) <gll9@cdc.gov>; Russell, Charles <Charles.Russell@STJUDE.ORG>; Cooper, Michael (NIH/NIAID) [E] <michael.cooper3@nih.gov>; Weiss, Susan <weisssr@pennmedicine.upenn.edu>; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina <weina.sun@mssm.edu>; Roberts, Chris (NIH/NIAID) [E] <paul.roberts@nih.gov>; Stephen M Tompkins <smt@uga.edu>; Uccellini, Melissa <melissa.uccellini@mssm.edu>; Thomas, Paul <Paul.Thomas@STJUDE.ORG>; B.H.G. Rockx <b.rockx@erasmusmc.nl>; Michael Chan <mchan@hku.hk>; S. Herfst <s.herfst@erasmusmc.nl>; Lane, Chelsea (NIH/NIAID) [E] <mary.lane@nih.gov>; Park, Eun-Chung (NIH/NIAID) [E] <epark@niaid.nih.gov>; Crozier, Ian (NIH) [C] <ian.crozier@nih.gov>; Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; andrea_sant@urmc.rochester.edu; Ellebedy, Ali <ellebedy@wustl.edu>; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E] <readsa@niaid.nih.gov>; Finzi, Diana (NIH/NIAID) [E] <dfinzi@niaid.nih.gov>; Turpin, Jim (NIH/NIAID) [E] <jturpin@niaid.nih.gov>; jae jung (jaeujung@med.usc.edu) <jaeujung@med.usc.edu>; SAMANTHA LOEBER <sloeber@wisc.edu>; Cherry, Sara <cherrys@pennmedicine.upenn.edu>; akuki@trudeauinstitute.org; Hui-Ling Yen <hyen@hku.hk>; Andrew Mesecar <amesecar@purdue.edu>; Jonsson, Colleen Beth <cjonsson@uthsc.edu>; Strome, Scott Eric <sstrome@uthsc.edu>; Fitzpatrick, Elizabeth A <efitzpat@uthsc.edu>; Ryan Langlois <langlois@umn.edu>; Seema Lakdawala <seemal@pitt.edu>; amesecar@gmail.com; Runstadler, Jonathan A. <Jonathan.Runstadler@tufts.edu>; Pruijssers, Ardina <ardina.pruijssers@vumc.org>; David.Renner@pennmedicine.upenn.edu; Fremont, Daved <fremont@wustl.edu>; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L. <anne.piantadosi@emory.edu>; Richt, Juergen <jricht@vet.k-state.edu>; Khurana, Surender (FDA/CBER) <Surender.Khurana@fda.hhs.gov>; Neu, Donna <Donna_Neu@URMC.Rochester.edu>; Golding, Hana (FDA/CBER) <Hana.Golding@fda.hhs.gov>

Cc: Hendricks, Tanya J <thendr19@uthsc.edu>; Hoffman, James <James.Hoffman@STJUDE.ORG>; Brooke, Christopher Byron <cbrooke@illinois.edu>

Subject: RE: SARS-CoV-2 Weekly Investigators Meeting

Hi All!

Thank you Dr. Richt for a wonderful presentation and to those who called in. I have attached my attendance tracker for your awareness.

Next week, Drs. Gaur and Hoffman will be presenting their research on testing asymptomatic healthcare workers.

Please reach out to me if you'd like to present during a future call.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

-----Original Appointment-----
From: Lampley, Rebecca (NIH/NIAID) [C]
Sent: Friday, May 15, 2020 11:52 AM
To: paul-mccray@uiowa.edu; Lampley, Rebecca (NIH/NIAID) [C]; Leo Poon; Webby, Richard; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Schultz-Cherry, Stacey; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; 'Krammer, Florian'; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; aneesh.mehta@emory.edu; Baric, Toni C; MASATO HATTA; Gabriele Neumann (gabriele.neumann@wisc.edu); Subbarao, Kanta; Mathur, Punam (NIH/NIAID) [E]; jmclellan@austin.utexas.edu; Mark Denison; MFrieman@som.umaryland.edu; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); zhuhuachen@gmail.com; Bozick, Brooke (NIH/OD) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Russell, Charles; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; Stephen M Tompkins; Uccellini, Melissa; Thomas, Paul; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); andrea_sant@urmc.rochester.edu; Ellebedy, Ali; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Juergen Richt; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana
Cc: Hendricks, Tanya J; Hoffman, James; Brooke, Christopher Byron
Subject: SARS-CoV-2 Weekly Investigators Meeting
When: Tuesday, June 2, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom; https://www.zoomgov.com/j/1609711373?pwd=MkhZdGN4UzhHT2s5VndqWTFBc2J0QT09

Hi Everyone,

Below you will find the updated meeting link for our weekly investigators call regarding COVID-19.

Our tentative agendas will be:

- COVID-19 research presentation given by PI
- Animal Model updates
- Assay discussion
- Other Needs/Issues
- Call for presenters

ZoomGov Meeting:
https://www.zoomgov.com/j/1609711373?pwd=552.136

Meeting ID: 160 971 1373
Password: 552.136

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Contact information obtained from public sources

ID	Industrial distributors	City
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6	Rexel	Paris
7	Wesco International	Greater Pittsburgh
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9	MSC Industrial Supply	Greater New York
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Deidre Cheeks	Vice President		
-	-		-
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Kelly Pelling	Director of Sales	630-833-0300	kelly.pelling@mcmaster.com
Edward Martin	SVP - Sales and	800-645-7270	martine@mscdirect.com
Will Lutz	SVP Sales	800-932-3746	-
Tom Armold	VP of Sales	877-279-2799	tarnold@applied.com
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Ron Stark	SVP, Sales and	855-625-5285	RON.STARK@AIRGAS.COM
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Michael G.	VP Sales	937-294-533	-
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Blades Bob	V. P. Sales	305-714-4100	bbob@watsco.com
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Keith Hanrahan	Purchasing/Count	214-343-1888	Khanrahan@hajoca.com
Chuch Fiorino	Director of	781-272-6600	chuck.fiorino@fwwebb.com
-	-	-	-
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Chris Moore	Director of Sales	1-818-686-9111	cmoore@rshughes.com
Jay Gilbert	Vice President,	1-214-358-5500	jay.gilbert@purvisindustries.com
Arnaud Le	Director, Sales &	1-919-838-4200	achatelier@dillonsupply.com

Charles T.	Chief Sales Officer	1-614-219-6100	charles.McCurdy@kimballmidwest.com

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Sources
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To: Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]
Cc: Hijano, Diego[Diego.Hijano@STJUDE.ORG]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Tue 6/9/2020 2:36:03 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting
nCoV PI call attendee list.xlsx

Hi!

Thank you all for attending this week's SARS-CoV-2 Investigators meeting and to Drs. Gaur and Hoffman from St. Jude for their

wonderful presentation.

Next week, we will have two presenters:

Laura Hughes, PhD (Scripps) – 10 minutes with Q and A
Efficiently collecting, sharing, and integrating COVID-19 data is critical to scientific research. Outbreak.info aggregates COVID-19 epidemiology, data, and resources into a single location.

And

Wes Van Voorhis, MD PhD and Isabelle Phan, 35 minutes with Q and A
Two topics:
1) a prediction method for sensitive and specific diagnostic epitopes for SARS-CoV-2 antibody detection and their validation in the ELISA format; and,
2) Compound screening of repurposing libraries of SARS-CoV-2 biochemical targets, nsp15 (endonuclease), nsp16/nsp10 (2'-O-Me-transferase), and nsp14 (Guanine-N7-Me-transferase).

Thank you,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Brooke Bozick	x		x	x	x	x	
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Diana Finzi						x	
Diane Post	x	x	x	x	x	x	
Diego Hijano							
Don Milton						x	
Donna Neu		x	x	x	x	x	
Elizabeth Fitzpatrick						x	

Erica Raterman						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jean Patterson						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 6/10/2020 1:49:11 PM (UTC-05:00)
Subject: SIG U19 conference call new instructions

Hi Everyone,
I am replacing our old monthly invitation with the details below. We will be having a call tomorrow, but it will be a short one.

https://zoom.us/j/91792514323?pwd= **552.136**
Meeting ID: 917 9251 4323
Password: **552.136**
One tap mobile
+19292056099,,91792514323#,,1# # US (New York)
+13017158592,,91792514323#,,1# **552.136** # US (Germantown)

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Ralph S[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Anne Beall[anne.beall@gmail.com]
Sent: Tue 1/7/2020 3:15:23 PM (UTC-06:00)
Subject: article - "Characteristics of Microbes Most Likely to Cause Pandemics and Global Catastrophes"
Adalja2019_Chapter_CharacteristicsOfMicrobesMostL.pdf

Happy New Year!
I hope that you are both doing well.
I just wanted to send along this article in case you hadn't already seen it - "Characteristics of Microbes Most Likely to Cause Pandemics and Global Catastrophes." It is attached. It specifically references coronaviruses, and I thought it might be useful as a citation in papers or grants.

Best Wishes,
Anne

Characteristics of Microbes Most Likely to Cause Pandemics and Global Catastrophes

Amesh A. Adalja, Matthew Watson, Eric S. Toner, Anita Cicero and Thomas V. Inglesby

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A. A. Adalja (✉) · M. Watson · E. S. Toner · A. Cicero · T. V. Inglesby
Johns Hopkins Center for Health Security, 621 E. Pratt Street Suite 201, Baltimore, MD 21202, USA
e-mail: aadalja1@jhu.edu

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Abstract Predicting which pathogen will confer the highest global catastrophic biological risk (GCBR) of a pandemic is a difficult task. Many approaches are retrospective and premised on prior pandemics; however, such an approach may fail to appreciate novel threats that do not have exact historical precedent. In this paper, based on a study and project we undertook, a new paradigm for pandemic preparedness is presented. This paradigm seeks to root pandemic risk in actual attributes possessed by specific classes of microbial organisms and leads to specific recommendations to augment preparedness activities.

1 Introduction

The recent global experience with severe infectious disease epidemics has triggered much interest in understanding the broader pandemic threat landscape. A substantial proportion of pandemic and biological threat preparedness activities have focused on list-based approaches that were in part based on pandemic influenzas of the past, historical biological weapon development programs, or recent outbreaks of emerging infectious diseases (e.g., SARS, MERS, Ebola) (Centers for Disease Control and Prevention 2017; Casadevall and Relman 2010). But such an approach inherently fails to account for agents not currently known or those without historical precedent. For that reason, preparedness activities that are limited to these approaches may hamper preparedness and lessen resilience.

The purpose of this study was to analyze the characteristics of pathogens that could be capable of causing a global catastrophic biological risk (GCBR). These would be events in which biological agents—whether naturally emerging or reemerging, deliberately created and released, or laboratory engineered and escaped—could lead to sudden, extraordinary, widespread disaster beyond the collective capability of national and international governments and the private sector to control. If unchecked, GCBRs would lead to great suffering, loss of life, and sustained damage to national governments, international relationships, economies, societal stability, or global security (Schoch-Spana et al. 2017).

Given the severe potential public health consequences of pandemic events, there needs to be a vital interest in developing and maintaining a flexible, rapid, and robust

response capability. Anticipating the forms of microbial threats that might cause future pandemics can help strengthen preparedness and response capacities. This paper proposes a framework for considering future pandemic threats and provides recommendations for how this framework should inform pandemic preparedness.

2 Methodology

Review of the published literature and previous reports: The project team surveyed the current biomedical literature on the topic of emerging infectious disease characteristics, the pathogenic potential of microbes, and related topics. The literature review was microbe- and species-agnostic, encompassing all classes of microorganisms and host species. The literature review was accomplished with extensive PubMed searches on these subjects. Relevant US government policy and strategy were reviewed.

Interviews: The project team interviewed more than 120 technical experts who work in and are intimately knowledgeable about this field. Interviewees were drawn from academia, industry, and government. Our goal was to ascertain the experts' views about the essential traits needed for a pathogen to become a GCBR, to contextualize historical outbreaks in light of these traits, and to determine which currently known infectious disease agents possess such characteristics.

Pandemic Pathogen Meeting: The project team completed a preliminary analysis that synthesized the results of our literature review and expert interviews. Those findings were used to design and facilitate a meeting held on November 9, 2017, that included many of those who had been interviewed for this project. The meeting was held at the Johns Hopkins Center for Health Security in Baltimore, MD. The purpose of the meeting was to gain additional insight and input into the project analysis, examine assumptions, and test possible recommendations. Participants included representatives of US and foreign academic institutions, the federal government, and other independent subject matter experts.

This paper is based on the findings of the project and is modification of the project report (Johns Hopkins Center for Health Security 2018).

3 Findings

3.1 Specific Microbial Characteristics Are Probably the Most Important Factors Regarding Global Catastrophic Biological Risks

3.1.1 The Alchemy of a Pandemic Pathogen

When a pathogen has the capacity to cause a pandemic, it will possess several attributes that other microbes, capable of causing only sporadic or limited human infections, will lack. These traits can be divided into several categories: spread via respiratory transmission; capable of spread during incubation period prior to symptom onset; no preexisting host immunity; and other possible intrinsic microbial characteristics. Many of these characteristics have been captured and are reflected, in equation form, by Casadevall (Casadevall 2017).

3.1.2 Modes of Transmission

Microbes have varied routes of transmission, ranging from blood and body fluids to vector-borne to fecal–oral to respiratory (airborne and respiratory droplet). While each mode of transmission is capable of causing large outbreaks if sustained human-to-human transmission is possible and left unchecked, certain modes of transmission are more amenable than others to intervention. For example, the transmission of an infectious disease caused by blood and body fluid transmission can be halted with infection control measures such as gloves or gowns.

Of the various modes of transmission, the respiratory route is the mechanism most likely to lead to pandemic spread. This is chiefly due to the fact that interventions to interrupt this method of spread are more difficult to implement when the simple and universal act of breathing can spread a pathogen. The prolific spread of influenza, pertussis, measles, and rhinoviruses is testament to this fact (Herfst et al. 2017).

By contrast, although pathogens spread by the fecal–oral route, such as *Vibrio cholera* and the hepatitis A virus, can generate explosive outbreaks, even a modicum of sanitary infrastructure can quench the outbreak.

Vector-borne outbreaks are a special case of a non-respiratory-spread agent. Indeed, the only postulated extinction of a mammalian species by an infectious organism, the Christmas Island rat, was caused by a vector-borne trypanosome (Wyatt et al. 2008). For most of the agents that use this class of transmission, the spread is limited by a geographically and climatologically restricted vector habitat. Humans can protect against vectors, and they can change where they live, but the Christmas Island rat could not. These factors have generally served to limit the pandemic potential of microbes that are spread by vectors.

Exceptions to this general limitation of vector-borne viruses include microbes spread by *Anopheles* and *Aedes* mosquitoes. Pathogens spread by these mosquitoes

have higher pandemic potential, given the geographic breadth of their spread. For example, most of sub-Saharan Africa is hospitable to the malaria-transmitting *Anopheles* mosquitoes, while residents in 75% of US counties—as well as half the world's population—are regularly exposed to *Aedes* mosquitoes that serve as vectors for high viremia flaviviruses and alphaviruses. Such phenomena are borne out by the prolific spread of dengue, chikungunya, and Zika (Sinka et al. 2012; Centers for Disease Control and Prevention 2017).

3.1.3 Timing of Transmission

The onset and duration of the period when a person is contagious during an infection also play a major role in spread. Diseases that are contagious during a late stage of infection, when infected people are very sick and therefore have more limited opportunities for spread, may be delimited in their spread. On the other hand, diseases that are contagious prior to symptom development, during the incubation period, or when only mild symptoms are present have greater opportunities for spread as infected individuals are able to conduct their activities of daily living with little or no interruption.

Modeling studies with simulated outbreaks have shown that the presence or absence of this timing of transmission factor can be decisive in whether an outbreak can or cannot be controlled. If a microbe is contagious before a person is seriously ill while the disease is still incubating, then there is higher potential for pandemic spread. Historical examples reinforce this idea, as the only human infectious disease to be vanquished from the planet—smallpox—was one that was not contagious during the incubation period (Fraser et al. 2004). By contrast, a microbe such as the influenza virus, which is contagious prior to symptom development and has a wide range of clinical severity, is able to infect widely and is not amenable to control (Brankston et al. 2007).

3.1.4 Host Population Factors and Intrinsic Microbial Pathogenicity Characteristics

Microbial pathogenicity cannot, in reality, be separated from host characteristics. As elucidated by Pirofsky and Casadevall's host damage framework, disease is a complex interplay between a host immune system and a microbe (Pirofski and Casadevall 2008). In congruity with this paradigm, host features and microbial pathogenicity are discussed together.

For a microbe to cause a GCBR-level pandemic, it will be necessary for a significant proportion of the human population to be immunologically naïve to the agent so that the microbe would have a high number of susceptible humans to infect. Additionally, large quantities of a sufficiently effective countermeasure (vaccine or antimicrobial agent) would not be available. Immunologic naïveté would be expected with a zoonotic pathogen. The microbe, correspondingly, would

have to possess the ability to evade the host immune response through virulence factors, immunological camouflage, or other features that allow a productive infection to ensue.

Additionally, human receptors that are utilized by a pandemic-causing microbe would likely be widespread in the population, facilitating permissive infection in the majority of humans. Receptors may also provide target organ tropism for the agent, allowing severe disease to occur (e.g., lower respiratory tract and central nervous system).

Case fatality rates (CFRs) need not be inordinately high to cause a GCBR-level event, as evidenced by the 2.5% CFR reported for the 1918 influenza pandemic—the event closest to an actual human GCBR in the modern era (Taubenberger and Morens 2006). A low but significant CFR adheres to the host density threshold theorem. According to this commonly held theorem, a microbe that kills too many of its hosts will run out of susceptible hosts and be extinguished (Cressler et al. 2016). While this may be true of pathogens that are closely linked to one host species, it is not applicable to sapronotic diseases such as amebic encephalitis and cholera (in certain contexts), which can infect and kill without jeopardizing future transmission or survival. Indeed, many extinction-level amphibian infectious diseases are sapronotic in nature, such as the chytrid disease of salamanders and frogs (Fisher 2017).

Additionally, a GCBR-level event may not confer direct mortality. Reproductive effects (i.e., in the manner of rubella or Zika) or carcinogenic effects (e.g., HTLV-1) could, in many ways, be highly detrimental to the future of humanity, as they could lead to significant curtailment of lifespans and diminishing birth rates, which could ultimately result in significant population collapse (Rasmussen et al. 2017; Tagaya and Gallo 2017).

3.2 *RNA Viruses Are the Class of Microbe that Could Cause a GCBR, Though Other Microbial Classes Could Evolve or Be Engineered in Ways that Pose These Risks*

Given the right context, any microbial organism could evolve or be engineered to be a GCBR. However, the most likely cause of a GCBR presently is a virus, with RNA viruses being the most probable (Woolhouse et al. 2013).

3.3 *Bacteria: Broad-Spectrum Antimicrobials Limit Pandemic Potential of Pathogens*

Historically, bacterially caused infections such as plague have had incredible impacts on the human species (Raoult et al. 2013). However, the development of antibacterial therapies, beginning with the sulfonamides in 1935 and then penicillin

in 1942, has severely limited the ability of this class of microbes to cause a GCBR-level pandemic. In addition, the relatively slower speed of replication and accumulation of mutations also disadvantages this class over viruses. For example, a human infected with the hepatitis C virus (an RNA virus) produces trillions of virions per day, whereas the doubling time of *Yersinia pestis*, the cause of plague, is 1.25 h (Neumann et al. 1998; Deng et al. 2002).

The public health crisis of multiple-drug-resistant bacteria, such as carbapenem-resistant enterobacteriaceae (CRE) and others, is very alarming (Logan and Weinstein 2017). The spread of these bacterial agents, for which few if any treatments exist, threatens the entire practice of modern medicine, from cancer chemotherapy to joint replacement therapy. However, these organisms, which have variable attributable mortality, tend to be unable to efficiently infect human hosts that are not compromised or hospitalized. As such, the risk to the general public is constrained.

Large outbreaks of cholera and plague have represented true public health emergencies in Yemen and Madagascar, but their spread reflects severe infrastructure deficiencies caused by war and supply constraints rather than true global pandemic risk (Qadri et al. 2017; Roberts 2017).

3.3.1 Fungi: Thermal Growth Restriction Limits Pandemic Potential

Fungi represent prolific pathogens outside of the mammalian species. Outbreaks of chytrid fungal disease in frogs and salamanders as well as snake fungal disease represent true existential threats to affected species (Fisher 2017). However, fungi are largely thermally restricted, and only limited members of this class of microbes can infect warm-blooded organisms such as mammals (Casadevall 2012). Indeed, a fungal filter is hypothesized to have existed and may be partly responsible for mammalian warm-bloodedness. The success of the mammalian-adapted fungus that causes white-nose syndrome in bats is facilitated by the lower body temperature that occurs during their hibernation (Foley et al. 2011).

Human infections with fungi tend to be severely damaging only in an immunocompromised host. The human innate immune system contends with countless fungal spores that are present in every breath of air. As such, many endemic fungal diseases, such as histoplasmosis or coccidioidomycosis, do not cause harm in the majority of immunocompetent humans infected. Even newly emerging fungi such as *Candida auris* and *Cryptococcus gattii* are largely subjected to this limitation (Chowdhary et al. 2017; Centers for Disease Control and Prevention 2010). One of the most widespread fungal outbreaks—the *Exserohilum* fungal meningitis outbreak—was abetted by direct injection of a contaminated medical product into the spinal region of humans, which is not a usual mechanism of infection (Casadevall and Pirofski 2013).

Without thermal adaptation (which might be feasible with deliberate manipulation), fungi, many of which are sapronotic and do not rely on or need mammalian hosts, will not constitute a pandemic threat to humans.

3.3.2 Prions: Select Transmission Characteristics Limit Pandemic Potential

Prions—transmissible infective proteins—are one of the most fascinating and understudied of infectious agents. These agents, which are responsible for diseases such as kuru and new variant Creutzfeldt-Jakob disease (vCJD, the human form of "mad cow disease") in humans, cause scrapie, chronic wasting disease, and bovine spongiform encephalopathy in other mammalian species (Chen and Dong 2016).

Though highly damaging to humans and other species they infect, prions require specific conditions for spread. New variant Creutzfeldt-Jakob disease was to date the most highly publicized outbreak of a human prion disease; it resulted in 229 human cases tied to the consumption of beef products primarily in England in the 1990s and the 2000s (Hilton 2006). Other modes of transmission of CJD tied to iatrogenic spread via contaminated surgical instruments or cadaveric hormone products ceased once protective measures were put in place (Bonda et al. 2016). Kuru, a geographically restricted prion disease, was spread via human cannibalism in Papua New Guinea, and the outbreak abated once that practice was ended in the 1960s (Liberski et al. 2012).

The transmission characteristics of prion diseases are such that very extraordinary circumstances, on a par with human cannibalism or massive food contamination, must be present for a GCBR-level risk to be present for humans. Additionally, and almost by definition, such an event would be slow-moving (prions were once known as "slow viruses").

3.3.3 Protozoa: Limited Pandemic Pathogen

Protozoal organisms have the distinction of being the only infectious disease to have caused the extinction of a mammalian species. The Christmas Island rat, unable to outrun its vector, was felled by a vector-borne trypanosome (*T. lewisi*) during the early twentieth century on the Australian island (Wyatt et al. 2008). Human forms of trypanosomiasis have not risen to such a level of concern.

Human protozoal infections have exerted tremendous pressure on the species, and it is hypothesized that half of all humans who have lived died of malaria, which still kills approximately half a million humans annually (World Health Organization 2017). However, the development of antimalarial compounds and vector avoidance strategies has proved successful when they are able to be employed appropriately, and they have relegated malaria to a pathogen whose impact is amenable to control. Nonetheless, one aspect of malaria is of particular concern: the development and spread of artemisinin-resistant forms, which render treatment extremely challenging with little to no effective antimalarial agents left for use. Largely confined to specific regions of Asia, such as Cambodia and Myanmar, this organism poses severe treatment challenges and, if artemisinin-resistant forms were to spread to Africa, could represent a continent-wide catastrophic biologic risk (Haldar et al. 2018).

3.3.4 Other Microbial Classes with Limited Pandemic Risk

Ameba, ectoparasites, and helminths all have limited pandemic risk, as they are constrained by pathogenicity, transmissibility, or both. Clonally transmissible tumors—such as the notable devil facial tumor disease in Tasmanian devils—are rare occurrences in humans, with restricted modes of transmission (maternal–fetal and organ transplantation).

Space-adapted organisms (e.g., salmonella that originates on Earth but spends time in the space station before coming back to earth) can exhibit enhanced virulence; however, they still are susceptible to antibiotic treatment and normal control measures: There is no evidence they pose greater epidemic risk than normal salmonella (Wilson et al. 2007). An alien microbe species that is obtained on Mars or meteorites and brought back to earth, one of the focuses of the planetary protection program at the National Aeronautics and Space Administration (NASA), was not deemed by our interviewees and meeting participants to be likely to pose a threat. And if such a species were found, it would be unlikely to be adaptable to an Earthlike planet environment, as adaptations to its home planet's markedly different environments would likely preclude adaptations to Earth. Even though the chances of serious biological risk posed by such a sample return are deemed to be low, there are many uncertainties, and the highest level biocontainment procedures are being considered for specimens that might harbor such non-Earth-based organisms (National Research Council 2009).

3.3.5 Viruses: Several Factors Contribute to Heightened Pandemic Risk

Traditionally, viruses have been ranked at the highest level of pandemic risk, and dedicated preparedness efforts often focus solely on viruses. A disproportionate focus on viruses is justified, however, based on several aspects unique to the viral class of microbes.

The high rate of replication of viruses—for instance, over 1 trillion hepatitis C virions are produced per day in a human infection—coupled with the mutability inherent in such short generation times gives viruses an unrivaled plasticity. This plasticity allows for host adaptability, zoonotic spillover, and immune system evasion.

The lack of a broad-spectrum antiviral agent—like ones available for bacterial and even fungal organisms—also confers a special status on viruses. With no off-the-shelf treatment available to contain a viral outbreak, and likely no vaccine, containment efforts, at least in the early stages, will likely need to be made in the absence of a medical countermeasure (Zhu et al. 2015).

There is a strong consensus that RNA viruses represent a higher pandemic threat than DNA viruses (Kreuder Johnson et al. 2015). This assessment is derived from the fact that the stability of RNA as a genomic material is less than that of DNA, giving more genomic pliability to the RNA viruses. DNA viruses such as smallpox

do challenge this assumption, and concern exists surrounding the related risks of monkeypox viruses, which are increasingly spreading in the absence of a smallpox vaccine campaign (Kantele et al. 2016). As monkeypox outbreaks continue to occur with longer chains of transmission, employing smallpox vaccines in target populations might be considered.

Another aspect of viral characterization is the location of replication. Viruses with greater capacity for widespread have been shown in studies to be more likely to replicate in the cytoplasm of a cell (Pulliam and Dushoff 2009; Olival et al. 2017). This is postulated to be due to the higher affinity a virus must have for a particular type of host in order to be permitted entry into its nucleus, and this greater affinity would limit its zoonotic potential because it would be likely to be strongly tied to its usual host. In general, it is DNA viruses that tend to have a nuclear replication cycle, while RNA viruses have a cytoplasmic cycle. Strikingly, smallpox—a DNA virus with proven ability to cause pandemics—is a cytoplasmic replicator, while influenza—an RNA virus with proven ability to cause pandemics—has a nuclear replication cycle. The exceptions to these rules argue against any overly strict adherence to them.

Other factors that may increase a virus' potential to cause a global catastrophic risk include a segmented genome (as exemplified by influenza viruses), a comparatively smaller genome size, and high host viremia (e.g., vector-borne flaviviruses). For example, the flu virus' segmented genome makes novel genetic assortment an eventuality, while a large genome may prevent nimble mutations. However, with each characteristic it is impossible to find a general rule, as exceptions abound.

Among currently studied viruses, the influenza A viruses are widely judged to pose the greatest pandemic risk based on historical outbreaks and viral characteristics (Silva et al. 2017; Imai et al. 2017). Analysis of influenza risks is made in the Centers for Disease Control and Prevention (CDC)'s Influenza Rapid Assessment Tool (IRAT) which ranks H7N9 as the most concerning influenza virus strain (Centers for Disease Control and Prevention 2017).

There are several viral groups other than the orthomyxoviruses (which include the H7N9 strain of influenza A) that are spread by respiratory routes, possess RNA genomes, and merit enhanced attention: paramyxoviruses (especially these three genera: respirovirus, henipavirus, and rubulavirus), pneumoviruses, coronaviruses, and picornaviruses (especially these two genera: enterovirus and rhinovirus). Based on our analysis and their inherent characteristics, these viral groups are the most likely source of a GCBR-level threat.

3.4 *Viral Catalogs Are Scientifically Valuable but Are not Themselves Able to Predict the Next Pandemic*

There are efforts under way to construct viral catalogs of as many viruses as possible. The explicit aim of these projects is to reduce the uncertainty of outbreaks by extensively cataloging as many viral species as possible, so that a virus that causes a disease is less likely to be truly unknown. At the meeting and interviews for this project, a number of experts expressed concern that, while efforts to catalog and broadly sequence viruses in the animal world would provide new scientific discovery, we should not expect that it will identify the source of the next pandemic or that it can change the work being done for pandemic preparedness. Broad viral sequencing would uncover many novel viruses. However, the vast majority of discovered viruses will not have the ability to infect humans let alone the prospect of widespread in the population. Only a few viruses possess this ability.

This work should be pursued with the objective of fundamental viral scientific discovery, rather than the goal of near-term improvement in pandemic preparedness.

3.5 *Increasing Specific Diagnoses of Infectious Disease Syndromes Would Provide Valuable Information and Increase the Chances of Identifying a Pathogen Capable of Causing a Major Epidemic or Pandemic*

In the clinical practice of medicine, syndromic diagnosis—that is, making a non-specific diagnosis, such as "sepsis," "pneumonia," or "viral syndrome," with little to minimal laboratory testing—is the norm. Specific diagnosis (i.e., sending patient samples for definitive laboratory diagnosis) is often eschewed if it does not affect clinical management, is costly, and is not revealed with routine tests, and/or if the patient recovers. This practice has become enshrined not only in resource-poor areas in which access to diagnostic testing may be limited, but also in resource-rich areas, like North America and Western Europe, where specific diagnoses are viewed as superfluous.

However, the yield from pursuing an etiologic diagnosis in infectious syndromes such as atypical pneumonia, sepsis, encephalitis, meningitis, and clinically significant fevers of unknown origin may be considerable, as it will provide important insight into the ongoing torrent of threats posed by the microbial world. By causing an infection with enough severity to come to medical attention, the culpable microbes have already established that they are damage-causing pathogens to humans—a feat that only a sliver of the microbial world can accomplish (Woolhouse et al. 2016). Many of these microbial diagnoses cannot be made through the routinely ordered diagnostics. Therefore, a special effort would need to

be made to get to a microbial diagnosis. If that were to be done more frequently and at a more strategic level around the world, it would provide an opportunity to develop new situational awareness regarding which microbes are circulating and infecting humans—information that is clinically valuable in its own right and more attuned to uncovering GCBR-level pathogens than broad viral cataloging.

Such efforts should not be limited to exotic "hot spots" of disease emergence but should be practiced in localities that are broadly representative of where these conditions occur. Particular hot spots of emergence due to the presence of unique risk factors may be higher yield overall, but they should not be the sole sites of investigation. Infectious disease emergence can occur anywhere, as evidenced by the 2009 H1N1 pandemic, which was first recognized as the etiology behind a mild pediatric upper respiratory infection in California and West Nile fever emerging in cases of undifferentiated encephalitis in the New York City metropolitan area in the late 1990s (Centers for Disease Control and Prevention 2009; Nash et al. 2001).

Such a program would have significant cost and infrastructure implications in resource-constrained regions, so it would be most logical to set up sentinel or strategic sites for pursuing this level of microbial diagnosis in ways that are broadly representative. In developed nations such as the USA, these programs are available but underutilized because of lack of awareness or perceived lack of value by clinicians, for whom it will often not likely change therapeutic decisions.

3.6 Human Factors and/or the Occurrence of Complex Disasters Can Elevate Pathogens to GCBR Levels

Many participants in the project voiced the view that any microbe's pandemic potential could be substantially enhanced by human factors and poor preparedness, which could exacerbate a pathogen's spread or damage-causing potential.

Specific issues identified included gaps in hospital preparedness, medical countermeasure manufacturing capacity, medical countermeasure manufacturing locations, impacts on critical workforce members, and cascading effects on vital programs such as food production. For example, concentration of intravenous fluid manufacturing plants in Puerto Rico created massive shortages after a hurricane took the plants offline in 2017 (Wong 2017). The inability of hospitals to surge to meet enhanced patient needs for ventilators or ICU beds is another potential constraint.

Human factors could also take the form of mistaken actions that are based on political considerations but are not supported by an evidence-based medical rationale, or scientific mistakes based on human error, such as misidentifying a microbe or misinterpretation of scientific or epidemiologic data. For example, early in the SARS outbreak, mistakes regarding the etiology of the viral agent occurred, and the 2014 West African Ebola outbreaks were initially thought to be cholera, delaying response efforts for months (World Health Organization 2014).

Some participants in this study were of the view that such factors as these could outweigh any intrinsic property possessed by a microbe or any physiologic vulnerability possessed by a human. Magnification by human error could cause delays in response or awareness, allowing a pathogen to spread wider and deeper into the population and rendering containment more difficult, sowing panic, and severely stressing the healthcare infrastructure of a region. The majority view, however, was that intrinsic microbial characteristics are the main driver of a microbe's ability to cause a pandemic.

4 Recommendations

4.1 Preparedness for Pandemic and Global Catastrophic Biological Threats Should Acknowledge the Microbial Characteristics that Pose the Greatest Dangers

Pandemic preparedness should place a high priority on preparing for RNA viral threats, given their frequent spread by respiratory route, cytoplasmic replication, and high mutability. Surveillance, science, and countermeasure development programs and efforts should logically allocate significant resources to this class of microbes. Except for influenza and certain coronaviruses, there are not major preparedness efforts being made for other viruses in this class of microbes.

While RNA viruses were at the top of the list of concerns, other classes of microbes, such as bacteria, fungi, and protozoa, should not be completely dismissed given characteristic that pose special concerns.

Cultivating and maintaining expertise in the epidemiology, surveillance, and pathogenicity of all classes of microbes, with explicit incorporation of a One Health approach—which incorporates and integrates information from infectious diseases of plants, amphibians, and reptiles—will help foster the broad capacities needed for emerging pandemic and global catastrophic biological risks.

4.2 Pathogen List-Based Approaches and Precedents Are not Sufficient to Address Pandemic and Catastrophic Biological Risks

Pathogen-based lists, both USA and global, based on influenza precedents, historical biological weapon programs, and emerging infectious diseases were responsible for galvanizing early activities in the field of pandemic preparedness and have helped drive many important contributions. But these lists could create a sense of confidence regarding the prediction of future pandemic threats.

Lists can become frozen in the minds of those in the field and may be viewed as exhaustive rather than as starting points. Additionally, inclusion in lists could also be sought for political (and not epidemiologic) reasons if inclusion carries with it the prospect of enhanced funding for a long-neglected endemic problem.

One of the chief rationales behind this project was to attempt to move away from a strict list-based approach when considering pandemic threats and to develop a framework grounded in the facts of a microbe's biology and epidemiology. We recommend that risk assessment be rooted in the actual traits that confer pandemic or global catastrophic biological risks as opposed to a pathogen's presence on some earlier developed list.

4.3 Improving Surveillance of Human Infections with Respiratory-Borne RNA Viruses Should Be a Higher Priority

As respiratory-borne RNA viruses have been identified as possessing heightened pandemic potential, it is important to strengthen surveillance activities around these viruses where they currently exist and establish them where they are not yet in place. Currently, of the respiratory-borne RNA viruses, only influenza and certain coronaviruses receive high priority for surveillance.

While some efforts to understand coronaviruses, in the wake of SARS and MERS, exist, there is no systematic laboratory surveillance of coronavirus infections in humans. Similarly, no such program exists for rhinoviruses, parainfluenza viruses, RSV, metapneumoviruses, and similar viruses. Since this class of viruses is most likely to hold the future pandemic pathogen, constructing an influenza-like surveillance approach that better characterizes the prevalence, patterns, and geographic distribution of these viruses should be a priority.

Such an approach would focus on human infections, characterizing the epidemiology, virologic features, antiviral susceptibility (if applicable), and clinical manifestations in a fashion that mimics the extensive influenza surveillance conducted by the CDC and other international entities.

4.4 An Increased Emphasis on Developing a Specific Pipeline of Various Antiviral Agents for RNA Respiratory Viruses—Both Broad Spectrum and Virus-Specific—Would Add Resilience Against Pathogens that Pose Pandemic and Global Catastrophic Biological Risks

Currently, outside of anti-influenza antivirals, there is only one FDA-approved antiviral for the treatment of respiratory-spread RNA viruses (ribavirin). Of the six FDA-approved influenza antivirals—amantadine, rimantadine, baloxavir, zanamivir, oseltamivir, and peramivir—all target influenza viruses specifically and have no activity outside influenza, with two influenza A-specific agents (amantadine and rimantadine) rendered virtually obsolete because of resistance. The other antiviral agent (inhaled ribavirin) is approved for the treatment of respiratory syncytial virus (RSV) but has very limited use due to poor efficacy and major toxicity concerns for both RSV and parainfluenza viruses.

There are currently no approved antivirals for any other respiratory-spread RNA viruses in the world. Prioritization of antiviral compounds against this group of viruses may lead to acceleration of drug development and (government and non-government) incentivizing programs. Such antiviral compounds would have an advantage over many other emerging infectious disease countermeasures: These viruses exact a considerable toll in the form of community infections each year, providing a basis for a traditional pharmaceutical market as well as one for emerging infectious disease.

Pursuing not only broad-spectrum RNA antivirals, but also those specifically targeted to specific viruses such as RSV, would increase the likelihood of yield.

Nontraditional molecules, such as monoclonal antibodies and immunomodulators, should also be investigated for a role in the treatment and prevention of RNA virus respiratory infections (Walker and Burton 2018). Such adjunctive treatments may lead to improved clinical outcomes. To date, only one virally targeted monoclonal antibody is FDA-approved: pavalizumab for prevention in high-risk infants.

4.5 Vaccines Against RNA Respiratory Viruses, Including a Universal Influenza Vaccine, Should Be Pursued with Increased Priority

As with the above discussion regarding antivirals, the need for vaccines against respiratory-borne RNA viruses should also be prioritized. Currently, aside from influenza, for which a moderately effective but technically limited vaccine exists, there are no other vaccines for respiratory-borne RNA viruses. Experimental vaccines targeting RSV have made it into late clinical development only to fail.

Several important initiatives in this realm do exist and could be augmented to move beyond specific targets that have already been recognized. For example, the Coalition for Epidemic Preparedness Innovations (CEPI) has selected a coronavirus (MERS-CoV) and a paramyxovirus (Nipah) for vaccine development incentivizing (Røttingen et al. 2017). Such a program could, in potential future initiatives, select additional vaccine targets from this group of viruses and even encourage the development of broadly protective vaccines against groups of viruses—for example, a vaccine that protects against all four strains of human parainfluenza viruses, both MERS and SARS CoVs, and both Hendra and Nipah viruses.

Additionally, the heightened interest at the National Institutes of Health (NIH) in a universal influenza vaccine in the wake of the moderately severe 2017–18 influenza season should be channeled to provide significantly increased resources to this endeavor (Paules et al. 2017). As certain avian influenza viruses are of the highest threat tier, a universal influenza vaccine (even one that just protects against A strains) could substantially hedge against an influenza virus attaining GCBR status.

4.6 A Clinical Research Agenda for Optimizing the Treatment of Respiratory-Spread RNA Viruses Should Be Funded by Pharmaceutical Companies, Governments, and Medical Device Companies and Pursued by Clinical Centers

As was evident during the 2009 influenza pandemic and subsequent influenza seasons, the treatment of influenza is suboptimal, despite evidence-based guidance. The status of the treatment for other respiratory viruses is even less defined.

While there currently is not a robust antiviral armamentarium against these viruses, there are important clinical questions that occur with their treatment that merit further study. For example, what adjunctive therapies are useful? What coinfections may be present? At what stage of illness are rescue oxygenation devices warranted? As many of these viruses are highly prevalent in the community and are frequently encountered by clinicians in both outpatient and inpatient settings, finding answers to these questions would render clinicians more adept at dealing with pandemic versions of these viruses.

With respect to influenza, there is a growing literature on the use of antiviral agents in combination with anti-inflammatory agents such as nonsteroidal anti-inflammatory agents (NSAIDs) and macrolide antibiotics (Hung et al. 2017). Untangling the nuances of these treatment effects in order to develop robust guidance would have an impact on the ability to cope with an influenza-driven GCBR.

4.7 *Special Review Is Warranted for Respiratory-Borne RNA Virus Research that Could Increase Pandemic Risks*

Because of the higher likelihood that a GCBR-level threat might emerge from the group of RNA viruses with respiratory-spread, special attention to research on these agents is warranted if such research could increase pandemic risks. While much research on this class of viruses would be low risk and managed by appropriate approaches to biosafety, experimentally engineered antiviral resistance, vaccine resistance, or enhanced transmission, for example, would raise major biosafety and biosecurity concerns. The 1977 appearance of the H1N1 influenza A strain was thought to have resulted from laboratory escape (Zimmer and Burke 2009). It is important to understand the kinds of work being performed with these agents and, in particular, to know of experiments that are being done or are being proposed that would result in increased pandemic risks. Those experiments should have their own special review and approval process that is consistent with the risks and assesses the risks and benefits of this work before approval or funding of this work.

4.8 *Pursuing Microbiologically Specific Diagnoses of Infectious Disease Syndromes Should Become More Routine Globally*

As unknown infectious syndromes abound in all locations, and any given infectious syndrome may have as its etiology a potentially unknown or unappreciated microbe, specific diagnosis should be a routine endeavor. Atypical pneumonias, central nervous system infections, and even upper respiratory infections often are treated without any etiologic agent being identified.

As diagnostic technologies and devices improve in breadth, speed, and ease of use, the increasing uptake of these devices will provide a new opportunity to enhance situational awareness of an infectious syndrome in any location where they are deployed. Such devices are currently being used in research projects in the developing world. The more routine use of devices, such as multi-analyte molecular diagnostic devices, has the capacity to provide a fuller picture of the microbiological epidemiology of any given syndrome, illuminating what has heretofore been biological dark matter (Doggett et al. 2016; Kozel and Burnham-Marusich 2017). Coupled with heightened surveillance of respiratory-borne RNA viruses, the ability to capture an early signal of a potential pandemic pathogen will be greatly enhanced.

To date, certain considerations have limited the uptake and use of these devices: cost, perceived lack of clinical impact, and constraints on hospital resources such as isolation beds. Impacts on hospitals might be noted in laboratory testing volume as

well as costs. However, when these devices are viewed in the context of pandemic preparedness, the cost-effectiveness calculation should change. These considerations could be moderated if they are considered part of a hospital's emergency preparedness activities and not exclusively as clinical (they also have benefit for antibiotic stewardship activities in both inpatient and outpatient settings). In fact, the use of these devices should be considered on a par with mechanical ventilators, vaccines, antivirals, and antibiotics in the context of pandemic preparedness. Pilot projects demonstrating the feasibility of procuring such devices for infectious disease emergency preparedness could be conducted.

5 Conclusion

Understanding the microbial characteristics most importantly regarding the risks of pandemic or global catastrophic biological threats can help strengthen pandemic preparedness activities. While RNA viruses pose the greatest risks, there are characteristics of other microbial classes that cause special concerns and are important to consider in scientific research agendas and in public health preparedness efforts. This analysis leads to a series of recommendations related to disease surveillance, antiviral and vaccine development, clinical research, and research oversight. Taken together, assessment of key microbial class characteristics plus the focused actions that follow this assessment can broadly help improve preparedness for pandemic and global catastrophic risks.

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To: Menachery, Vineet[vimenach@UTMB.EDU]; Baric, Ralph S[rbaric@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Fri 6/19/2020 10:36:01 AM (UTC-05:00)
Subject: RE: R01

Thanks great news! Congratulations.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, June 19, 2020 11:31 AM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: R01

Got my R01. Guess I'll have to keep doing this. Thanks for the support.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 6/19/2020 11:58:03 AM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - 06/23/2020
nCoV PI call attendee list.xlsx

Happy Friday!!!

Hope everyone enjoyed the two presentations on Tuesday, June 16th given by Dr. Hughes and Drs. Van Voorhis and Phan.

Drs. Thomas and Ellebedy will be presenting their research updates next Tuesday, June 23rd on the topic of:
Comparing COVID-19 to influenza: immunological insights from a cohort of moderate and severe infections

Have a great weekend!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Brooke Bozick	x		x	x	x	x	
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Diana Finzi						x	
Diane Post	x	x	x	x	x	x	
Diego Hijano							
Don Milton						x	

Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jean Patterson						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Marlene Espinoza		x	x	x	x	x
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						

Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x

Wesley C Van Voorhis					
William Karesh	x				
Willy Valdivia					
Wolfgang Leitner					
Xizhi Guo	x				
Yoshihiro Kawaoka	x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun
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To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Fri 6/19/2020 10:44:29 AM (UTC-05:00)
Subject: RE: R01

Hi Congrats! Welcome to Life is great in 5 year blocks. Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, June 19, 2020 11:31 AM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: R01

Got my R01. Guess I'll have to keep doing this. Thanks for the support.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 1/8/2020 12:38:59 PM (UTC-06:00)
Subject: SIG U19 monthly call

Hi everyone,
Just a reminder that we will have our monthly SIG U19 call on Thursday January 9, 1:30 ET/10:30 PT. Mark will be presenting.

Calling numbers:

Phone: 1-800-747-5150
Passcode: 552.136
Germany, calling number below:
08001014525

access code **552.136**

Best regards,

Toni Baric
Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292
Office: 919-966-3507
tcbaric@med.unc.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]; Ralph Baric[rbaric@email.unc.edu]
Cc: Frieman, Matthew[MFrieman@som.umaryland.edu]
From: Diamond, Michael[mdiamond@wustl.edu]
Sent: Tue 6/30/2020 10:06:48 PM (UTC-05:00)
Subject: Re: CoV question

Thanks...
We definitely see anti-ORF8 Abs in mice...
Testing if they do anything....
M

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 30, 2020 10:04 PM
To: Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>
Cc: Frieman, Matthew <MFrieman@som.umaryland.edu>
Subject: Re: CoV question

HKU1 and OC43 don't have a known ORF3b or ORF8. The accessory ORFs don't have much homology across families.

I do question if there is sufficient abundance of those proteins to generate ab response against them. Dont' know much about it or if anyone has really looked. I'd think 8 before 3B.

From: Diamond, Michael <mdiamond@wustl.edu>
Sent: Tuesday, June 30, 2020 7:01 PM
To: Ralph Baric <rbaric@email.unc.edu>
Cc: Menachery, Vineet <vimenach@UTMB.EDU>; Frieman, Matthew <MFrieman@som.umaryland.edu>
Subject: CoV question

Ralph/Matt/Vineet

Reviewing a paper (what else is new). Quick question....

Do OC43 and HKU1 (other betacoronaviruses) have ORF3b and ORF8 proteins?

I don't think so, but I want to be sure

This is about potential X-reactivity of these antigens to anti-SARS-CoV-2 sera....if the OC43 and HKU1 don't have these proteins, the SARS-2 proteins might be useful for SARS-CoV-2 diagnostics (apart from MERS-CoV and SARS-CoV)

Yes?

Mike

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To: Gralinski, Lisa E[lgralins@email.unc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Hampton, Brea Kaseanna-Lanae[hamptb10@email.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; McWeeney, Shannon [mcweeney@ohsu.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
Cc: mtferris[mtferris@email.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]
From: Schaefer, Alexandra[aschaefe@email.unc.edu]
Sent: Wed 7/1/2020 11:31:27 AM (UTC-05:00)
Subject: Re: CC manuscript

Hi All,

also, can everybody please add people who need to be on the paper -
make sure that names and middle initials are spelled correctly
and add the correct affiliations?

That would be great!

Thanks,
Alex

From: Schaefer, Alexandra
Sent: Wednesday, July 1, 2020 11:48 AM
To: Gralinski, Lisa E <lgralins@email.unc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Hampton, Brea Kaseanna-Lanae <hamptb10@email.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Menachery, Vineet D <vineet@email.unc.edu>
Cc: mtferris <mtferris@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: CC manuscript

Hi all,

please find attached our draft discussing Group-2b coronavirus infection in the CC-RIX and 2 independent CC-F2 screens.

It would be great if you could have a look at it and give me comments back by next Wednesday (July 8th).

Thanks and wishing everybody a (hopefully) restful holiday weekend,
Alex

To: Strome, Scott Eric[sstrome@uthsc.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 7/3/2020 1:37:04 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - July 7, 2020
nCoV PI call attendee list.xlsx

Happy Friday, Everyone!

Thank you to all that called in (attendee list attached) and to our presenter, Dr. Krammer, for his presentation last Tuesday.

On Tuesday, July 7th, Dr. Michael Chan will be reviewing "**Experimental platforms to study SARS-CoV-2**".

Have a safe and wonderful weekend.

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Brooke Bozick	x		x	x	x	x	
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Diana Finzi						x	
Diane Post	x	x	x	x	x	x	
Diego Hijano							

Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jean Patterson						
Jeremy Crawford						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Marlene Espinoza		x	x	x	x	x
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x

Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x

Viviana Simon				x	x
Walt Orenstein		x	x	x	x
Weina Sun	x	x	x	x	x
Wesley C Van Voorhis					
William Karesh	x				
Willy Valdivia					
Wolfgang Leitner					
Xizhi Guo	x				
Yoshihiro Kawaoka	x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	23-Jun	30-Jun
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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 1/9/2020 12:49:45 PM (UTC-06:00)
Subject: Call for Pilot Proposals
System Immunogenetics U19 Pilot Research Funds Available.docx

Good afternoon,
Attached please find the call for pilot grants for the SIG U19. As requested on the phone call, if you are going to post on social media, please include the website for further information.

Thanks!

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

Pilot Research Funds Available.

The Center for Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross at the University of North Carolina at Chapel Hill conducts innovative research focused on the identification of immune regulatory genes and variant alleles that regulate disease outcomes following SARS-CoV, Ebola, Influenza, Chikungunya and West Nile Virus infections and/or vaccinations. The program uses systems genetic based approaches in the Collaborative Cross Genetic Reference Population to map genes that regulate protective or pathogenic immune outcomes following infection or vaccination. Pilot research program goals should fall within one or more of the following areas, including: building collaborative interactions with existing Projects that extend the breadth of the Program; developing new models of human immunity and/or disease; mapping novel immune regulatory genes; responding to emerging public health emergencies; and/or translating murine immune discoveries to human disease and improved public health. Approximately $115,000 **total** dollars will be available for a 1-year pilot program. Interested applicants are encouraged to submit:

1. Specific aims (1 page)
2. Research Approach (2 page) application outlining research goals
3. NIH Biosketch
4. Budget
5. Budget Justification
6. Scope of Work (1/2 page)
7. Unsigned PHS 398 Face Page

Budget period: 9/1/2020-8/31/21

The candidate selected would need to submit a signed, PHS 398 face page. All interested parties should submit their grant applications to Antoinette Baric, Program Manager (antoinette_baric@med.unc.edu) by March 1, 2020 at 5 PM ET. For more information on the Systems Immunogenetics program, please visit the website [HYPERLINK "http://www.systemsimmunogenetics.org"]

To: Gralinski, Lisa E[lgralins@email.unc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Hampton, Brea Kaseanna-Lanae[hamptb10@email.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Shannon McWeeney[mcweeney@ohsu.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Graham, Rachel[rlgraham@ad.unc.edu]
Cc: mtferris[mtferris@email.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]
From: Schaefer, Alexandra[aschaefe@email.unc.edu]
Sent: Wed 7/1/2020 1:07:59 PM (UTC-05:00)
Subject: Re: CC manuscript
Fig4A.pdf

Hi All,

I just realized,
that a phenotype plot got duplicated in the figures--- specifically Fig4Aiii

please find attached to this email the corrected version:

Sorry about that!
Alex

From: Schaefer, Alexandra <aschaefe@email.unc.edu>
Sent: Wednesday, July 1, 2020 12:31 PM
To: Gralinski, Lisa E <lgralins@email.unc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Hampton, Brea Kaseanna-Lanae <hamptb10@email.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; vimenach@utmb.edu <vimenach@utmb.edu>
Cc: mtferris <mtferris@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: CC manuscript

Hi All,

also, can everybody please add people who need to be on the paper -
make sure that names and middle initials are spelled correctly
and add the correct affiliations?

That would be great!

Thanks,
Alex

From: Schaefer, Alexandra
Sent: Wednesday, July 1, 2020 11:48 AM
To: Gralinski, Lisa E <lgralins@email.unc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Hampton, Brea Kaseanna-Lanae <hamptb10@email.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; McWeeney, Shannon <mcweeney@ohsu.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Menachery, Vineet D <vineet@email.unc.edu>
Cc: mtferris <mtferris@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: CC manuscript

Hi all,

please find attached our draft discussing Group-2b coronavirus infection in the CC-RIX and 2 independent CC-F2 screens.

It would be great if you could have a look at it and give me comments back by next Wednesday (July 8th).

Thanks and wishing everybody a (hopefully) restful holiday weekend,
Alex

To: Efrem Lim[Efrem.Lim@asu.edu]; Brenda Hogue[Brenda.Hogue@asu.edu]; Alexandra Lucas[arlucas5@asu.edu]; Matthew Frieman[mfrieman@som.umaryland.edu]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; Ralph Baric[rbaric@email.unc.edu]; Ralph Baric[ralph_baric@unc.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]; Mark Denison[mark.denison@vanderbilt.edu]; Kanta Subbarao[Kanta.Subbarao@mh.org.au]; Gallagher, Thomas[tgallag@luc.edu]; Paul Keim[Paul.Keim@nau.edu]; Janko Nikolich[jnikolich@medadmin.arizona.edu]; Janko Nikolich-Zugich[nikolich@email.arizona.edu]
Cc: Erika Arch[earch@asu.edu]; Ian Hogue[ihogue@asu.edu]
From: Grant McFadden[grantmcf@asu.edu]
Sent: Thur 7/9/2020 12:16:02 PM (UTC-05:00)
Subject: FW: Viroholics COVID-19 Seminar Series, ASV Virtual Workshops, and getting involved with ASV

Viroholics Speakers:

This is just to confirm that all of the 2020 ASU Viroholics COVID seminar recordings for which we had permission have now been posted on the ASV website.

Thank you all for your support, and let us collectively defeat this pandemic!

And stay safe, everyone.....

Grant

Grant McFadden
Director, Center for Immunotherapy, Vaccines, and Virotherapy (B-CIVV)
Biodesign Institute
727 E Tyler Street, Room A330E
Arizona State University
Tempe, AZ, 85287

Ph: 480-727-3388
FAX: 480-965-1844
Cell: 352-672-2263
Email: grantmcf@asu.edu
--

From: ASV Membership Administration <noreply@members.asv.org>
Sent: Thursday, July 9, 2020 9:53 AM
To: Ian Hogue <ihogue@asu.edu>
Subject: Viroholics COVID-19 Seminar Series, ASV Virtual Workshops, and getting involved with ASV

Virtual Workshops 2020. A BIG thank you is due to the volunteers who made the virtual workshops a huge success. We are especially grateful to Stephanie Karst, ASV Program Chair, and Andréa Garcia and Hailey Goran in the ASV Office. There were 56 organizers who planned and hosted 46 different workshops. Among the workshops, 430 abstracts were presented with approximately 5900 total participants from at least 40 different countries.

Viroholics Seminar Series. The Viroholics Seminar Series, hosted by Arizona State University, recorded a COVID-19 edition with many experts in the field. You can see the program and watch the seminars here: Viroholics Seminar Series

Get involved with ASV! Dedicated ASV members volunteer their time to run the Society and plan the annual meeting. ASV is made up of several committees, and the following committees are looking for new members. This is a great way to contribute to ASV and network with other scientists.

- Travel Award
- Communications
- Education and Career Development

If you are interested, contact the committee chair or the ASV Office. Find committee information here.

ASV 2021 Satellites. There will not be a call for satellite proposals for ASV 2021. The satellites originally selected for ASV 2020 are now planned for ASV 2021.

Time sensitive public affairs matter for ASV members. A rule has been proposed by the current US administration that, if finalized would severely restrict asylum. The ASV and other scientific societies (such as the American Academy of Pediatrics, AAP) have been approached to comment on the rule change. This rule change is part of larger issues that affect how research science is done, and the ASV Executive Committee wanted to make you aware of this. **The public has until July 15, 2020 to comment on the proposal.**

If you would like to comment, a Toolkit document from the AAP and a document from the American Immigration Lawyers Association is linked here. The instructions for how to comment are here (scroll down to “addresses.”)

Questions or concerns? Please email asv@asv.org

To: Gralinski, Lisa E[lgralins@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Baric, Ralph S[rbaric@email.unc.edu]
From: Schaefer, Alexandra[aschaefe@email.unc.edu]
Sent: Fri 7/10/2020 10:35:09 AM (UTC-05:00)
Subject: Comments from Mike Diamond

HI all,

Just got comments from Mike back----
he thinks FACS downstream analysis and gating schemes need to be in the suppemental

Do you have this data available?

Alex

To: Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Webby, Richard[Richard.Webby@STJUDE.ORG]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Schultz-Cherry, Stacey[Stacey.Schultz-Cherry@STJUDE.ORG]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; 'Krammer, Florian'[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Subbarao, Kanta[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; jmclellan@austin.utexas.edu[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Russell, Charles[Charles.Russell@STJUDE.ORG]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Stephen M Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Thomas, Paul[Paul.Thomas@STJUDE.ORG]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; andrea_sant@urmc.rochester.edu[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 7/10/2020 11:31:44 AM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting
nCoV PI call attendee list.xlsx

Hi All,

Thank you all who joined (attendance attached) and to our presenter, Dr. Michael Chan. Next Tuesday, July 14th, Dr. Vineet Menachery will be giving a presentation on "Exploration of the SARS-CoV-2 furin cleavage site".

Towards the end of the call, the question was asked "if there was the hACE2 ad-vector available in BEI". Dr. Stemple followed up after the call with the response that this one is available: https://www.beiresources.org/Catalog/animalviruses/NR-52390.aspx

Have a great weekend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Brooke Bozick	x		x	x	x	x	
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Diana Finzi						x	
Diane Post	x	x	x	x	x	x	
Diego Hijano							

Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jean Patterson						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Marlene Espinoza		x	x	x	x	x

Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
mprabhudas						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x

Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	23-Jun	30-Jun
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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Heise, Mark T[mark_heisem@med.unc.edu]
Sent: Thur 1/9/2020 11:32:30 AM (UTC-06:00)
Subject: RE: SIG U19 monthly call
SIGU19 Presentation Jan 2020-1.pdf

Hi everyone.
Please find a PDF of today's presentation attached.
Thanks
Mark

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, January 8, 2020 1:39 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: SIG U19 monthly call

Hi everyone,
Just a reminder that we will have our monthly SIG U19 call on Thursday January 9, 1:30 ET/10:30 PT. Mark will be presenting.

Calling numbers:

Phone: 1-800-747-5150
Passcode: **552.136**
Germany, calling number below:
08001014525

access code **552.136**

Best regards,

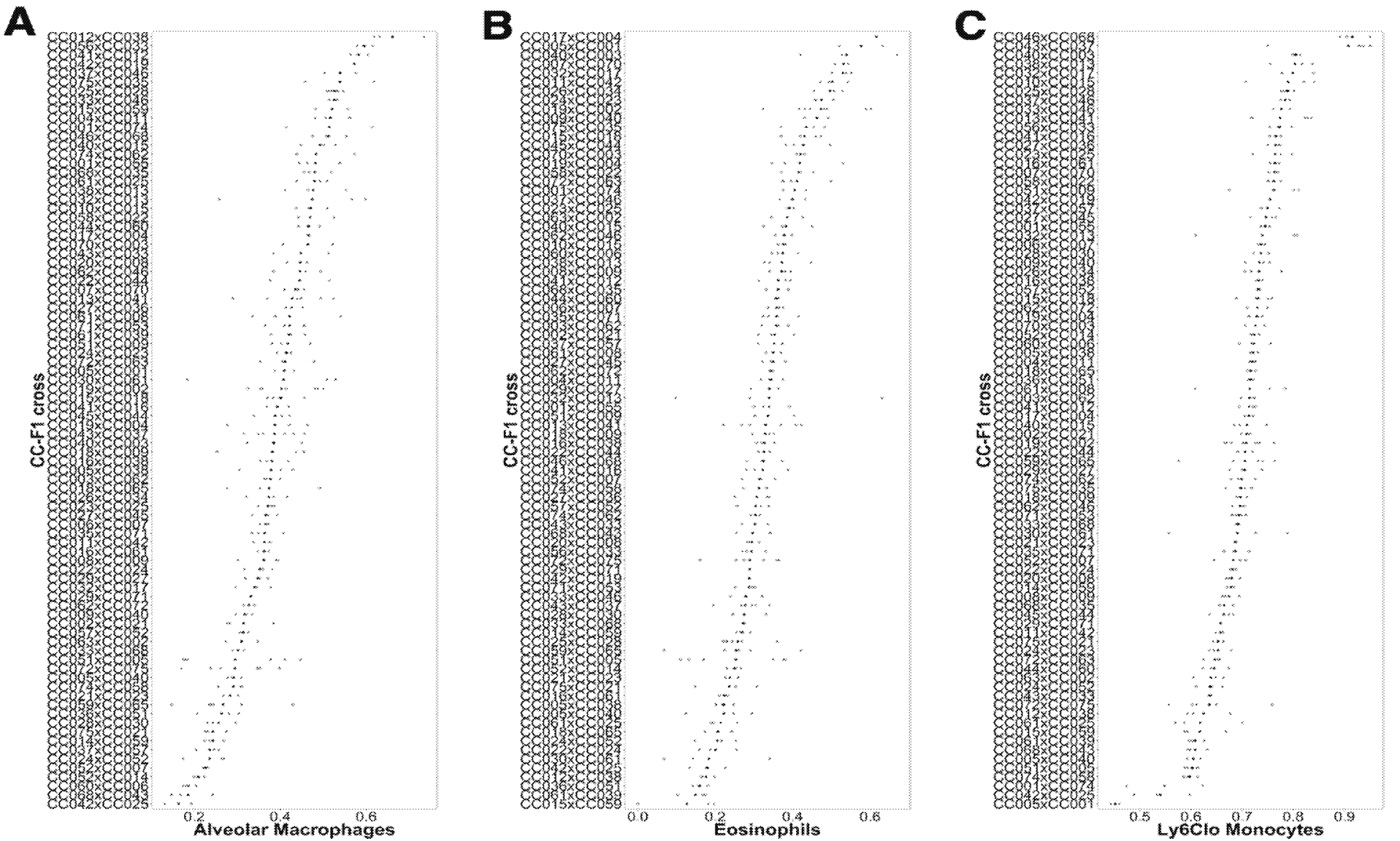
Toni Baric

Department of Microbiology and Immunology
9025 Burnett Womack
CB# 7292
Chapel Hill, NC 27599-7292

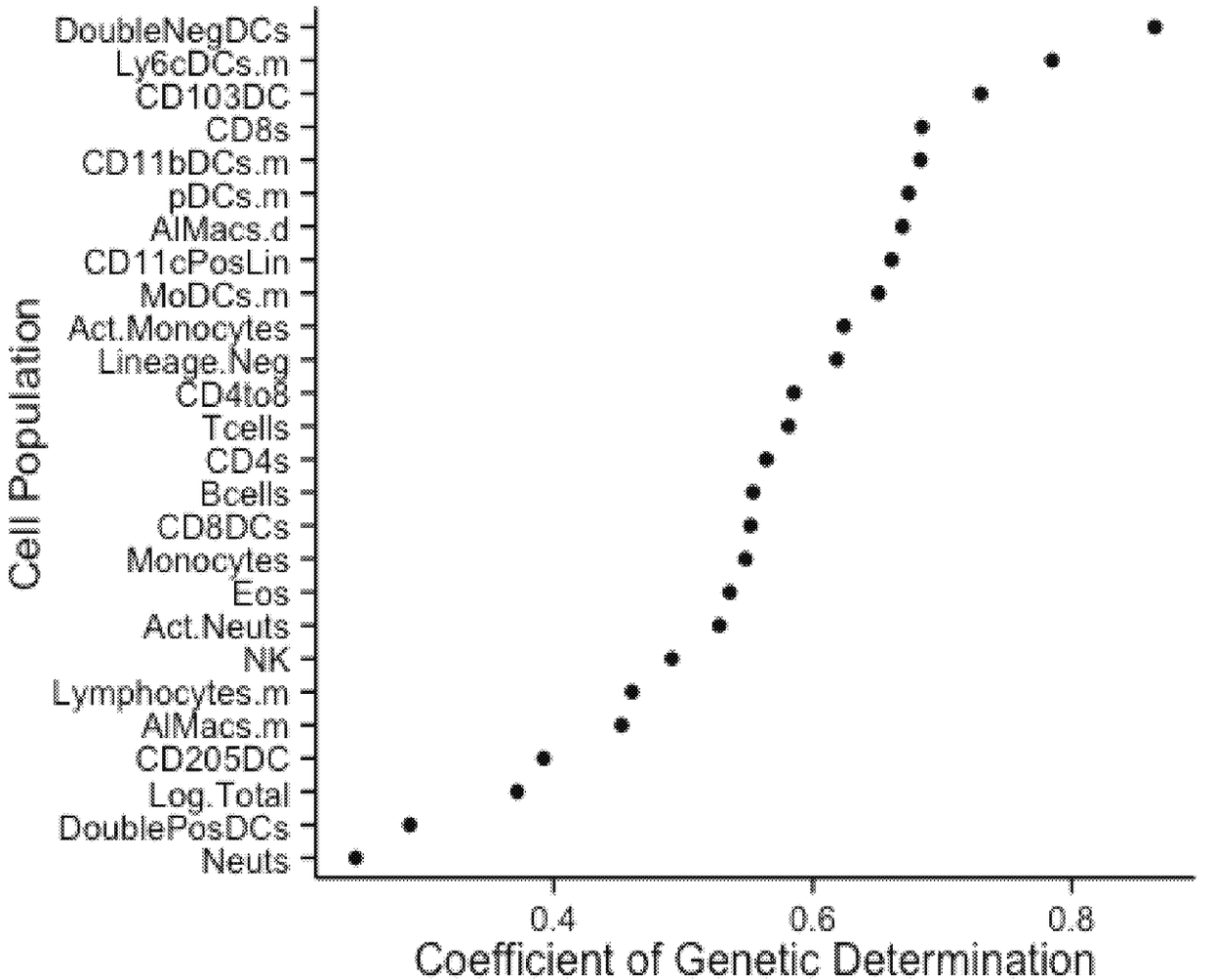
Office: 919-966-3507
tcbaric@med.unc.edu

Do Baseline Immune Loci Affect Virus-Induced Disease or Immunity?

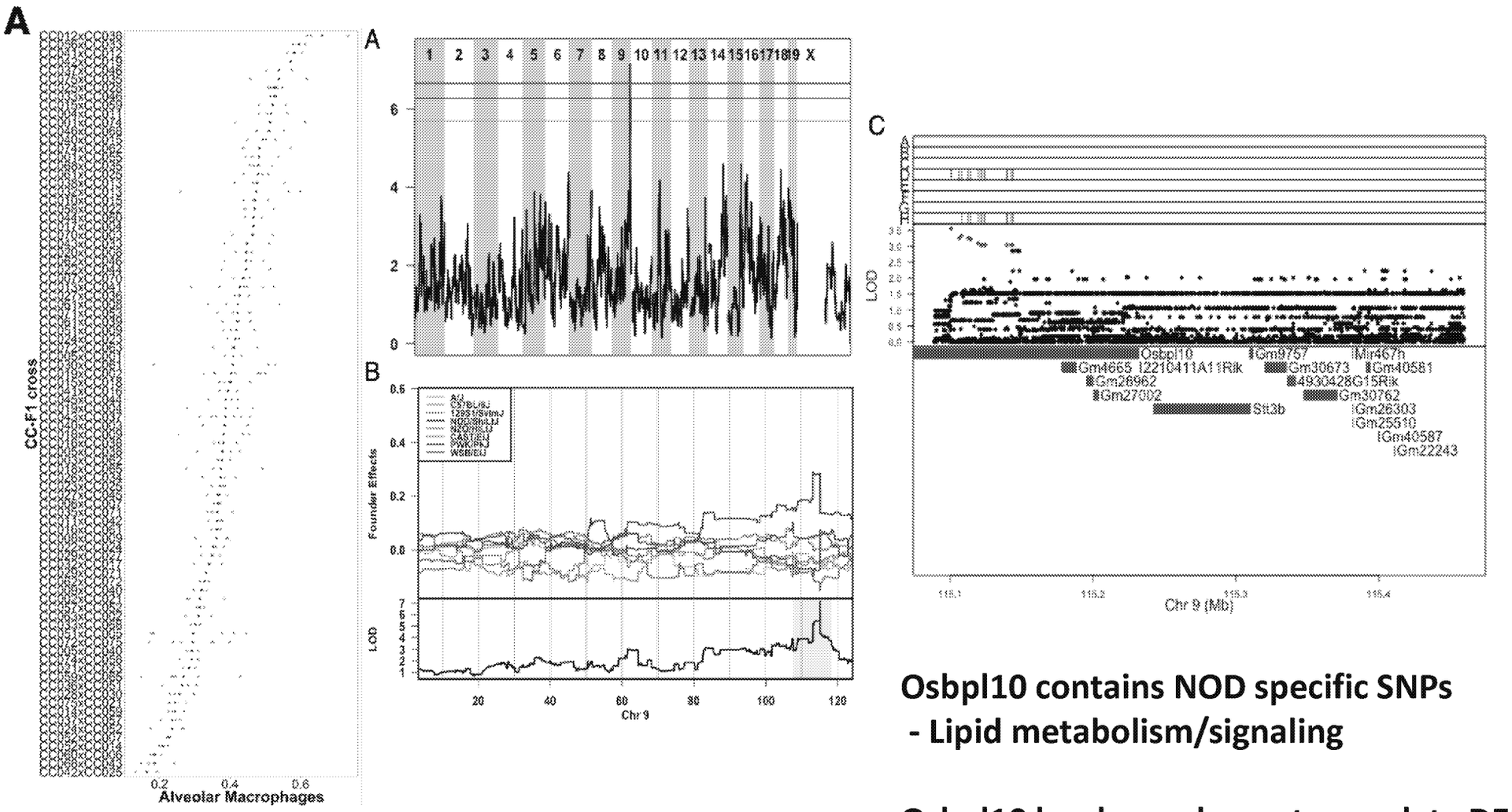
Lung Leukocyte Populations are highly variable across CC RIX lines



Heritability of Baseline Lung Cell Populations



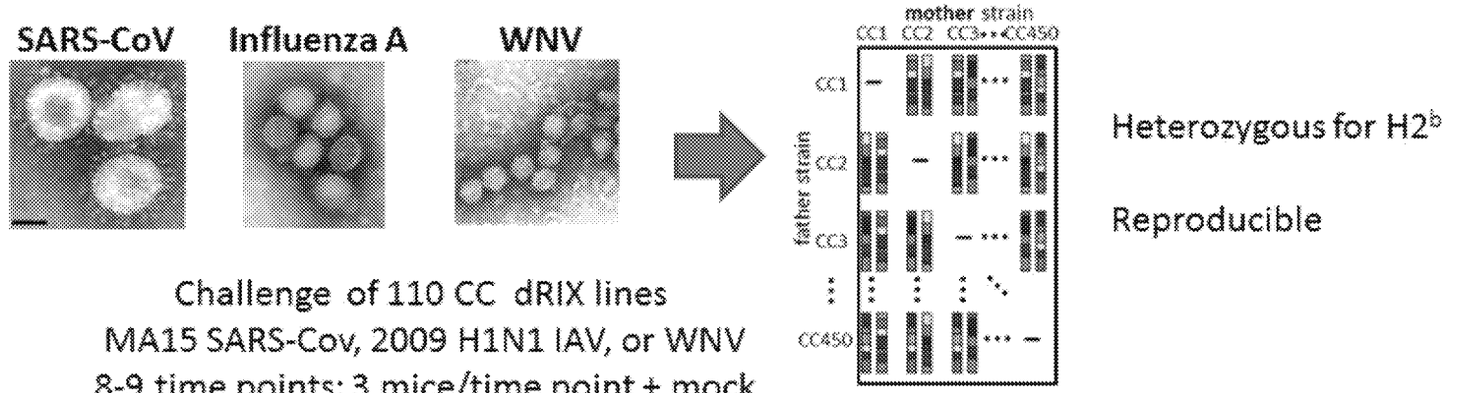
A QTL On Chr. 9 Regulates Alveolar Macrophage #s in the Lung

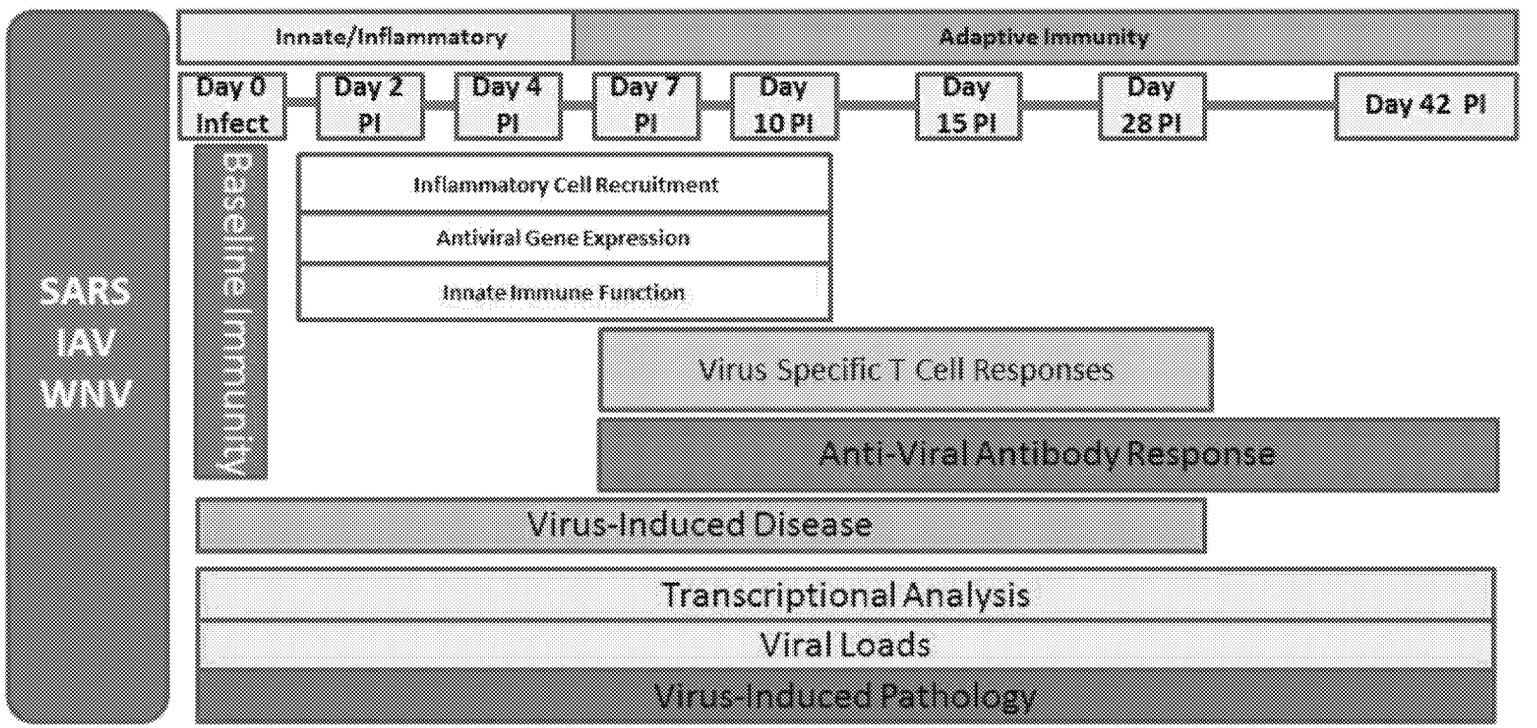


Osbpl10 contains NOD specific SNPs
- Lipid metabolism/signaling

Osbpl10 has been shown to regulate DENV replication
PLoS Path. DOI:10.1371/journal.ppat.1006220 February 27, 2017

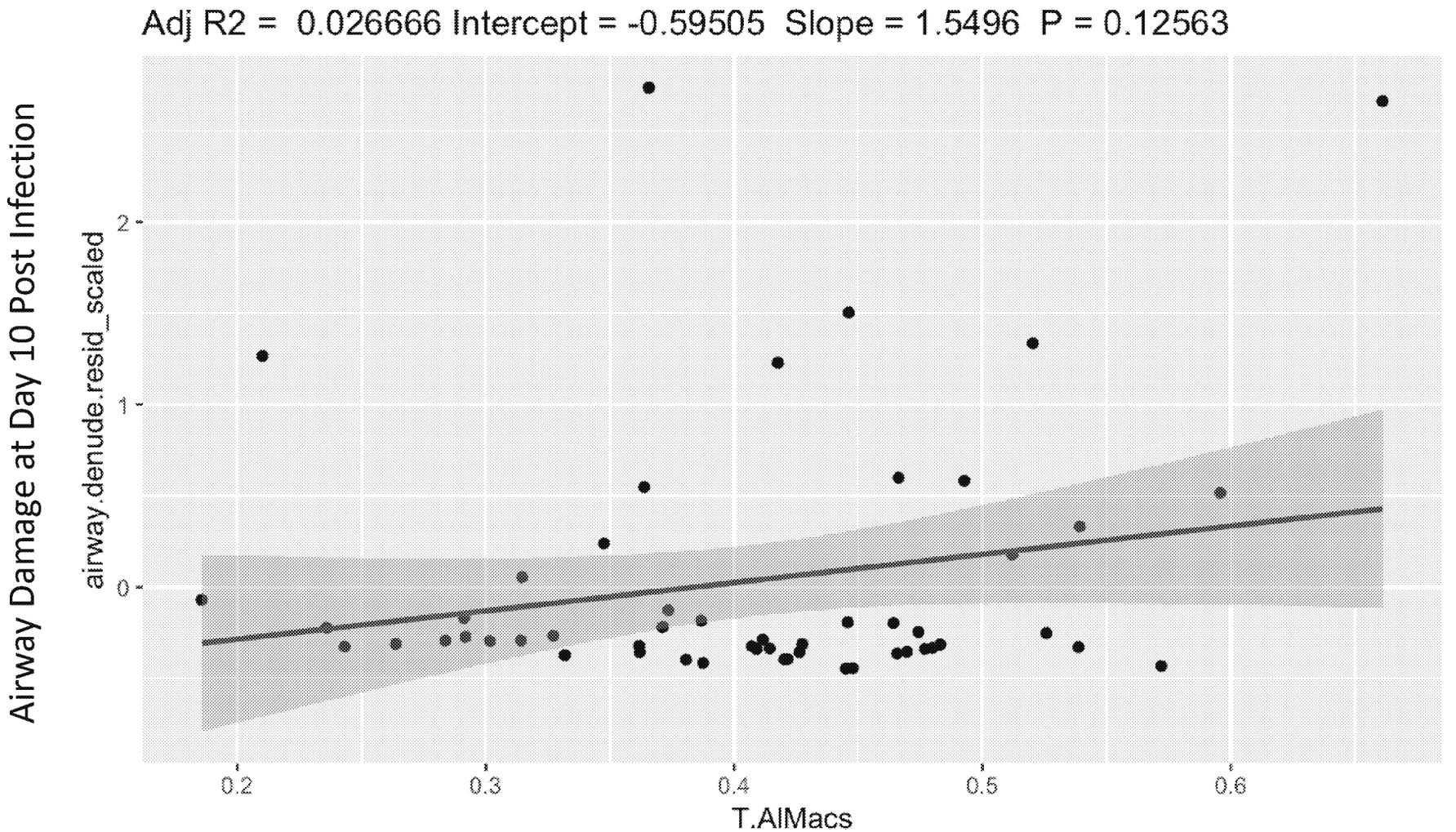
Brea Hampton





- Challenge groups of animals (n=3 mice/dRIX line/time point)
- Compare immune responses to 3 viruses across 110+ CC RIX lines
- Map QTL and identify candidate genes

Does Variation in Baseline Lung Leukotyes Correlate With Susceptibility to Virus-induced Disease?



Brea Hampton

Using Nested Models to Test Whether Specific Loci/Haplotypes Correlate with Other Phenotypes

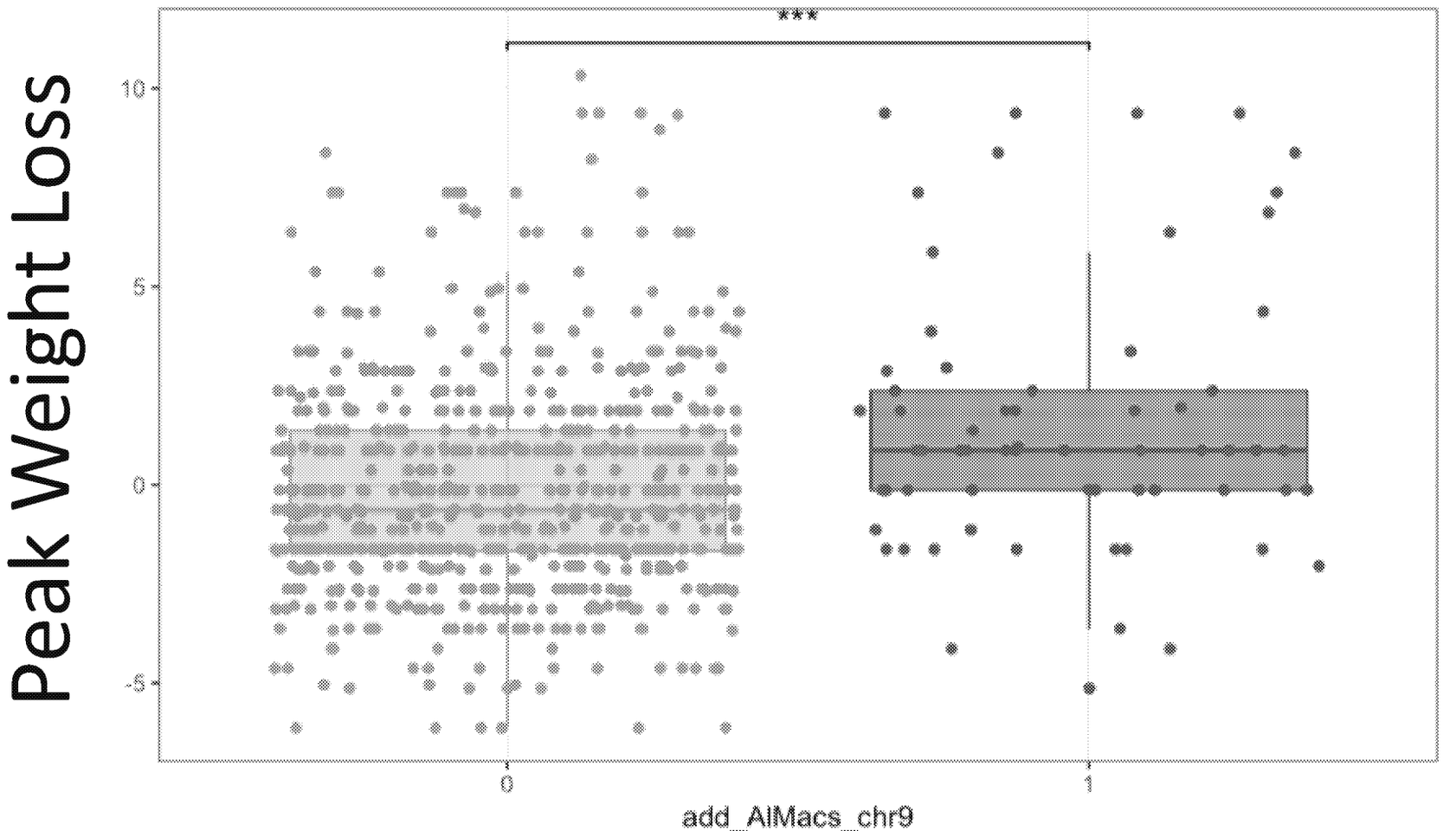
We use an ANOVA framework to test whether there is an increase in statistical fit when we include information on baseline QTL haplotypes, relative to variation already explained by RIX and other factors included in the base model.

Base model: virus-induced phenotype = RIX + error
Full model: virus-induced phenotype = RIX + baselineQTL + error

***For IAV-induced phenotypes we include Mx1 status in the models.**

Brea Hampton
Marty Ferris

Alveolar Macrophage Variation is Associated with IAV Susceptibility



Mock lung leukocyte QTL

Name	Phenotype	Phenotypic Range	Heritability Estimate	QTL	Effect size	Haplotype Effects
*QLH1***	Alveolar Macrophages	0.1631 – 0.6610	0.536	Chr. 9: 115.0Mb – 115.2Mb	0.128	NOD/ShiLtJ – high
*QLH7***	CD4$^+$ T cells	0.1309 – 0.8740	0.868	Chr. 5: 41.9Mb – 48.4Mb	0.240	C57BL/6J – high
*QLH6***	CD8$^+$ T cells (as a fraction of all T cells)	0.0012 – 0.5230	0.748	Chr. 14: 46.9Mb – 58.6Mb	0.228	A/J – high NZO/SH1LtJ – low
*QLH8***	CD11c$^+$ dendritic cells	0.1339 – 0.9032	0.526	Chr. 15: 86.8Mb – 91.4Mb	0.027	CAST/EiJ – low
*QLH9***	CD103$^+$, CD205$^+$ dendritic cells (as a fraction of lineage$^-$ cells)	0.0003 – 0.6561	0.358	Chr. 19: 38.2Mb – 61.3Mb		NZO/SH1LtJ – low
*QLH10***	Lineage$^-$ cells	0.3811 – 0.9971	0.782	Chr. 12: 106.3Mb – 108Mb	0.322	WSB/EiJ – low
*QLH5***	Ly6C^{lo} 'patrolling' monocytes (as a fraction of all Ly6C$^{+/lo/-}$ monocytes)	0.3164 – 0.9414	0.509	Chr. 7: 12.8Mb – 29.4Mb	0.499	C57BL/6J, WSB/EiJ – low
*QLH2****	Ly6C$^-$ 'patrolling' monocytes (as a fraction of all Ly6C$^{+/lo/-}$ monocytes)	0.1075 – 0.9067	0.739	Chr. 15: 72.4Mb – 78.2Mb	0.515	CAST/EiJ – high WSB/EiJ – low
*QLH3****	Ly6C$^-$ 'patrolling' monocytes	0.1708 – 0.6377	0.667	Chr. 15: 48.3Mb – 63.2Mb	0.522	CAST/EiJ – high
*QLH2****	Ly6C$^+$ 'inflammatory' monocytes (as a fraction of all Ly6C$^{+/lo/-}$ monocytes)	0.2438 – 0.8819	0.497	Chr. 15: 72.4Mb – 77.8Mb	0.490	WSB/EiJ – high
*QLH2**** *QLH4****	Ly6C$^+$ 'inflammatory' monocytes	0.0838 – 0.6365	0.566	Chr. 15: 72.4Mb – 78.1Mb Chr. 2 : 18.3Mb – 33.2Mb	0.399 0.422	WSB/EiJ – high
*QLH11*** *QLH12***	Plasmacytoid dendritic cells	0.0529 – 0.4206	0.600	Chr. 15: 71.4Mb – 79.1Mb Chr. 14: 119.3Mb – 123.3Mb	0.422 0.051	WSB/EiJ – high WSB/EiJ – low

IAV-induced phenotypes	***QLH1*** (Alveolar macrophages)	***QLH2*** (Ly6C- fraction) Patrolling Monocytes	***QLH3*** (Ly6C-) Patrolling Monocytes	***QLH4*** (Ly6C+) Inflammatory Monocytes	***QLH5*** (Ly6Clo fraction) Patrolling Monocytes	***QLH6*** (CD8+ T cells)	***QLH10*** (Lineage$^-$)
Lowest day	**0.004488** **	0.464	0.6324	0.4786	**0.0006994** ***	0.6108	
Lowest weight	0.5167	0.1611	**0.03534** *	0.2915	0.84	**0.04531** *	0.8609
Airway debri	0.1014	0.3873	0.3286	0.3143	0.9627	0.8408	0.9447
Airway denude	**0.0009429** ***	0.4081	0.589	0.370	0.6049	0.6102	0.9661
Vascular cuffing	0.1857	0.2743	0.5673	0.5543	0.3875	0.136	0.7154
Airway cuffing	0.8738	0.4756	0.5011	0.6288	0.9659	0.4435	0.01354 *
Alveolar inflammation	0.2171	0.9762	0.7598	0.3426	0.5899	0.8601	0.2623
Pulmonary edema	0.1298	0.9426	0.249	0.6811	0.4317	0.5147	0.2821
Hyalin membrane	**0.07385** .	0.1249	0.495	0.2904	0.2756	0.6223	0.1486
Lymphocytes	0.2032	0.8032	0.5899	0.6963	0.4305	0.6299	0.1092
Neutrophils	0.8928	0.9317	0.6942	0.7509	0.344	**0.01586** *	0.3666
Macrophages	0.1332	0.6181	0.5791	0.7742	0.1861	0.7879	0.7364
Exudate	0.9139	0.7621	**0.000679** ***	0.2319	0.741	0.376	0.4356
D4 weight loss	0.6874	0.5417	**0.04316** *	0.9805	0.3984	**0.09069** .	0.4671
D7 weight loss	0.4629	0.5612	**0.00715** **	0.2011	0.8032	0.131	0.6845
D10 weight loss	0.3536	0.2078	0.1964	0.3071	0.8577	0.1739	0.5346

IAV-Induced Changes in Respiratory Function

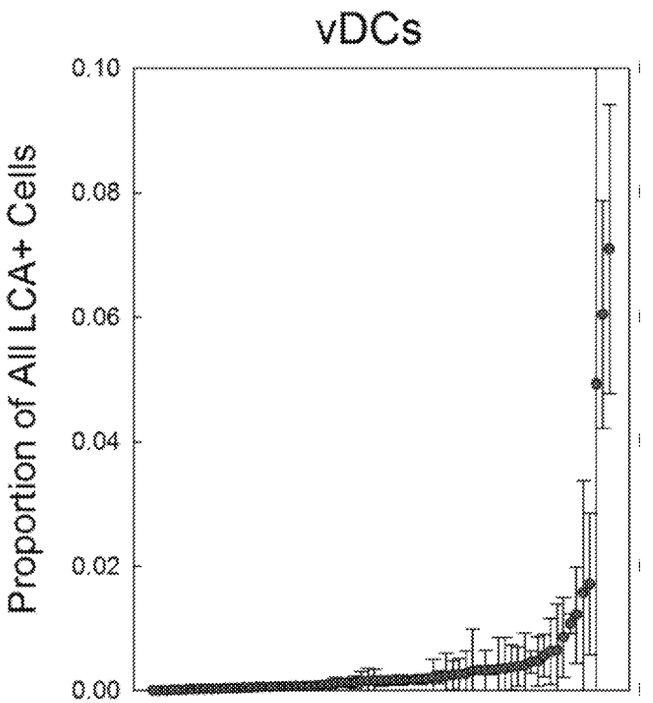
IAV-induced phenotypes	*QLH1* (Alveolar macrophages)	*QLH2* (Ly6C- fraction)	*QLH3* (Ly6C-)	*QLH4* (Ly6C+)	*QLH5* (Ly6Clo fraction)	*QLH6* (CD8+ T cells)	*QLH10* (Lineage$^-$)
EF50	**0.05572 .**	0.161	0.1964	**0.0824 .**	0.01278 *	0.6376	0.1162
Rpef	0.4584	0.434	0.906	**0.05338 .**	0.008862 **	0.5426	0.1717
Penh	0.5134	0.2036	**0.08369 .**	0.3799	0.1598	0.9792	0.7747

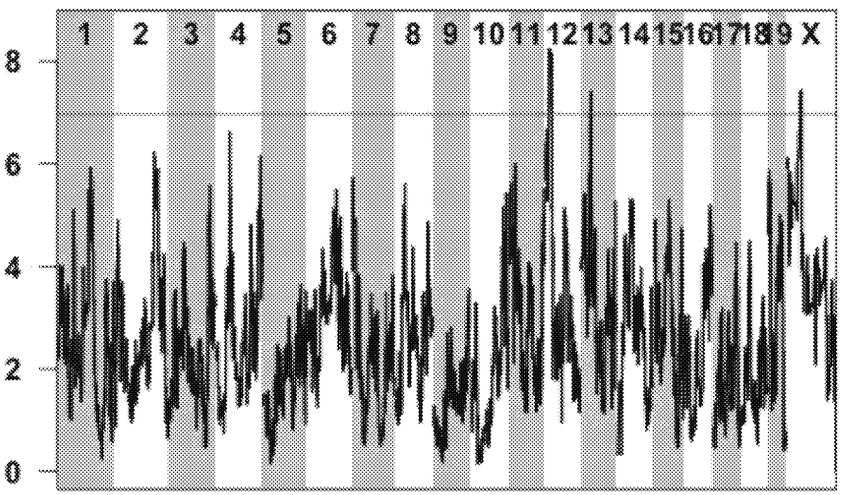
Now for Something Completely New (A Novel Cell Population in the CC?)

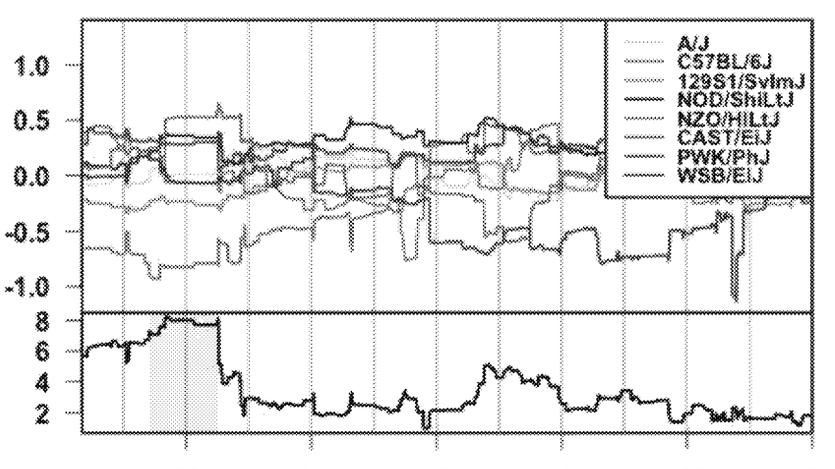
"variable DCs" identified in a subset of samples

CD11c^{+}, CD11b^{++}, GR-1^{lo}, SiglecF^{-}, B220^{-}, MHC-IIc^{var}

Present in some strains, not in others







Alan Whitmore/Marty Ferris

Now for Something Completely New (A Novel Cell Population in the CC?)

"variable DCs" identified in a subset of samples

$CD11c^{+}$,

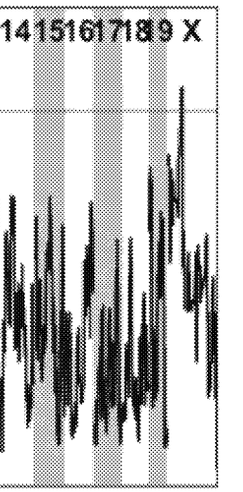
Present

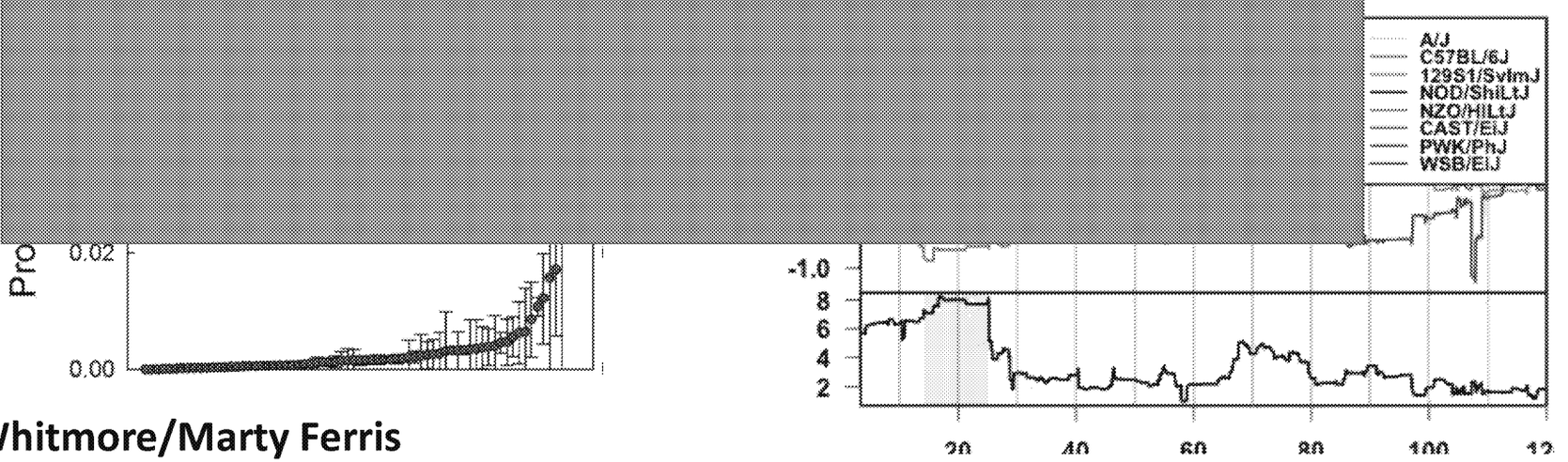
Chromosome 12 vDC QTL is Associated with:

Hyalin Membrane (p = 0.02)

Day 4 Weight Loss (p = 0.019)

Rpef (p = 0.036)





Alan Whitmore/Marty Ferris

SARS-CoV

SARS-induced phenotype	*QLH1* (Alveolar macrophages)	*QLH2* (Ly6C- fraction)	*QLH3* (Ly6C-)	*QLH4* (Ly6C+) Inflammatory Monocytes	*QLH5* (Ly6Clo fraction)	*QLH6* (CD8+ T cells)	*QLH10* (Lineage$^-$)
D2 titer	0.1969	**0.03316 ***	0.9041	**0.02485 ***	0.8698	0.5627	0.6677
D4 titer	0.7141	0.9483	0.1755	**0.01524 ***	0.3522	0.3787	0.9528
Severe weight loss	0.8053	0.8825	0.5064	0.6202	0.209	0.5998	0.9157
Severe disease	0.4272	0.7944	0.2453	**7.53e-12 *** **	0.25	0.7164	0.8639
Mortality	0.1813	0.8947	0.7664	**0.02948 ***	0.249	0.7512	0.9025
EF50	0.596	0.5062	0.9067	**0.009634 ** **	0.771	0.8759	0.7052
Rpef	0.5456	0.9541	0.5441	**0.08519 .**	0.9791	0.5856	0.2824
Penh	**0.08444 .**	0.8003	0.4851	0.3286	0.3225	0.3282	0.9787

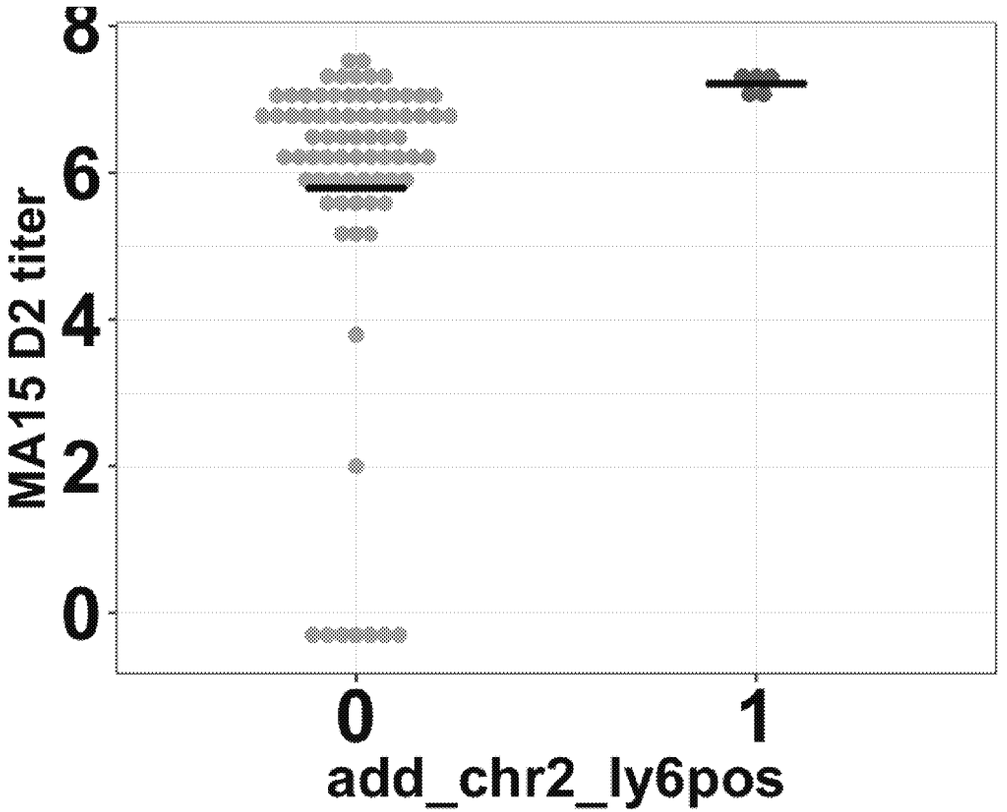
Inflammatory Macrophages and SARS-CoV

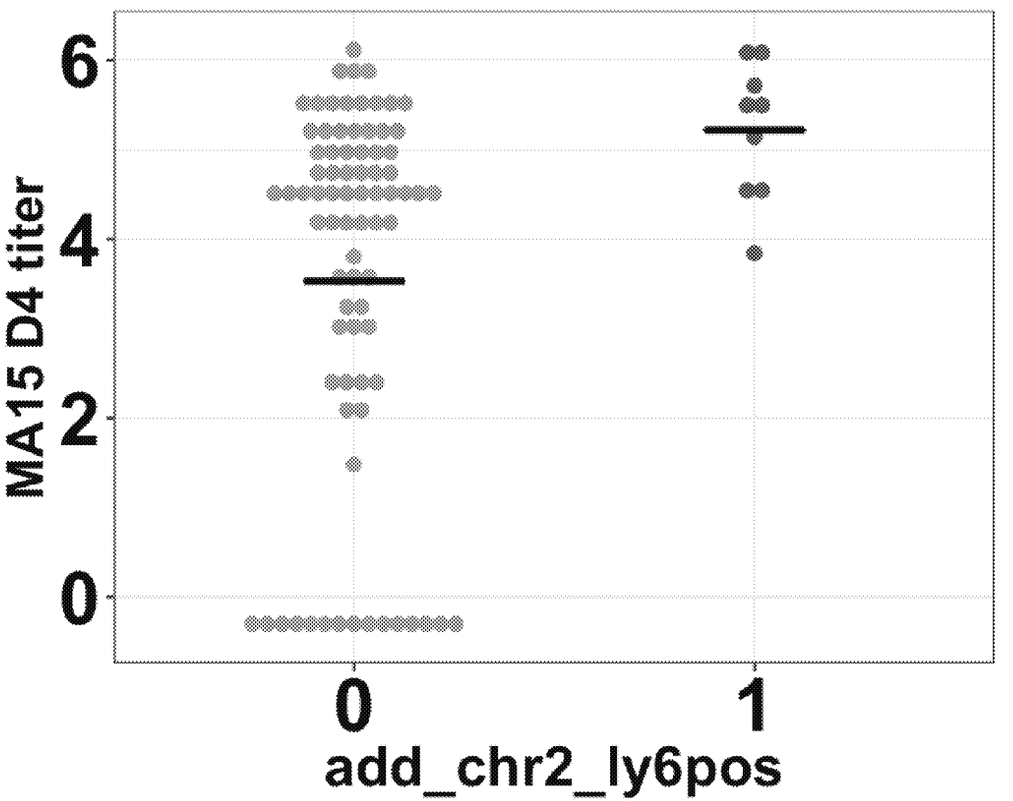
Cell Host Microbe. 2016 Feb 10;19(2):181-93. doi: 10.1016/j.chom.2016.01.007.
Dysregulated Type I Interferon and Inflammatory Monocyte-Macrophage Responses Cause Lethal Pneumonia in SARS-CoV-Infected Mice.
Channappanavar R[1], Fehr AR[1], Vijay R[2], Mack M[3], Zhao J[4], Meyerholz DK[5], Perlman S[6].

1) Type I interferon expression leads to recruitment of inflammatory Macs (Ly6c+, CD11b+)

2) Inflammatory Macs promote lung damage and disease, while also impairing T cell responses without affecting viral loads

3) Depletion of inflammatory Macs with anti-CCR2 protects from disease





Presence of at least one WSB/EiJ allele at this locus is associated with increased viral titer at early timepoints post-infection.

Conclusions

- Baseline lung leukocyte populations are highly variable across the CC
- This variation is highly heritable and we have identified a number of QTL associated with variation in these populations.
- Several genetic loci associated with baseline leukocyte variation are also associated with variation in virus-induced disease.
  - Is this association due to effects on baseline leukocytes or other effects of the causal variant under the locus?
  - Are any of these loci broadly associated with virus-susceptibility?

Acknowledgements

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Ralph Baric
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Alexandra Schaefer
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Ginger Shaw
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U19 AI 109761
R21 AI119933

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; McWeeney, Shannon [mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Mooney, Michael [mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Fri 1/10/2020 7:00:24 AM (UTC-06:00)
Subject: RE: Call for Pilot Proposals

Good morning everyone,
I wanted to let you know that Mike Mooney has uploaded the call for pilots to the SIG website.

http://www.systemsimmunogenetics.org/announcement.html

Thanks
Toni

From: Baric, Toni C
Sent: Thursday, January 9, 2020 1:50 PM
To: Baric Toni <tcbaric@med.unc.edu>; Baric, Ralph <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; Ferris Martin <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@email.unc.edu>; Gralinski Lisa <lgralins@email.unc.edu>; Heise Mark <heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; McWeeney, Shannon <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Mooney, Michael <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Subject: Call for Pilot Proposals

Good afternoon,
Attached please find the call for pilot grants for the SIG U19. As requested on the phone call, if you are going to post on social media, please include the website for further information.

Thanks!

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 7/27/2020 3:14:50 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - July 28, 2020

nCoV PI call attendee list.xlsx

Hi All,

Apologies for the last minute email.

Last week, Dr. Benjamin Miller gave a fantastic presentation on "**Analyzing the Human SARS-CoV-2 Antibody Response Using Arrayed Imaging Reflectometry**." I have attached the attendee list for review.

Tomorrow, Dr. Jens Wrammert, will be giving a presentation on "**Antibody and B cell Responses in Acute and Convalescent COVID-19 patients**."

Hope everyone can attend!

Thanks,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					
David Topham	x	x		x	x		
David Wentworth		x	x	x	x	x	
Deborah Lynn Fuller							

Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x

Malik Peiris		x				
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mindy Davis						
mprabhudas						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x

Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	23-Jun	30-Jun
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To: Menachery, Vineet[vimenach@UTMB.EDU]; Schaefer, Alexandra[aschaefe@email.unc.edu]
Cc: Gralinski, Lisa E[lgralins@email.unc.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Sun 8/2/2020 6:40:49 AM (UTC-05:00)
Subject: RE: HKU3 data

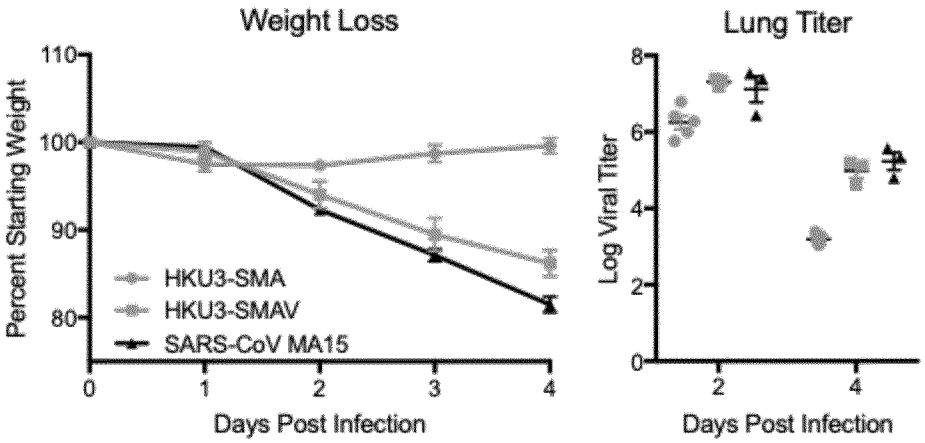
Thanks Vineet, very helpful. I'm obviously way behind in my email. Hope your doing well. ralph

---

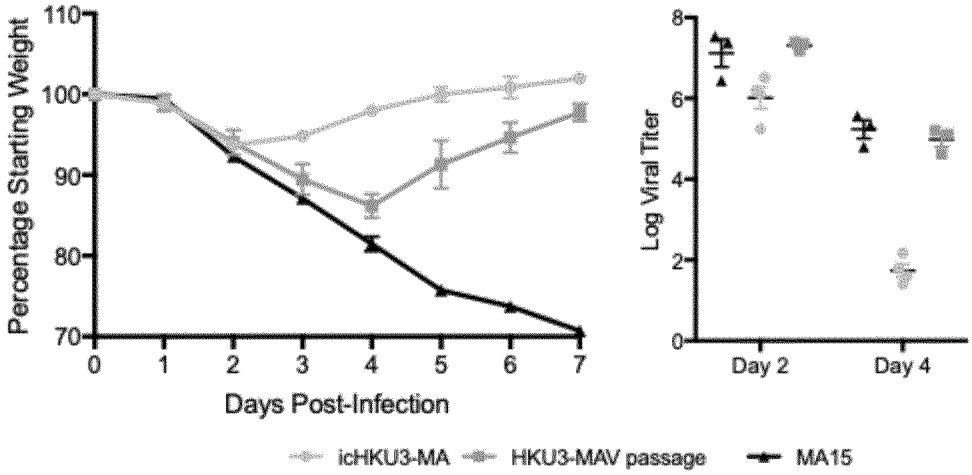
From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, July 24, 2020 10:55 PM
To: Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Gralinski, Lisa E <lgralins@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: HKU3 data

Hey Alex, Ralph, and Lisa,

I tried to thumb through what I had from Sudhakar. Haven't been able to decipher it all. What I do have is the following graph I made. The Bat-SRBD-MA is from Rachel's original experiment (circa 2008) that she gave to me. The Bat-SRBD-MAv is an experiment that I did compared to MA15 before I left in 2017. If you want this data, I can send you the PRISM file. This study was done with plaque purified stock that Sudhakar made as far as I understand.



This data is from the same experiment where i compared it with the icHKU3-SMAv and found that the ic version was attenuated compared to plaque purified virus



Let me know if this is what you want and I'll try to find the raw data and PRISM file to send. I have files from Sudhakar,

but not really sure the conditions/ages, etc for those. I can try to decipher, but it will take some time.

As far as I know, the histology for these experimetns was still at UNC for this experiment. Likely still in formalin if I had to bet. I can send you the labels if you think we need to have the histology.

VDM

From: Schaefer, Alexandra <aschaefe@email.unc.edu>
Sent: Thursday, July 23, 2020 4:12 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: HKU3 data

Hi Vineet,

Lisa mentioned that you might have some in vivid or in vitro data with the HKU3 Virus Sudharkar passaged?

It would be great if you could send me the data, we might put it into the manuscript as supplement data characterizing the HKU3 virus?

Thanks,
Alex

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To: Gralinski, Lisa E[lgralins@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; rlgraham@email.unc.edu[rlgraham@email.unc.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]
From: Totura, Allison (OS/ASPR/BARDA)[Allison.Totura@hhs.gov]
Sent: Thur 8/6/2020 7:25:03 AM (UTC-05:00)
Subject: ACTIV Discussion: Viral Stocks

Hi,

ACTIV would like to request someone from the Baric Lab or who has significant CoV experience to participate on a call today at 1pm (EDT) regarding the growth of SARS-CoV-2 stocks.

The immediate purpose of these stocks would primarily be for in vivo animal challenge studies, so the objective is to grow high titer stocks that also have few AA changes in the spike glycoprotein.

Please let me know if you can participate or have someone in mind, and Clint (NIAID) or I will forward the invite.

Thanks,
Allison

Allison Totura, PhD
Biologist | Division of Nonclinical Development
Biomedical Advanced Research and Development Authority (BARDA)
Office of the Assistant Secretary for Preparedness and Response (ASPR)
Phone: (202)774-8586

To: Baric, Ralph S[rbaric@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Gralinski, Lisa E[lgralins@email.unc.edu]
From: Schaefer, Alexandra[aschaefe@email.unc.edu]
Sent: Sun 8/2/2020 8:15:02 AM (UTC-05:00)
Subject: Re: HKU3 data

Hi Vineet,

thanks for digging out your HKU3 data---

We decided to go ahead and sequence the isolate that we have in the BSL3 first, and then eventually add all the HKU3 information into the paper in the revised version.

It would be great if you could provide the Prism files for the data comparing Rachel's original virus with Bat-SRBD-MAv; we could add that to the paper together with the sequences of both viruses (Rachel has submitted hers to GenBank already; Bat-SRBD-MAv will be added as soon as we have the seq.).

Thanks and Happy Sunday,
Alex

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Sunday, August 2, 2020 7:40 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Gralinski, Lisa E <lgralins@email.unc.edu>
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To: Schaefer, Alexandra <aschaefe@email.unc.edu>
Cc: Gralinski, Lisa E <lgralins@email.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>
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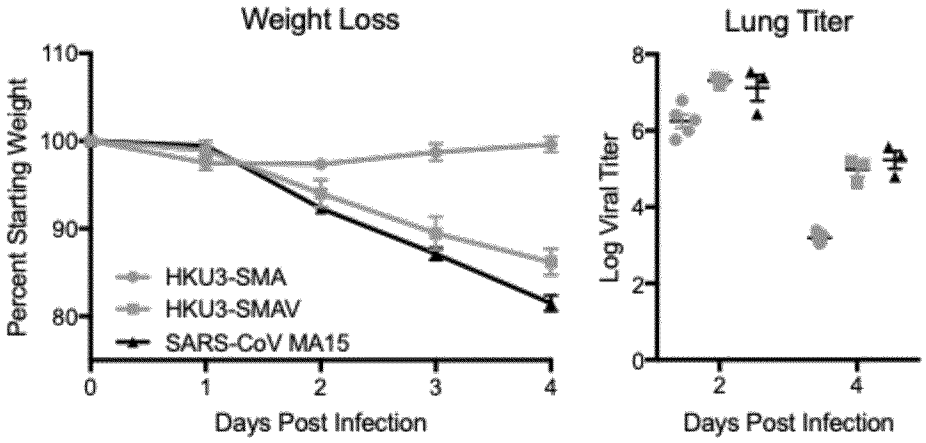

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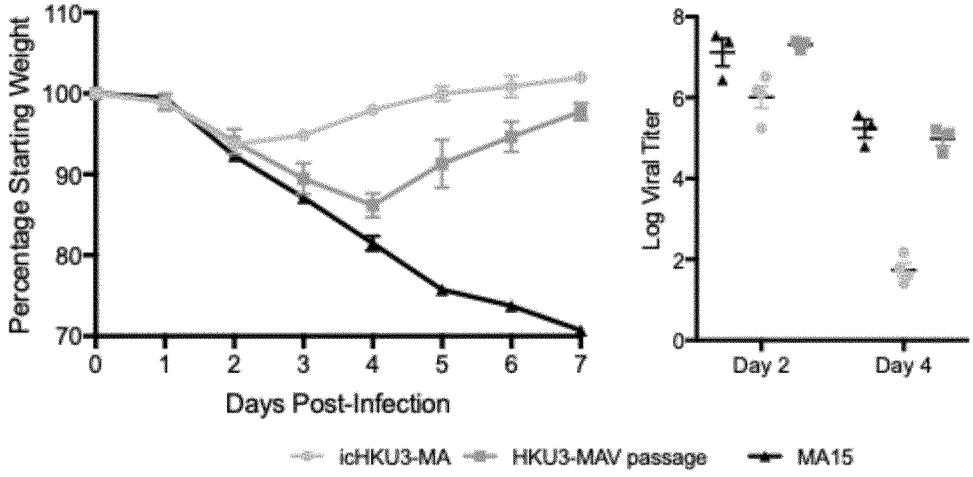

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From: Schaefer, Alexandra <aschaefe@email.unc.edu>
Sent: Thursday, July 23, 2020 4:12 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
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It would be great if you could send me the data, we might put it into the manuscript as supplement data characterizing the HKU3 virus?

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To: Totura, Allison (OS/ASPR/BARDA)[Allison.Totura@hhs.gov]; Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]
From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Thur 8/6/2020 9:00:19 AM (UTC-05:00)
Subject: RE: ACTIV Discussion: Viral Stocks

Hi Allison,
I can participate in this call from the Baric laboratory side of things.
thanks,
Lisa

Lisa Gralinski
Assistant Professor
Department of Epidemiology
University of North Carolina
919-966-3890

From: Totura, Allison (OS/ASPR/BARDA) <Allison.Totura@hhs.gov>
Sent: Thursday, August 6, 2020 8:25 AM
To: Gralinski, Lisa E <lgralins@email.unc.edu>; Menachery, Vineet <vimenach@UTMB.EDU>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Graham, Rachel <rlgraham@ad.unc.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; Florence, Clint (NIH/NIAID) [E] <clint.florence@nih.gov>
Subject: ACTIV Discussion: Viral Stocks

Hi,

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Thanks,
Allison

Allison Totura, PhD
Biologist | Division of Nonclinical Development
Biomedical Advanced Research and Development Authority (BARDA)
Office of the Assistant Secretary for Preparedness and Response (ASPR)
Phone: (202)774-8586

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ellebedy, Ali[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; jim.heath@isbscience.org[jim.heath@isbscience.org]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID)

[E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Tue 8/4/2020 2:00:38 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - August 11, 2020
ViPR_IRD_WorkShop2020.pdf
nCoV PI call attendee list.xlsx

Hi All,

Today, we were treated to a double feature brought to you by:

Dr. Sabra Klein
"Defining the causes of heterogeneity in antibody responses against SAR-CoV-2"
-and-
Dr. Weina Sun
"Newcastle disease viruses (NDV) expressing the spike protein of SARS-CoV-2 as vaccine candidates"

Thank you both for presenting on such short notice and to everyone that attended the meeting. The attendance is attached for your reference. I've also attached a flyer for the ViPR Workshop. If interested in attending, the registration link is embedded in the PDF.

On Tuesday, August 11th, Dr. Sara Cherry will be giving a presentation titled "**COVID-19: Can we identify new antivirals?**"

Have a great week!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

ViPR
Virus Pathogen Resource

BV-BRC Virtual Workshops for SARS-CoV-2 and the Coronaviridae virus family

The BRC team will be offering a series of online webinars and workshops, with a focus on SARS-CoV-2 and the Coronaviridae virus family. Each session will include a short 15 minute live demo of ViPR tools, followed by an optional mini-tutorial. The ViPR team will then remain online for the remainder of the hour for hands on Q&A. Each session will be accompanied by tutorial documents that will allow the users to walk through the exercises on their own even after the sessions have ended.

Users will learn how to search for data, use comparative analysis tools, and save data to their workbench for later analyses.

Registration links for individual sessions can be found below. Registered users will receive an online meeting link, along with a mini-tutorial exercise shortly before the start of webinar/workshop.

Tues Aug 4, 2020, 8:00 AM PDT	I- Genomes and Annotation.	Registration
Tues Sep 1, 2020, 8:00 AM PDT	II- Comparative genomics.	Registration
Tues Oct 6, 2020, 8:00 AM PDT	III- SARS-CoV-2 Assembly & Annotation.	Registration
Tues Nov 3, 2020, 8:00 AM PDT	IV- Host response omics data.	Registration
Tues Dec 1, 2020, 8:00 AM PDT	V- Coronaviridae orthologue group prediction.	Registration

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							
David Renner (Susan Weiss lab)		x					

David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Lambert						

Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
mprabhudas						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x

Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
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4-Aug

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To: Gralinski, Lisa E[lgralins@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]
From: Totura, Allison (OS/ASPR/BARDA)[Allison.Totura@hhs.gov]
Sent: Thur 8/6/2020 9:33:23 AM (UTC-05:00)
Subject: RE: ACTIV Discussion: Viral Stocks

Great, thank you Lisa.

I will forward the invite, it may say that it is from Rosa Maria Alvarez because she organized the meeting.

Allison Totura, PhD
Biologist | Division of Nonclinical Development
Biomedical Advanced Research and Development Authority (BARDA)
Office of the Assistant Secretary for Preparedness and Response (ASPR)
Phone: (202)774-8586

From: Gralinski, Lisa E <lgralins@email.unc.edu>
Sent: Thursday, August 6, 2020 10:00 AM
To: Totura, Allison (OS/ASPR/BARDA) <Allison.Totura@hhs.gov>; Menachery, Vineet <vimenach@UTMB.EDU>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Graham, Rachel <rlgraham@ad.unc.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; Florence, Clint (NIH/NIAID) [E] <clint.florence@nih.gov>
Subject: RE: ACTIV Discussion: Viral Stocks

Hi Allison,
I can participate in this call from the Baric laboratory side of things.
thanks,
Lisa

Lisa Gralinski
Assistant Professor
Department of Epidemiology
University of North Carolina
919-966-3890

From: Totura, Allison (OS/ASPR/BARDA) <Allison.Totura@hhs.gov>
Sent: Thursday, August 6, 2020 8:25 AM
To: Gralinski, Lisa E <lgralins@email.unc.edu>; Menachery, Vineet <vimenach@UTMB.EDU>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Graham, Rachel <rlgraham@ad.unc.edu>
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Cc: Baric, Ralph[rbaric@email.unc.edu]
From: Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]
Sent: Thur 8/6/2020 9:45:27 AM (UTC-05:00)
Subject: Re: ACTIV Discussion: Viral Stocks

All –

We are working to re-schedule. Kara (key member of the ACTIV team) wasn't available today.

Thanks –

Clint

From: "Totura, Allison (OS/ASPR/BARDA)" <Allison.Totura@hhs.gov>
Date: Thursday, August 6, 2020 at 10:33 AM
To: "Gralinski, Lisa E" <lgralins@email.unc.edu>, "Menachery, Vineet" <vimenach@UTMB.EDU>, "Sheahan, Timothy Patrick" <sheahan@email.unc.edu>, "Graham, Rachel" <rlgraham@ad.unc.edu>
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Phone: (202)774-8586

To: Efrem.Lim@asu.edu[Efrem.Lim@asu.edu]; Brenda.Hogue@asu.edu[Brenda.Hogue@asu.edu]; mfrieman@som.umaryland.edu[mfrieman@som.umaryland.edu]; darryl.falzarano@usask.ca[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; adolfo.garcia-sastre@mssm.edu[adolfo.garcia-sastre@mssm.edu]; ryan.camping@mssm.edu[ryan.camping@mssm.edu]; rbaric@email.unc.edu[rbaric@email.unc.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; mark.denison@vanderbilt.edu[mark.denison@vanderbilt.edu]; kanta.subbarao@influenzacentre.org[kanta.subbarao@influenzacentre.org]; jallen19@luc.edu[jallen19@luc.edu]; falonzo@luc.edu[falonzo@luc.edu]; sbaker1@luc.edu[sbaker1@luc.edu]; ecampbell@luc.edu[ecampbell@luc.edu]; tgallag@luc.edu[tgallag@luc.edu]; miwashima@luc.edu[miwashima@luc.edu]; kknight@luc.edu[kknight@luc.edu]; dlannin@luc.edu[dlannin@luc.edu]; ple@luc.edu[ple@luc.edu]; hmathew@luc.edu[hmathew@luc.edu]; bmounce@luc.edu[bmounce@luc.edu]; cosipo@luc.edu[cosipo@luc.edu]; lqiao@luc.edu[lqiao@luc.edu]; aulijasz@luc.edu[aulijasz@luc.edu]; kvisick@luc.edu[kvisick@luc.edu]; awolfe@luc.edu[awolfe@luc.edu]; ywu24@luc.edu[ywu24@luc.edu]; suprichard@luc.edu[suprichard@luc.edu]; kradek1@lumc.edu[kradek1@lumc.edu]; cputonti@luc.edu[cputonti@luc.edu]; kforma@luc.edu[kforma@luc.edu]; adingwall@luc.edu[adingwall@luc.edu]; mdiaz2@luc.edu[mdiaz2@luc.edu]; mchoudhry@lumc.edu[mchoudhry@lumc.edu]; jclanc1@luc.edu[jclanc1@luc.edu]; rschult@luc.edu[rschult@luc.edu]; pwitte@luc.edu[pwitte@luc.edu]; nikolich@email.arizona.edu[nikolich@email.arizona.edu]; mabecassis@email.arizona.edu[mabecassis@email.arizona.edu]; elizabeth.aitken@unimelb.edu.au[elizabeth.aitken@unimelb.edu.au]; nicole.allard@mh.org.au[nicole.allard@mh.org.au]; cdos@unimelb.edu.au[cdos@unimelb.edu.au]; lokanayaki.anguswamy@mh.org.au[lokanayaki.anguswamy@mh.org.au]; melinda.ashcroft@unimelb.edu.au[melinda.ashcroft@unimelb.edu.au]; jennifer.audsley@unimelb.edu.au[jennifer.audsley@unimelb.edu.au]; anna.ayres@mh.org.au[anna.ayres@mh.org.au]; abachem@unimelb.edu.au[abachem@unimelb.edu.au]; ann-marie.baker@mh.org.au[ann-marie.baker@mh.org.au]; jemma.bakos@mh.org.au[jemma.bakos@mh.org.au]; susan.ballard@unimelb.edu.au[susan.ballard@unimelb.edu.au]; laura.bannerman@unimelb.edu.au[laura.bannerman@unimelb.edu.au]; ian.barr@influenzacentre.org[ian.barr@influenzacentre.org]; alexanderdav@unimelb.edu.au[alexanderdav@unimelb.edu.au]; sbedoui@unimelb.edu.au[sbedoui@unimelb.edu.au]; markdb@unimelb.edu.au[markdb@unimelb.edu.au]; Noleen.bennett@mh.org.au[Noleen.bennett@mh.org.au]; babiggs@unimelb.edu.au[babiggs@unimelb.edu.au]; michael.bramhall@unimelb.edu.au[michael.bramhall@unimelb.edu.au]; simone.bittmann@mh.org.au[simone.bittmann@mh.org.au]
From: Romel john Garrido[rmjmg@yahoo.com]
Sent: Fri 8/14/2020 5:21:48 AM (UTC-05:00)
Subject: A Hypothesis: The Receptor Site Removing Virus
ABA1A8EE-AA0D-43FF-A77A-5E8C95648572.jpeg

Good Day Doctor,

In line with the call of the times, I am inclined to submit a hypothesis(although not back-up by evidence) regarding what I think is the real mechanism of action Sars CoV virus which makes it so elusive.

Hypothesis of Sars CoV 2 and similar viruses upon early entry to host. Evolution of viruses which are zoonotic in nature(The Glycoprotein Receptor Site Removing Virus).

Congratulations to the scientific community for breakthrough Doctor about Dexamethasone. I have an inkling as to how steroids help. My hypothesis closely resembles that study Doctor. Because steroids help in immunosuppression especially the role of macrophages.

My Hypothesis approaches to paradox and is not likely to be generally accepted. Please read my hypothesis Doctor. Thank you.

I am so puzzled by its(SARS CoV2) mechanism, that I hypothesized:

SARS CoV 2 during the early phase of entry

The Sars CoV 2 virus, is like all viruses attack by the immune system during the early phase of entry. However, It is a unique Virus. During humoral and cell mediated response in the early phase of entry, Sars CoV 2 can easily elude immune response whenever threatened by removing off its receptor sites composing of S epitopes. Leaving the virus with only the capsid. And in its absence, the immune system is thought to have shut down, then Sars CoV 2 S epitopes from the capsids start to agglutinate or regenerate (this removing and attaching / regenerating of epitopes is my hypothesis Doctor) and the whole process starts again and again. ''Many years ago Doctor, in the year 2000, I read an old scientific American journal saying that some scientist remove the receptor sites of a similar to HIV virus in caterpillars and what astonished them is that the immune system instead of attacking it, it instead shut off''. Doctor normally when a virus enters the host, it will be recognized through membrane-bound Pattern Recognition Receptors (PRRs), the complement system and other mechanisms (including cross-reactive antibodies to previously encountered structures that are cross-reactive, such as related viruses). Membrane-bound PRRs will trigger direct phagocytosis while soluble PRR will opsonize (tag) the particle for uptake by phagocytic cells. They will ingest the particle and degrade it (proteolytic enzymes, reactive oxygen species such as H2O2). However, I believe with my hypothesis, viral capsid with no epitopes, its molecular pattern will still be recognized thru Pathogen Associated Molecular Patterns (PAMP), TLR 3 and TLR 7 together with Rig-1. But it cannot make the membrane bound PRRs phagocitized the viral capsid without epitopes...everything is over functioning but no complete phagocytosis will happen and that's why cytokine storm occur. The process continue until SARS-CoV-2 reaches and uses the SARS-CoV receptor ACE2 for entry and the serine protease TMPRSS2 for S protein priming. I believe the SARS CoV 2 is doing a self defense mechanism of detaching its own S epitopes in order not to be phagocitized, soluble PRRs will tag the particle for uptake by phagocytic cells but it will not be phagocitized since it can easily remove its epitopes. I also know that viruses cannot synthesize proteins on their own (when it is still outside the target cell),but somehow SARS CoV 2 is able to do this removing and attaching / or regenerating its epitopes at a faster rate than the immune system. I believe there is an enzymes or acid that causes it but is still unknown....somehow it removes its own receptor S epitopes immediately after opsonization and when the Phagocytic cell is about engulf it.

As to the treatment, I can only speculate , but I really believe this phenomenon of viral removal of glycoprotein is cause by chemical reactions from phagocytic cells...theoretically, e.g during classical pathway of complement activation, if somehow we can inhibit phagocytic cells for a while so that the epitopes will not be detached and allow normal antigen cell death to be tag and opsonized thru C5b-9 (C4bC2aC3bC5bC6C7C8C9 thru Membrane Attack Complex to occur), then it would have been tricked(but this is only speculations and causes immunosuppression). Somehow we must develop a mechanism to fight back receptor site removing viruses, assuming of course-only if my hypothesis is correct...but again this(Treatment) is only speculation. But the principle is not to allow the antigen to remove its epitopes. Doctor, this idea is very unique and original. No literature, in my very limited resources has ever been written about this hypothesis - virus shedding its epitopes. However, I really believe this is the piece of the puzzle that really fits. Although no literature exist to prove it's an

epitope shedding virus, still no literature also says it's not either. I really think- please forgive me to be so blunt Doctor, but no vaccines in the classical sense can solve this pandemic...still, I am praying my theory is wrong and an effective vaccine can be found...but if not, we really need a different approach. This is the reason, I think why reinfection (is thought to occur) happens and why development of effective antibodies is quite impossible for now. I'm just glad to have told my hypothesis to you Doctor. Doctor, I believe this is the evolution of some viruses which are zoonotic in nature even the Sars-CoV-2, "the receptor site removing viruses". And we are entering to a new era in Science. Thank you for your time Doctor. Forgive me for bothering you again but I really believe we can give supportive care now and reduce a large percentage of death. Please I request for anonymity.

''Some findings suggest they have found T cells but no antibodies".

Membrane bound PRR's triggers direct phagocytosis. Although opsonize it never reaches C5b-9 since SARS CoV 2 manage to remove its epitopes. APC still interacts with T Cells though ...e.g macrophages who cannot destroy the SARS CoV 2 Virus (since it's an epitope shedding virus...from my earlier hypothesis) still tries to communicate with T Cells and since there are some particle from shed epitope- they are being shown and communicated by APC...that's why T Cells are activated and mediated per se. PAMP, TLR 3, TLR 7 and Rig-1 still recognizes the capsid with no epitope and the immune system attacks thru T Cells. Cytotoxic T cells becomes present in large numbers in convalescent individuals because SARS CoV 2 already invaded a lot of cells which activated Program Cell Death. Over time, in convalescent individuals antibody rapidly declined to undetectable levels but T Cells keep on recognizing the Capsid. It makes perfect sense.

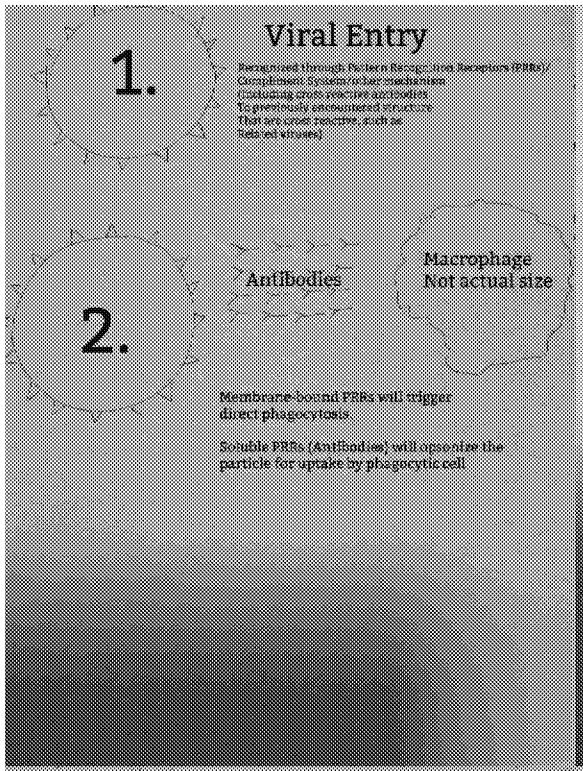
Please study my Hypothesis Doctor. I really believe Dexamethasone is thought to be effective not because of its anti inflammatory effect but because it can inhibit monocytes and thus macrophages migration. It's a paradox...from my hypothesis- the more you inhibit macrophages the more the virus dies. You may want to look at other macrophage inhibiting drugs. I'll just attach a picture for better understanding of my hypothesis. I have no other agenda. I request for anonymity Doctor.

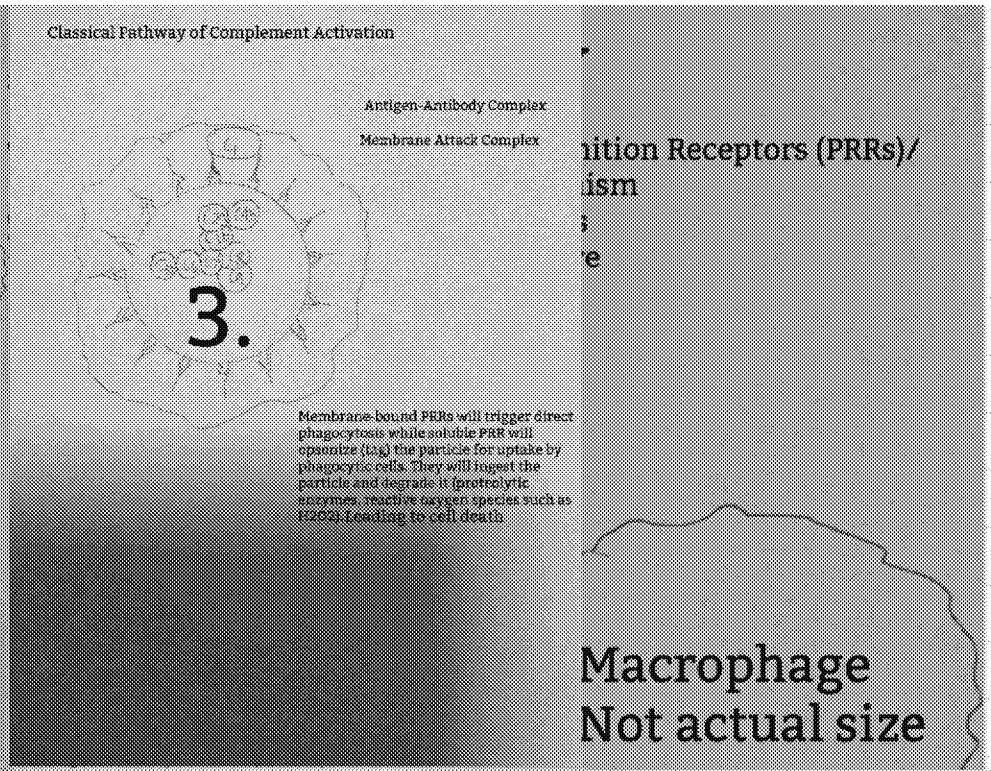
Antibodies are supposed to be cross reactive to same strain SARS CoV 2 Virus. Reinfection doesn't make sense. I hope somebody can solve this paradox soonest. Just maybe this is pointing to the right direction and by some miracle you may want to investigate this further since there is no advance science in my part of the world. My name is Romel, I am currently working as an Agricultural Pilot. I also have a BS in Biology many years ago. I have no other agenda Doctor.

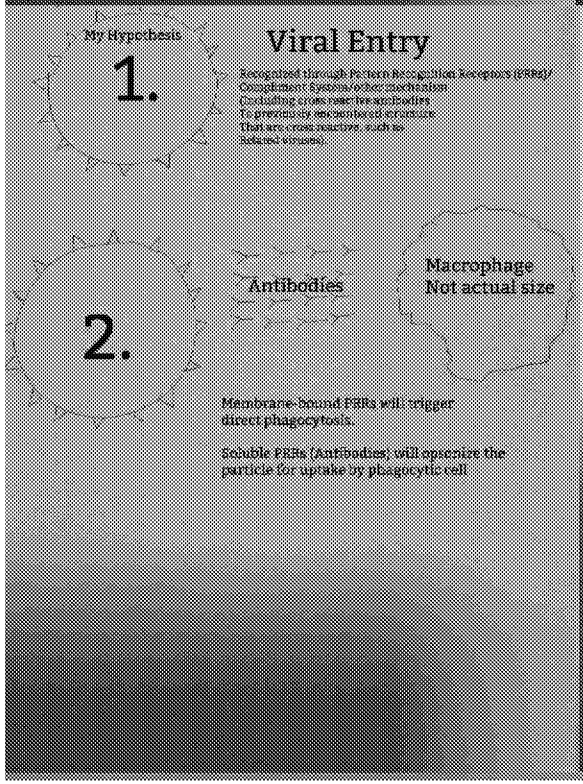
Thank you again Doctor

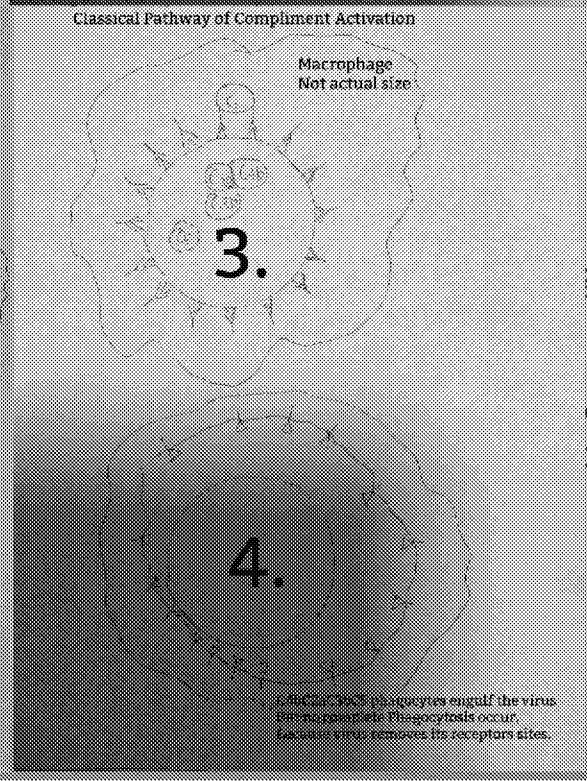
Respectfully,

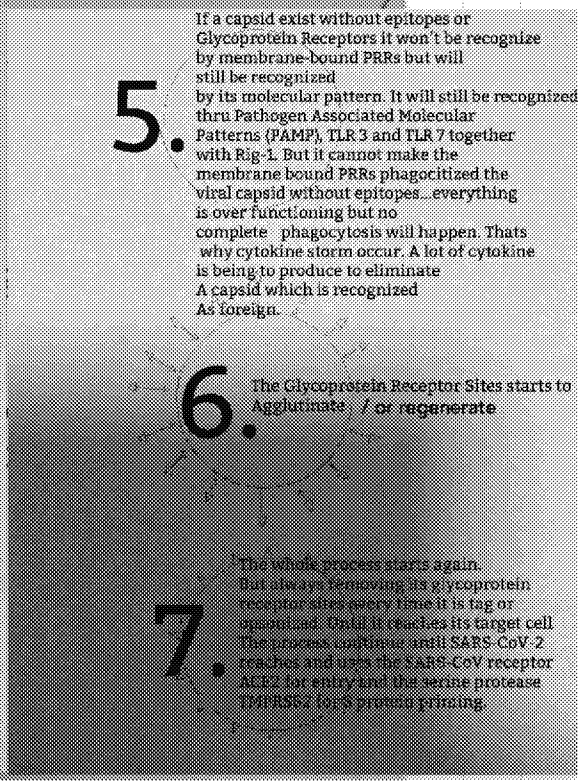
Romel











To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 8/20/2020 8:15:25 AM (UTC-05:00)
Subject: FW: Drafted agenda for the Systems Immunology U19 Program Annual Meeting on Oct. 8-9
Systems Immun_2020_Agenda_draft1.docx

Hi All,
Please see attached.
Toni

From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Wednesday, August 19, 2020 3:37 PM
To: Ulevitch, Richard <Ulevitch@scripps.edu>; Bruce Beutler <Bruce.Beutler@utsouthwestern.edu>; Garry Nolan (gnolan@stanford.edu) <gnolan@drowlab.com>; Diercks, Alan <Alan.Diercks@seattlechildrens.org>; Baric, Ralph S <rbaric@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Michael Gale <mgale@u.washington.edu>; mtferris <mtferris@email.unc.edu>; Shannon McWeeney <mcweeney@ohsu.edu>; Arlene Sharpe <arlene_sharpe@hms.harvard.edu>; Vijay Kuchroo <vkuchroo@evergrande.hms.harvard.edu>; Jonathan Kagan <jonathan.kagan@childrens.harvard.edu>; nhacohen@mgh.harvard.edu; John Doench <jdoench@broadinstitute.org>
Subject: Drafted agenda for the Systems Immunology U19 Program Annual Meeting on Oct. 8-9
Importance: High

Dear Colleagues,

Thank you very much for sending me the titles of your presentations.

Attached please find the drafted agenda for our Systems Immunology U19 Program Annual Meeting on Oct. 8-9. Please let me know if you have any questions or suggestions. Once you think it is ok, I will finalize the agenda.

Thank you.

Best,
Joy

Systems Immunology U19 Annual Meeting

October 8-9, 2020

National Institutes of Allergy and Infectious Diseases

Agenda

October 8:

12:00 – 12:10 PM	**Welcome/Introductory Remarks** **Joy Liu/Daniel Rotrosen,** NIAID
12:10 – 2:10 PM	*Systems Approach to Immunity and Inflammation*
12:10 – 12:50 PM	*Germline Mutagenesis with Automated Meiotic Mapping to Study Immunity in Mice* **Bruce Beulter**, UT Southwestern Medical Center
12:50 – 1:20 PM	*Systems Analysis of Innate Immune Responses to Infection* **Alan Diercks**, Seattle Children's Research Institute
1:20 – 1:55 PM	*The Hierarchical Structures of Immune Neighborhoods* **Garry Nolan**, Stanford University
1:55 – 2:10 PM	*Inflammasomes and Inflammation in Health and Disease* **Richard Ulevitch,** The Scripps Research Institute
2:10 – 2:20 PM	**Discussion**
2:20 – 2:40 PM	**Break**
2:40 – 4:40 PM	*Systems Immunogenetics of Biodefense and Emerging Pathogens in the Collaborative Cross*
2:40 – 2:45 PM	*Introduction: SIG U19 and the Collaborative Cross* **Ralph Baric**, University of North Carolina at Chapel Hill
2:45 – 3:20 PM	*Project 1: Emerging Coronaviruses and SARS-CoV2* **Ralph Baric**, University of North Carolina at Chapel Hill
3:20 – 3:50 PM	*Project 2: Influenza Virus* **Mark Heise**, University of North Carolina at Chapel Hill
3:50 – 4:20 PM	*Project 3: West Nile Virus* **Michael Gale**, University of Washington
4:20 – 4:30 PM	*Core B: Mouse Genetics Core* **Marty Ferris**, University of North Carolina at Chapel Hill
4:30 – 4:40 PM	*Core C: Systems Genetics and Bioinformatics Core* **Shannon McWeeney,** Oregon Health & Science University
4:40 – 4:50 PM	**Discussion**

4:50 – 4: 55 PM	**End of Day 1**

October 9:

12:55 – 1:00 PM	**Welcome back** **Joy Liu, NIAID**
1:00 – 3:00 PM	*Defining Regulators of Immunity to Acute Infection Using CRISPR Screens*
1:00 – 1:10 PM	*Program Overview and Updates* **Arlene Sharpe**, Harvard University Medical School
1:10 – 1:25 PM	*CHIME Technology Updates and CD8 T Cell Screens* **Martin LaFleur**, Harvard University Medical School
1:25 – 1:45 PM	*Project 1: CRISPR Screens to Discover Regulators of CD4 T cells* **Vijay Kuchroo**, Brigham and Women's Hospital
1:45 – 2:05 PM	*Project 2: CRISPR Screens to Discover Regulators of DC* **Jon Kagan,** Children's Hospital Corporation
2:05 – 2:25 PM	*Project 2: CRISPR Screens to Discover Regulators of DC/T Cell Interactions* **Nir Hacohen,** The Board Institute
2:25 – 2:40 PM	*Core B: Bioinformatics and Data Management* **Orr Ashenberg,** The Board Institute
2:40 – 2:50 PM	*Core C: CRISPR Library* **John Doench,** The Board Institute
2:50 – 3:00 PM	*CRISPR Technology Development* **Katie Geiger-Schuller,** The Board Institute
3:00 – 3:10 PM	**Discussion**
3:10 – 3:15 PM	**Adjourn General Meeting**
3:15 – 3:35 PM	**Break**
3:35 – 4:35 PM	**Systems Immunology Steering Committee Meeting** **(closed session, Steering Committee members and NIAID staff only)**
4:35 – 4:40 PM	**End of Meeting**

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; aneesh.mehta@emory.edu[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]

Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov];

Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDPHSIS/CGH/DGHT)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 8/21/2020 12:43:02 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - August 25th
nCoV PI call attendee list.xlsx

Hi All,

On Tuesday, August 11th, Dr. Sara Cherry gave a wonderful presentation titled "**COVID-19: Can we identify new antivirals?**". Thank to all who attended the meeting and to Dr. Cherry for her presentation.

Our next presenter will be Dr. Mehul Suthar on Tuesday, August 25th. Dr. Suthar's presentation is titled "**Immunity to SARS-CoV-2 infection in humans**". Hope everyone can join!

Have a great weekend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						
Daved Fremont							

David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						

Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						

Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
William Florence						
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
x	x	x	x	x	x	x	x	x
x	x	x	x					
x	x	x	x	x	x	x	x	x
					x			
x	x	x	x	x	x		x	x
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							x	x
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	x							

						x		
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	x				x	x	x	x
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x	x
x	
	x
x	x

To: Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; qtan@pathology.wustl.edu[qtan@pathology.wustl.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]
From: Purvine, Emilie[Emilie.Purvine@pnnl.gov]
Sent: Fri 8/21/2020 7:29:05 PM (UTC-05:00)
Subject: hypergraphs paper ready to submit
Hyperbio_centrality_paper.pdf

Hello all,

Thank you for your patience as my project team worked on revisions to the hypergraph paper you all saw back in January (wow has it been that long already?!). In our opinion we are ready to submit to BMC Bioinformatics but I am sending you all a copy now in case anybody has any final changes, acknowledgements, etc. that need to be included. In addition to anything in the content of the paper you wish to comment on, I ask that you please double check the following:

*) Your affiliation(s) - is this up to date? Any changes needed?
*) Author contributions - please make sure what I have listed for you is appropriate and adequate
*) Acknowledgements - please let me know what grants should be acknowledged for any of your experimental or analysis work

I will be submitting this for our internal approval process on Monday. Once that is approved, unless there are any objections, I will submit to the journal. Please try to get me comments before COB Friday, August 28. I hope to submit the following week.

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Data Science and Analytics Group

Pacific Northwest National Laboratory
PNNL/Battelle Suite 500
1100 Dexter Ave. N
Seattle, WA 98109
Phone: 206-528-3461

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Baric, Ralph S[rbaric@email.unc.edu]
From: Jacob Kocher[jake.kocher22@gmail.com]
Sent: Tue 1/21/2020 3:24:43 PM (UTC-06:00)
Subject: Re:
B cell paper figures 10062019 - JK neut.docx

Hi Ralph and Vineet,
My apologies for the delayed response. The first 6 weeks were a bit difficult (adjusting is a good word for that time), but now we're past that and have a happy baby. Couldn't be happier!

I attached the neut curves that I got for D15. This confirms that HELMET mice have some neutralizing response (Tem Morrison's group has also shown this previously).

Given VDM's last email, I'm curious what the next step is - I don't have time in the immediate future to address the reviewer's comments to send back to JVI.

-Jake

On Mon, Jan 6, 2020 at 5:02 PM Menachery, Vineet <vimenach@utmb.edu> wrote:

> Hey Jake and Ralph,
>
> Happy new year to you both. Congrats on the baby. Hopefully you are adjusting well. You have so much to look forward to.
>
> In regards to the paper, I have read through it, skimming and looking through the figures. I still think that the manuscript needs a lot of work. Anne did not address the reviewer comments and I still find the paper confusing and sloppy.
>
> Based on what is here, I do not think it can go back to JVI. It still needs to be cleaned up quite a bit in the text for clarity. I would recommend dropping figure 3 altogether, as the point is lost and not especially clear. Similarly, I would take the HELMET data out of figure 4 and have it on its own as figure 5. FInally, figure 5-6 should be combined. The text needs to be modified here too to be much more careful in the discussion.
>
> Overall, there is good data here and a clear story. Unfortunately, in the current form, it is very difficult to get to that conclusion.
>
> VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, January 2, 2020 12:15 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Jacob Kocher <jake.kocher22@gmail.com>
Subject:

Hi Jacob and Vineet, Here is the version of Anne's B cell paper with her final comments. Jake, can you take a look to make sure the new data you generated is appropriately presented. Vineet, I appreciate your comments. I'd also like your thoughts on where to submit this. Its been a year plus since it was reviewed at JV-should we go back or chase a sure

thing. Jake, congrats on the new baby! Hope you both had a Happy Holiday and New Year. Ralph

FIGURES

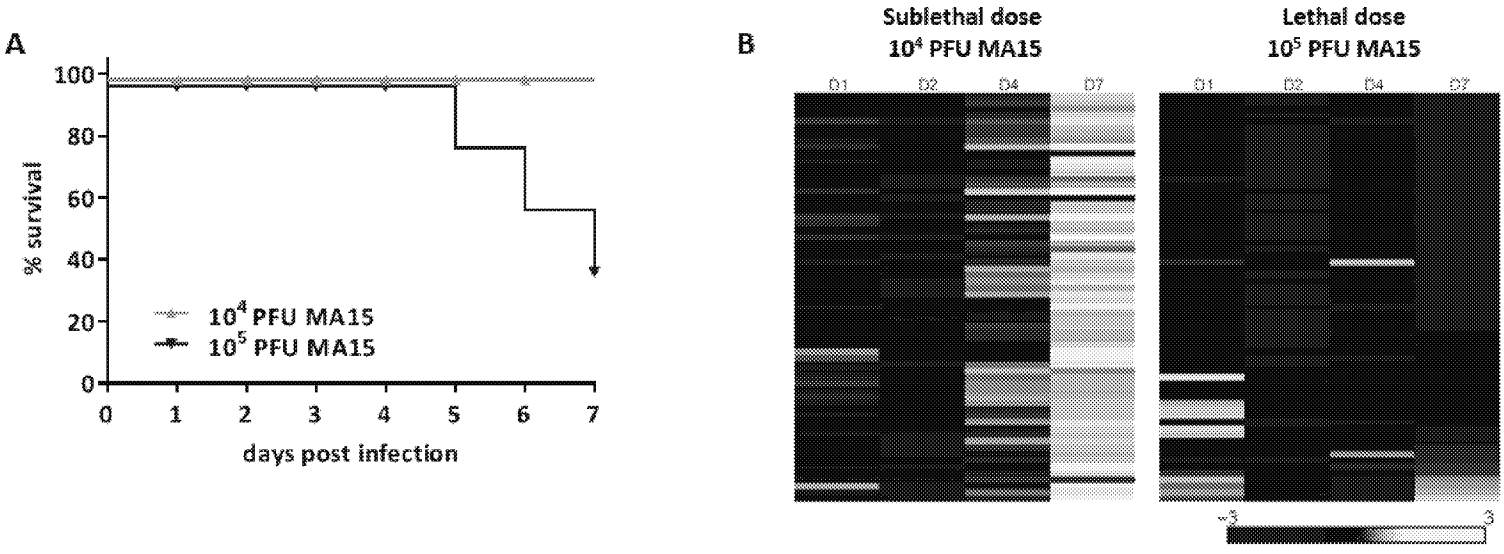
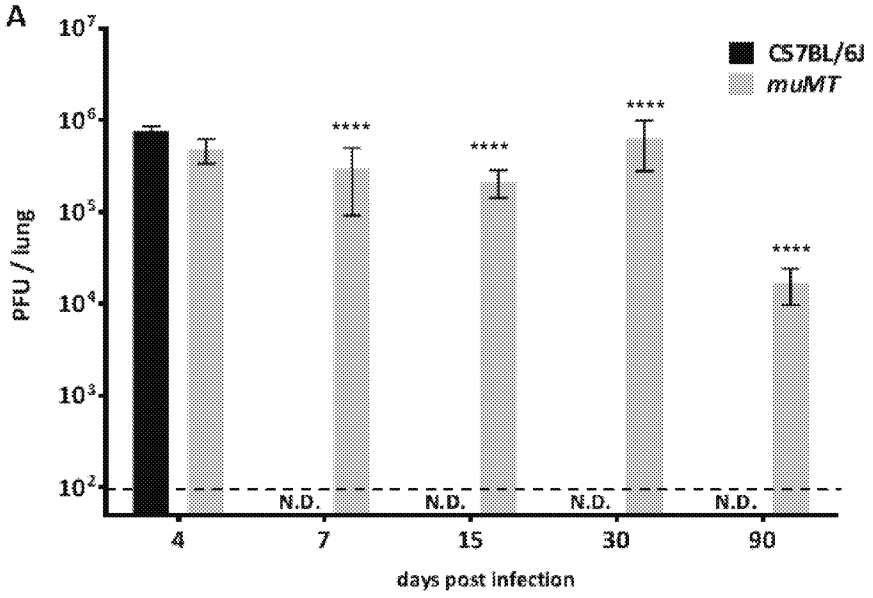
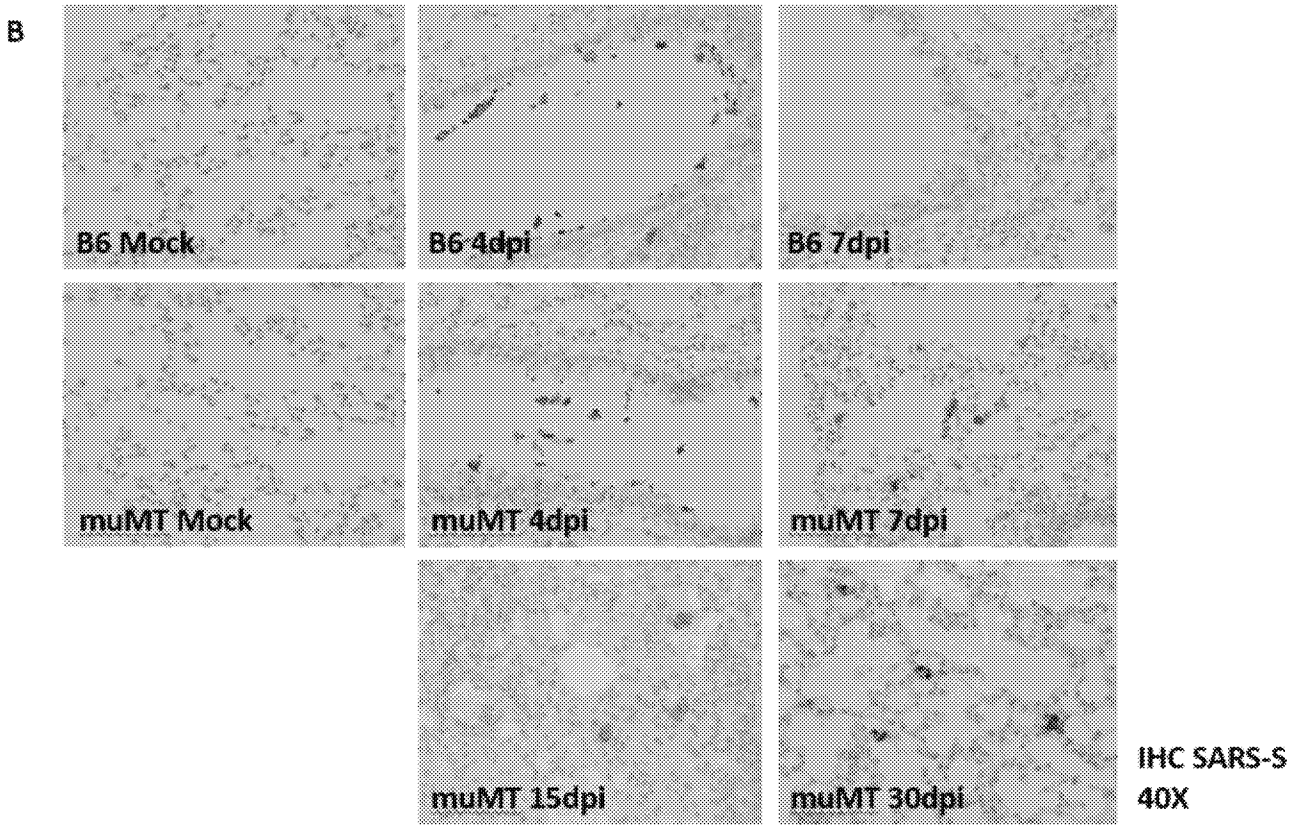
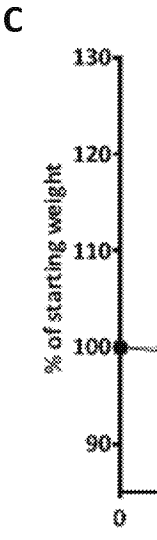
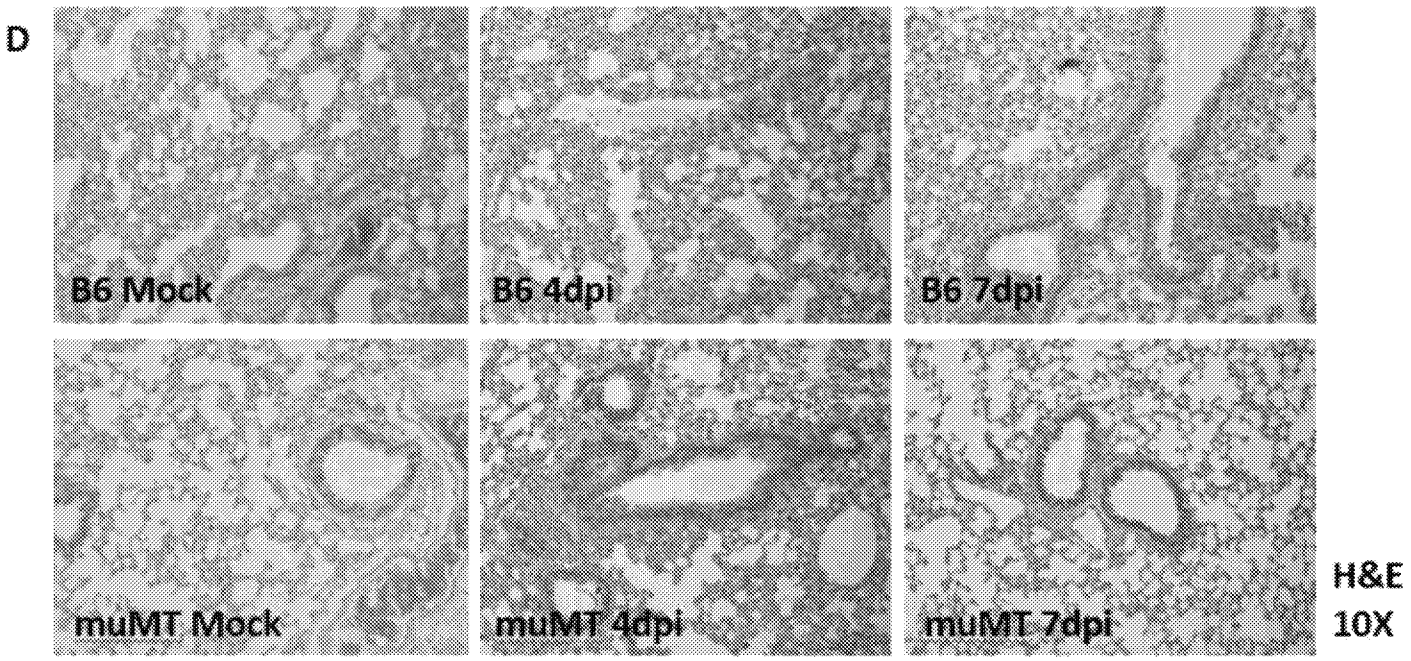


Fig 1. Bioinformatics points to an important role for B cells. 20 week old C57BL/6J mice were infected intranasally with a 50uL sublethal (10^4 PFU/mouse) or lethal (10^5 PFU/mouse) dose of MA15 SARS-CoV diluted in PBS. (A) Survival curves for infected mice. Mice dropping below 70% weight loss were humanely sacrificed and counted as succumbing to disease for the purposes of the experiment. All mice were sacrificed at 7 dpi. n=5 per group. (B) Log_2 fold change ratio of immunoglobulin family-related gene expression from the lungs of MA15 SARS-CoV-infected C57BL/6J mice after infection compared to mock infected mice. Yellow indicates increased gene expression compared to mock. Blue indicates decreased expression compared to mock. Probe and gene descriptions provided in Fig S1.


A
C57BL/6J
muMT
PFU / lung
10^7
10^6
10^5
10^4
10^3
10^2
****
****
****
****
N.D.
N.D.
N.D.
N.D.
4
7
15
30
90
days post infection


B
B6 Mock
B6 4dpi
B6 7dpi
muMT Mock
muMT 4dpi
muMT 7dpi
muMT 15dpi
muMT 30dpi
IHC SARS-S
40X


C
% of starting weight
130
120
110
100
90
0



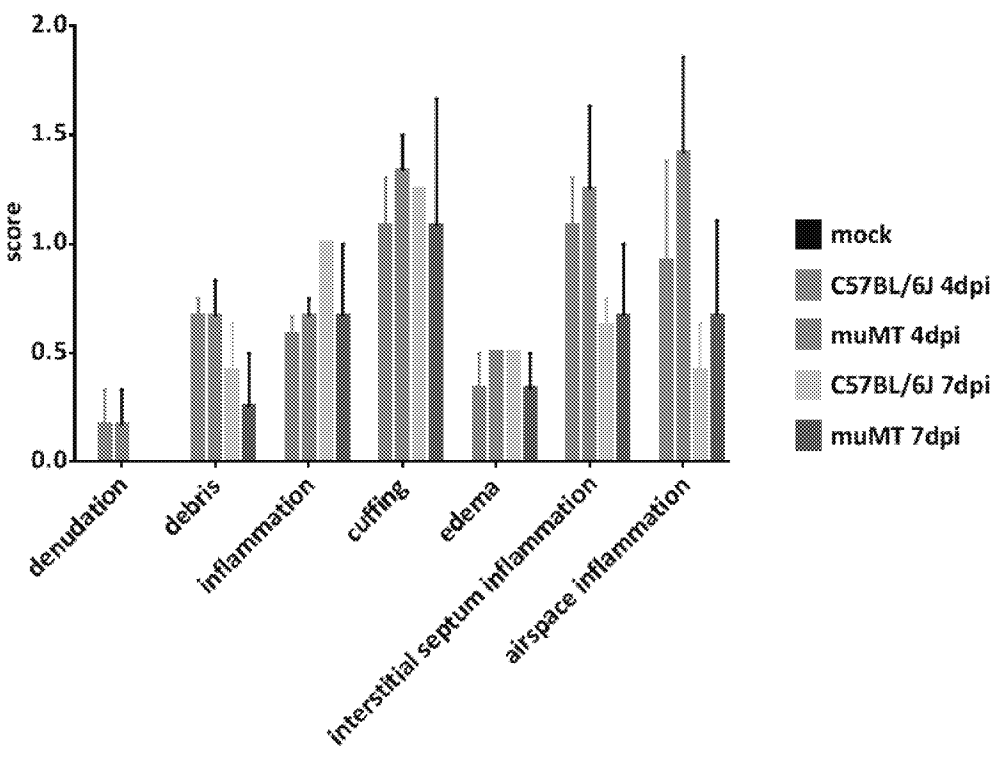
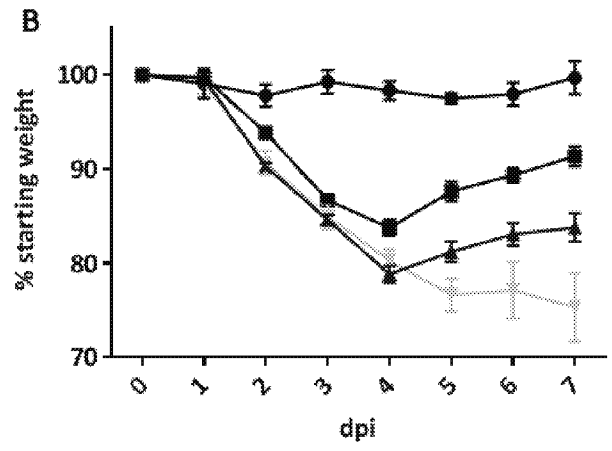
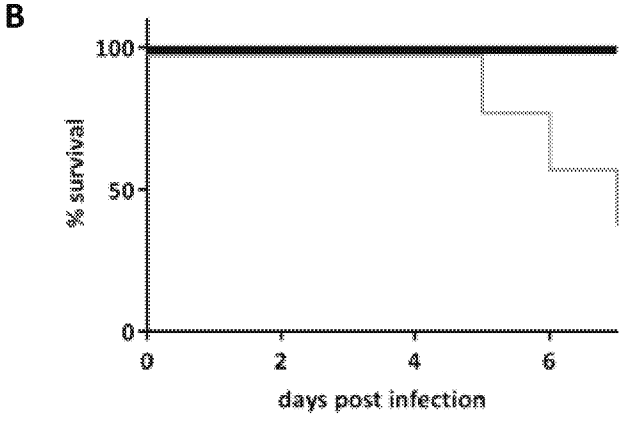


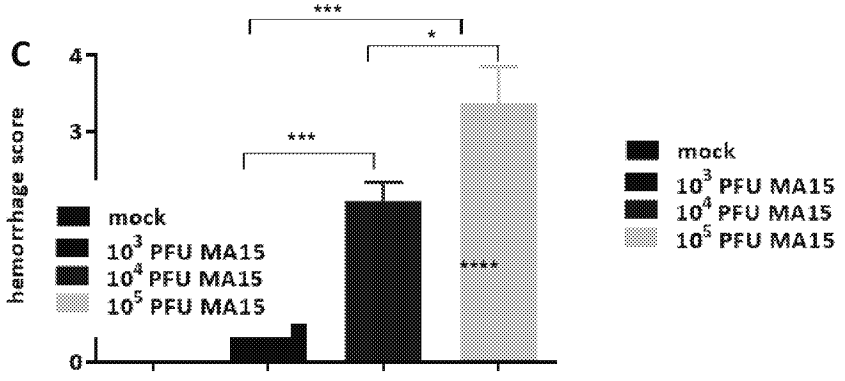
Fig 2. B cells are required to clear SARS-CoV. 10 week old C57BL/6J or muMT B cell deficient mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. (A) Lung mean virus load was quantitated by plaque

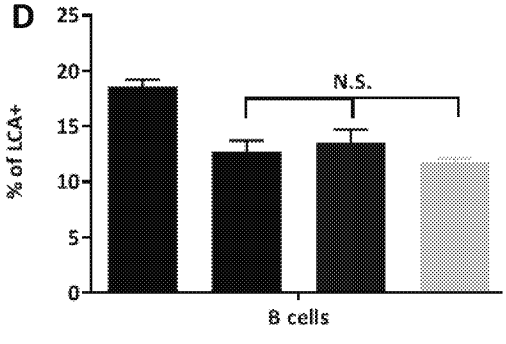
assay. Statistical significance determined using ANOVA analysis, with **** signifying $p<0.0001$. (B) Representative images of lung sections at indicated timepoints post-infection. SARS-CoV staining was performed via immunohistochemistry using anti-SARS-N and is shown in brown. (C) Mean weight loss per group is represented as a percent of starting weight for each mouse. Mice were weighed daily. (D) Representative images of lung sections at indicated timepoints post-infection. H&E staining is shown. (E) Lung injury scores from mice at indicated times. None show significant differences between C57BL/6J and *muMT* mice at matched timepoints.

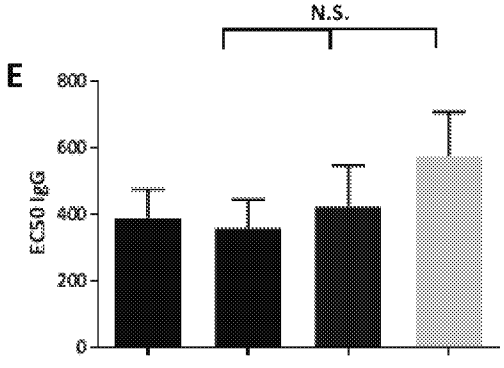

B
% starting weight
100
90
80
70
0
1
2
3
4
5
6
7
dpi

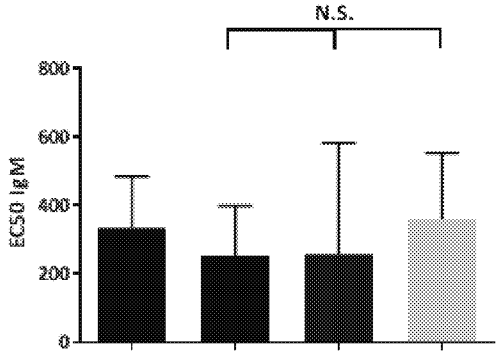

A
****
****
****


B
% survival
100
50
0
0
2
4
6
days post infection


C
hemorrhage score
4
3
0
***
*
***
****
mock
10^3 PFU MA15
10^4 PFU MA15
10^5 PFU MA15
mock
10^3 PFU MA15
10^4 PFU MA15
10^5 PFU MA15


D
% of LCA+
25
20
15
10
5
0
N.S.
B cells


E
EC50 IgG
800
600
400
200
0
N.S.


EC50 IgM
800
600
400
200
0
N.S.

F

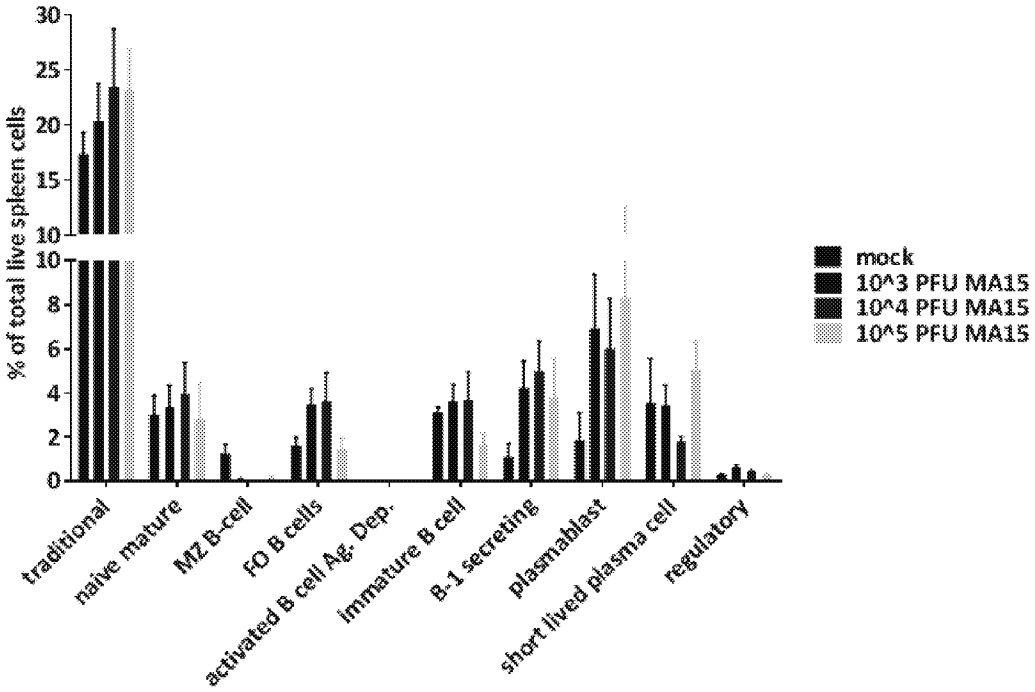


Fig 3. B cell and antibody responses do not correlate with pathogenesis. 20 week old mice were infected intranasally with a lethal (10^5 PFU/mouse) or sublethal (10^3 or 10^4 PFU/mouse) dose of MA15 SARS-CoV. n=5/group. (A) Mean weight loss per group is represented as a percent of starting weight for each mouse. Weights at each dose significantly differed from each other group at 5, 6, and 7 dpi. (B) Survival curves of infected mice. (C) Mean hemorrhage score of mouse lungs taken during 7 dpi harvest. (E) Mean total B cells as a percent of LCA+ cells. B cells are defined as B220+ and CD20+. (E) Mean SARS-S reactive immunoglobulin levels represented as EC50. (F) Splenic B cell populations after MA15 SARS-CoV infection at mock, sub-lethal, and lethal infection doses in 10 week old C57BL/6J mice – no significant differences were seen in B cell populations. All statistics performed by t test. * $p<0.01$. *** $p<0.0001$. ****$p<0.00001$.

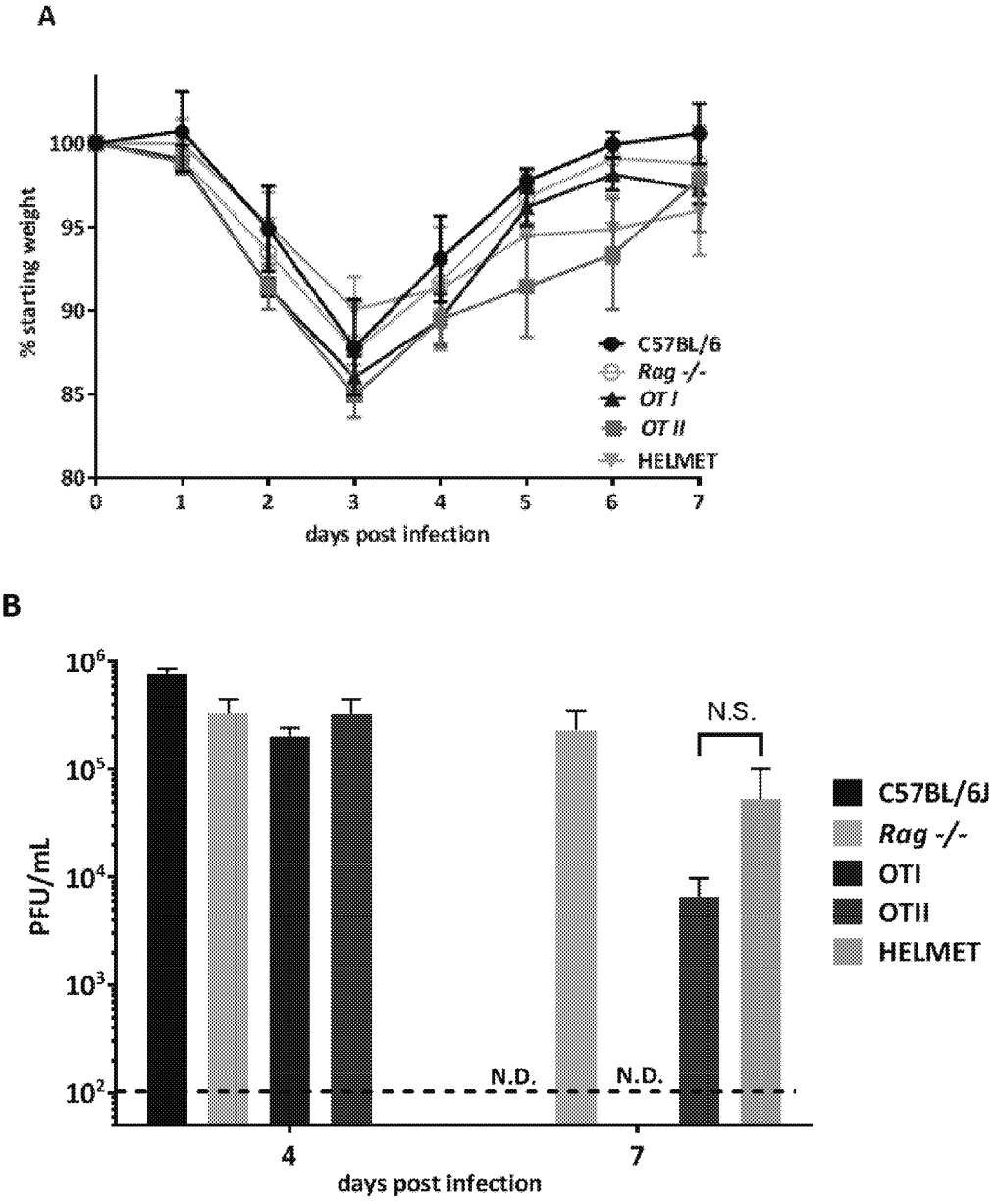


Fig 4. Lack of antigen-specific CD4+T cell responses results in delayed SARS-CoV clearance. 10 week old mice were infected with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group at 4 and 7 dpi. n=3/group at 15 dpi. (A) Mean weight loss per group is represented as a percent of starting weight for each mouse. Mice were weighed daily. No significant difference between weight groups. (B) Lung mean virus load was quantitated by plaque assay. All statistics performed by t test.

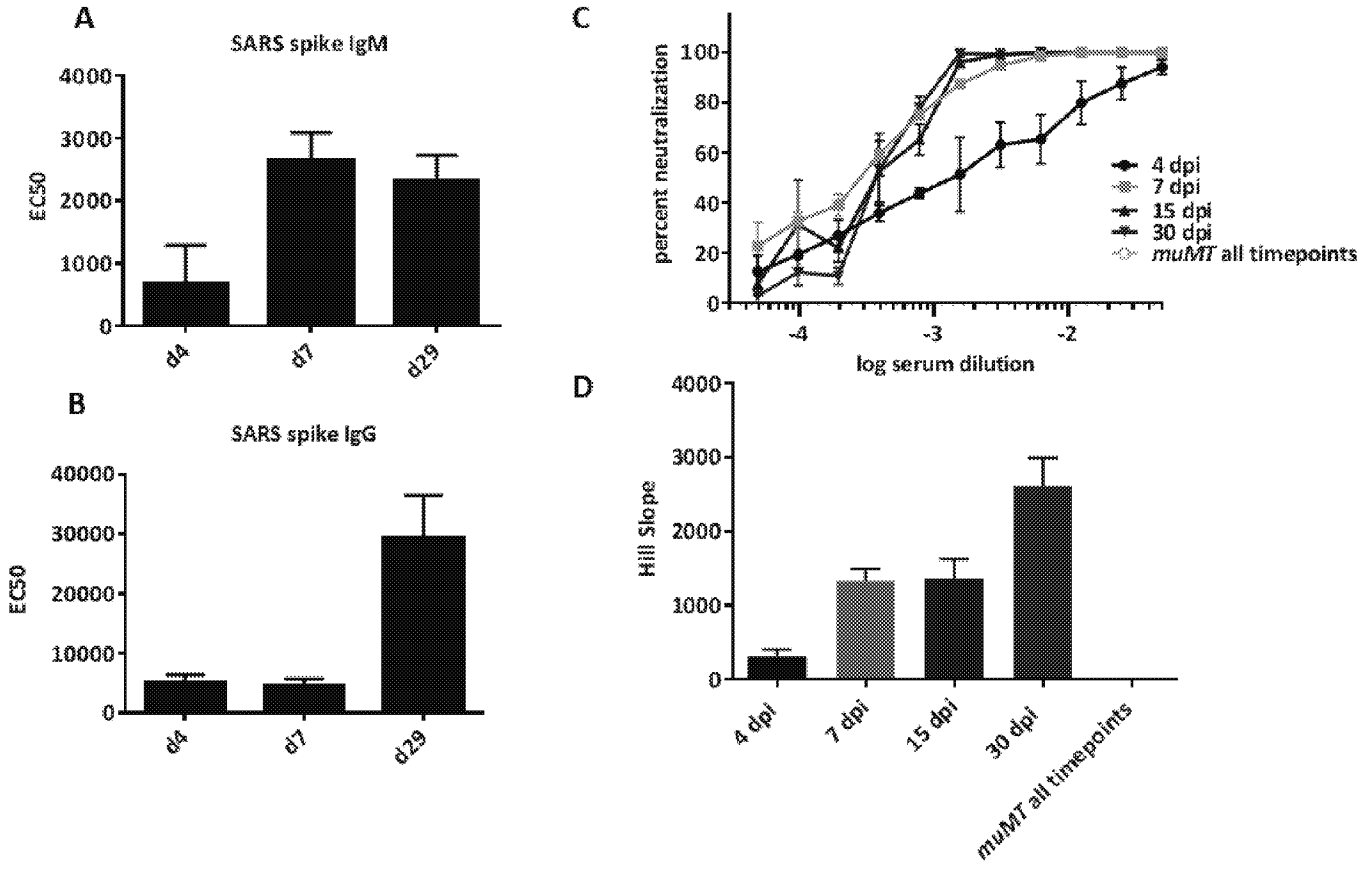


Fig 5. Serum antibodies at 7 days post infection can efficiently neutralize SARS-CoV *in vitro*. 10 week old mice were infected intranasally with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. (A-B) Mean serum IgM (A) and IgG (B) EC50 against SARS-CoV spike protein. n=5 mice/group. (C) SARS-CoV plaque neutralization and (D) hill slopes of neutralization curves were determined by plaque assay using serum taken from MA15 SARS-infected mice at the indicated timepoints.

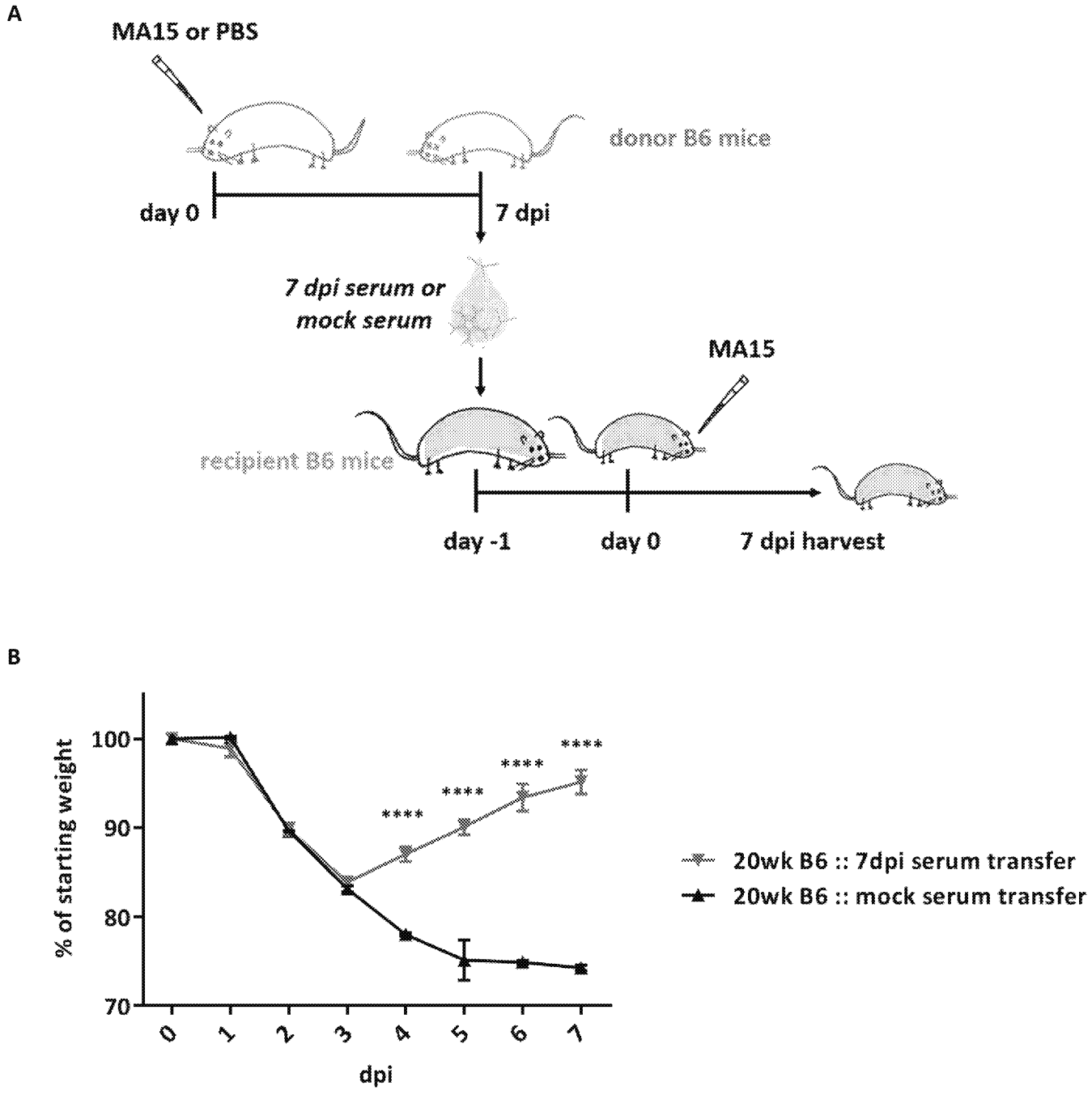


Fig 6. Prophylactic transfer of early antibody prevents mortality during lethal SARS-CoV infection through viral neutralization *in vivo*. Experimental set up of serum transfer experiments. C57BL/6J mice were infected with SARS-CoV at a sublethal dose and serum was harvested at the indicated time point after infection. Serum was transferred at a 1:1 ratio i.p. to the experimental mouse, which was infected with a lethal dose of SARS-CoV 24 hours later. Mice were weighed daily and harvested 7dpi. (A) Mean weight loss of mock serum of 7dpi serum transfer to 12 week or 20 week old C57Bl/6J mice. (B) :: shorthand for received. Statistical significance determined using ANOVA analysis, with **** signifying $p<0.0001$.

SUPPLEMENTARY FIGURES

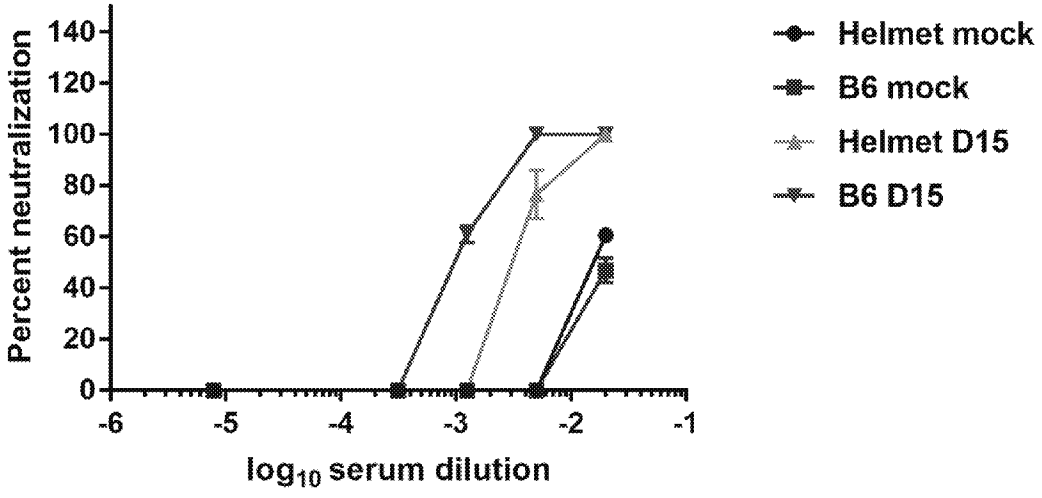
SUPPLEMENT 1. Heat map genes in order of display in Figure 1.

Probe	Gene	Description
A_51_P103364	ENSMUST00000103552	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S12] [ENSMUST00000103552]
A_51_P104768	ENSMUST00000103498	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S55] [ENSMUST00000103498]
A_51_P128248	Igh	Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody [M20831]
A_51_P150705	Igj	Mus musculus immunoglobulin joining chain (Igj), mRNA [NM_152839]
A_51_P150710	Igj	Mus musculus immunoglobulin joining chain (Igj), mRNA [NM_152839]
A_51_P183581	Pou2af1	Mus musculus POU domain, class 2, associating factor 1 (Pou2af1), mRNA [NM_011136]
A_51_P203148	AB017433	Mus musculus mRNA for anti-IL-18 IgG heavy chain, clone 125-2H, partial cds. [AB017433]
A_51_P230716	Igh-VJ558	K0727F04-5N NIA Mouse Hematopoietic Stem Cell (Lin-[CA578712]
A_51_P270807	Tnfrsf17	Mus musculus tumor necrosis factor receptor superfamily, member 17 (Tnfrsf17), mRNA [NM_011608]
A_51_P272341	EG211331	BY724721 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530011I23 5'. [BY724721]
A_51_P288295	ENSMUST00000103496	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-7] [ENSMUST00000103496]
A_51_P298802	Bfsp2	Mus musculus beaded filament structural protein 2, phakinin (Bfsp2), mRNA [NM_001002896]
A_51_P328275	ENSMUST00000103505	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S45] [ENSMUST00000103505]
A_51_P346681	AY090902	Mus musculus clone GN-2-M1 monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial cds [AY090902]
A_51_P405638	LOC544905	601217727F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586566 5'. [BE371942]
A_51_P442889	LOC639988	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC639988), mRNA [XM_916675]
A_51_P452153	2010001M09Rik	Mus musculus RIKEN cDNA 2010001M09 gene (2010001M09Rik), mRNA [NM_027222]
A_51_P461902	L22886	Mus musculus rearranged IgH mRNA, V-region, cell line Cyd-1. [L22886]
A_51_P476757	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_51_P503757	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010004G10 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008094]
A_51_P513770	ENSMUST00000103535	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S5] [ENSMUST00000103535]
A_51_P515985	U55685	Mus musculus anti-DNA immunoglobulin light chain IgG, antibody 452s.36, partial cds. [U55685]
A_52_P1054013	AK041235	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530093J23 product:immunoglobulin heavy chain 4 (serum IgG1), full insert sequence. [AK041235]
A_52_P139027	Igh-VJ558	Mus musculus J558+ IgM heavy chain mRNA, hybridoma clone ME2B7, partial cds. [U39781]
A_52_P14626	Igk-V33	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830304C16 product:Ig kappa chain V-VI region XRPC 44 homolog

		[Mus musculus], full insert sequence [AK157689]
A_52_P149235	Mel13	Mouse anti-idiotype antibody-resistant variant IgK (Vk-Ox1 gene family) mRNA, VJ5 region [M57586]
A_52_P151887	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_52_P174000	AB070542	Mus musculus VH186.2-D-J-IgG1 mRNA, partial cds, sequence:kec-5. [AB070542]
A_52_P213483	Ighv1-77	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC619994), mRNA [XM_138377]
A_52_P214437	EG668544	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC668544), mRNA [XM_001002167]
A_52_P225158	NAP113251-1	Unknown
A_52_P238230	AF152371	Mus musculus kappa light chain of Mab7 mRNA, partial cds. [AF152371]
A_52_P246248	AF240166	Mus musculus MRP3 mRNA, complete cds. [AF240166]
A_52_P259779	LOC631531	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1S4] [ENSMUST00000103523]
A_52_P30641	Gm459	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE_DB;Acc:IGKV4-86] [ENSMUST00000103337]
A_52_P358406	ENSMUST00000103518	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-47] [ENSMUST00000103518]
A_52_P383114	Igl-V1	Mus musculus anti-deoxynivalenol scFv lambda light chain variable region mRNA, partial cds. [AY151141]
A_52_P385767	BC055911	Mus musculus cDNA clone MGC:68301 IMAGE:3662102, complete cds. [BC055911]
A_52_P449214	Gm1418	PREDICTED: Mus musculus gene model 1418, (NCBI) (Gm1418), mRNA [XM_357683]
A_52_P450276	Igl-V1	Mus musculus immunoglobulin lambda chain (IgL) mRNA, complete cds. [M94350]
A_52_P463637	AY895789	Mus musculus clone RLS1478F immunoglobulin heavy chain (Igh) mRNA, partial cds. [AY895789]
A_52_P469009	AY182513	Mus musculus clone BaFL-P40 immunoglobulin heavy chain variable region mRNA, partial cds. [AY182513]
A_52_P476989	AF210281	Mus musculus isolate B880 immunoglobulin heavy chain variable region mRNA, partial cds. [AF210281]
A_52_P47786	AB069910	Mus musculus V303-D-J-C mu mRNA, partial cds, sequence:R2-10. [AB069910]
A_52_P479163	NAP106724-1	Unknown
A_52_P480019	L48666	Mus musculus (cell line C3H/F2-15) chromosome 12 anti-DNA antibody heavy chain mRNA. [L48666]
A_52_P490470	NP614311	GB|AF459850.1|AAO59848.1 immunoglobulin heavy chain VDJ region [Mus musculus] [NP614311]
A_52_P492532	Gm189	Mus musculus single chain Fv antibody (E4(Fv)) mRNA, partial cds [AF025535]
A_52_P532769	Igh	Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody [M20831]
A_52_P544090	AF218659	Mus musculus clone nMeV21 immunoglobulin heavy chain variable region mRNA, partial cds. [AF218659]
A_52_P559566	ENSMUST00000103527	Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE_DB;Acc:IGHV1-56] [ENSMUST00000103527]
A_52_P565106	NAP107273-1	Unknown

A_52_P565636	AY172876	Mus musculus clone BApecB1a-P3 immunoglobulin heavy chain variable region mRNA, partial cds. [AY172876]
A_52_P578436	Gm1418	PREDICTED: Mus musculus gene model 1418, (NCBI) (Gm1418), mRNA [XM_357683]
A_52_P582068	ENSMUST00000103351	Immunoglobulin Kappa light chain V gene segment [Source:IMGT/GENE_DB;Acc:IGKV4-63] [ENSMUST00000103351]
A_52_P58543	Gm1524	AGENCOURT_10055965 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6479347 5', mRNA sequence [BQ937284]
A_52_P614207	BC080787	Mus musculus immunoglobulin kappa chain complex, mRNA (cDNA clone MGC:91220 IMAGE:4206216), complete cds. [BC080787]
A_52_P622355	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]
A_52_P638100	AB070552	Mus musculus V102-D-J-IgG1 mRNA, partial cds, sequence:lec-8. [AB070552]
A_52_P648824	X12388	Mouse hybridoma 10B10S mRNA for IgM(b) heavy chain variable region V(H)-J(H)2. [X12388]
A_52_P672903	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]
A_52_P686392	Igh-VJ558	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700110L11 product:immunoglobulin heavy chain, (J558 family), full insert sequence. [AK007163]
A_52_P829408	Igl-V1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010007E08 product:immunoglobulin lambda chain, variable 1, full insert sequence. [AK008145]

Supplementary Figure 2.



Supp Figure 2. HELMET mice have decreased neutralizing antibody responses. 10 week old mice were infected intranasally with a sublethal dose of MA15 SARS-CoV (10^4 PFU/mouse). n=5/group. SARS-CoV plaque neutralization and were determined by plaque assay using serum taken from MA15 SARS-infected mice at 15 days post-infection.

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Wed 8/26/2020 6:02:52 PM (UTC-05:00)
Subject: storm

Hi Vineet, Thanks for all this, I was a lot later. Great progress,go for it. Glad to hear your R21 came through along with the RO1. I know it's a relief. Just hoping you and **552.117** are in a safe location as Laura comes on shore. Stay safe, hope the **552.117** **552.117** are doing well.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Sunday, June 14, 2020 10:29 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Baric, Toni C <antoinette_baric@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>
Subject: Progress report

Hey Ralph,

Sorry, I lost track of time with the progress report. See attached with some of the progress with the PARP9 story my student Craig is working on. We had a fundable score on my aging CC R21 but NOA. If it is funded, I was going to do a F2 with CC032XCC072. This will help resolve the SARS titer qtl. I will plan on doing it with SARS2 if the MA virus also causes age dependent disease; otherwise I'll do SARS1.

I added the publications that cited U19 funding which might not already overlap with what you have. Let me know if I need anything else. Again, sorry it is late.

VDM

To: R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Sabra Klein[sklein2@jhu.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]; Andrea Cox[acox@jhmi.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID)

[E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDPHSIS/CGH/DGHT)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 8/27/2020 11:13:31 AM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - September 1
nCoV PI call attendee list.xlsx

Hi All,

On Tuesday, August 25th, Dr. Mehul Suthar gave a wonderful presentation titled "**Immunity to SARS-CoV-2 infection in humans".** Thank you all who attend (attendee list attached) and to Dr. Suthar for his presentation.

On Tuesday, September 1st, we will be treated to a double feature brought to you by:

Dr. Natalie Thornburg
"Using virus isolation from clinical specimens to understand the transmission potential and dynamics of SARS-CoV-2"
-and-
Dr. Yu (Lucy) Cong
"Characterization of SARS-CoV-2 Induced Disease in Golden Syrian Hamsters by ^{18}F-FDG PET/CT"

Looking forward to another set of great presentations!

Have a great rest of the week!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Mesecar							
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Conrad Mallia							
Colleen Jonsson						x	
Connie Schmaljohn		x	x		x		
Courtney Comar (Susan Weiss lab)	x						

Daved Fremont						
David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Jim Chappell				x	x	
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x

Kristina Lu						
Kris Emo						
Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Mehul Suttar						
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x

Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
William Florence						
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
x	x	x	x	x	x	x	x	x	
x	x	x	x						
x	x	x	x	x	x	x	x	x	
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4-Aug	11-Aug	25-Aug
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x	x	x

To: fullerdh@uw.edu[fullerdh@uw.edu]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Sabra Klein[sklein2@jhu.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Jain, Sanjay[sjain5@jhmi.edu]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; michael.martin2@emory.edu[michael.martin2@emory.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Andrea Cox[acox@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; david.vaninsberghe@emory.edu[david.vaninsberghe@emory.edu]

Cc: Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Weston, Stuart[SWeston@som.umaryland.edu]; Hammond, Holly[HHammond@som.umaryland.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDPHSIS/CGH/DGHT)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 9/4/2020 9:11:41 AM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - September 8, 2020
nCoV PI call attendee list.xlsx

Hi All,

On Tuesday, September 1st, were treated to a double feature brought to you by:

Dr. Natalie Thornburg
"Using virus isolation from clinical specimens to understand the transmission potential and dynamics of SARS-CoV-2"
-and-
Dr. Yu (Lucy) Cong
"Characterization of SARS-CoV-2 Induced Disease in Golden Syrian Hamsters by ^{18}F-FDG PET/CT"

Thank you both for presenting and for those that attended.

On Tuesday, September 8th, Dr. Katia Koelle will be giving a presentation titled "**Phylodynamic and recombinant analysis of circulating SARS-CoV-2 diversity**".

Hope you all have a wonderful holiday weekend!

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Alvaro Ordonez							
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Mesecar							
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Clint Florence							
Conrad Mallia							
Colleen Jonsson						x	

Connie Schmaljohn		x	x		x	
Courtney Comar (Susan Weiss lab)	x					
Daved Fremont						
David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Glen Abedi						
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Ji Lee						
Jim Chappell				x	x	
jmankow1						
Jonathan Runstadler						x
Judy Hewitt						
Juergen Richt				x	x	x

Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Emo						
Kris Lambert						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Lucy Cong						
Mackenzie Zendt						
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Mehul Suttar						
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						

Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Robert Johnson						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Sanjay Jain						
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Sharon Saydah						
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
William Florence						

Willy Valdivia					
Wolfgang Leitner					
Xizhi Guo	x				
Yoshihiro Kawaoka	x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
x	x	x	x	x	x	x	x	x	
x	x	x	x						
x	x	x	x	x	x	x	x	x	
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4-Aug	11-Aug	25-Aug	1-Sep
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x			x
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		x	x
	x		
	x	x	x
x	x		
			x
x			x
	x	x	

x x x x

To: Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]
Cc: Renee Ireton[rireton@uw.edu]; Graham PhD, Jessica B[jgraham@fredhutch.org]; Michael J Gale[mgale@uw.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]
From: Shaw, Ginger[ginger_shaw@med.unc.edu]
Sent: Thur 9/10/2020 12:27:19 PM (UTC-05:00)
Subject: Re: SIG U19 recurring monthly call

Got it, thanks!

Sent from my U.S.Cellular© Smartphone
Get Outlook for Android

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Thursday, September 10, 2020 1:26:31 PM
To: Shaw, Ginger <ginger_shaw@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>
Subject: RE: SIG U19 recurring monthly call

I am resending a new link. There is apparently a problem with the last one.

From: Shaw, Ginger <ginger_shaw@med.unc.edu>
Sent: Thursday, September 10, 2020 1:23 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>

Subject: Re: SIG U19 recurring monthly call

Toni,
I am getting a message Meeting ID is invalid.
Ginger

Ginger D Shaw
Department of Genetics
120 Mason Farm Road
5041 Genetic Medicine Building CB#7264
University of North Carolina at Chapel Hill
Chapel Hill NC 27599
cellphone 865-661-2696
shawg@email.unc.edu

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, September 9, 2020 7:31 PM
To: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>
Subject: SIG U19 recurring monthly call
When: Thursday, September 10, 2020 1:30 PM-2:30 PM.
Where: https://zoom.us/j/91792514323?pwd= **552.136**

Reminder that we will have our monthly SIG U19 call. The topic of discussion is the upcoming October meeting.

SIG U19 monthly calling information

Join Zoom Meeting
https://zoom.us/j/91792514323?pwd= **552.136**

Meeting ID: 917 9251 4323
Password: **552.136**
One tap mobile
+19292056099,,91792514323#,,1#, **552.136** # US (New York)
+13017158592,,91792514323#,,1#, **552.136** # US (Germantown)

Dial by your location
+1 929 205 6099 US (New York)
+1 301 715 8592 US (Germantown)
+1 312 626 6799 US (Chicago)
+1 669 900 6833 US (San Jose)
+1 253 215 8782 US (Tacoma)
+1 346 248 7799 US (Houston)
Meeting ID: 917 9251 4323

Password: **552.136**
Find your local number: https://zoom.us/u/a5ntKItyA

Join by SIP
91792514323@zoomcrc.com

Join by H.323
162.255.37.11 (US West)
162.255.36.11 (US East)
Meeting ID: 917 9251 4323
Password: **552.136**

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
Cc: Renee Ireton[rireton@uw.edu]; Graham PhD, Jessica B[jgraham@fredhutch.org]; Michael J Gale[mgale@uw.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]
From: Shaw, Ginger[ginger_shaw@med.unc.edu]
Sent: Thur 9/10/2020 12:23:07 PM (UTC-05:00)
Subject: Re: SIG U19 recurring monthly call

Toni,
I am getting a message Meeting ID is invalid.
Ginger

Ginger D Shaw
Department of Genetics
120 Mason Farm Road
5041 Genetic Medicine Building CB#7264
University of North Carolina at Chapel Hill
Chapel Hill NC 27599
cellphone 865-661-2696
shawg@email.unc.edu

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, September 9, 2020 7:31 PM
To: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>
Subject: SIG U19 recurring monthly call
When: Thursday, September 10, 2020 1:30 PM-2:30 PM.
Where: https://zoom.us/j/91792514323?pwd= **552.136**

Reminder that we will have our monthly SIG U19 call. The topic of discussion is the upcoming October meeting.

SIG U19 monthly calling information

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From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/91792514323?pwd= **552.136**
Importance:	Normal
Subject:	Canceled: SIG U19 recurring monthly call
Start Time:	Thur 6/11/2020 12:30:00 PM (UTC-05:00)
End Time:	Thur 6/11/2020 1:30:00 PM (UTC-05:00)
Required Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Optional Attendees:	Renee Ireton; Graham PhD, Jessica B; Michael J Gale; Cornett, Cathy; Michael Davis

Cancelling this occurrence to remove from your calendar because the link is bad

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Password: **552.136**

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/91792514323?pwd= **552.136**
Importance:	Normal
Subject:	Canceled: SIG U19 recurring monthly call
Start Time:	Thur 9/10/2020 12:30:00 PM (UTC-05:00)
End Time:	Thur 9/10/2020 1:30:00 PM (UTC-05:00)
Required Attendees:	Schughart, Klaus; Lund, Jennifer; Graham, Rachel; Fischer, William A. II; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Graham, Jessica ; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Optional Attendees:	Lund PhD, Jennifer; Michael Davis; Graham PhD, Jessica B; Renee Ireton; Michael J Gale; Cornett, Cathy

Reminder that we will have our monthly SIG U19 call. The topic of discussion is the upcoming October meeting.

SIG U19 monthly calling information

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To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 9/10/2020 2:00:58 PM (UTC-05:00)
Subject: FW: Registration site for Systems Immunology U19 Annual Meeting

Dear Colleagues,

I hope that you had a great Labor Day weekend.

This is to inform you that the registration site for our Systems Immunology U19 Annual Meeting on October 9th has been open. Please feel free to use the following link to register and forward it to your colleagues if you need. Please note that this meeting is only limited to the three U19 groups.

https://www.cvent.com/d/v7qsxw.

If you have any question, please let me know. We will send out the Zoom link later.

Best regards,
Joy Liu

Qian"Joy" Liu, MD, MSc
Division of Allergy, Immunology, and Transplantation
National Institute of Allergy and Infectious Diseases
5601 Fishers Lane, Rm 7B54, Rockville, MD 20852
(E) liujoy@mail.nih.gov| (P) 301-761-6621

To: Shaw, Ginger[ginger_shaw@med.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Noll, Kelsey[kenoll@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
Cc: Renee Ireton[rireton@uw.edu]; Graham PhD, Jessica B[jgraham@fredhutch.org]; Michael J Gale[mgale@uw.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 9/10/2020 12:26:31 PM (UTC-05:00)
Subject: RE: SIG U19 recurring monthly call

I am resending a new link. There is apparently a problem with the last one.

From: Shaw, Ginger <ginger_shaw@med.unc.edu>
Sent: Thursday, September 10, 2020 1:23 PM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton <colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>
Subject: Re: SIG U19 recurring monthly call

Toni,
I am getting a message Meeting ID is invalid.
Ginger

Ginger D Shaw
Department of Genetics
120 Mason Farm Road
5041 Genetic Medicine Building CB#7264
University of North Carolina at Chapel Hill
Chapel Hill NC 27599
cellphone 865-661-2696
shawg@email.unc.edu

From: Baric, Toni C <antoinette_baric@med.unc.edu>
Sent: Wednesday, September 9, 2020 7:31 PM
To: Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Berhorst, Jackie <jdao@uw.edu>; D. Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; mtferris <mtferris@email.unc.edu>; Fischer, William A. II <william_fischer@med.unc.edu>; Graham, Jessica <jgraham@fhcrc.org>; Graham, Rachel <rlgraham@ad.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Ireton, Renee <rireton@u.washington.edu>; Kathleen Voss <katvoss@uw.edu>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; Linnertz, Colton

<colton_linnertz@med.unc.edu>; Lund, Jennifer <jlund@fredhutch.org>; Shannon McWeeney <mcweeney@ohsu.edu>; mgale@u.washington.edu <mgale@u.washington.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Noll, Kelsey <kenoll@email.unc.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Shaw, Ginger <ginger_shaw@med.unc.edu>; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>; Swarts, Jessica <jswarts@fredhutch.org>; West, Ande <westande@email.unc.edu>
Cc: Renee Ireton <rireton@uw.edu>; Graham PhD, Jessica B <jgraham@fredhutch.org>; Michael J Gale <mgale@uw.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>
Subject: SIG U19 recurring monthly call
When: Thursday, September 10, 2020 1:30 PM-2:30 PM.
Where: https://zoom.us/j/91792514323?pwd= **552.136**

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SIG U19 monthly calling information

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To: Orenstein, Walter[worenst@emory.edu]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG];

rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Sun 9/13/2020 9:53:59 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - September 15th
nCoV PI call attendee list.xlsx

Hi All,

Thank you all for attending the Dr. Koelle's presentation on Tuesday, September 8th and to Katia for presenting.

On Tuesday, September 15th, Dr. Jim Heath will be giving a presentation titled: "**The origins of immune dysfunction in severe COVID-19**."

Hope you all can attend!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Alvaro Ordonez							
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Mesecar							
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Clint Florence							
Conrad Mallia							
Colleen Jonsson						x	

Connie Schmaljohn		x	x		x	
Courtney Comar (Susan Weiss lab)	x					
Daved Fremont						
David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Glen Abedi						
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Holly Hammond						
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Ji Lee						
Jimmy Logue						
Jim Chappell				x	x	
jmankow1						
Jonathan Runstadler						x

Joseph Mankowski						
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Coca						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Emo						
Kris Lambert						
Kristen Hildebrand						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Lucy Cong						
Mackenzie Zendt						
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Mehul Suttar						
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Michael Martin						
Mike Cooper		x	x			x
Mike H						
Mindy Davis						
Natalie Thornburg						
Pamela McKenzie	x	x	x	x	x	x

Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Robert Johnson						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Sanjay Jain						
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Sharon Saydah						
Shiho Chiba						
Simon Anthony					x	x
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x
Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x

Viviana Simon				x	x
Walt Orenstein		x	x	x	x
Weina Sun	x	x	x	x	x
Wesley C Van Voorhis					
William Karesh	x				
William Florence					
Willy Valdivia					
Wolfgang Leitner					
Xizhi Guo	x				
Yoshihiro Kawaoka	x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
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To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Gabriele Neumann (gabriele.neumann@wisc.edu)[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Griffith, Andrew James[agriff51@uthsc.edu]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID)

[E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]
Cc: Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 9/23/2020 2:05:18 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - September 29, 2020
nCoV PI call attendee list.xlsx

Hi All,

On Tuesday, September 22nd, Dr. Biao He gave a wonderful presentation titled: "**A single dose intranasal immunization with parainfluenza virus 5-based COVID-19 vaccine generates sterilizing immunity in nasal cavities of ferrets and cats**". Thank you Dr. He for presenting and to those who attended.

Coming up on September 29th, Dr. Susan Weiss will be giving a presentation on "**Coronavirus Activation and Antagonism of dsRNA Induced Antiviral Pathways**".

I am looking for presenters starting on October 13th. Please let me know if you're interested in presenting.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	24-Mar	31-Mar	7-Apr	14-Apr	21-Apr	28-Apr
Erik Stemmy	x	x	x	x	x	x	
Marciela DeGrace	x	x	x	x	x	x	
Rebecca Lampley	x	x	x	x	x	x	
Aditya Gaur							
Adolfo Garcia-Sastre	x	x	x	x	x	x	
Aisha Souquette							
Alan Embry	x	x	x	x	x	x	
Ali Ellebedy					x	x	
Alicia Fry							
Alison Augustine				x			
Alvaro Ordonez							
Amy Krafft							
Andrea Pruijssers						x	
Andrea Sant				x	x	x	
Andrew Mesecar							
Andrew Pekosz	x	x	x	x	x	x	
Andy Mesecar						x	
Aneesh Mehta							
Angela Rasmussen							
Ann Eakin			x				
Anice Lowen	x	x	x	x	x	x	
Anita McElroy							
Anne Piantadosi							
Atsuo Kuki						x	
Aubree Gordon	x	x	x	x		x	
Barry Rockx		x					
Ben Cowling	x						
Ben Larman							
Benjamin Miller							
Bin Zhou							
Biao He							
Brooke Bozick	x		x	x	x	x	
Carly Dillen							
Carlie Williams							
Catherine Luke							
Claire Midgley							
Charles Russell	x	x	x	x	x	x	
Chelsea Lane			x	x		x	
Chris Brooke							
Christopher Hsu							
Chris Roberts	x	x	x	x	x	x	
Clint Florence							

Conrad Mallia						
Colleen Jonsson						x
Connie Schmaljohn		x	x		x	
Courtney Comar (Susan Weiss lab)	x					
Daved Fremont						
David Renner (Susan Weiss lab)		x				
David Topham	x	x		x	x	
David Wentworth		x	x	x	x	x
Deborah Lynn Fuller						
Diana Finzi						x
Diane Post	x	x	x	x	x	x
Diego Hijano						
Don Milton						x
Donna Neu		x	x	x	x	x
Elizabeth Fitzpatrick						x
Erica Raterman						
Evans						
Eunchung Park				x	x	x
Florian Krammer	x	x	x	x	x	x
Francisco Chaves						
Frederic Bushman	x			x		x
Gabriele Neumann	x	x	x	x	x	x
Gavin Smith		x				x
Ghazi Kayali	x	x		x	x	x
Glen Abedi						
Greg Deye						
Hana Golding						x
Harm van Bakel	x	x		x	x	x
Holly Hammond						
Hui-Ling Yen		x	x			x
Ian Crozier				x	x	x
Ian Plumb						
Isabelle Phan						
Ishwar Chandramouliswaran						
Jae Jung						x
James Hoffman						
James Kobie		x	x		x	x
Jared Evans						
Jean Patterson						
Jens Wrammert						
Jeremy Crawford						
Jesse Erasmus						
Ji Lee						
Jimmy Logue						
Jim Chappell				x	x	

jmankow1						
Jonathan Runstadler						x
Joseph Mankowski						
Judy Hewitt						
Juergen Richt				x	x	x
Kanta Subbarao		x			x	x
Katharina Koelle						
Katy Shaw-Saliba	x	x	x	x	x	x
Katherine Fenstermacher						
Kimberly Coca						
Kimberly Stemple	x	x	x	x	x	x
Kristina Lu						
Kris Emo						
Kris Lambert						
Kristen Hildebrand						
Laura Hughes						
Lauren Sauer						
Larry Anderson	x	x	x	x	x	x
Leo Poon		x				
Liliana Brown						
Lisa Hensley	x	x	x	x	x	x
Lucy Cong						
Mackenzie Zendt						
Malik Peiris		x				
Marie Killerby						
Mark Challberg						
Mark Denison	x	x	x	x	x	x
Mark Pallansch						x
Mark Sangster		x	x	x	x	x
Mark Williams						
Marlene Espinoza		x	x	x	x	x
Marta Gaglia						
Martin Linster		x	x	x		x
Masato Hatta (UW)	x	x		x	x	
Matt Frieman		x	x	x	x	x
Maureen McGargill					x	x
Mehul Suttar						
Melissa Uccellini	x				x	x
Mercy Prabhudas						
Michael Bryan						
Michael Chan		x				
Michael Martin						
Mike Cooper		x	x			x
Mike H						
Mindy Davis						

Natalie Thornburg						
newmanlm						
Pamela McKenzie	x	x	x	x	x	x
Patrice Becker						
Paul McCray						
Paul Thomas	x			x	x	x
Peter Daszak		x	x	x	x	x
Peter H						
Peter Myler						
Peter Palese	x	x	x	x	x	x
Phuong Nguyen-Contant						
Punam Mathur	x	x	x	x	x	x
Ralph Baric		x			x	
Randall Tressler						
Raul Andino						
Reed Johnson	x	x	x	x	x	x
Reed Shabman						
Richard Rothman		x	x	x	x	x
Richard Sciotti						
Richard Webby	x	x	x			x
Rick Bushman						
Robert Johnson						
Ron Fouchier		x		x	x	
Rudra Goudavet						
Ryan Langlois						x
Sabra Klein						
Sander Herfst		x	x	x	x	x
Sanjay Jain						
Samantha Loeber						x
Sara Cherry						x
Sara Woodson						
Scott Hensley						
Scott Strome						x
Seema Lakdawala						x
Sharon Saydah						
Shiho Chiba						
Simon Anthony					x	x
Sonnie Kim						
Stacey Schultz-Cherry	x	x	x	x	x	x
Stanley Perlman					x	x
Stephen Tompkins	x	x	x	x	x	x
Steve Smiley						
Surender Khurana						x
Susan Gerber			x	x	x	x
Susan Weiss		x	x	x	x	x

Theresa Fitzgerald						
Troy Sutton		x	x		x	x
Tom Fabrizio	x			x	x	
Vineet Menachery					x	x
Viviana Simon					x	x
Walt Orenstein			x	x	x	x
Weina Sun		x	x	x	x	x
Wesley C Van Voorhis						
William Karesh		x				
William Florence						
Willy Valdivia						
Wolfgang Leitner						
Xizhi Guo		x				
Yoshihiro Kawaoka		x	x	x	x	x

5-May	12-May	19-May	26-May	2-Jun	9-Jun	16-Jun	21-Jul	28-Jul
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From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Attendees:	Gralinski, Lisa E; Menachery, Vineet; Baric, Ralph S; Ralph Baric
Location:	https://zoom.us/j/91896758073?pwd= **552.136**
Importance:	Normal
Subject:	Call to discuss SIG Annual Meeting
Start Time:	Sun 10/4/2020 7:30:00 AM (UTC-05:00)
End Time:	Sun 10/4/2020 8:00:00 AM (UTC-05:00)
Required Attendees:	Gralinski, Lisa E; Menachery, Vineet; Baric, Ralph S
Optional Attendees:	Ralph Baric

Antoinette Baric is inviting you to a scheduled Zoom meeting.

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To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony,

Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; jmankows[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Sat 10/3/2020 5:28:36 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - October 6, 2020
nCoV PI call attendee list.xlsx

Hi All,

On September 29th, Dr. Susan Weiss gave a wonderful presentation on "**Coronavirus Activation and Antagonism of dsRNA Induced Antiviral Pathways**". Thank you to our presenter and all who attended.

Dr. Martha Nelson will be giving a presentation on "**How Coronavirus Took Hold in North America and in Europe**" during our next Tuesday SARS-CoV-2 Investigators call on October 6th.

Hope everyone has a great weekend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	29-Sep
Erik Stemmy	x
Marciela DeGrace	x
Rebecca Lampley	x
Aditya Gaur	
Adolfo Garcia-Sastre	x
Aisha Souquette	
Alan Embry	x
Ali Ellebedy	
Alicia Fry	
Alison Augustine	x
Alvaro Ordonez	x
Amy Krafft	
Andrea Pruijssers	
Andrea Sant	
Andrew Mesecar	
Andrew Pekosz	
Andy Mesecar	
Aneesh Mehta	
Angela Rasmussen	x
Ann Eakin	
Anice Lowen	x
Anita McElroy	x
Anne Piantadosi	
Atsuo Kuki	x
Aubree Gordon	
Barry Rockx	
Becky Dutch	x
Ben Cowling	
Ben Larman	
Benjamin Miller	x
Bin Zhou	
Biao He	
Brooke Bozick	x
Carly Dillen	x
Carlie Williams	
Catherine Luke	
Claire Midgley	
Charles Russell	x
Chelsea Lane	
Chris Brooke	
Christopher Hsu	
Chris Roberts	

Clint Florence	x
Conrad Mallia	
Colleen Jonsson	
Connie Schmaljohn	
Courtney Comar (Susan Weiss lab)	
Daved Fremont	
David Renner (Susan Weiss lab)	
David Topham	
David Wentworth	
Deborah Lynn Fuller	
Diana Finzi	
Diane Post	x
Diego Hijano	
Don Milton	
Donna Neu	x
Elizabeth Fitzpatrick	
Erica Raterman	
Evans	
Eunchung Park	
Florian Krammer	x
Francisco Chaves	x
Frederic Bushman	
Gabriele Neumann	x
Gavin Smith	
Ghazi Kayali	
Glen Abedi	
Greg Deye	
Hana Golding	x
Harm van Bakel	x
Holly Hammond	x
Hui-Ling Yen	x
Ian Crozier	x
Ian Plumb	
Isabelle Phan	
Ishwar Chandramouliswaran	
Jae Jung	
James Hoffman	
James Kobie	
Jared Evans	
Jean Patterson	
Jens Wrammert	
Jeremy Crawford	
Jesse Erasmus	
Ji Lee	
Jimmy Logue	

Jim Chappell	
jmankow1	
Joe Breen	x
Jonathan Runstadler	x
Joseph Mankowski	
Judy Hewitt	
Juergen Richt	x
Kanta Subbarao	
Katharina Koelle	
Katy Shaw-Saliba	
Katherine Fenstermacher	x
Kimberly Coca	
Kimberly Stemple	x
Kristina Lu	
Kris Emo	
Kris Lambert	
Kristen Hildebrand	x
Laura Hughes	
Lauren Sauer	x
Larry Anderson	
Larry Wolfraim	x
Leo Poon	
Liliana Brown	
Lisa Hensley	
Lisa Miorin	x
Lori Newman	x
Lucy Cong	x
Mackenzie Zendt	x
Malik Peiris	x
Marie Killerby	
Mark Challberg	
Mark Denison	x
Mark Pallansch	x
Mark Sangster	
Mark Williams	
Marlene Espinoza	x
Marta Gaglia	
Martin Linster	
Masato Hatta (UW)	
Matt Frieman	x
Maureen McGargill	x
Mehul Suttar	x
Melissa Uccellini	x
Mercy Prabhudas	
Michael Bryan	

Michael Chan	
Michael Martin	
Mike Cooper	
Mike H	
Mindy Davis	
Natalie Thornburg	
newmanlm	
Pamela McKenzie	x
Patrice Becker	
Paul McCray	x
Paul Thomas	
Peter Daszak	
Peter H	x
Peter Myler	
Peter Palese	x
Phuong Nguyen-Contant	x
Punam Mathur	x
Ralph Baric	
Randall Tressler	
Raul Andino	
Reed Johnson	
Reed Shabman	
Richard Rothman	x
Richard Sciotti	
Richard Webby	
Rick Bushman	
Robert Johnson	
Ron Fouchier	
Rudra Goudavet	
Ryan Langlois	x
Sabra Klein	
Sander Herfst	
Sanjay Jain	
Samantha Loeber	x
Sara Cherry	x
Sara Woodson	x
Scott Hensley	
Scott Strome	x
Seema Lakdawala	x
Sharon Saydah	
Shiho Chiba	x
Simon Anthony	
Sonnie Kim	
Stacey Schultz-Cherry	x
Stanley Perlman	

Stephen Tompkins	
Steve Smiley	
Surender Khurana	x
Susan Gerber	
Susan Weiss	x
Theresa Fitzgerald	
Troy Sutton	
Tom Fabrizio	
Vineet Menachery	
Viviana Simon	
Walt Orenstein	
Weina Sun	x
Wesley C Van Voorhis	x
William Karesh	
William Florence	
Willy Valdivia	
Wolfgang Leitner	
Xizhi Guo	
Yoshihiro Kawaoka	x

To: Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; qtan@pathology.wustl.edu[qtan@pathology.wustl.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; Adam Cockrell[asmcockrell@gmail.com]; Jacob Kocher[jake.kocher22@gmail.com]
From: Purvine, Emilie[Emilie.Purvine@pnnl.gov]
Sent: Tue 10/6/2020 5:57:38 PM (UTC-05:00)
Subject: FW: arXiv submission submit/3403313

Hello all,

The BMC Bioinformatics submission was completed on 10/1 and I received a subsequent request from the journal to post the preprint on arXiv or bioRxiv because of the relevance with the current SARS-CoV-2 outbreak. I submitted to arXiv today and it will go live on Thursday. Check out the information below. If you see anything wrong with the submission let me know ASAP and I'll edit the submission if I can. I'll pass along the paper password, once I receive it, for you to "claim" it if you like.

_____

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Pacific Northwest National Laboratory
Phone: 206-528-3461

-----Original Message-----
From: e-prints@arxiv.org <e-prints@arxiv.org>
Sent: Tuesday, October 6, 2020 3:45 PM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Subject: arXiv submission submit/3403313

Dear arXiv user,

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arXiv:submit/3403313
From: Emilie Purvine <emilie.purvine@pnnl.gov>
Date: Tue, 6 Oct 2020 18:45:19 EST (1180kb,D)

Title: Hypergraph Models of Biological Networks to Identify Genes Critical to Pathogenic Viral Response
Authors: Song Feng, Emily Heath, Brett Jefferson, Cliff Joslyn, Henry Kvinge, Hugh D. Mitchell, Brenda Praggastis, Amie J. Eisfeld, Amy C. Sims, Larissa B. Thackray, Shufang Fan, Kevin B. Walters, Peter J. Halfmann, Danielle Westhoff-Smith, Qing Tan, Vineet D. Menachery, Timothy P. Sheahan, Adam S. Cockrell, Jacob F. Kocher, Kelly G. Stratton, Natalie C. Heller, Lisa M. Bramer, Michael S. Diamond, Ralph S. Baric, Katrina M. Waters, Yoshihiro Kawaoka, Jason E. McDermott, Emilie Purvine
Categories: q-bio.QM math.CO
MSC-class: 92C42, 92-08, 05C65
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Background: Representing biological networks as graphs is a powerful approach to reveal underlying patterns, signatures, and critical components from high-throughput biomolecular data. However, graphs do not natively capture the multi-way relationships present among genes and proteins in biological systems.
Hypergraphs are generalizations of graphs that naturally model multi-way relationships and have shown promise in modeling systems such as protein complexes and metabolic reactions. In this paper we seek to understand how hypergraphs can more faithfully identify, and potentially predict, important genes based on complex relationships inferred from genomic expression data sets.
Results: We compiled a novel data set of transcriptional host response to pathogenic viral infections and formulated relationships between genes as a hypergraph where hyperedges represent significantly perturbed genes, and vertices represent individual biological samples with specific experimental conditions. We find that hypergraph betweenness centrality is a superior method for identification of genes important to viral response when compared with graph centrality.
Conclusions: Our results demonstrate the utility of using hypergraphs to represent complex biological systems and highlight central important responses in common to a variety of highly pathogenic viruses.
\\

To: Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony,

Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; jmankows[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 10/7/2020 1:09:19 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - October 13

Hi All,

Please let me know if you are interested in presenting on Tuesday, October 13th or during future meetings.

Thanks,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 10/8/2020 6:06:19 PM (UTC-05:00)
Subject: RE: Slides

Student or postdoc pic to put on the slides and name if anyone working on CC?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, October 8, 2020 10:32 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Gralinski, Lisa E <lgralins@email.unc.edu>
Subject: Slides

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Michael Davis[madphd@uw.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Tue 10/13/2020 11:23:04 AM (UTC-05:00)
Subject: SIG U19 Meeting Update

Hi Everyone,
Ralph and I would like to thank everyone for all the work on the SIG-U19 reverse site visit. The presentations were well received and Program was very happy with the U19's progress and productivity. They were especially impressed with the level of collaboration within this program, as well as the new collaborations between the different U19 groups.

However, there is some bad news. During the steering committee meeting Program announced that they will not be putting the U19 program forward for renewal due to changing funding priorities. Therefore, the program will end after the current 5 year funding period in 2022. This is clearly disappointing, but they did want to give all three groups as much lead time as possible to explore other funding opportunities. Given the expertise and resources that our groups have built over the past 8+ years, Ralph and I both think that there are several different options that we can pursue with respect to R01's or even PPGs. Therefore, we would like to set up a call amongst the PIs to discuss the results of the steering committee meeting, as well as ways to go forward. Therefore, Toni will follow up with everyone to schedule a call.

Thank you again for all the work on the program and we are looking forward to talking further.

Ralph and Mark

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony,

Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; jmankows[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][picketttte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 10/15/2020 1:56:38 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - October 20th
nCoV PI call attendee list.xlsx

Hi All,

On October 13th, Dr. Ben Tenoever gave a wonderful presentation on "**Leveraging the Host Response to SARS-CoV-2 to Identify Effective Antivirals**". Thank you to our presenter and all who attended.

Dr. Jacob Hou will be giving a presentation on "**SARS-CoV-2 D614G Variant Exhibits Enhanced Replication ex vivo and Earlier Transmission in vivo**" during our next Tuesday SARS-CoV-2 Investigators call on October 20th.

Hope everyone has a great rest of the week!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		29-Sep	6-Oct	13-Oct
Erik Stemmy	x	x	x	
Marciela DeGrace	x	x	x	
Rebecca Lampley	x	x	x	
Aditya Gaur				
Adolfo Garcia-Sastre	x	x	x	
Aisha Souquette				
Alan Embry	x			
Ali Ellebedy				
Alicia Fry		x		
Alison Augustine	x	x		
Alvaro Ordonez	x	x	x	
Amanda Perofsky		x		
Amy Krafft			x	
Andrea Pruijssers				
Andrea Sant			x	
Andrew Mesecar			x	
Andrew Pekosz		x		
Andy Mesecar				
Aneesh Mehta				
Angela Rasmussen	x	x	x	
Ann Eakin				
Anice Lowen	x		x	
Anita McElroy	x	x	x	
Anne Piantadosi				
Aron Hall			x	
Atsuo Kuki	x			
Aubree Gordon		x		
Barry Rockx				
Becky Dutch	x			
Ben Cowling				
Ben Larman				
Benjamin Miller	x	x		
Ben Tenoever			x	
Bin Zhou				
Biao He				
Brooke Bozick	x	x	x	
Carly Dillen	x	x	x	
Carlie Williams		x		
Catherine Luke				
Claire Midgley				
Charles Russell	x	x		
Chelsea Lane				

Chris Brooke			
Christopher Hsu			
Chris Roberts			
Clint Florence	x	x	
Conrad Mallia			
Colleen Jonsson		x	x
Connie Schmaljohn		x	
Courtney Comar (Susan Weiss lab)			
Daved Fremont			
David Renner (Susan Weiss lab)			
David Topham			
David Wentworth		x	
Deborah Lynn Fuller			
Diana Finzi		x	
Diane Post	x		x
Diego Hijano			
Don Milton			
Donna Neu	x	x	x
Elizabeth Fitzpatrick			
Erica Raterman			
Evans			x
Eunchung Park		x	x
Eun Mi Lee		x	
Florian Krammer	x	x	x
Francisco Chaves	x		
Frederic Bushman		x	
Gabriele Neumann	x		x
Gavin Smith			
Ghazi Kayali		x	
Glen Abedi			
Grace Tietz		x	
Greg Deye			
Hana Golding	x	x	x
Harm van Bakel	x	x	x
Holly Hammond	x	x	
Hui-Ling Yen	x		
Ian Crozier	x	x	
Ian Plumb		x	x
Isabelle Phan			
Ishwar Chandramouliswaran			
Jacob Hou			x
Jae Jung			
James Hoffman		x	
James Kobie		x	x
Jared Evans			

Jean Patterson			
Jenni		x	
Jennifer Gordon		x	x
Jens Wrammert			
Jeremy Crawford			
Jesse Erasmus			
Ji Lee			
Jimmy Logue			
Jim Chappell			
jmankow1			
Joe Breen	x		x
Jonathan Runstadler	x	x	x
Joseph Mankowski		x	
Judy Hewitt			
Juergen Richt	x	x	x
Kanta Subbarao			
Katharina Koelle		x	
Katy Shaw-Saliba			
Katherine Fenstermacher	x	x	x
Kimberly Coca			
Kimberly Stemple	x	x	
Korin Bullen		x	x
Kristina Lu			
Kris Emo			
Kris Lambert			
Kristen Hildebrand	x	x	x
Laura Hughes			
Lauren Sauer	x		x
Larry Anderson		x	x
Larry Wolfraim	x		
Leo Poon			
Liliana Brown		x	
Lisa Hensley		x	
Lisa Miorin	x		
Liz		x	x
Lori Newman	x		x
Lucy Cong	x	x	x
Mackenzie Zendt	x	x	x
Malik Peiris	x		x
Marie Killerby			
Mark Challberg			
Mark Denison	x		
Mark Pallansch	x	x	
Mark Sangster		x	x
Mark Williams			

Marlene Espinoza	x	x	x
Marta Gaglia		x	
Martha Nelson		x	
Martin Linster		x	x
Masato Hatta (UW)			
Matt Frieman	x		x
Maureen McGargill	x	x	
Mehul Suttar	x		
Melissa Uccellini	x	x	x
Mercy Prabhudas			
Michael Bryan			
Michael Chan			
Michael Martin		x	
Mike Cooper			
Mike Holbrook			x
Mindy Davis			
Natalie Thornburg			
newmanlm		x	
Nidia Trovao		x	
Pamela McKenzie	x	x	x
Patrice Becker			
Paul McCray	x	x	x
Paul Thomas			
Peter Daszak		x	x
Peter Halfmann	x		x
Peter Myler			
Peter Palese	x		
Phuong Nguyen-Contant	x	x	x
Punam Mathur	x	x	
Rachel Graham			x
Ralph Baric			
Randall Tressler			
Raul Andino			
Reed Johnson		x	
Reed Shabman		x	
Richard Rothman	x	x	x
Richard Sciotti			
Richard Webby			x
Rick Bushman			
Robert Johnson			
Ron Fouchier			x
Rudra Goudavet			
Russell Ray			x
Ryan Langlois	x		
Sabra Klein		x	

Sander Herfst			
Sanjay Jain			x
Samantha Loeber	x		
Sara Cherry	x	x	
Sara Woodson	x	x	
Scott Hensley			
Scott Strome	x	x	x
Seema Lakdawala	x	x	
Sharon Saydah			
Shiho Chiba	x	x	x
Simon Anthony		x	x
Sonnie Kim		x	
Stacey Schultz-Cherry	x	x	x
Stanley Perlman			
Stephen Tompkins			
Steve Smiley			
Surender Khurana	x		x
Susan Gerber			
Susan Weiss	x	x	
Theresa Fitzgerald			x
Troy Sutton		x	
Tom Fabrizio			
Vineet Menachery		x	x
Viviana Simon			
Walt Orenstein			x
Weina Sun	x	x	
Wesley C Van Voorhis	x	x	x
William Karesh			
William Florence			
Willy Valdivia			
Wolfgang Leitner			
Xizhi Guo			
Yoshihiro Kawaoka	x		x

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony,

Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/FIC) [E][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][picketttte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]
Cc: Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 10/22/2020 2:10:31 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - October 27
nCoV PI call attendee list.xlsx

Hi All,

On October 20th, Dr. Jacob Hou gave a presentation on "**SARS-CoV-2 D614G Variant Exhibits Enhanced Replication ex vivo and Earlier Transmission in vivo**". Thank you to our presenter and all who attended.

Next Tuesday, October 27th, Drs. Ralph Baric and Mark Heise giving a presentation on "**Countermeasure testing in SARS-CoV2 Mouse Models**".

Hope everyone is able to attend!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		13-Oct		20-Oct
Erik Stemmy	x		x	
Marciela DeGrace	x		x	
Rebecca Lampley	x		x	
Aditya Gaur				
Adolfo Garcia-Sastre	x		xx	
Aisha Souquette				
Alan Embry				
Ali Ellebedy				
Alicia Fry				
Alison Augustine			x	
Alvaro Ordonez	x		x	
Amanda Perofsky				
Amy Krafft	x		x	
Andrea Pruijssers				
Andrea Sant	x		x	
Andrew Mesecar	x		x	
Andrew Pekosz			x	
Andy Mesecar				
Aneesh Mehta				
Angela Rasmussen	x		x	
Ann Eakin				
Anice Lowen	x		x	
Anita McElroy	x			
Anne Piantadosi			x	
Aron Hall	x			
Atsuo Kuki			x	
Aubree Gordon				
Barry Rockx				
Becky Dutch				
Ben Cowling				
Ben Larman				
Benjamin Miller				
Ben Tenoever	x		x	
Bin Zhou			x	
Biao He				
Brooke Bozick	x		x	
Carly Dillen	x		x	
Carlie Williams			x	
Catherine Luke				
Claire Midgley				
Charles Russell				
Chelsea Lane			x	

Chris Brooke		
Christopher Hsu		
Chris Roberts		
Clint Florence		
Conrad Mallia		
Colleen Jonsson	x	x
Connie Schmaljohn		
Courtney Comar (Susan Weiss lab)		
Daved Fremont		
David Renner (Susan Weiss lab)		
David Topham		
David Wentworth		
Deborah Lynn Fuller		
Diana Finzi		x
Diane Post	x	
Diego Hijano		
Don Milton		x
Donna Neu	x	x
Elizabeth Fitzpatrick		
Erica Raterman		
Evans	x	
Eunchung Park	x	x
Eun Mi Lee		
Florian Krammer	x	x
Francisco Chaves		x
Frederic Bushman		
Gabriele Neumann	x	x
Gavin Smith		
Ghazi Kayali		
Glen Abedi		
Grace Tietz		
Greg Deye		
Hana Golding	x	x
Harm van Bakel	x	
Holly Hammond		
Hui-Ling Yen		
Ian Crozier		x
Ian Plumb	x	
Isabelle Phan		
Ishwar Chandramouliswaran		
Jacob Hou	x	x
Jae Jung		
James Hoffman		
James Kobie	x	
Jared Evans		x

Jean Patterson		
Jenni		x
Jennifer Gordon	x	
Jens Wrammert		
Jeremy Crawford		
Jesse Erasmus		
Ji Lee		
Jimmy Logue		
Jim Chappell		
jmankow1		
Joe Breen	x	
Jonathan Runstadler	x	x
Joseph Mankowski		
Judy Hewitt		
Juergen Richt	x	x
Kanta Subbarao		
Katharina Koelle		
Katy Shaw-Saliba		
Katherine Fenstermacher	x	
Kimberly Coca		
Kimberly Stemple		
Korin Bullen	x	
Kristina Lu		
Kris Emo		
Kris Lambert		
Kristen Hildebrand	x	x
Laura Hughes		
Lauren Sauer	x	
Larry Anderson	x	x
Larry Wolfraim		
Leo Poon		
Liliana Brown		x
Lisa Hensley		
Lisa Lindesmith		x
Lisa Miorin		
Liz	x	x
Lori Newman	x	
Lucy Cong	x	x
Mackenzie Zendt	x	x
Malik Peiris	x	x
Marie Killerby		
Mark Challberg		
Mark Denison		
Mark Pallansch		x
Mark Sangster	x	x

Mark Williams		
Marlene Espinoza	x	x
Marta Gaglia		x
Martha Nelson		
Martin Linster	x	x
Masato Hatta (UW)		
Matt Frieman	x	x
Maureen McGargill		x
Mehul Suttar		
Melissa Uccellini	x	x
Mercy Prabhudas		
Michael Bryan		
Michael Chan		
Michael Martin		
Mike Cooper		
Mike Holbrook	x	x
Mindy Davis		
Natalie Thornburg		
newmanlm		
Nidia Trovao		
Pamela McKenzie	x	x
Patrice Becker		
Paul McCray	x	x
Paul Thomas		
Peter Daszak	x	x
Peter Halfmann	x	
Peter Myler		
Peter Palese		
Phuong Nguyen-Contant	x	
Punam Mathur		x
Rachel Graham	x	x
Ralph Baric		
Randall Tressler		
Raul Andino		
Rebecca Dutch		x
Reed Johnson		x
Reed Shabman		
Richard Rothman	x	
Richard Sciotti		
Richard Webby	x	
Rick Bushman		
Robert Johnson		
Ron Fouchier	x	x
Rudra Goudavet		
Russell Ray	x	x

Ryan Langlois		
Sabra Klein		
Sander Herfst		
Sanjay Jain	x	x
Samantha Loeber		
Sara Cherry		
Sara Woodson		x
Scott Hensley		
Scott Strome	x	x
Seema Lakdawala		
Sharon Saydah		
Shiho Chiba	x	x
Simon Anthony	x	x
Sonnie Kim		
Stacey Schultz-Cherry	x	
Stanley Perlman		
Stephen Tompkins		x
Steve Smiley		
Surender Khurana	x	x
Susan Gerber		
Susan Weiss		
Theresa Fitzgerald	x	x
Troy Sutton		x
Tom Fabrizio		
Vineet Menachery	x	x
Viviana Simon		
Walt Orenstein	x	
Weina Sun		x
Wesley C Van Voorhis	x	
William Karesh		
William Florence		
Willy Valdivia		
Wolfgang Leitner		
Xizhi Guo		
Yoshihiro Kawaoka	x	x

To: Michael J Gale[mgale@uw.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Jackie V. Berhorst[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 11/2/2020 10:29:36 AM (UTC-06:00)
Subject: RE: Nov and Dec SIG U19 call conflicts

Thanks Mike. Put a hold on that slot. It looks like everyone can make it.

From: Michael J Gale <mgale@uw.edu>
Sent: Monday, November 2, 2020 11:28 AM
To: Baric, Toni C <antoinette_baric@med.unc.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Jackie V. Berhorst <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney <mcweeney@ohsu.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>
Subject: RE: Nov and Dec SIG U19 call conflicts

Dec 3 call works for me. M

From: Baric, Toni C [mailto:antoinette_baric@med.unc.edu]
Sent: Monday, November 02, 2020 7:34 AM
To: Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Jackie V. Berhorst <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; Michael J Gale <mgale@uw.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney <mcweeney@ohsu.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>
Subject: Nov and Dec SIG U19 call conflicts

Good morning,
Looking ahead on the calendar for November and December, both Mark and Ralph have 2 day long meetings for another center grant. We are proposing to cancel November call and have the call Dec 3 at 1:30 EST/10:30 PST.

Please let me know if it is possible for you to make this call.

Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Jennifer Hyde[jlhyde4@uw.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Nelson, Martha (NIH/FIC) [C][nelsonma@mail.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Florian Krammer[florian.krammer@mssm.edu]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; Baric, Toni C[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Martinez, David Rafael[davidmar@email.unc.edu]; Luke, Catherine (NIH/NIAID) [E][catherine.luke@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDPHSIS/CGH/GID)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu];

Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@jhu.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@jhmi.edu]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 10/28/2020 4:43:26 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - November 3rd
nCoV PI call attendee list.xlsx

Hi!

On October 27th, members from Dr. Ralph Baric and Dr. Mark Heise laboratories gave two great presentations on "**Countermeasure testing in SARS-CoV2 Mouse Models**". Thank you to both presenters and to those that attended.

Next week, on November 3rd, Dr. Bin Zhou or Dr. David Wentworth will be giving a presentation titled "**SARS-CoV-2 spike D614G variant confers enhanced replication and transmissibility**".

Have a great rest of the week!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		13-Oct	20-Oct	27-Oct
Erik Stemmy	x	x	x	
Marciela DeGrace	x	x	x	
Rebecca Lampley	x	x		
Aditya Gaur				
Adolfo Garcia-Sastre	x	x	x	
Aisha Souquette				
Alan Embry				
Ali Ellebedy			x	
Alicia Fry				
Alison Augustine		x	x	
Alvaro Ordonez	x	x		
Amanda Perofsky				
Amy Krafft	x	x		
Andrea Pruijssers			x	
Andrea Sant	x	x		
Andrew Mesecar	x	x	x	
Andrew Pekosz		x	x	
Andy Mesecar				
Andrzej Joachimiak			x	
Aneesh Mehta				
Angela Rasmussen	x	x	x	
Ann Eakin				
Anice Lowen	x	x	x	
Anita McElroy	x		x	
Anne Piantadosi		x		
Aron Hall	x			
Atsuo Kuki		x	x	
Aubree Gordon				
Barry Rockx				
Becky Dutch				
Ben Cowling				
Ben Larman				
Benjamin Miller			x	
Ben Tenoever	x	x	x	
Bin Zhou		x	x	
Biao He				
Brooke Bozick	x	x		
Carly Dillen	x	x	x	
Carlie Williams		x		
Catherine Luke			x	
Claire Midgley				
Charles Russell			x	

Chelsea Lane		x	
Chris Brooke			
Christopher Hsu			
Chris Roberts			
Clint Florence			
Conrad Mallia			
Colleen Jonsson	x	x	
Connie Schmaljohn			x
Courtney Comar (Susan Weiss lab)			
Daved Fremont			
David Martinez			x
David Renner (Susan Weiss lab)			
David Topham			
David Wentworth			x
Deborah Lynn Fuller			
Diana Finzi		x	
Diane Post	x		x
Diego Hijano			
Don Milton		x	x
Donna Neu	x	x	x
Elizabeth Fitzpatrick			
Erica Raterman			
Evans	x		
Eunchung Park	x	x	x
Eun Mi Lee			
Florian Krammer	x	x	x
Francisco Chaves		x	x
Frederic Bushman			
Gabriele Neumann	x	x	x
Gavin Smith			
Ghazi Kayali			x
Glen Abedi			
Grace Tietz			
Greg Deye			
Hana Golding	x	x	x
Harm van Bakel	x		
Holly Hammond			
Hui-Ling Yen			
Ian Crozier		x	x
Ian Plumb	x		
Isabelle Phan			
Ishwar Chandramouliswaran			
Ivan			x
Jacob Hou	x	x	x
Jae Jung			x

James Hoffman			
James Kobie	x		x
Jared Evans		x	x
Jean Patterson			
Jenni		x	
Jennifer Gordon	x		
Jens Wrammert			
Jeremy Crawford			
Jesse Erasmus			
Ji Lee			
Jimmy Logue			
Jim Chappell			
jmankow1			
Joe Breen	x		
Jonathan Runstadler	x	x	x
Joseph Mankowski			
Judy Hewitt			
Juergen Richt	x	x	x
Kanta Subbarao			
Katharina Koelle			
Katy Shaw-Saliba			
Katherine Fenstermacher	x		x
Kimberly Coca			
Kimberly Stemple			
Korin Bullen	x		
Kristina Lu			
Kris Emo			
Kris Lambert			
Kristen Hildebrand	x	x	x
Laura Hughes			
Lauren Sauer	x		
Larry Anderson	x	x	x
Larry Wolfraim			
Leo Poon			
Liliana Brown		x	
Lisa Hensley			
Lisa Lindesmith		x	
Lisa Miorin			
Liz	x	x	x
Lori Newman	x		
Lucy Cong	x	x	x
Mackenzie Zendt	x	x	x
Malik Peiris	x	x	
Marie Killerby			
Mark Challberg			

Mark Denison			x
Mark Heism			x
Mark Pallansch		x	
Mark Sangster	x	x	x
Mark Williams			x
Marlene Espinoza	x	x	x
Marta Gaglia		x	x
Martha Nelson			
Martin Linster	x	x	x
Masato Hatta (UW)			
Matt Frieman	x	x	x
Maureen McGargill		x	x
Mehul Suttar			x
Melissa Uccellini	x	x	x
Mercy Prabhudas			
Michael Bryan			
Michael Chan			
Michael Martin			
Mike Cooper			
Mike Holbrook	x	x	
Mindy Davis			
Nat Moorman			x
Natalie Thornburg			x
newmanlm			x
Nidia Trovao			
Pamela McKenzie	x	x	
Patrice Becker			
Paul McCray	x	x	x
Paul Thomas			
Peter Daszak	x	x	
Peter Halfmann	x		x
Peter Myler			
Peter Palese			x
Phuong Nguyen-Contant	x		
Punam Mathur		x	x
Rachel Graham	x	x	
Ralph Baric			x
Randall Tressler			
Raul Andino			
Rebecca Dutch		x	x
Reed Johnson		x	
Reed Shabman			
Richard Rothman	x		
Richard Sciotti			
Richard Webby	x		

Rick Bushman			
Robert Johnson			
Ron Fouchier	x	x	
Rudra Goudavet			
Russell Ray	x	x	x
Ryan Langlois			
Sabra Klein			x
Sander Herfst			
Sanjay Jain	x	x	x
Samantha Loeber			
Sara Cherry			x
Sara Woodson		x	
Scott Hensley			
Scott Strome	x	x	x
Seema Lakdawala			
Sharon Saydah			
Shiho Chiba	x	x	x
Simon Anthony	x	x	x
Sook Ho			x
Sonnie Kim			
Stacey Schultz-Cherry	x		x
Stanley Perlman			x
Stephen Tompkins		x	
Steve Smiley			
Surender Khurana	x	x	x
Susan Gerber			
Susan Weiss			x
Thames P			x
Theresa Fitzgerald	x	x	
Timothy Sheahan			x
Troy Sutton		x	
Tom Fabrizio			
Tori Baxter			x
Vineet Menachery	x	x	
Viviana Simon			
Walt Orenstein	x		x
Weina Sun		x	x
Wesley C Van Voorhis	x		
William Karesh			
William Florence			
Willy Valdivia			
Wolfgang Leitner			
Xizhi Guo			
Yoshihiro Kawaoka	x	x	x

To: Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; JACKIE V. BERHORST (jdao@uw.edu)[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Mon 11/2/2020 9:34:02 AM (UTC-06:00)
Subject: Nov and Dec SIG U19 call conflicts

Good morning,
Looking ahead on the calendar for November and December, both Mark and Ralph have 2 day long meetings for another center grant. We are proposing to cancel November call and have the call Dec 3 at 1:30 EST/10:30 PST.

Please let me know if it is possible for you to make this call.

Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Cornett, Cathy[catherine_cornett@med.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Jackie V. Berhorst[jdao@uw.edu]; Jennifer M. Lund[jlund@fhcrc.org]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; mtferris[mtferris@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shannon McWeeney[mcweeney@ohsu.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]
From: Michael J Gale[mgale@uw.edu]
Sent: Mon 11/2/2020 10:28:13 AM (UTC-06:00)
Subject: RE: Nov and Dec SIG U19 call conflicts

Dec 3 call works for me. M

From: Baric, Toni C [mailto:antoinette_baric@med.unc.edu]
Sent: Monday, November 02, 2020 7:34 AM
To: Baric, Ralph S <rbaric@email.unc.edu>; Cornett, Cathy <catherine_cornett@med.unc.edu>; Gralinski, Lisa E <lgralins@email.unc.edu>; Heise, Mark T <mark_heisem@med.unc.edu>; Jackie V. Berhorst <jdao@uw.edu>; Jennifer M. Lund <jlund@fhcrc.org>; Klaus Schughart (kschugha@uthsc.edu) <kschugha@uthsc.edu>; Leist, Sarah Rebecca <leist@email.unc.edu>; mtferris <mtferris@email.unc.edu>; Menachery Vineet (vimenach@utmb.edu) <vimenach@utmb.edu>; Michael J Gale <mgale@uw.edu>; Miller, Darla <darla_miller@med.unc.edu>; Michael Mooney <mooneymi@ohsu.edu>; Pardo Manuel de Villena, Fernando <fernando_pardo-manuel@med.unc.edu>; Schaefer, Alexandra <aschaefe@email.unc.edu>; Schughart, Klaus <Klaus.Schughart@helmholtz-hzi.de>; Shannon McWeeney <mcweeney@ohsu.edu>; Suthar, Mehul S. (mehul.s.suthar@emory.edu) <mehul.s.suthar@emory.edu>
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Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Paul Leon[paul@autonomoustherapeutics.com]; Timothy Notton[tim@autonomoustherapeutics.com]; Ariel Weinberger[ariel@autonomoustherapeutics.com]; tcbaric@med.unc.edu[tcbaric@med.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 3/7/2019 5:46:47 PM (UTC-06:00)
Subject: DARPA Project

Ralph,
I have been working on a DARPA proposal with Autonomous Therapeutics on MERS-CoV with a quick turn around.

Ariel and Pau (CCed) are funded for another DARPA project to generate therapeutic interferring particles and are looking to apply their approach for MERS on this specific supplement call.

We have been chatting for a few weeks and they are interested in both in vitro and in vivo experiments with their MERS-CoV targeted TIPs. I am currently planning to work with them on the in vitro side, but suggested they talk directly with you about the DPP4 288/330 model.

I do not think my lab has the capacity to do the in vivo mouse experiments and they prefer the 288/330 model. If the TIPs work in mice, we would extend the work to marmosets at UTMB.

They will contact you directly and I know they are on a short turn around time; I cced Toni as well to see if you'd have time in your schedule. I'll be doing harvests in the morning, so no need to include me on any of the calls.

Thanks

VDM

To: jgraham@fredhutch.org[jgraham@fredhutch.org]; Lund, Jennifer[jlund@fredhutch.org]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; lgralins@email.unc.edu[lgralins@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 4/11/2019 11:49:30 AM (UTC-05:00)
Subject: All virus Paper
AllVirus_Manuscript-rsb (1)_VDM.docx

Hey Jenny and Jess,
I mentioned some of my thoughts to Jess at the meeting. I also cced Lisa so that she can comment on my comments.

Let me know if you want me to look at it again. I think its a nice study.

VDM

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 4/25/2019 9:12:23 PM (UTC-05:00)
Subject: RE:

Ralph,
I don't appreciate being accused of things that I didn't do.

I did not share any QTL mapping or any other data from the U19 with them. I did share that Trim6 might be a target under the QTL for Ebola and that genetic diversity might be important. I did this in context of one of their students presenting their Ebola data on Trim6 KO mice. If that was inappropriate, I apologize.

I did share with Lisa that we have infected the Trim6KO mice with SARS and found a phenotype. Perhaps this was inappropriate as well. The researcher had offered their Ebola Trim6KO data as preliminary data if we wanted to use it in the U19 presentation. Again, perhaps this was inappropriate.

I agree that there are norms in behaviors to be followed, but accusing me of sharing data with direct competitors without knowing the full story also results in a loss of trust between members of the group.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Thursday, April 25, 2019 8:41 PM
To: Menachery, Vineet
Subject:

Hi Vineet, Lisa had mentioned that you had shared our Ebola Mapping data and candidate genes with researchers at UTMB who do Ebola research, and who also happen to have a Trim6 KO. If so, this is inappropriate. It was not your data and not yours to share. As a collaborator on the U19 there are norms in behavior that have to be followed or it results in a complete loss of trust between members of the group. Ralph

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Fri 4/26/2019 7:02:44 AM (UTC-05:00)
Subject: RE:

Ralph,
I apologize. I shared that Trim6 was a potential target under the QTL for Ebola. I shouldn't have. It won't happen again.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Friday, April 26, 2019 5:53 AM
To: Menachery, Vineet
Subject: RE:

Vineet, I appreciate the full story. However, your second paragraph is still at odds with your first sentence. If some data is shared without the courtesy of discussing it first with the lab that generated the data, it is flat out inappropriate. Consequently, I don't believe I accused you incorrectly, as you seem to be arguing scope. How can you offer their data for our U19 without discussing this with the PI who is directing the student? Why wasn't I brought into this discussion beforehand. If you can't understand my frustration, then you are correct and we have a problem.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, April 25, 2019 10:12 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE:

Ralph,

I don't appreciate being accused of things that I didn't do.

I did not share any QTL mapping or any other data from the U19 with them. I did share that Trim6 might be a target under the QTL for Ebola and that genetic diversity might be important. I did this in context of one of their students presenting their Ebola data on Trim6 KO mice. If that was inappropriate, I apologize.

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I agree that there are norms in behaviors to be followed, but accusing me of sharing data with direct competitors without knowing the full story also results in a loss of trust between members of the group.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Thursday, April 25, 2019 8:41 PM
To: Menachery, Vineet
Subject:

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a collaborator on the U19 there are norms in behavior that have to be followed or it results in a complete loss of trust between members of the group. Ralph

To: kdinnon@email.unc.edu[kdinnon@email.unc.edu]; Yount, Boyd L Jr[byount@email.unc.edu]; McAnarney, Eileen T.[etmcanar@UTMB.EDU]; lgralins@email.unc.edu[lgralins@email.unc.edu]; andrew_hale@unc.edu[andrew_hale@unc.edu]; rlgraham@email.unc.edu[rlgraham@email.unc.edu]; trevor.scobey@unc.edu[trevor.scobey@unc.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; davide.corte@humabs.ch[davide.corte@humabs.ch]; bgraham@mail.nih.gov[bgraham@mail.nih.gov]; wil2001@columbia.edu[wil2001@columbia.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Thur 5/30/2019 12:07:30 PM (UTC-05:00)
Subject: RE: MERS-Uganda Virus Manuscript

Good afternoon,
We are still hoping to get comments on the draft back today or tomorrow. If you need more time than tomorrow, please let me know, otherwise we will proceed incorporating the suggestions and submit next week.

Thanks

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Menachery, Vineet
Sent: Friday, May 24, 2019 1:41 PM
To: kdinnon@email.unc.edu; Yount, Boyd L Jr; McAnarney, Eileen T.; lgralins@email.unc.edu; andrew_hale@unc.edu; rlgraham@email.unc.edu; trevor.scobey@unc.edu; Anthony, Simon J.; davide.corte@humabs.ch; bgraham@mail.nih.gov; wil2001@columbia.edu
Cc: Baric, Ralph S
Subject: MERS-Uganda Virus Manuscript

Good afternoon,
Please find attached the following manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection." The manuscript describes our efforts to recover a virus expressing the bat spike protein from PDF2180-CoV. Each of you has contributed to this work and have been included as an author.

We are planning to submit the manuscript to PNAS in the next few weeks. Please take a look over it, paying close attention to the accuracy of your name and affiliation. Also, please add any authors that might be missing and their email contact information.

My apologies for emailing Friday before a US holiday weekend. Ideally, we would like to have the comments back by next Thursday, May 30th. With the busy time of year, we understand if you require more time to look over it; please just let us know that you need more time.

I will email a reminder on Tuesday. If I do not hear from you by Thursday afternoon, I will assume you are satisfied with the manuscript in its current state.

Thank you again for your contributions to this work. We look forward to hearing from you.

Vineet D. Menachery

Vineet D. Menachery, Ph.D.

Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Wed 6/5/2019 3:05:31 PM (UTC-05:00)
Subject: U19 Progress Report Blurb UTMB
U19 Progress Report UTMB 060519.docx

U19 Progress Report- UTMB

During the reporting period, we have focused on identifying the causitive gene associated with HrS2, a QTL associated with low viral titer following infection of preCC mice with SARS-CoV. This region, spanning 5.4bMb on chromosome 16 explains 22% of the variation in day 4 titer. Allele effects indicated low titer was associatd with the PWK allele and subsequent analysis narrowed gene targets to genes with SNPs private to PWK. The resulting list identified 48 genes including several mucins, genes involved in apoptosis and T cell activation, and two members of the poly (ADP-ribose) polymerase (PARP) family, PARP9 and PARP14. Previous efforts had identified Muc4 as a priority candidate and studies in Muc4 KO mice revealed changes in pathogenesis. However, no change in viral titer was observed, arguing that Muc4 did not drive changes in viral titer.

We subsequently focused on Parp9 and Parp14 as a potential candidate genes. Previous work by our collaborator, Matthew Daugherty (UCSD), had identified PARP9 and PARP14 as highly evolving genes in the mamamlian genome. His work had predicted that viruses target these PARP proteins driving their diversity in primates. Similarly, previous studies had implicated a role for PARP9 in modifying STAT1 signaling following IFN stimulations. In additions, PARP9 and PARP14 are reported to regulate each other and driving Th1 and Th2 responses respectively. We used *in silico* measures to predict that PARP9 may be cleaved by coronavirus 3CLpro [ADDIN EN.CITE <EndNote><Cite><Author>Kiemer</Author><Year>2004</Year><IDText>Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology</IDText><DisplayText>(26)</DisplayText><record><dates><pub-dates><date>Jun 6</date></pub-dates><year>2004</year></dates><keywords><keyword>Artificial Intelligence</keyword><keyword>Binding Sites/genetics</keyword><keyword>Coronavirus 229E, Human/enzymology/pathogenicity</keyword><keyword>Cysteine Endopeptidases/*metabolism</keyword><keyword>Humans</keyword><keyword>Neural Networks (Computer)</keyword><keyword>Proteins/*metabolism</keyword><keyword>SARS

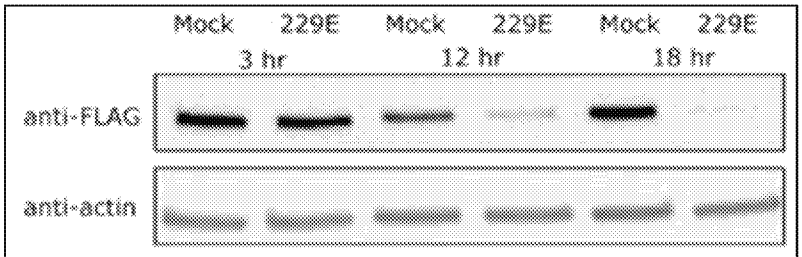


Figure X: PARP9 protein degraded over the course of CoV infection. Huh7 cells were transfected with FLAG-tagged human PARP9 protein 24 hours prior to infection. Cells were subseqeuntly infected with Human CoV-229E at MOI 1 and protein collected at indicated times and probed fof protein expression.

Virus/*enzymology/pathogenicity</keyword><keyword>Sequence Analysis, DNA/methods</keyword><keyword>Severe Acute Respiratory Syndrome/*pathology/virology</keyword></keywords><urls><related-urls><url>http://dx.doi.org/10.1186/1471-2105-5-72</url></related-urls></urls><isbn>1471-2105</isbn><custom2>PMC442122</custom2><titles><title>Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology</title><secondary-title>BMC Bioinformatics</secondary-title></titles><pages>72</pages><contributors><authors><author>Kiemer, L.</author><author>Lund, O.</author><author>Brunak, S.</author><author>Blom, N.</author></authors></contributors><edition>2004/06/08</edition><language>eng</language

><added-date format="utc">1557863848</added-date><ref-type name="Journal Article">17</ref-type><auth-address>Center for Biological Sequence Analysis BioCentrum-DTU, Technical University of Denmark DK-2800 Lyngby. lars@cbs.dtu.dk</auth-address><remote-database-provider>NLM</remote-database-provider><rec-number>164</rec-number><last-updated-date format="utc">1557863848</last-updated-date><accession-num>15180906</accession-num><electronic-resource-num>10.1186/1471-2105-5-72</electronic-resource-num><volume>5</volume></record></Cite></EndNote>]. We first overexpressed human PARP9 in human hepatoma cells (Huh7), a suitable cell line for infection with human CoV 229E (HCoV-229E). Over a time course of 3 hr to 18 hr post infection, we observed a decrease in overexpression of PARP9 in the context of HCoV-229E infection (**Fig. 2**), compared to a housekeeping control (β-actin). These results provide the first example that CoVs are capable of antagonizing PARP9 protein, and provide additional evidence that CoVs have developed mechanisms to combat host PARPs, subverting an otherwise protective role of PARPs in CoV infection. Similar down regulation of human PARP9 has been observed following MERS-CoV infection of Vero cells overexpressing PARP9 (data not shown), indicating that targeting is conserved across multiple CoVs. Ongoing studies will extend these finding to SARS-CoV and explore changes in mouse Parp9 with alleles from CC lines inlcuding B6 and PWK. We predict that the PWK allele of Parp9 may be resistant to degradation resulting in the lower titer QTL found in the original CC screen. We will also characterize CoV targeting of human PARP14 using similar over expression and infection approaches.

From: Menachery, Vineet [/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: 5/28/2019 5:22:14 PM
To: Baric, Ralph S [rbaric@email.unc.edu]
CC: kdinnon@email.unc.edu
Subject: PNAS cover letter
Attachments: PNAS cover letter Uganda Paper 052819.docx

Here is my first go at PNAS cover letter. Feel free to modify, not my best effort.

Also, I didn't include Scott Randell as an author, but we did infect HAE. Do you want him as an author?

VDM

UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL

DEPARTMENT OF EPIDEMIOLOGY
MCGAVRAN-GREENBERG HALL
CAMPUS BOX 7435
CHAPEL HILL, NC 27599-7435

F 919.966.2689

To the Editors,

Please find enclosed manuscript, "Trypsin treatment unlocks barrier for zoonotic coronaviruses infection" by Menachery, Dinnon, et al. In this work, we describe the restriction of two MERS-like bat coronaviruses and the use of exogenous trypsin to overcome this block. The results demonstrate that proteolytic activation of spike, not receptor binding, is the major barrier to emergence of these two group 2C coronaviruses. With implications for virus emergence and surveillance, we believe the work is both appropriate and timely for publication in PNAS.

The recent outbreaks of Zika, Ebola, and MERS-CoV highlight a significant threat posed by cross-species transmission leading to human disease. Coupled with global air travel and unequal public health infrastructures, the impact of emerging viral outbreaks is potentially devastating in terms of human health as well as economic impact. However, despite a wealth of metagenomics data identifying novel coronavirus strains, correlates to evaluate emergence potential are still lacking. Therefore, in this manuscript, we use metagenomics data and reverse genetic systems to generate chimeric virus strains in order to identify and prepare for potential pre-pandemic viruses.

Focusing on PDF-2180 CoV, a MERS-like virus sequence isolated in Uganda, we generated a chimeric strain expressing the PDF-2180 spike in the context of MERS-CoV. While initially not viable, we found that the addition of exogenous trypsin rescued viral replication in Vero and human cells. The chimeric virus could replicate in human gut cells, but not in human airway cells. Notably, blockade of the MERS-CoV receptor DPP4 had no impact on replication of the chimeric, bat-spike expressing virus suggesting use of an alternative receptor. Monoclonal antibodies targeted against MERS-CoV had no efficacy against this chimeric MERS-Uganda spike virus. Importantly, exogenous trypsin also rescued a second group 2C coronavirus, HKU5-CoV, indicating that proteolytic cleavage, not receptor binding, was the primary barrier for emergence of these two zoonotic coronaviruses in human cells. Overall, the results of our studies demonstrate that host protease cleavage may be a primary barrier for coronavirus emergence. Coupled with receptor binding, spike activation offers a new parameter to evaluate emergence potential of coronavirus. In addition, the finding offers a novel means to recover previously uncultivable zoonotic coronavirus strains.

Considering these factors, we believe that the manuscript will be of interest to a wide range of readers including those interested in translation of metagenomics data, emerging infectious disease, and public health preparedness. We would like to suggest that Drs. Yoshihiro Kawaoka, Peter Palese, or Linda Saif serve as editors for this manuscript. We would also like to recommend Drs. Luis Enjuanes, Thomas Gallagher, and Peter Daszak as potential reviewers.

Sincerely,

Ralph Baric, Professor of Epidemiology
Principle Investigator,
University of North Carolina at Chapel Hill
Chapel Hill, North Carolina 27599-7435
Ph: 919-966-3895
rbaric@ad.unc.edu

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Tue 6/25/2019 1:39:40 PM (UTC-05:00)
Subject: RE: PNAS MS# 2019-09188 Decision Notification

It was ok. Not much in terms of CoV stuff other than structure from Veesler. Good networking and lots of ideas.
I'll send a draft of the presubmission inquiry today. I am heading to my parents tomorrow, so I will try and send it tonight or in the morning if you can make comments (or if you want to send). I'll CC you on the email and work toward reformatting as needed.

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Tuesday, June 25, 2019 1:34 PM
To: Menachery, Vineet
Subject: RE: PNAS MS# 2019-09188 Decision Notification

Okay, how was the meeting?

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 2:17 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: PNAS MS# 2019-09188 Decision Notification

I talked to both the Nat Micro and CHM editors at the plus strand meeting. I will put in a presubmission inquiry to Cell Host and see what they say. Since I didn't talk about it at the +strand meeting, they wouldn't be familiar with the story.

I'll work on reformating; size wise we should be good for either journal. Editor told me that they wouldnt say yes in the respone, but they will say no if they aren't interested.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Tuesday, June 25, 2019 1:07 PM
To: Menachery, Vineet
Subject: RE: PNAS MS# 2019-09188 Decision Notification

And I agree, sometimes this profession just sucks

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, June 25, 2019 2:05 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: FW: PNAS MS# 2019-09188 Decision Notification

Such bull shit.

Where do you want to go? Nature Micro or Cell Host is my thought.

From: journalstaff@pnascentral.org [journalstaff@pnascentral.org]
Sent: Tuesday, June 25, 2019 10:48 AM
To: Menachery, Vineet
Cc: vineet@email.unc.edu
Subject: PNAS MS# 2019-09188 Decision Notification

June 25, 2019

Title: "**Trypsin treatment unlocks barrier for zoonotic coronaviruses infection.**"
Tracking #: 2019-09188
Authors: Menachery et al.

Dear Dr. Menachery,

I regret to inform you that the PNAS Editorial Board has declined your manuscript [MS# 2019-09188] for further consideration. We receive many more good papers than we can publish and the Board must carefully weigh which papers merit external review. The expert who served as editor concluded that although this work is interesting, it does not have the broad appeal needed for PNAS and is better suited for a more specialized journal.

Thank you for submitting your manuscript to PNAS. I am sorry we cannot be more encouraging this time, and I hope you will consider submitting future work to PNAS.

Sincerely yours,
May R. Berenbaum
Editor-in-Chief

From: Menachery, Vineet [/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: 6/25/2019 8:40:21 PM
To: hostmicrobe@cell.com
CC: Baric, Ralph S [rbaric@email.unc.edu]
Subject: Presubmission Inquiry: Barrier to Coronavirus Emergence
Attachments: Presubmission Abstract.pdf

Dear Editors at Cell Host & Microbe:

Please find our presubmission inquiry for our manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection", by Menachery, Dinnon, et al.

In this work, we describe the restriction of two MERS-like bat coronaviruses and the use of exogenous trypsin to overcome this barrier. Employing a MERS-CoV reverse genetic system, we constructed a chimeric virus replacing the wild-type spike with the PDF2180-CoV spike, a MERS-like virus found in an Ugandan bat. While initially not viable, we found that the addition of exogenous trypsin rescued viral replication in Vero and human cells. The chimeric MERS virus could replicate in human gut cells, but not in human airway cells. Notably, blockade of MERS-CoV receptor DPP4 had no impact on chimeric virus replication, suggesting use of an alternate receptor. Testing of monoclonal antibodies designed against the RBD and S2 portions of the MERS-CoV spike showed no efficacy against the PDF2180-chimeric virus. Importantly, exogenous trypsin also rescued replication of a second group 2C CoV, full-length HKU5-CoV. These results indicate host protease cleavage of spike constitutes a primary barrier for group 2C CoV emergence. Coupled with receptor binding, spike activation offers a new parameter to evaluate emergence potential of coronavirus. In addition, the finding offers a means to recover previously uncultivable zoonotic coronavirus strains.

We have attached our abstract and a graphical description of our findings for you to review. We look forward to your response.

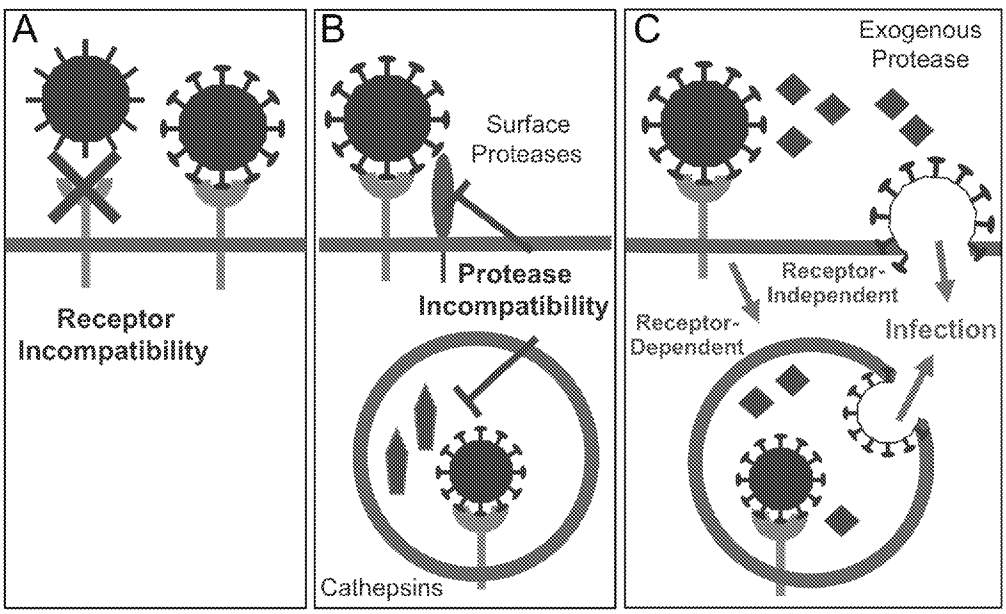
Sincerely,

Vineet D. Menachery & Ralph S. Baric

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

Abstract

Using an ever-expanding database of viral metagenomics sequences, we are positioned to identify high-risk pathogens poised to seed future outbreaks and probe molecular mechanisms associated with emergence. In this work, we examine restriction of a MERS-like CoV sequence isolated from a Ugandan bat, PREDICT/PDF-2180. Using reverse genetics, a chimeric virus expressing the spike ecto-domain of PDF-2180 within the MERS-CoV backbone had been generated, but had failed to recover infectious virions. However, addition of exogenous trypsin facilitated virus recovery and passage in Vero cells and productive infection of human cells. Importantly, blocking DPP4, the receptor for MERS-CoV, did not ablate infection of the PDF-2180 chimeric virus. In addition, therapeutics targeting the MERS-CoV spike proved ineffective in limiting the PDF-2180 chimeric virus. Notably, trypsin treatment also rescued replication of a related group 2C bat CoV, HKU5-CoV, suggesting that proteolytic spike activation may broadly limit zoonotic coronavirus infection. Together, these results indicate that proteolytic processing is a critical factor for infection and represents an important barrier in the emergence of zoonotic coronaviruses in new animal populations.



To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Tue 6/25/2019 3:31:22 PM (UTC-05:00)
Subject: presubmission draft
Presubmission Abstract.pdf

Dear Editors at Cell Host & Microbe:

Please find our presubmission inquiry for our manuscript, "Trypsin treatment unlocks barrier for zoonotic coronavirus infection", by Menachery, Dinnon, et al.

In this work, we describe the restriction of two MERS-like bat coronaviruses and the use of exogenous trypsin to overcome this barrier. Employing a MERS-CoV reverse genetic system, we constructed a chimeric virus replacing the wild-type spike with the PDF2180-CoV spike, a MERS-like virus found in an Ugandan bat. While initially not viable, we found that the addition of exogenous trypsin rescued viral replication in Vero and human cells. The chimeric MERS virus could replicate in human gut cells, but not in human airway cells. Notably, blockade of MERS-CoV receptor DPP4 had no impact on chimeric virus replication, suggesting use of an alternate receptor. Testing of monoclonal antibodies designed against the RBD and S2 portions of the MERS-CoV spike showed no efficacy against the PDF2180-chimeric virus. Importantly, exogenous trypsin also rescued replication of a second group 2C CoV, full-length HKU5-CoV. These results indicate host protease cleavage of spike constitutes a primary barrier for group 2C CoV emergence. Coupled with receptor binding, spike activation offers a new parameter to evaluate emergence potential of coronavirus. In addition, the finding offers a means to recover previously uncultivable zoonotic coronavirus strains.

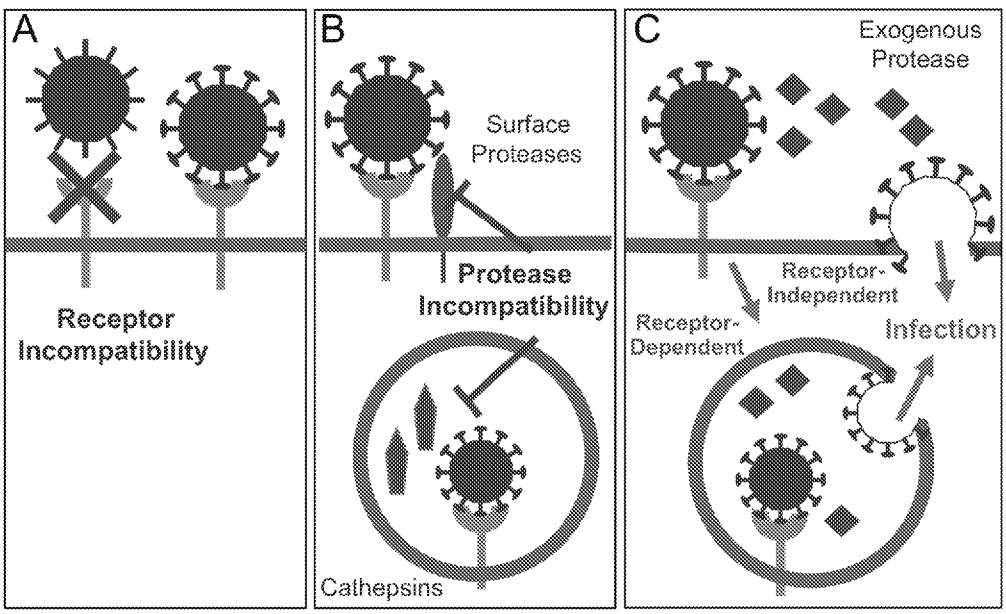
We have attached our abstract and a graphical description of our findings for you to review. WE look forward to your response.

Sincerely,

Vineet D. Menachery & Ralph S. Baric

Abstract

Using an ever-expanding database of viral metagenomics sequences, we are positioned to identify high-risk pathogens poised to seed future outbreaks and probe molecular mechanisms associated with emergence. In this work, we examine restriction of a MERS-like CoV sequence isolated from a Ugandan bat, PREDICT/PDF-2180. Using reverse genetics, a chimeric virus expressing the spike ecto-domain of PDF-2180 within the MERS-CoV backbone had been generated, but had failed to recover infectious virions. However, addition of exogenous trypsin facilitated virus recovery and passage in Vero cells and productive infection of human cells. Importantly, blocking DPP4, the receptor for MERS-CoV, did not ablate infection of the PDF-2180 chimeric virus. In addition, therapeutics targeting the MERS-CoV spike proved ineffective in limiting the PDF-2180 chimeric virus. Notably, trypsin treatment also rescued replication of a related group 2C bat CoV, HKU5-CoV, suggesting that proteolytic spike activation may broadly limit zoonotic coronavirus infection. Together, these results indicate that proteolytic processing is a critical factor for infection and represents an important barrier in the emergence of zoonotic coronaviruses in new animal populations.



To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=UTMB/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MENACHERY, VINEET30F]
Sent: Mon 7/1/2019 10:29:52 PM (UTC-05:00)
Subject: RE: ASM nomination
Menachery CV ASM 2019.pdf

See attached CV.

From: Menachery, Vineet
Sent: Sunday, June 30, 2019 11:01 AM
To: Baric, Ralph S
Subject: RE: ASM nomination

I'll send the CV Monday or Tuesday.
Thanks again. Hopefully Diamond and Yoshi will do it. I know Mike has written most of my letters for this. Yoshi did the one for the Star award. They only have to write it if I make the first cut.

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Saturday, June 29, 2019 4:24 PM
To: Menachery, Vineet
Subject: RE: ASM nomination

Hi Vineet, Okay thisis very helpful. I will be delighted to lead it and get the nominating letter together, send cv next week. I had been concerned a bout contacting other referee's at the last minute and wasn't aware they had draft letters already available.
Ralph

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, June 28, 2019 11:26 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: RE: ASM nomination

Hey Ralph,

The nomination is a webform (in the link) and has a slot (4000 characters) for defining why I am deserving of the award. They only contact the references (Diamond or Yoshi or Scott) if I am a finalist. Both have already written a letter on my behalf for the Texas Star award, so I think they have text already.

I can ask Scott, but based on what I have heard, it really needs to be someone that can put the nominee's accomplishments in the perspective of your field. The people who have won that I know (Nick Heaton and Stacy Horner) had their post-doc PI nominate (Gale and Palese) them.

It has been implied that the nomination is about your record, the stature of the people who are your references, and the nominator highlighting your importance to your specific field. I think you are probably most qualified to do that.

The award does not always get many people applying. The nomination is due almost a year before the next meeting and most people miss the deadline and forget. That being said, my biggest strike for the award will be not having an independent pub from my own lab. Best is the number of papers I've published. We got favorable reviews on our JVI paper this month, but won't be back in til later in July.

I can send my CV next week, but you can also send it at a later date, that might help.

Thanks for participating.

VDM

From: Baric, Ralph S [rbaric@email.unc.edu]
Sent: Friday, June 28, 2019 2:58 PM
To: Menachery, Vineet
Subject: RE: ASM nomination

Hi Vineet, I'd be delighted to participate. Given the timeline, it might be better for me to write a letter and scott to nominate, as I can address why your deserving of this award for early career basic research, which I think you'd be competitive for. Not sure how quickly diamond and kawaoka can respond or whether they have made other commitments, although they are both familiar with your work. Does scott have a feel for the mechanism here? Is it better for your former mentor or current chair to nominate you for this award? Some insight into this would help. Ralph

---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, June 27, 2019 10:07 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: ASM nomination

Hey Ralph,

Would you be willing to nominate me for the ASM early career award. https://www.asm.org/Academy/ASM-Award-for-Early-Career-Basic-Researchhttps://www.asm.org/Academy/ASM-Award-for-Early-Career-Basic-Research

The application requires 1 nominator and 2 references. I'd suggest that Mike Diamond and Yoshi would be good for the nomination. You could also use Scott Weaver. I put their emails down below. The hardest part of the form is the following prompt:

Describe the nominee's outstanding contributions to the microbial sciences. Please be as specific as possible, with particular focus on why the nominee is deserving of this specific award (*no more than 4000 characters*). For more information regarding specific awards descriptions, please visit: https://www.asm.org/Academy/ASM-Awards.

If you are willing, the nomination is due by July 9th. If you don't have time, I can ask Scott Weaver or another person to nominate me. Let me know and I will send you and updated CV.ThanksVDM

mdiamond@wustl.edu
yoshihiro.kawaoka@wisc.edu
sweaver@UTMB.EDU

552.117

VINEET DAVID MENACHERY

Assistant Professor
Dept. of Microbiology and Immunology
University of Texas Medical Branch

Vimenach@utmb.edu
[redacted]
themenacherylab.com

Galveston National Laboratory
301 University Blvd., Route 0610
Galveston, Texas 77555
Office Phone 409.266.6934

RESEARCH INTERESTS

Utilizing severe coronavirus infections, the Menachery Lab seeks to define virus-host interactions that dictate disease outcomes taking advantage of three cutting edge platforms: 1) reverse genetic systems for virus generation, 2) a refined systems biology approach, and 3) diverse model systems for infection. Described below, the current projects provide insight into our approach and explore areas with implications for understanding infection and disease.

- **Examine the dynamics of host-virus interactions within and between diverse viral families.** Employing uniform experimental platforms, these systems based studies seek to identify common host pathways induced and/or antagonized by various pathogenic viruses. The approach also leverages differences between wild-type and mutant viruses to identify key processes that drive pathogenic outcomes. The overall goal is to derive mechanistic insight and develop novel avenues for antiviral treatment.
- **Explore the pathogenic and emergence potential of novel CoVs.** The outbreaks of both SARS and MERS-CoV underscore the need for continued surveillance of zoonotic viruses. While CoV sequences have been identified, minimal translational work has been undertaken. These studies evaluate the likelihood of emergence, pathogenic potential, and efficacy of current therapeutic platforms against existing coronavirus strains.
- **Define age dependent changes to host immunity via viral infection**. Infectious disease in the context of aging represents an opportunity to explore changes to immunity as well as gain insights into a leading cause of death among the elderly. Importantly, both SARS and MERS-CoV induce more severe infection and increased mortality in aged human patients. This phenotype is recapitulated in young and aged mouse models, allowing exploration of host virus interaction that change as a product of aging. These studies seek to identify, confirm, and validate changes in pathway activation as well as develop treatments to mitigate disease in the aged hosts.
- **Examine the role of host diversity in susceptibility to infection.** In addition to aging, host genetic diversity plays a critical role in the response to respiratory virus infection. Employing the Collaborative Cross (CC), a panel of recombinant inbred mice that captures genetic diversity similar to the human population, we observe a wide spectrum of phenotypes. These readouts can be dysregulated from each other, allowing fine mapping to define specific genetic components that drive phenotypic responses.

EDUCATION

University of North Carolina at Chapel Hill — May 2017
Post-doctoral Fellowship — Chapel Hill, North Carolina

Washington University in Saint Louis — May 2010
Doctorate of Philosophy in Biological Sciences, concentration in Immunology — Saint Louis, Missouri

Clemson University — May 2004
Bachelors of Science in Microbiology, *Minor* in Business Administration — Clemson, South Carolina

LABORATORY POSITIONS

Menachery Laboratory
Dept. of Microbiology and Immunology, University of Texas Medical Branch — Galveston, TX
Assistant Professor — May 2017- Present

Laboratory of Dr. Ralph S. Baric
Dept. of Epidemiology, University of North Carolina — Chapel Hill, NC
Post-doctoral fellow — August 2010- May 2017

Laboratory of Dr. David Leib
Dept. of Ophthalmology and Vision Sciences, Washington University — Saint Louis, MO
Graduate Student — May 2005- May 2010

Laboratory of Dr. Timothy Sparer
Microbiology Dept., University of Tennessee — Knoxville, TN
Research Technician — June 2003 – August 2003

PUBLICATIONS

2019

1. **Menachery VD***, Dinnon KH*, Yount BL, McAnarney ET, Gralinski LE, Hale A, Graham RL, Scobey T, Anthony SJ, Corti D, Graham B, Lipkin WI, Baric RS. Trypsin treatment unlocks barrier for zoonotic coronavirus infection. ***Nature Microbiology***. Submitted July 2019.
2. Johnson BA, Hage A, Kalveram B, Mears M, Plante JA, Rodriguez SE, Ding Z, Bente D, Bradrick S, Freiberg AN, Popov V, Rajsbaum R, Rossi S, Russell WK, **Menachery VD**. Peptidoglycan associated cyclic lipopeptide disrupts viral infectivity. ***Journal of Virology.*** Revision July 2019.
3. Dinnon KH, Gallichotte EN, Fritch EJ, **Menachery VD**, Baric RS. Shortening of Zika virus CD-loop reduces neurovirulence while preserving antigenicity. . PLOS Neglected Tropical Diseases. 019 Mar 7;13(3):e0007212.
4. Schindewolf C, **Menachery VD**. Middle East Respiratory Syndrome Vaccine Candidates: Cautious Optimism. **Viruses.** 2019 Jan 17; 11(1). Pii: E74.

2018

5. Van Doremalen N, Schaefer A, **Menachery VD**, Letko M, Bushmaker T, Fischer R, Figueroa D, Hanley P, Saturday G, Baric RS, Munster V. SARS-like coronavirus WIV1-CoV does not replicate in Egyptian fruit bats (*Rousettus aegyptiacus*). ***Viruses***. 2018 Dec 19; 10(12). Pii:E727
6. Gralinski LE, Sheahan TP, Morrison TE, **Menachery VD**, Jensen K, Whitmore A, Heise MT, Baric RS. Complement activation contributes to SARS-Coronavirus pathogenesis. **MBio**. 2018 Oct 9;9(5). pii: e01753-18.
7. **Menachery VD**, Gralinski LE, Mitchell HD, Dinnon KH, Leist SR, Yount BL, McAnarney ET, Graham RL, Waters KM, Baric RS. Combination attenuation offers strategy for live-attenuated coronavirus vaccines. **J Virol.** 2018 Aug 16;92(17). pii: e00710-18.
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9. **Menachery VD*,** Agnihothram S*, Yount BL, Lindesmith LC, Whitmore A, Schaefer A, Heise MT, Baric RS. Development of a broadly accessible VEE Replicon Particle Vaccine Platform. **J Virol**. 2018 May 14;92(11). pii: e00027-18. *Co-first authors.
10. **Menachery VD***, Schaefer A*, Burnum-Johnson, KE, Mitchell HD, Eisfeld AJ, Walters KB, Nocra CD, Purvine SO, Casey CP, Monroe ME, Weitz KK, Stratton KG, Webb-Robertson BM, Gralinski LE, Metz TO, Smith RD, Waters KM, Sims AC, Kawaoka Y, Baric RS. MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. **PNAS**. 2018 Jan 30;115(5):E1012-E1021.
11. Johnson BA, Graham RL, **Menachery VD**. Metagenomics, structure, and reverse genetics: Key platforms for emerging coronavirus research. **Virology.** 2017 Dec 23. pii: S0042-6822(17)30414-2.

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12. **Menachery VD**, Gralinski LE, Dinnon KH, Mitchell HD, Dinnon KD, Leist SR, Yount BL, Graham RL, McAnarney ET, Stratton KG, Debbink K, Sims AC, Waters KM, Baric RS. MERS-CoV NSP16 necessary for IFN resistance and viral pathogenesis. **MSphere.** 2017 Nov 15;2(6). pii: e00346-17.
13. Gallichotte EN, Dinnon KH, Lim XN, Ng TS, Lim E, **Menachery VD**, Kok SM Lok, Baric RS. CD-loop extension in Zika virus envelope key for stability and pathogenesis. **J Infect Dis.** 2017 Sep 8.
14. **Menachery VD,** Mitchell HD, Cockrell AS, Gralinski LE, Yount BL, Graham RL, McAnarney ET, Douglas MG, Scobey T, Beall A, Dinnon K, Kocher JF, Hale AE, Stratton KG, Waters KM, Baric RS. MERS-CoV Accessory ORFs play key role for infection and pathogenesis. **MBio**. 2017 Aug 22;8(4). pii: e00665-17.
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16. Gralinski LE, **Menachery VD**, Morgan AP, Totura AL, Beall A, Kocher J, Plante J, Harrison-Shostak DC, Schaefer A, Pardo-Manuel de Vilena F, Ferris MT, Baric RS. Allelic Variation in *Ticam2* contributes to SARS-CoV pathogenesis. **G3** (Bethesda), 017 Jun 7;7(6):1653-1663.
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18. **Menachery VD*,** Gallichotte EN*, Dinnon KH, Yount BL, Hartman S, Widman D, Messer W, de Silva A, Baric RS. Epitope Addition and Ablation via Manipulation of a Dengue Virus Serotype 1 Infectious Clone. **mSphere**. 2017 Feb 22;2(1). pii: e00380-16. *Co-first authors.

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2016

20. **Menachery VD,** Yount BL, Sims AC, Agnihothram SA, Gralinski LE, Plante JA, Graham RL, Scobey T, Royal S, Pickles RJ, Randell SH, Lanzavecchia A, Marasco WA, Baric RS. SARS-like WIV1-CoV poised for human emergence, but may lack epidemic potential. **PNAS**. 2016 Mar 14. pii: 201517719. PMC4801244

2015

21. **Menachery VD.** MERS vaccine candidate offers promise, but questions remain. **E-Biomedicine.** 2015 Sep 25;2(10):1292-3. PMC4634784.
22. **Menachery VD**, Yount BL, Debbink K, Agnihothrum SA, Gralinski LE, Graham RL, Plante JA, Scobey T, Donaldson E, Ge XY, Randell SH, Lanzavecchia A, Marasco WA, Shi ZL, Baric RS. SARS-like cluster of circulating bat coronavirus pose a threat for human emergence. **Nature Medicine.** Dec;21(12):1508-13. PMC4797993.
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24. **Menachery VD***, Gralinski LE*, Baric RS, Ferris MT. New Metrics for Evaluating Respiratory Pathogenesis. **PlosOne.** 2015 June 26; 10(6): e0131451. PMC4482571,

2014

25. Selinger C, Tisoncik-Go J, **Menachery VD,** Agnihothrum S, Law GL, Chang J, Kelly SM, Sova P, Baric RS, Katze MG. Cytokine systems approach demonstrates differences in innate and pro-inflammatory host responses between genetically distinct MERS-CoV isolates. **BMC Genomics**. 2014 Dec 22;15(1):1161. PMC4522970.
26. **Menachery VD,** Debbink K, Baric RS. Coronavirus Non-Structural Protein 16: Evasion, Attenuation, and Possible Treatments. **Virus Research**. 2014 Sep 30; pii: S0168-1702(14)00396-7. PMC3993736.
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28. **Menachery VD***, Eisfeld AJ*, Josset L, Sims AC, Schaefer A, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Matzke MM, Webb-Robertson BJ, Shukula AK, Burkett S, Metz TO, Pickles R, Smith RD, Waters KM, Katze MG, Kawaoka Y, Baric RS. Pathogenic influenza and coronaviruses utilize similar and contrasting approaches to control global interferon stimulated gene responses. **MBio**. 2014 May 20; 5(3): e1174-14. PMC4030454.
29. Agnihothram S, Yount BL Jr, Donaldson EF, Huynh J, **Menachery VD**, Gralinski LE, Graham RL, Becker MM, Tomar S, Scobey TD, Osswald HL, Whitmore A, Gopal R, Ghosh AK, Mesecar A, Zambon M, Heise M, Denison MR, Baric RS. A mouse model for Betacoronavirus subgroup 2c using a bat coronavirus strain HKU5 variant. **MBio**. 2014 Mar 25; 5(2): e00047-14. PMC3977350.
30. **Menachery VD**, Yount BL, Josset L, Gralinski LE, Scobey T, Agnihothram S, Katze M, Baric RS. Attenuation and Restoration of SARS-CoV Mutant lacking 2'O Methyltransferase Activity. **J Virol**. 2014 Apr;88(8):4251-64. PMC4260984.

2013

31. Agnihothram S, Gopal R, Yount B Jr, Donaldon EF, **Menachery VD**, Graham RL, Scobey TD, Gralinski LE, Denison MR, Zambon M, Baric RS. 2013. Evaluation of Serologic and Antigenic Relationships Between Middle Eastern Respiratory Syndrome Coronavirus and Other Coronaviruses to Develop Vaccine Platforms for the Rapid Response to Emerging Coronaviruses. **J Infect Dis.** 2013 Dec 30. PMC3952667.
32. Scobey T, Yount BL, Sims AC, Donaldson EF, Agnihothram SS, **Menachery VD**, Graham RL, Swanstrom J, Bove PF, Kim JD, Grego S, Randell SH, Baric RS. Reverse genetics with a full-length infectious cDNA of the Middle East respiratory syndrome coronavirus. **Proc Natl Acad Sci** U S A. 2013 Oct 1;110(40):16157-62. PMC3791741.
33. **Menachery VD,** Baric RS. Bugs in the System. **Immunol Rev**. 2013 Sep: 255(1):256-74. PMC3748621.
34. Gralinski LE, Bankhead A, Jeng S, **Menachery VD**, Proll S, Belisle SE, Matzke M, Webb-Robertson BJ, Luna ML, Shukla AK, Ferris MT, Bolles M, Chang J, Aicher L, Waters KM, Smith RD, Metz TO, Law GL, Katze MG,

McWeeney S, Baric RS. Mechanisms of severe acute respiratory syndrome coronavirus-induced acute lung injury. **MBio**. 2013 Aug 6;4(4). PMC3747576.

35. **Menachery VD***, Josset L*, Gralinski LE, Agnihothram S, Sova P, Carter VS, Yount BL, Graham RL, Baric RS, Katze MG. Cell Host Response to Infection with Novel Human Coronavirus EMC Predicts Potential Antivirals and Important Differences with SARS Coronavirus. **MBio**. 2013 Apr 30; 4(3). PMC3663187. *Co-first authors.
36. Sims AC, Tilton SC, **Menachery VD**, Gralinski LE, Schäfer A, Matzke MM, Webb-Robertson BJ, Chang J, Luna ML, Long CE, Shukla AK, Bankhead AR 3rd, Burkett SE, Zornetzer G, Tseng CT, Metz TO, Pickles R, McWeeney S, Smith RD, Katze MG, Waters KM, Baric RS. Release of SARS-CoV nuclear import block enhances host transcription in human lung cells. **J Virol**. 2013 Apr; 87(7):3885-902. PMC3624188.

2008-2012

37. Pasieka, TJ, **Menachery VD**, Rosato PC, Leib DA. Corneal replication is an interferon response-independent bottleneck for virulence of herpes simplex virus type 1 in the absence of virion host shutoff. **J Virol**. 2012 Jul; 86(14):7692-5. PMC3416281.
38. **Menachery VD**, Pasieka TJ, Leib DA. Interferon regulatory factor 3-dependent pathways are critical for control of herpes simplex virus type 1 central nervous system infection. **J Virol**. 2010 Oct; 84(19): 9685-94. PMC2937762.
39. **Menachery VD**, Leib DA. Control of herpes simplex virus replication is mediated through an IRF-3 dependent pathway. **J Virol**. 2009 Dec; 83(23): 12399-406. PMC2786705.
40. Pasieka TJ, Lu B, Crosby SD, Wylie KM, Morrison LA, Alexander DE, **Menachery VD**, Leib DA. Herpes simplex virus virion host shutoff attenuates establishment of the antiviral state. **J Virol**. 2008 Jun;82(11):5527-35. PMC2395185.

AWARDS & HONORS

- American Association of Immunologist Early Career Faculty Travel Grant (2019)
- UTMB Nominee, Pew Scholars Program (2019)
- University of Texas System Rising STARs Award (2017)
- Pathway to Independence Award (K99/R00, NIA) (2015-2020)
- Ruth L. Kirschstein National Research Service Award (F32, NIAID) (2013-2015)
- Postdoctoral Award for Research Excellence, University of North Carolina (2014)
- Millstein Young Investigator Award, International Society of Interferon and Cytokine Research (2016)
- UTMB Nominee, Searle Scholar Program (2017, 2018)
- Best Talk, UNC Microbiology & Immunology Postdoc Symposium (2016)
- Selection to Virus and Cell, Gordon Research Conference (2013, 2015, 2017)
- Milstein Travel Award, International Society of Interferon and Cytokine Research (2012)
- National Eye Institute Research Training Grant in the Visual Sciences (2008-2010)
- American Society of Virology Travel Award (2009, 2011, 2015)
- Selection to 4th Annual NIH National Graduate Student Research Festival (2009)
- Magna Cum Laude, Clemson University (2004)
- Prince Alumni Scholar, Clemons University (2000-2004)
- Campbell Young Leader Scholar, Clemson University (2000-2002)
- Eagle Scout, Boy Scouts of America

PROFESSIONAL SERVICE

Session Chair

- Annual Meeting, American Society of Virology, College Park, Maryland (2018)
- Positive Sense RNA Virus Meeting, Keystone Symposia, Killarney, Ireland (2019)
- Annual Meeting, American Society of Virology, Minneapolis, Minnesota (2019)
- Biology of Acute Respiratory Infection, Gordon Research Conference, Galveston, Texas (2020)

Journal Reviewer

- *Virus Research* (2014 – present)
- *Virology* (2014 – present)
- *Viruses* (2019 – present)
- *Journal of Virology* (2016 – present)
- *PlosPathogen* (2016 – present)
- *Cell Host Microbe* (2018 – present)
- *Clinical Microbiology Reviews* (2014 – present)

- *Journal of Molecular Biology* (2019 – present)
- *American Journal of Physiology - Lung Cellular and Molecular* (2016 – present)
- *Ebiomedicine* (2015 – present)
- *PlosOne* (2014 – present)

Grant Reviewer
- Hong Kong Research Grants Council (2015 – present)
- Systems Immunogenetics Pilot Program (2018 – present)

Panel & Committee Membership
- Oliver Smithies Nobel Symposium Committee (2014)
- Panelist K-Series Information Session (2015, 2016)
- Poster Judge, McLaughlin Symposia (2018, 2019)

Science Communication
- Guest, *This Week In Virology* Podcast Episode 364: "It's not SARS 2.0" (2015).
- Research Featured, STAT News, "SARS-like virus in bats shows potential to infect humans, study finds" (2015).
- Interview, Infectious Disease Hub, "Emerging technologies to investigate coronavirus emergence" (2019).

RESEARCH SUPPORT

Ongoing Research Support

4R00AG049092-03 (PI- Menachery) June 2017- May 2020
Pathway to Independence Award (K99/R00), National Institute of Aging
Title: Systems Based Analysis of Host Factors that Contribute to Aging Pathogenesis
This grant utilizes systems biology and the SARS-CoV mouse model to identify target host pathways that contribute to differential disease outcomes in the aged host compared to young.
Role: PI

University of Texas Rising STARs Award (PI- Menachery) May 2017- April 2020
Award granted for recruitment of promising faculty members for the purposes of equipment and renovation expenditures for establishment of their new laboratory.
Role: PI

U19AI100625 (PI- Baric/Heise) May 2017 – April 2022
Title: Systems Immunogenetics of SARS-CoV Infection
This program uses the Collaborative Cross to study complex genetic interactions in diverse populations, to identify novel polymorphic genes regulating immune responses to SARS and gain insights into genetic interactions that shape immune phenotypes in mice and humans.
Role: Project 1 Co-I

Claude Pepper Pilot Award (PI- Menachery) September 2018 – August 2019
Claude D. Pepper Older American Independence Center
Title: Parabiosis and Age-dependent Viral Pathogenesis
Goal: Project explores feasibility of using parabiosis to study aging in the context of SARS-CoV infection.
Role: PI

Completed Research Support

Pilot Award Oklahoma Nathan Shock Center (PI- Menachery) July 2017- June 2018
Award by an NIA Center of Excellence in Biology of Aging to analyze aging systems biology data in the context of infection; funds support collaboration with the with the Discovery Bioinfomatics Core housed within the Oklahoma Nathan Shock Center.
Role: PI

1K99AG049092-01A1 (PI- Menachery) June 2015- May 2017
Pathway to Independence Award (K99/R00), National Institute of Aging
Title: Systems Based Analysis of Host Factors that Contribute to Aging Pathogenesis
This grant utilizes systems biology and the SARS-CoV mouse model to identify target host pathways that contribute to differential disease outcomes in the aged host compared to young.
Role: PI

5F32AI102561-02-09 (PI- Menachery) January 2013- June 2015
Ruth L. Kirschstein National Research Service Award, National Institute of Allergy and Infectious Disease, NIH
Title: Evaluation of SARS-CoV 2'O Methyltransferase Mutants
The major goal is to examine the role of NSP16 in the context of infection, host responses, and therapeutics.
Role: PI

Postdoctoral Awards for Research Excellence (PI- Menachery) September 2014- July 2015
Office of Postdoctoral Affairs, University of North Carolina at Chapel Hill
The award recognizes research excellence and provides support for materials or further training opportunities.
Role: Awardee

T32EY013360-09 (PI- Beebe) September 2008- May 2010
National Eye Institute Research Training Grant in Visual Science
Title: The Impact of Interferon Regulatory Factor 3 on the Immune Response to Herpes Simplex Virus-1 Infection
This project examined the role of interferon regulatory factor 3 in controlling HSV-1 infection in vitro and in vivo.
Role: Trainee

INVITED SEMINARS

2019

Seminar Speaker

Infection and Immunity Seminar Series 2019 — Imperial College London
London, UK — June 2019

Plenary Speaker

Annual Conference 2019 — UK Microbiology Society
Belfast, Northern Ireland, UK — April 2019

2018

Seminar Speaker

Infectious Disease Division — Washington University School of Medicine
St. Louis, MO — June 2018

Microbiology Department Seminar — Ichan School of Medicine, Mount Sinai Hospital
New York, NY — March 2018

Center for Infection and Immunity — Mailman School of Public Health, Columbia University
New York, NY — March 2018

Plenary Speaker

4th Medical Conference — Instituto de Medicina Tropical Pedro Kouri
Havanna, Cuba — December 2018

2016

Seminar Speaker

Microbiology Department — University of Pennsylvania
Philadelphia, PA — March 2016

Microbiology Department — Columbia University
New York, NY — March 2016

Biochemistry and Molecular Biology Department — Penn State University
State College, PA — February 2016

Microbiology, Immunology, and Cancer Department — University of Virginia
Charlottesville, VA — February 2016

Laboratory of Infectious Disease — National Institute of Health
Bethesda, MD — February 2016

Microbiology and Immunology — University of Iowa
Iowa City, IA — January 2016

PROFESSIONAL DEVELOPMENT

- Positive-Strand RNA Virus Keystone Meeting (2016, 2019)
- Virus and Cell Gordon Conference (2013, 2015, 2017)

- American Society of Virology Annual Meeting (2006, 2008, 2009, 2011-2019)
- American Association of Immunologist Annual Meeting (2018, 2019)
- Aging and Immunity Symposium (2017)
- International Nidovirales Symposium (2014, 2017)
- Cytokines Meeting (2016, 2018)
- Biology of Acute Respiratory Infection Gordon Conference (2016)
- NIH Systems Biology U19 Annual Meeting (2015, 2016, 2017, 2019)
- "Omics" Systems Biology Program Meeting (2015)
- Responsible Conduct & Human Subjects Research Training, Collaborative Institutional Training Initiative (2014)
- Pathogenesis of Respiratory Viruses, Keystone Symposia (2014)
- Systems Immunogenetics Bi-Annual Meeting, Chapel Hill, NC (2013, 2014, 2015, 2016)
- Systems Genetics Workshop, Chapel Hill, NC (2013)
- North Carolina State 2nd Annual Postdoctoral Research Symposium (2013)
- Microbiology and Immunology Reunion, University of North Carolina (2013)
- Annual Oliver Smithies Nobel Symposium (2013, 2014)
- Virology in Progress, UNC (2011- 2017)
- 3rd Annual Systems Biology Programmatic and Systems Biology Working Group Meeting (2011)
- Systems Biology Approaches to Virus-Host Interaction Conference, Chapel Hill (2011, 2012)
- University of North Carolina Virology Colloquium (2010, 2011, 2012, 2015)
- Responsible Conduct of Research Training (2010)
- Triangle Immunology Interest Group (2010- Present)
- Immunology Program Retreat (2004 – 2008)
- International Herpes Workshop (2007)

TEACHING AND MENTORING EXPERIENCE

Microbial Pathogenesis: Viruses
Biological and Biomedical Sciences Program, University of North Carolina Chapel Hill, NC
Guest Lecturer April 2014

- Senior level graduate course exploring microbial pathogenesis of viruses.
- Delivered lecture on host-virus interactions as well as providing and grading final exam questions.

Preparing for the Postdoctoral Process
The Graduate School, University of North Carolina Chapel Hill, NC
Panelist September 2013

- Served as contributor for panel to prepare graduate students for researching, finding, and getting a post-doctoral opportunity in their area of interest.

Undergraduate Research
Dept. of Biology, University of North Carolina Chapel Hill, NC
Research Mentor August 2011- May 2012

- Senior level undergraduate course in biology that seeks to provide students with research experience while working on a relevant question of current biological interest to a UNC research laboratory.
- Responsibilities included direct training and supervision of a senior undergraduate, Jordan Best. Provided guidance for projects that included construction of over expression vectors, stable cell lines, and chimeric mutant viruses. Reviewed lab notebook, aided final summary report, and provided context and recommendations for final grade.

Principles of Biology III: Physiology
Dept. of Biology, Washington University in St. Louis Saint Louis, MO
Teaching Assistant January 2007- May 2007

- Sophomore undergraduate class of 360-390 students with strong interest in biology; subject matter focuses on molecular and cellular bases of systems physiology.
- Responsibilities included leading 3 one-hour discussion sections per week; writing and grading weekly quizzes; attending lectures and holding office hours; leading final exam preparation sessions; and proctoring all exams.

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Dinnon, Kenneth Harold III[kdinnon@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 12/16/2019 9:42:33 AM (UTC-06:00)
Subject: Re: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!
JVI Spotlight Text.docx

Here is the draft of the spotlight text. I'd like to have it sent to JV by the end of the day if possible.

Also, with Amy gone, who is handling the publication bills.

Thanks

VDM

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, December 11, 2019 2:07 PM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Dinnon, Kenneth Harold III <kdinnon@email.unc.edu>
Subject: Fw: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

guess somebody thought it was interesting.

I"ll work on this and send you a draft by Friday.

VDM

From: Dutch, Rebecca <rebecca.dutch@uky.edu>
Sent: Wednesday, December 11, 2019 12:44 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Dear Vineet,

Congratulations! Your article, "Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection " (JVI01774-19) has been selected by the editors of the Journal of Virology for inclusion in "Spotlight," a feature in the Journal that highlights research articles of significant interest from the current issue. This section follows the table of contents and includes short descriptions of five especially meritorious articles.

If you wish your article to be included in this section, please draft a short, declarative title and a brief summary of your manuscript (between 50-100 words) and forward these to me. The summary should be composed in general terms, highlighting the broad biological significance of the work. Also, please select a panel of one figure from your paper to display alongside the text in the Spotlight section. Please crop the figure file so that it includes only the portion of the figure to be published in the Spotlight, and send the resulting high-resolution (300dpi) TIF (preferred), EPS, or PPT file to me. The figure can convey the most important experimental result of your study or an interesting image. Do not send a multi-panel figure. We only have space for a single panel. Please include a short descriptive title for the figure. The title used in the legend for the chosen figure may suffice. You will find an example of what we are aiming for in this section, attached.

As our printing deadlines are very tight, we must receive your material – the headline, paragraph of text,

cropped figure file, and brief figure legend by 5 pm (Eastern Standard Time) on Tuesday the 17th of December. Please let me know if I can help you with any questions. Thank you for contributing to the Journal of Virology Spotlight.

Sincerely,
Becky Dutch
Editor, Journal of Virology

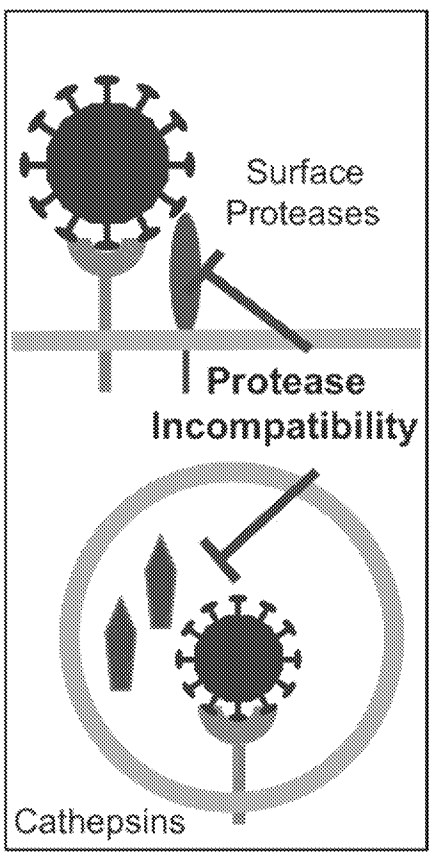
Rebecca Dutch
Professor and Chair, Molecular and Cellular Biochemistry
University of Kentucky College of Medicine
143 BBSRB
741 S. Limestone St.
Lexington, KY 40536-0509

JVI Spotlight
Menachery, Dinnon et al.

Reconsidering the Primary Barriers to Coronavirus Emergence

Traditionally, the emergence of coronaviruses (CoVs) has been attributed to a gain in receptor binding in a new host. In this study, we rescued replication of two MERS-like bat viruses through the addition of exogenous trypsin. Our results argue that proteolytic cleavage of the spike, not receptor binding, is the primary replication barrier for these CoVs. Importantly, the majority of zoonotic virus sequences are isolated from guano, suggesting an enteric replication cycle in bats. Thus, the presence of exogenous protease may be required for the replication of bat viruses and a key barrier to emergence in a new host.

Spotlight Figure: **Absence of compatible host proteases restricts bat CoV infection.**



UNC
GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL

DEPARTMENT OF EPIDEMIOLOGY F 919.966.2689
McGAVRAN-GREENBERG HALL
CAMPUS BOX 7435
CHAPEL HILL, NC 27599-7435

November 25, 2019

To the Editors,

Please find our revised manuscript, "Trypsin treatment unlocks barrier for zoonotic bat coronaviruses infection" by Menachery, Dinnon, et al.

We take this opportunity to thank the reviewer for the comments and suggestions. We have responded to all the comments of the reviewer and feel that the improved manuscript is now appropriate for publication. Detailed modifications have been highlighted in the manuscript, and the significant changes are described in the response to reviewers.

Both reviewers recognized the significance and importance of our findings. However, both reviewers asked for clarification and elaboration on specific points and additional experiments to support our conclusions. Specifically, Reviewer 1 requested modification of the text and expansion on several points of interest. In addition, we revised our description of the HAE infections to more clearly describe the experiments. Reviewer 2 requested documentation of spike cleavage and examination of the proteolytic cleavage site sequences. Each has been added to the manuscript and figures have been modified as outlined in the response to reviews.

Overall, we believe that these responses have improved the quality of the manuscript and made it more appropriate for publication in Journal of Virology. Thank you for your consideration of this revised manuscript..

Sincerely,

Ralph S. Baric, PhD
Professor
University of North Carolina at Chapel Hill
Chapel Hill, North Carolina
[HYPERLINK "mailto:rbaric@email.unc.edu"]

Vineet D. Menachery, Ph.D.
Assistant Professor
University of Texas Medical Branch
Galveston, Texas
[HYPERLINK "mailto:vimenach@utmb.edu"]

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Dinnon, Kenneth Harold III[kdinnon@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 12/11/2019 2:07:38 PM (UTC-06:00)
Subject: Fw: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!
JVI Spotlight Sample with Figure and Title.pdf

guess somebody thought it was interesting.

I"ll work on this and send you a draft by Friday.

VDM

From: Dutch, Rebecca <rebecca.dutch@uky.edu>
Sent: Wednesday, December 11, 2019 12:44 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Congratulations! Your Article Has Been Chosen as a JVI Spotlight!

Dear Vineet,

Congratulations! Your article, "Trypsin Treatment Unlocks Barrier to Zoonotic Bat Coronaviruses Infection " (JVI01774-19) has been selected by the editors of the Journal of Virology for inclusion in "Spotlight," a feature in the Journal that highlights research articles of significant interest from the current issue. This section follows the table of contents and includes short descriptions of five especially meritorious articles.

If you wish your article to be included in this section, please draft a short, declarative title and a brief summary of your manuscript (between 50-100 words) and forward these to me. The summary should be composed in general terms, highlighting the broad biological significance of the work. Also, please select a panel of one figure from your paper to display alongside the text in the Spotlight section. Please crop the figure file so that it includes only the portion of the figure to be published in the Spotlight, and send the resulting high-resolution (300dpi) TIF (preferred), EPS, or PPT file to me. The figure can convey the most important experimental result of your study or an interesting image. Do not send a multi-panel figure. We only have space for a single panel. Please include a short descriptive title for the figure. The title used in the legend for the chosen figure may suffice. You will find an example of what we are aiming for in this section, attached.

As our printing deadlines are very tight, we must receive your material – the headline, paragraph of text, cropped figure file, and brief figure legend by 5 pm (Eastern Standard Time) on Tuesday the 17th of December. Please let me know if I can help you with any questions. Thank you for contributing to the Journal of Virology Spotlight.

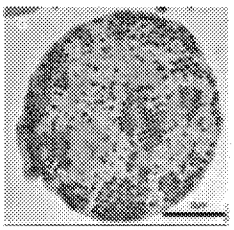
Sincerely,
Becky Dutch
Editor, Journal of Virology

Rebecca Dutch
Professor and Chair, Molecular and Cellular Biochemistry
University of Kentucky College of Medicine
143 BBSRB
741 S. Limestone St.
Lexington, KY 40536-0509

Faustovirus, a Virus of Amoebae Closely Related to the Mammalian Pathogen, Asfarvirus
(Reteno et al.)

African swine fever virus (ASFV) is the unique mammalian pathogen among the nucleocytoplasmic large DNA viruses (NCLDVs). Reteno et al. (#0115-15) report the isolation of Faustovirus, a new lineage of NCLDV phylogenetically close to ASFV. Faustovirus encodes about three times more mosaic gene complements than ASFV, of which two-thirds do not show significant similarity to known proteins. The isolation of this new giant virus provides a blueprint for finding new pathogenic or commensal viruses and for deciphering the dark matter in metagenomic databases.

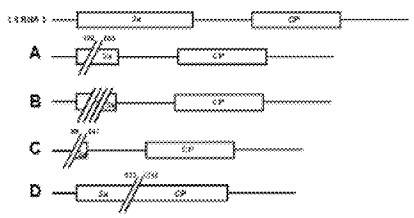
Electron microscopy imaging of the faustovirus.



Mutation and Recombination, Opposing Properties of a Viral Polymerase
(Pita et al.)

RNA virus polymerases display high mutation rates and have a tendency to generate recombinant viruses. In this study, Pita et al (#0040-15) show that cucumber mosaic virus strains with high levels of mutation frequency have low levels of recombination frequency, whereas those with low levels of mutation frequency have high levels of recombination frequency. These findings may reflect different effects of the capacity of the polymerase to remain associated with its template.

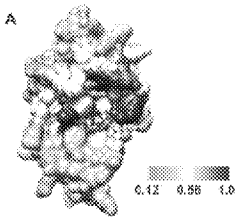
Structure of RNA 3 deletion mutants.



Structural Basis of Rotavirus RNase L Antagonism
(Ogden, Hu, et al.)

Some rotaviruses and coronaviruses encode a phosphodiesterase that cleaves 2',5'-oligoadenylates, which activate cellular RNase L, thereby shutting down a potent innate antiviral pathway. Ogden, Hu, et al. (#0701-15) present crystal structures of the rotavirus phosphodiesterase domain alone and in complex with 2',5'-oligoadenylate. This new structure enabled identification of the ligand-binding site, which is conserved among phosphodiesterases that cleave this substrate. This work points the way forward in the design of small-molecule inhibitors of viral RNase L antagonists.

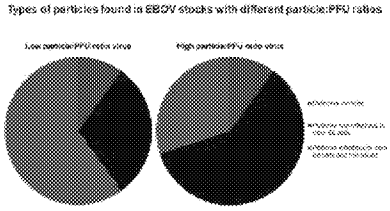
Surface representation of the rotavirus VP3 C-terminal domain with bound substrate.



Insights into Ebola Virus Lethality in an Animal Model
(Alfson et al.)

Ebola virus (EBOV) plaque-forming-units (PFUs) are usually quantified by plaque assay using Vero E6 cells. Alfson et al. (#0649-15) infected cynomolgus macaques with equivalent doses of two EBOV stocks possessing different particle-to-PFU ratios. A dose of 0.01 PFU from a high particle-to-PFU ratio stock was 100% lethal, while the same dose from a low particle-to-PFU ratio stock exhibited no lethality. This finding suggests that viral particles not quantified by plaque assay retain the capacity to cause lethal disease and should be considered when modelling EBOV disease and testing EBOV countermeasures.

Hypothesized composition of EBOV stocks with different particle:PFU ratios.



To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Jacob Kocher[jake.kocher22@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 1/6/2020 4:02:53 PM (UTC-06:00)
Subject: Re:

Hey Jake and Ralph,

Happy new year to you both. Congrats on the baby. Hopefully you are adjusting well. You have so much to look forward to.

In regards to the paper, I have read through it, skimming and looking through the figures. I still think that the manuscript needs a lot of work. Anne did not address the reviewer comments and I still find the paper confusing and sloppy.

Based on what is here, I do not think it can go back to JVI. It still needs to be cleaned up quite a bit in the text for clarity. I would recommend dropping figure 3 altogether, as the point is lost and not especially clear. Similarly, I would take the HELMET data out of figure 4 and have it on its own as figure 5. FInally, figure 5-6 should be combined. The text needs to be modified here too to be much more careful in the discussion.

Overall, there is good data here and a clear story. Unfortunately, in the current form, it is very difficult to get to that conclusion.

VDM

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, January 2, 2020 12:15 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Jacob Kocher <jake.kocher22@gmail.com>
Subject:

Hi Jacob and Vineet, Here is the version of Anne's B cell paper with her final comments. Jake, can you take a look to make sure the new data you generated is appropriately presented. Vineet, I appreciate your comments. I'd also like your thoughts on where to submit this. Its been a year plus since it was reviewed at JV-should we go back or chase a sure thing. Jake, congrats on the new baby! Hope you both had a Happy Holiday and New Year. Ralph

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Baric, Toni C[antoinette_baric@med.unc.edu]; lgralins@email.unc.edu[lgralins@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Sun 6/14/2020 9:29:19 PM (UTC-05:00)
Subject: Progress report
U19 Progress Report UTMB 060520.docx

Hey Ralph,

Sorry, I lost track of time with the progress report. See attached with some of the progress with the PARP9 story my student Craig is working on. We had a fundable score on my aging CC R21 but NOA. If it is funded, I was going to do a F2 with CC032XCC072. This will help resolve the SARS titer qtl. I will plan on doing it with SARS2 if the MA virus also causes age dependent disease; otherwise I'll do SARS1.

I added the publications that cited U19 funding which might not already overlap with what you have. Let me know if I need anything else. Again, sorry it is late.

VDM

To: Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]
Cc: Frieman, Matthew[MFrieman@som.umaryland.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 6/30/2020 10:04:18 PM (UTC-05:00)
Subject: Re: CoV question

HKU1 and OC43 don't have a known ORF3b or ORF8. The accessory ORFs don't have much homology across families.

I do question if there is sufficient abundance of those proteins to generate ab response against them. Dont' know much about it or if anyone has really looked. I'd think 8 before 3B.

From: Diamond, Michael <mdiamond@wustl.edu>
Sent: Tuesday, June 30, 2020 7:01 PM
To: Ralph Baric <rbaric@email.unc.edu>
Cc: Menachery, Vineet <vimenach@UTMB.EDU>; Frieman, Matthew <MFrieman@som.umaryland.edu>
Subject: CoV question

Ralph/Matt/Vineet

Reviewing a paper (what else is new). Quick question....

Do OC43 and HKU1 (other betacoronaviruses) have ORF3b and ORF8 proteins?

I don't think so, but I want to be sure

This is about potential X-reactivity of these antigens to anti-SARS-CoV-2 sera....if the OC43 and HKU1 don't have these proteins, the SARS-2 proteins might be useful for SARS-CoV-2 diagnostics (apart from MERS-CoV and SARS-CoV)

Yes?

Mike

To: Baric, Ralph S[rbaric@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 10/8/2020 8:59:37 PM (UTC-05:00)
Subject: Re: Slides + funding

You can cite my R00 and this U19.

R00AG049092

It is going forward on the R21 that I mentioned.

Craig Schindewolf did the PARP work
Eileen McAnarney did the CC work with me.

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, October 8, 2020 6:04 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Slides + funding

Hi Vineet, thanks. Did you get some funding for CC work that I can site as productivity on the U19 or your RO1? Can you send the grant number and title, my recollection is that you did (doesn't have to be NIH funding). Slides look good. ralph

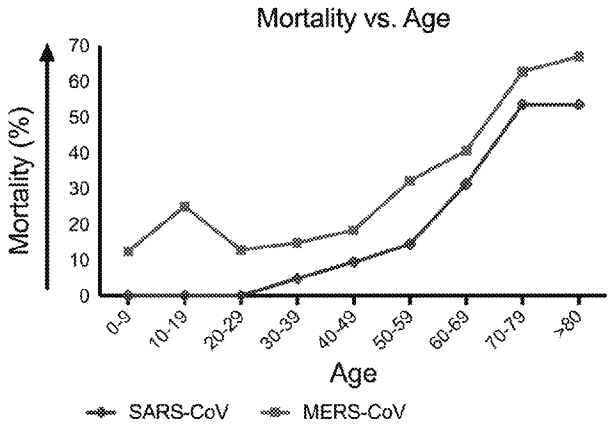
---

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Thursday, October 8, 2020 10:32 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Cc: Gralinski, Lisa E <lgralins@email.unc.edu>
Subject: Slides

To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: lgralins@email.unc.edu[lgralins@email.unc.edu]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 10/8/2020 9:32:13 AM (UTC-05:00)
Subject: Slides
Aging CC for RSB 100820.pptx
PARP9 summary for RSB 100820.pptx

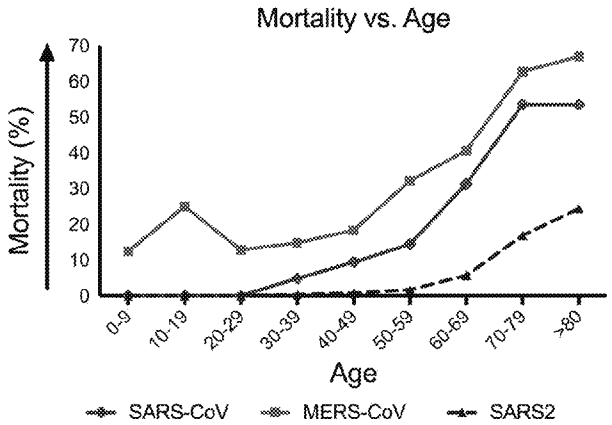
Aging, Genetic Diversity, and CoVs

Aging & Infection



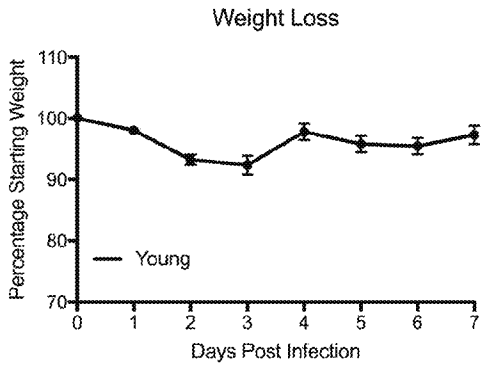
- Major age dependent disease with CoVs in humans

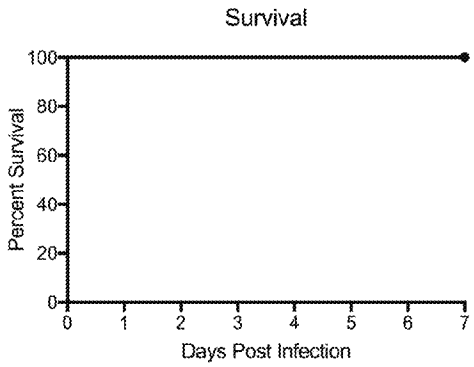
Aging & Infection



- Major age dependent disease with CoVs in humans

Age Related Pathogenesis to SARS





- SARS-CoV age-dependent disease conserved in mice

Genetic Diversity and Aging

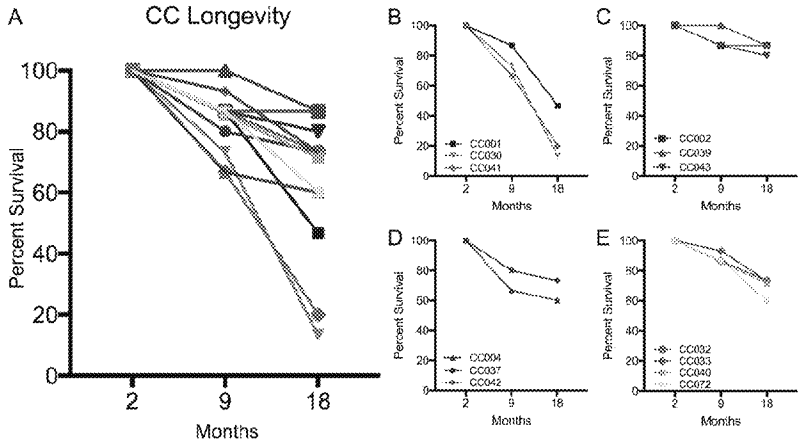
- How does genetic diversity impact the aging process?

- Is age dependent susceptibility to CoVs driven by genetic correlates?

Premise

- 8-12 mice from 13 CC lines were aged to >18 months
- Mice were challenged with SARS-CoV and compared to young (2.5 months)

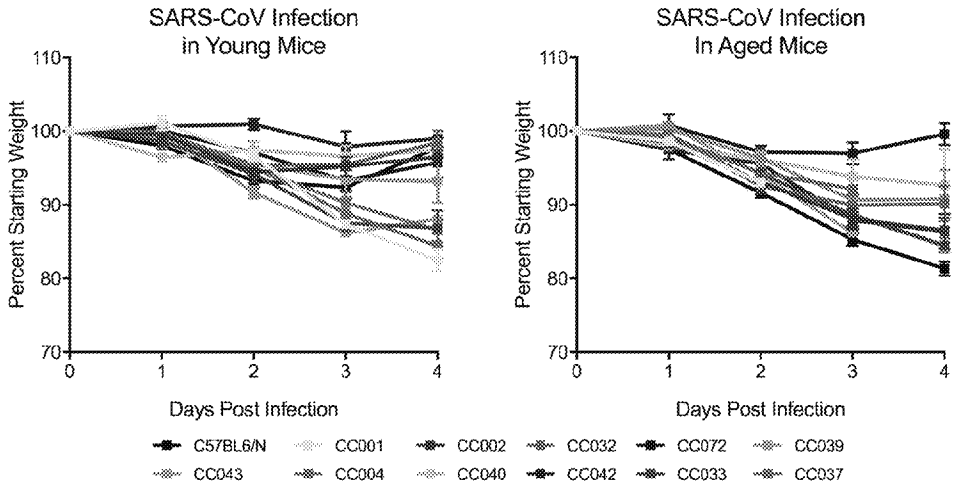
Longevity



- Range of survival for CC to 18 months of age

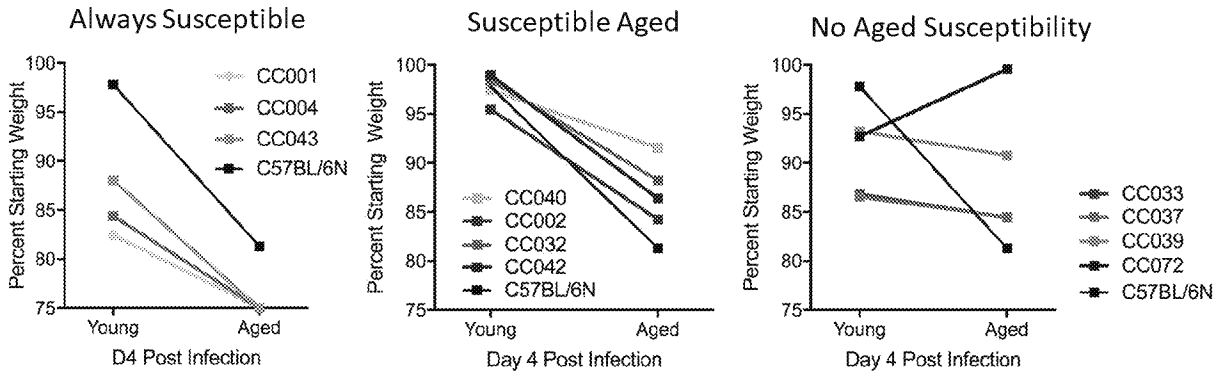
All the B6 mice survived to this point with no lethality.
No cause of deaths noted, mice surveyed for prseence at 9 and 18 months

Age-dependent Susceptibility



- Range of disease observed in young and aged

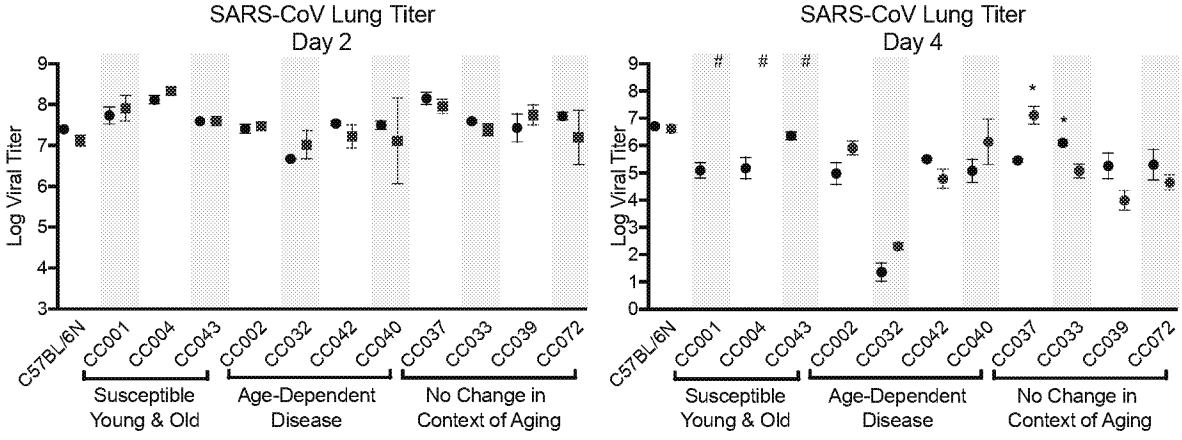
Age-dependent Susceptibility



- Age dependent CoV susceptibility conserved in most CC lines

Lines susceptible young and old
Lines susceptible just aged
Lines indifferent or resistant as they age

Age-dependent Susceptibility



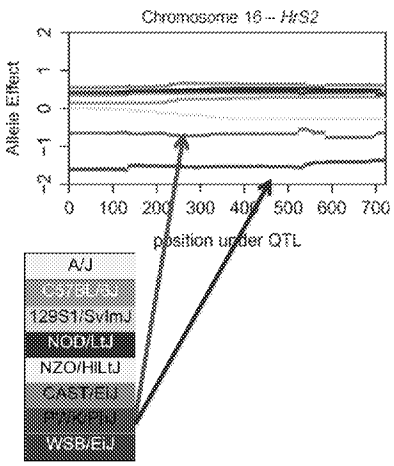
- Age dependent CoV susceptibility not driven by change in viral loads

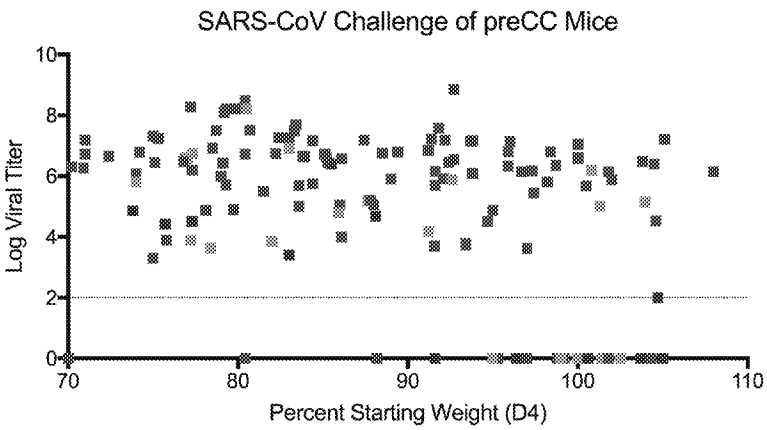
No significant changes in D2 titers between young and old
Day 4 has only CC037 with higher load in old;
represent animals groups that did not survive to the the d4 time point or did not have enough animals to graph

Mapping Age-Dependent Susceptibly

- Work on defining age-dependent QTL alleles
  - F2 cross
    - CC032 (susceptible aged) vs CC072 (resistant aged)
    - Examine young and aged F2 mice in screen
  - Funded on R21AI145400

SARS Viral Titer QTL: Chr. 16 (26%)





- Low titer phenotype driven by PWK/PhJ allele
- Cast/EiJ allele also had lower viral loads

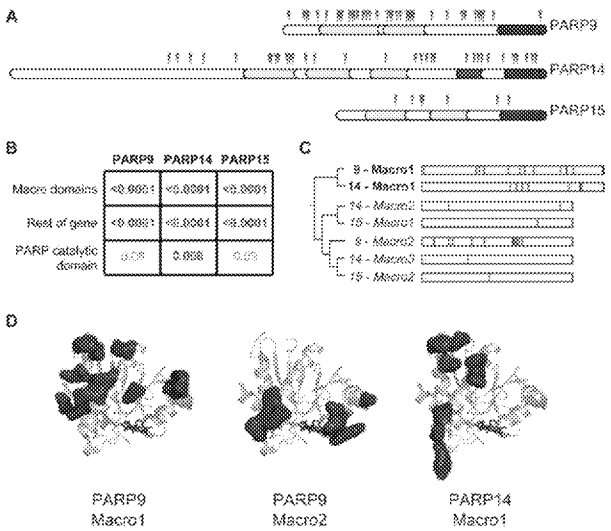
Gralinski et al. PLoS Genet. 2015 Oct 9;11(10):e1005504.

SARS Viral Titer QTL: Chr. 16

- 5.4Mb QTL region contains
  - 92 total coding genes
  - 30 non-coding RNA
- Narrowing to the PWK allele
  - 48 candidate genes with impactful mutation
  - Apoptosis, T-cell activation, mucins
  - Also include Parp9 and Parp14

PARP Proteins

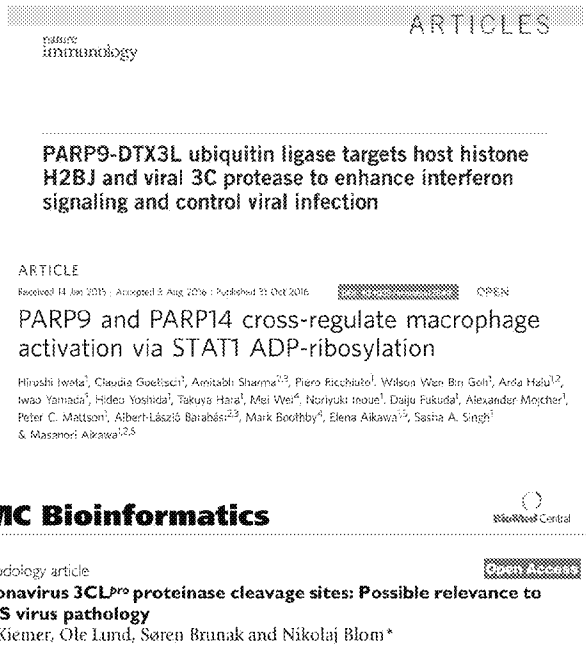
- Family of proteins associated with ADP ribosylation
- PARP genes found to be under heavy positive selection in primates and rodents



Daugherty et al. PLoS Genet. 2014 May; 10 (5):e1004403.

PARP Proteins

- PARP9 found to play role in interferon stimulated gene induction via STAT1
- PARP9 and PARP14 co-regulate each other in macrophage activation
- Prediction software suggest that CoV 3CL-protease may cleave PARP9 or PARP14



ARTICLES

nature immunology

PARP9-DTX3L ubiquitin ligase targets host histone H2BJ and viral 3C protease to enhance interferon signaling and control viral infection

ARTICLE

Received 14 Jan 2015 | Accepted 3 Aug 2016 | Published 31 Oct 2016 OPEN

PARP9 and PARP14 cross-regulate macrophage activation via STAT1 ADP-ribosylation

Hiroshi Iwata[1], Claudia Goettsch[1], Amitabh Sharma[1,2], Piero Ricchiuto[1], Wilson Wen Bin Goh[3], Arda Halu[1,2], Iwao Yamada[1], Hideo Yoshida[1], Takuya Hara[1], Mei Wei[4], Noriyuki Inoue[1], Daiju Fukuda[1], Alexander Mojcher[1], Peter C. Mattson[1], Albert-László Barabási[2,3], Mark Boothby[4], Elena Aikawa[1,2], Sasha A. Singh[1] & Masanori Aikawa[1,2,5]

BMC Bioinformatics

BioMed Central

Methodology article

Coronavirus 3CL^{pro} proteinase cleavage sites: Possible relevance to SARS virus pathology

Lars Kiemer, Ole Lund, Søren Brunak and Nikolaj Blom*

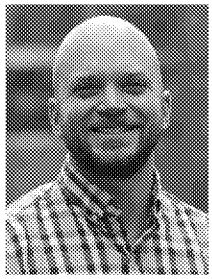
PARP Protein

- Hypothesis: PARP9 and/or PARP14 are targeted by coronavirus 3CL-proteases
  - Highly evolving gene in primates and rodents
  - Predicted cleavage sites for 3CL-protease in PARP9/14
  - PWK allele may be resistant to cleavage, allowing augmented ISG response, reducing CoV titer

PARP Proteins

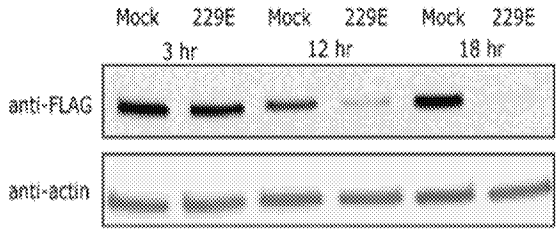
- Provided PARP9, DTX3L, and PARP14 constructs from human and other NHPs

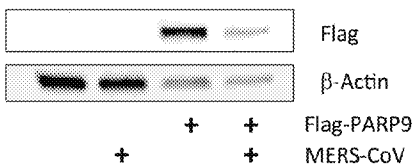
- We partnered to test CoVs



Daugherty Lab, UCSD

PARP9 degraded during CoV infection





- 229E-CoV and MERS-CoV show reduced tagged PARP9 expression

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis; Michael J Gale; Renee Ireton; Graham PhD, Jessica B; Graham PhD, Jessica B; Lund PhD, Jennifer

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 12/3/2020 12:30:00 PM (UTC-06:00)

End Time: Thur 12/3/2020 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton; Graham PhD, Jessica B; Graham PhD, Jessica B; Lund PhD, Jennifer

This is a reminder that we will be having our December call today.

Thank you

Toni

Join Zoom Meeting
https://zoom.us/j/95848751377?pwd= **552.136**

Meeting ID: 958 4875 1377
Passcode: **552.136**
One tap mobile
+19292056099,,95848751377#,,,,,,0#, **552.136** US (New York)
+13017158592,,95848751377#,,,,,,0#, US (Germantown)

Dial by your location
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To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; craig_cameron@med.unc.edu[craig_cameron@med.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Oki, Noffisat (NIH/OD) [E][noffisat.oki@nih.gov]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; David Tribble[dtribble@idcrp.org]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Timothy Burgess[timothy.burgess@usuhs.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Rafael Medina Silva[rmedinas@med.puc.cl]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Sabra Klein[sklein2@JHU.EDU]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Jennifer Hyde[jlhyde4@uw.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Emma Hodcroft[emmahodcroft@gmail.com]; andrzejj@anl.gov[andrzejj@anl.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry,

Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; kuhnr@purdue.edu[kuhnr@purdue.edu]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 12/9/2020 1:28:33 PM (UTC-06:00)
Subject: FW: Conversation with CDC's Dr. Redfield

Hi Everyone!

Dr. Scott Strome sent this along thinking some of you might be interest. Please keep in mind that all times are CST.

[redacted]

[redacted]

Please join the UT Health Science Center College of Medicine and Faculty Senate for a virtual conversation with Dr. Robert Redfield, director of the Centers for Disease Control and Prevention (CDC).

Monday, December 14

11:00 am – 12:00 pm CST

Zoom link: *https://zoom.us/j/91716864333*

Passcode: 901901

Dr. Scott Strome, Dean of the College of Medicine, has arranged this conversation so that the campus and community can hear Dr. Redfield's perspectives on COVID-19 – perspectives that will be directly applicable to health care providers, patients, businesses, and our community.

Dr. Redfield has more than 30 years of experience in research and clinical care of viral infections and infectious diseases, particularly HIV. He was a member of the President's Advisory Council on HIV/AIDS from 2005 to 2009, chair of the International Subcommittee, and past member of the Office of AIDS Research Advisory Council at the National Institutes of Health.

Our mailing address is:

UTHSC Communications and Marketing

920 Madison Avenue, Suite 810

Memphis, Tennessee 38163

To: Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; craig_cameron@med.unc.edu[craig_cameron@med.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Oki, Noffisat (NIH/OD) [E][noffisat.oki@nih.gov]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; David Tribble[dtribble@idcrp.org]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Timothy Burgess[timothy.burgess@usuhs.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Rafael Medina Silva[rmedinas@med.puc.cl]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Karla Satchell[k-satchell@northwestern.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Sabra Klein[sklein2@JHU.EDU]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Jennifer Hyde[jlhyde4@uw.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Emma Hodcroft[emmahodcroft@gmail.com]; andrzejj@anl.gov[andrzejj@anl.gov]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry,

Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; kuhnr@purdue.edu[kuhnr@purdue.edu]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Wed 12/9/2020 1:28:23 PM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - December 15th
nCoV PI call attendee list.xlsx

Hi Everyone,

On Tuesday, December 8th, Dr. Ben Tenoever gave a wonderful seminar on **"Single virion tracking of SARS-CoV-2 in vivo to better understand systemic inflammation associated with COVID-19".** Thank you to Dr. Tenoever for presenting and to those that attended.

Next up, Dr. Ivan Marazzi will be giving a presentation on "**A potential cure for severe COVID-19, in animal models, thus far**." Hope everyone is able to tune in! Please let me know if you know of anyone who would like to attend or present in future meetings.

Speaking of future meetings, the holidays are quickly approaching. Please complete the poll as to whether you are planning to attend the webinar on Tuesday, December 22nd so we have an idea of the number of attendees. If you want to email me your answer instead, that's ok too. Keep in mind, we will be canceling this meeting on December 29th (holiday vacation) and January 12th (CEIRS Annual Meeting).

Doodle poll: https://doodle.com/poll/kveqgffkyqfrk22z?utm_source=poll&utm_medium=link

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		8-Dec
Erik Stemmy	x	
Marciela DeGrace	x	
Rebecca Lampley	x	
Aditya Gaur		
Adolfo Garcia-Sastre	x	
Aisha Souquette		
Alan Embry	x	
Ali Ellebedy		
Alicia Fry		
Alison Augustine	x	
Alvaro Ordonez	x	
Amanda Perofsky		
Amy Kuehn	x	
Amy Krafft	x	
Andrea Pruijssers		
Andrea Sant		
Andrew Mesecar		
Andrew Pekosz		
Andy Mesecar		
Andrzej Joachimiak		
Aneesh Mehta		
Angela Rasmussen		
Ann Eakin		
Anice Lowen	x	
Anita McElroy		
Anne Piantadosi		
Aron Hall	x	
Atsuo Kuki		
Aubree Gordon		
Barry Rockx		
Becky Dutch		
Ben Cowling		
Ben Larman		
Benjamin Miller	x	
Ben Tenoever	x	
Bernard Lafont		
Bin Zhou	x	
Biao He		
Brooke Bozick	x	
Carly Dillen	x	
Carlie Williams		
Catherine Luke		

Catherine Sutcliffe	x
Claire Midgley	x
Charles Russell	x
Chelsea Lane	x
Chris Brooke	
Christopher Hsu	x
Chris Roberts	
Clint Florence	x
Conrad Mallia	
Colleen Jonsson	x
Connie Schmaljohn	
Courtney Comar (Susan Weiss lab)	
Daniel Blanco-Melo	x
Daved Fremont	
David Martinez	
David Renner (Susan Weiss lab)	
David Topham	x
David Tribble	x
David Wentworth	
Deborah Lynn Fuller	
Diana Finzi	
Diane Post	x
Diego Hijano	
Don Milton	x
Donna Neu	x
Edwin Asturias	x
Elizabeth Fitzpatrick	
Emma Hodcroft	
Erica Raterman	
Evans	
Eunchung Park	x
Eun Mi Lee	
Florian Krammer	x
Francisco Chaves	x
Frederic Bushman	
Gabriele Neumann	x
Gavin Smith	
Ghazi Kayali	
Glen Abedi	
Grace Tietz	
Greg Deye	
Hana Golding	x
Harm van Bakel	
Holly Hammond	
Hui-Ling Yen	

Ian Crozier	x
Ian Plumb	
Isabelle Phan	
Ishwar Chandramouliswaran	
Ivan Marazzi	x
Jacob Hou	
Jacques Banchereau	x
Jae Jung	
James Hoffman	
James Kobie	
Jared Evans	x
Jason Goldstein	x
Jean Patterson	
Jenni	
Jennifer German	
Jennifer Gordon	
Jennifer Hyde	x
Jennifer Kishimori	x
Jens Wrammert	
Jeremy Crawford	
Jesse Erasmus	
Ji Lee	
Jimmy Logue	
Jim Chappell	
jmankow1	
Joe Breen	
Jonathan Runstadler	x
Joseph Mankowski	
Judy Hewitt	
Juergen Richt	x
Julia Biggins	x
Kanta Subbarao	
Karla Satchell	x
Katharina Koelle	
Katy Shaw-Saliba	
Katherine Fenstermacher	
Kimberly Coca	
Kimberly Stemple	x
Korin Bullen	
Kristina Lu	
Kris Emo	
Kris Lambert	
Kristen Hildebrand	x
Laura Hughes	
Lauren Sauer	

Larry Anderson	x
Larry Wolfraim	
Leo Poon	
Liliana Brown	x
Lisa Hensley	
Lisa Lindesmith	
Lisa Miorin	
Liz	x
Lori Newman	
Lucy Cong	x
Mackenzie Zendt	
Malik Peiris	
Marie Killerby	
Marina Lee	x
Mark Challberg	
Mark Denison	
Mark Heism	
Mark Pallansch	x
Mark Sangster	
Mark Simons	x
Mark Williams	
Marlene Espinoza	x
Marta Gaglia	x
Martha Nelson	
Martin Blaser	x
Martin Linster	
Masato Hatta (UW)	
Matt Frieman	x
Maureen McGargill	x
Mehul Suttar	
Melissa Uccellini	x
Mercy Prabhudas	x
Michael Bryan	
Michael Chan	
Michael Martin	
Mike Cooper	
Mike Holbrook	x
Mindy Davis	
Missy	
Monica McNeal	x
Nat Moorman	
Natalie Thornburg	
newmanlm	
Nidia Trovao	
Noffisat Oki	x

Octavio Ramilo	x
Oluwasanmi Adenaiye	x
Pamela McKenzie	x
Patrice Becker	
Paul McCray	
Paul Jacob Bueno de Mesquita	
Paul Thomas	
Peter Daszak	
Peter Halfmann	x
Peter Myler	
Peter Palese	x
Phuong Nguyen-Contant	
Punam Mathur	x
Qifang Bi	
Rachel Graham	
Rafael Medina	x
Ralph Baric	
Randall Tressler	
Raul Andino	
Rebecca Dutch	x
Reed Johnson	
Reed Shabman	
Richard Rothman	
Richard Sciotti	
Richard Webby	x
Rick Bushman	
Robert Johnson	
Ron Fouchier	x
Rudra Goudavet	
Russell Ray	
Ryan Langlois	x
Ryan Ranallo	x
Sabra Klein	
Sander Herfst	
Sanjay Jain	
Sanmi Adenaiye	
Samantha Loeber	x
Sara Cherry	x
Sara Woodson	
Scott Hensley	
Scott Strome	x
Seema Lakdawala	x
Shahida Baqar	x
Sharon Saydah	
Sheldon Tai	x

Shiho Chiba	x
Simon Anthony	x
Sook Ho	
Sonnie Kim	
Stacey Schultz-Cherry	
Stacy Ferguson	
Stanley Perlman	x
Stephen Tompkins	x
Steve Smiley	
Steve Tsang	
Surender Khurana	x
Susan Gerber	
Susan Weiss	x
Teresa Hauguel	
Thames P	x
Theresa Fitzgerald	
Tim Burgess	x
Timothy Sheahan	
Tristan	x
Troy Sutton	
Tom Fabrizio	
Tori Baxter	
Vanessa Merino	x
Vineet Menachery	
Viviana Simon	
Walt Orenstein	x
Weina Sun	
Wesley C Van Voorhis	x
William Karesh	
William Florence	
William Morgenlander	
Willy Valdivia	
Wiriya Rutvisuttinunt	x
Wolfgang Leitner	
Xizhi Guo	
Yoshihiro Kawaoka	

To: Orenstein, Walter[worenst@emory.edu]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Keri Althoff[kalthoff@jhu.edu]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; SAMANTHA LOEBER[sloeber@wisc.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Sabra Klein[sklein2@JHU.EDU]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Jennifer Hyde[jlhyde4@uw.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Emma Hodcroft[emmahodcroft@gmail.com]; Robert E. Schwartz[res2025@med.cornell.edu]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Thomas Friedrich[tfriedri@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu];

'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Saydah, Sharon (CDC/DDNID/NCCDPHP/DDT)[zle0@CDC.GOV]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]

Cc: Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; cobeywork@gmail.com[cobeywork@gmail.com]; ODSET Pro[ODSETPro@mail.nih.gov]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Oki, Noffisat (NIH/OD) [E][noffisat.oki@nih.gov]; Caniza, Miguela[Miguela.Caniza@STJUDE.ORG]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Mark Mulligan[Mark.Mulligan@nyulangone.org]; Rafael Medina Silva[rmedinas@med.puc.cl]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Sent: Wed 12/16/2020 10:04:16 AM (UTC-06:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

nCoV PI call attendee list.xlsx

Hi Everyone!

On Tuesday, December 15th, Dr. Ivan Marazzi gave a presentation on "**A potential cure for severe COVID-19, in animal models, thus far**." Thank you, Ivan, for presenting and those that were able to join.

As a reminder, this call will be cancelled December 22nd and 29th. I will send an email closer to the new year with the presentation details for the January 4th meeting.

Hope everyone has a safe and joyful holiday season.

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892

Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name		8-Dec	15-Dec
Erik Stemmy	x	x	
Marciela DeGrace	x	x	
Rebecca Lampley	x	x	
Aditya Gaur			
Adolfo Garcia-Sastre	x		
Adrienne Randolph		x	
Aisha Souquette			
Alan Embry	x		
Ali Ellebedy		x	
Alicia Fry			
Alison Augustine	x		
Alvaro Ordonez	x	x	
Amanda Perofsky			
Amy Kuehn	x	x	
Amy Krafft	x		
Andrea Pruijssers			
Andrea Sant			
Andrew Mesecar			
Andrew Pekosz		x	
Andy Mesecar			
Andrzej Joachimiak		x	
Aneesh Mehta			
Angela Rasmussen			
Ann Eakin			
Anice Lowen	x	x	
Anita McElroy			
Anne Piantadosi			
Aron Hall	x	x	
Atsuo Kuki			
Aubree Gordon		x	
Barry Rockx			
Becky Dutch			
Ben Cowling			
Ben Larman			
Benjamin Miller	x		
Ben Tenoever	x	x	
Bernard Lafont			
Bin Zhou	x		
Biao He			
Brooke Bozick	x		
Carly Dillen	x	x	
Carlie Williams			

Catherine Luke		
Catherine Sutcliffe	x	x
Claire Midgley	x	x
Charles Russell	x	
Chelsea Lane	x	
Chris Brooke		
Christopher Hsu	x	
Chris Roberts		
Clint Florence	x	
Conrad Mallia		
Colleen Jonsson	x	x
Connie Schmaljohn		x
Courtney Comar (Susan Weiss lab)		
Daniel Blanco-Melo	x	
Daved Fremont		
David Martinez		
David Renner (Susan Weiss lab)		
David Topham	x	x
David Tribble	x	x
David Wentworth		
Deborah Lynn Fuller		
Diana Finzi		
Diane Post	x	x
Diego Hijano		
Don Milton	x	
Donna Neu	x	x
Doris Strome		x
Edwin Asturias	x	
Elizabeth Fitzpatrick		
Emma Hodcroft		
Erica Raterman		
Evans		
Eunchung Park	x	x
Eun Mi Lee		
Florian Krammer	x	x
Francisco Chaves	x	
Frederic Bushman		
Gabriele Neumann	x	x
Gage Moreno		x
Gavin Smith		
Ghazi Kayali		
Glen Abedi		
Grace Tietz		
Greg Deye		
Hana Golding	x	x

Harm van Bakel		
Holly Hammond		
Hui-Ling Yen		
Ian Crozier	x	x
Ian Plumb		
Isabelle Phan		
Ishwar Chandramouliswaran		
Ivan Marazzi	x	x
Jacob Hou		
Jacques Banchereau	x	
Jae Jung		
James Hoffman		
James Kobie		x
Jared Evans	x	x
Jason Goldstein	x	x
Jayeeta Dutta		x
Jean Patterson		
Jenni		
Jennifer German		
Jennifer Gordon		
Jennifer Hyde	x	
Jennifer Kishimori	x	
Jens Wrammert		
Jeremy Crawford		
Jesse Erasmus		
Jessica Ho		x
Ji Lee		
Jimmy Logue		
Jim Chappell		
jmankow1		
Joe Breen		
Jonathan Runstadler	x	x
Joseph Mankowski		x
Judy Hewitt		
Juergen Richt	x	x
Julia Biggins	x	x
Kanta Subbarao		
Karla Satchell	x	
Katarina Braun		x
Katharina Koelle		
Katy Shaw-Saliba		
Katherine Fenstermacher		x
Kimberly Coca		
Kimberly Stemple	x	x
Korin Bullen		

Kristina Lu		
Kris Emo		
Kris Lambert		
Kristen Hildebrand	x	x
Laura Hughes		
Lauren Sauer		
Larry Anderson	x	x
Larry Wolfraim		
Leo Poon		
Liliana Brown	x	
Lisa Hensley		
Lisa Lindesmith		
Lisa Miorin		
Liz	x	
Lori Newman		
Lucy Cong	x	x
Mackenzie Zendt		
Malik Peiris		
Marie Killerby		
Marina Lee	x	
Mark Challberg		
Mark Denison		
Mark Heism		
Mark Pallansch	x	
Mark Robien		x
Mark Sangster		
Mark Simons	x	
Mark Williams		x
Marlene Espinoza	x	x
Marta Gaglia	x	x
Martha Nelson		
Martin Blaser	x	x
Martin Linster		
Masato Hatta (UW)		
Mathew Esona		x
Matt Frieman	x	x
Maureen McGargill	x	x
Mehul Suttar		
Melissa Rolfes		x
Melissa Uccellini	x	x
Mercy Prabhudas	x	
Michael Bryan		
Michael Chan		
Michael Martin		
Mike Cooper		

Mike Holbrook	x	x
Mindy Davis		
Missy		
Monica McNeal	x	x
Nat Moorman		
Natalie Thornburg		
newmanlm		
Nidia Trovao		
Noffisat Oki	x	
Octavio Ramilo	x	
Oluwasanmi Adenaiye	x	
Pamela McKenzie	x	x
Patrice Becker		
Paul McCray		x
Paul Jacob Bueno de Mesquita		
Paul Thomas		
Peter Daszak		
Peter Halfmann	x	x
Peter Myler		
Peter Palese	x	
Phuong Nguyen-Contant		
Punam Mathur	x	x
Qifang Bi		
Rachel Graham		
Rafael Medina	x	x
Ralph Baric		
Randall Tressler		
Raul Andino		
Rebecca Dutch	x	
Reed Johnson		x
Reed Shabman		x
Richard Rothman		
Richard Sciotti		
Richard Webby	x	
Rick Bushman		
Robert Johnson		
Robert Schwartz		x
Ron Fouchier	x	x
Rudra Goudavet		
Russell Ray		
Ryan Langlois	x	
Ryan Ranallo	x	x
Sabra Klein		
Sander Herfst		x
Sanjay Jain		x

Sanmi Adenaiye		
Samantha Loeber	x	
Sara Cherry	x	x
Sara Woodson		x
Scott Hensley		
Scott Strome	x	x
Seema Lakdawala	x	
Shahida Baqar	x	x
Sharon Saydah		
Sheldon Tai	x	x
Shiho Chiba	x	x
Simon Anthony	x	
Sing Sing		x
Sook Ho		
Sonnie Kim		
Stacey Schultz-Cherry		x
Stacy Ferguson		x
Stanley Perlman	x	
Stephen Tompkins	x	x
Steve Smiley		
Steve Tsang		
Surender Khurana	x	x
Susan Gerber		
Susan Weiss	x	
Teresa Hauguel		
Thames P	x	x
Theresa Fitzgerald		
Tim Burgess	x	x
Timothy Sheahan		
Tristan	x	
Troy Sutton		
Tom Fabrizio		x
Tori Baxter		
Vanessa Merino	x	
Vernon Musale		x
Vineet Menachery		x
Viviana Simon		
Walt Orenstein	x	
Weina Sun		
Wesley C Van Voorhis	x	x
William Karesh		
William Kilembe		x
William Florence		
William Morgenlander		
Willy Valdivia		

Wiriya Rutvisuttinunt	x	x
Wolfgang Leitner		
Xizhi Guo		
Yoshihiro Kawaoka		

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 12/22/2020 8:00:00 AM (UTC-06:00)

End Time: Tue 12/22/2020 9:00:00 AM (UTC-06:00)

Required Attendees: Orenstein, Walter; Martinez, David Rafael; Goldstein, Jason (CDC/DDID/NCEZID/DSR); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Mark Mulligan; Rafael Medina Silva; Asturias, Edwin; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Davis, Mindy (NIH/NIAID) [E]; Martin Blaser; ZHANG, JIAJIA; Ferguson, Stacy (NIH/NIAID) [E]; cobeywork@gmail.com; ODSET Pro; Lockmuller, Jane (NIH/NIAID) [E]; Oki, Noffisat (NIH/OD) [E]; Caniza, Miguela; Gergen, Peter (NIH/NIAID) [E]; Timothy Burgess; Thompson, Mark (CDC/DDID/NCIRD/ID); Monica McNeal; Siriruk Changrob; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Read, Sarah (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Olson, Daniel; Keri Althoff; Biggins, Julia E CTR (USA); Miller, Benjamin; Pickett, Thames (NIH/NIAID) [E]; SAMANTHA LOEBER; McKenzie, Pamela; WVanVoorhis@medicine.washington.edu; Peter Halfmann; Sabra Klein; tenOever, Benjamin; Isabelle.Phan@seattlechildrens.org; Matthew Frieman; Jennifer Hyde; viviana.simon; Emma Hodcroft; Robert E. Schwartz; gavin.smith@duke-nus.edu.sg; Thomas Friedrich; Gage Moreno; Katarina Braun; DAVID H O'CONNOR; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); jwramme@emory.edu; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. 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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager

Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 1/12/2021 8:00:00 AM (UTC-06:00)

End Time: Tue 1/12/2021 9:00:00 AM (UTC-06:00)

Required Attendees: R.A.M. Fouchier; Read, Sarah (NIH/NIAID) [E]; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Miller, Benjamin; Matthew Frieman; Sabra Klein; jheath@systemsbiology.org; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Ferguson, Stacy (NIH/NIAID) [E]; ODSET Pro; Lockmuller, Jane (NIH/NIAID) [E]; Marcum, Chris (NIH/NHGRI) [E]; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Timothy Burgess; Randolph, Adrienne; cobeywork@gmail.com; Ranallo, Ryan (NIH/NIAID) [E]; Aubree Gordon; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Ben Cowling; larry.anderson@emory.edu; jwramme@emory.edu; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. 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Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch

DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Location: Zoom; https://www.zoomgov.com/j/1609711373?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Weekly Investigators Meeting

Start Time: Tue 12/29/2020 8:00:00 AM (UTC-06:00)

End Time: Tue 12/29/2020 9:00:00 AM (UTC-06:00)

Required Attendees: gavin.smith@duke-nus.edu.sg; Thomas Friedrich; Katarina Braun; DAVID H O'CONNOR; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. 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and know the content is safe.

CANCELLING for the holidays

Hi Everyone,

We will be incorporating COVID-19 Cohort presentations to our arsenal of talks. As a reminder, the goal for the weekly SARS-CoV-2 Investigators meeting is to provide a platform that is informative and encourages collaboration.

If you would like to present your research, please let me know. *

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If you have any questions, please feel free to reach out.

Stay safe,

Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis; Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Location: https://zoom.us/j/95848751377?pwd= **552.136**

Importance: Normal

Subject: Reminder SIG U19 Monthly Meeting

Start Time: Thur 1/14/2021 12:30:00 PM (UTC-06:00)

End Time: Thur 1/14/2021 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis

Optional Attendees: Michael J Gale; Renee Ireton; Graham PhD, Jessica B

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To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Ferris, Martin Thomas[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Michael Davis[madphd@uw.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 1/20/2021 9:44:35 AM (UTC-06:00)
Subject: Change in date for SIG U19 call

Hi All,
The time that works for most is the 4th Thursday of every month, 1:30 pm ET/10:30 PT. I will cancel the old invitation and send a new one.
Thanks for your cooperation.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/95848751377?pwd=552.136
Importance:	Normal
Subject:	Canceled: SIG U19 Monthly Meeting
Start Time:	Thur 9/10/2020 11:30:00 AM (UTC-06:00)
End Time:	Thur 9/10/2020 12:30:00 PM (UTC-06:00)
Required Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis
Optional Attendees:	Michael J Gale; Renee Ireton; Graham PhD, Jessica B

Resending the invitation.

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From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric

Location: https://zoom.us/j/99380423092?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 2/25/2021 12:30:00 PM (UTC-06:00)

End Time: Thur 2/25/2021 1:30:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric

This invitation replaces any previous invitation.

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Meeting ID: 993 8042 3092
Passcode: **552.136**

From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: Second Webinar for Systems Immunology Program

Start Time: Tue 3/23/2021 2:00:00 PM (UTC-06:00)

End Time: Tue 3/23/2021 3:00:00 PM (UTC-06:00)

Required Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Hi All,
This year's Systems Immunology meeting will be split in 3 separate 1 hour sessions. I will be forwarding 3 invitations. Our group presents on March 23.
Best regards,
Toni

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 9:56 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Diercks, Alan; Bruce Beutler; Leitner, Wolfgang (NIH/NIAID) [E]
Subject: Second Webinar for Systems Immunology Program
When: Tuesday, March 23, 2021 4:00 PM-5:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

According to your availability, our second webinar will be held from 4:00 to 5:00 PM EDT on March 23th. **Ralph Baric's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

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.....

To: cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; smarinop@umd.edu[smarinop@umd.edu]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; jwramme@emory.edu[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCEZID/DFWED)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; gabriele.neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; viviana.simon[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][jturpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves,

Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Jennifer Hyde[jlhyde4@uw.edu]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; Keri Althoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Thomas Friedrich[tfriedri@wisc.edu]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; hteitelb@umd.edu[hteitelb@umd.edu]; Jeffrey W. Herrmann[jwh2@umd.edu]; Ranallo, Ryan (NIH/NIAID) [E][ryan.ranallo@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Graham, Rachel[rlgraham@ad.unc.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Haslam, David[David.Haslam@cchmc.org]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Fri 1/29/2021 9:37:05 AM (UTC-06:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - February 2nd
nCoV PI call attendee list.xlsx

TGIF Everyone!

What a great discussion we had on Tuesday, January 26th following the presentation given by Drs. Dave O'Connor and Thomas Friedrich titled "**SARS-CoV-2 variants in Wisconsin**". Thank you to our presenters and to those who were able to join.

Next Tuesday, February 2nd, we will have a double feature from the following investigators:

Drs. Dave O'Connor and Thomas Friedrich
"COVID on campus: investigating links between SARS-CoV-2 transmission among college students and the broader community"

And

Dr. Denis Nash
"Serologic outcomes in a national, community-based cohort of U.S. adults: the CHASING COVID Cohort Study"

Hope you all are able to join!
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

nCoV PI call attendee list

Name	5-Jan	19-Jan	26-Jan
Erik Stemmy	x	x	x
Marciela DeGrace	x		x
Rebecca Lampley	x	x	x
Aditya Gaur			
Adolfo Garcia-Sastre	x	x	
Adrienne Randolph			x
Aisha Souquette			
Alan Embry			
Alexander Misharin		x	
Ali Ellebedy	x		
Alicia Fry	x		
Alison Augustine			
Alvaro Ordonez		x	x
Amanda Perofsky			
Amy Kuehn	x	x	x
Amy Krafft			
Andrea Pruijssers			
Andrea Sant			
Andrew Mesecar			
Andrew Pekosz	x	x	x
Andy Mesecar			
Andrzej Joachimiak	x	x	x
Aneesh Mehta			
Angela Rasmussen			
Ann Eakin			
Anice Lowen	x		x
Anita McElroy			
Anne Piantadosi			
Aron Hall	x	x	
Asun Mejias	x		
Atsuo Kuki		x	
Aubree Gordon	x	x	x
Barry Rockx			
Becky Dutch			
Ben Cowling			
Ben Larman			
Benjamin Miller		x	
Ben Singer		x	
Ben Tenoever		x	
Bernard Lafont			x
Bin Zhou			
Biao He			

Brooke Bozick	x		x
Carly Dillen	x	x	x
Carlie Williams		x	x
Catherine Luke			
Catherine Sutcliffe	x		
Claire Midgley	x		x
Charles Russell	x	x	
Chelsea Lane	x		
Chris Brooke			
Christopher Hsu			
Chris Marcum			x
Chris Roberts			
Clint Florence			
Conrad Mallia			
Colleen Jonsson	x	x	
Connie Schmaljohn	x	x	
Courtney Comar (Susan Weiss lab)			
Daniel Blanco-Melo			
Daniel Olson	x		
Daved Fremont			
David Martinez			
David Meekins			x
David O'Connor			x
David Renner (Susan Weiss lab)			
David Topham		x	
David Tribble			
David Wentworth			
Deborah Lynn Fuller			
Denis Nash	x		
Derek Eisnor		x	x
Diana Finzi			
Diane Post			
Diego Hijano			
Don Milton	x	x	x
Donna Neu	x	x	x
Doris Strome			x
Edwin Asturias		x	
Elizabeth Bartom		x	
Elizabeth Fitzpatrick	x		
Emma Hodcroft			
Erica Raterman			
Evans			
Eunchung Park	x	x	x
Eun Mi Lee			
Florian Krammer	x	x	

Francisco Chaves	x		
Frederic Bushman			
Gabriele Neumann	x	x	x
Gage Moreno			
Gavin Smith			
Ghazi Kayali	x		
Glen Abedi			
Grace Tietz			
Greg Deye			
Hana Golding		x	x
Harm van Bakel			x
Holly Hammond		x	
Hui-Ling Yen			
Ian Crozier	x	x	x
Ian Plumb			
Isabelle Phan			
Ishwar Chandramouliswaran			
Ivan Marazzi			
Jacob Hou			
Jacques Banchereau			
Jae Jung			
James Hoffman			x
James Kobie	x	x	
Jared Evans	x		x
Jason Goldstein			
Jayeeta Dutta			
Jean Patterson			
Jenni			
Jennifer German			
Jennifer Gordon			
Jennifer Hyde			x
Jennifer Kishimori			
Jens Wrammert			x
Jeremy Crawford			
Jesse Erasmus			
Jessica Ho			
Ji Lee			
Jimmy Logue			
Jim Chappell			
jmankow1			
Joe Breen			
Jonathan Runstadler	x	x	x
Joseph Mankowski		x	x
Judy Hewitt			
Juergen Richt	x		x

Julia Biggins		x	x
Kanta Subbarao			
Karla Satchell			
Katarina Braun			
Katharina Koelle	x		
Katie Mulka		x	
Katy Shaw-Saliba			
Katherine Fenstermacher	x	x	x
Keri Althoff			x
Kimberly Coca			
Kimberly Stemple			x
Korin Bullen			
Kristina Lu			
Kris Emo			
Kris Lambert			
Kristen Hildebrand	x	x	x
Laura Hughes			
Lauren Sauer			
Larry Anderson		x	x
Larry Wolfraim			
Leo Poon			
Liliana Brown	x		x
Lisa Hensley			x
Lisa Lindesmith			
Lisa Miorin			
Liz			x
Lori Newman			
Lucy Cong		x	x
Luis Martinez-Sobrido	x		
Mackenzie Zendt			
Malik Peiris			x
Marie Killerby			
Marina Lee	x		x
Mark Challberg			
Mark Denison	x	x	x
Mark Heism			
Mark Pallansch			x
Mark Robien	x	x	x
Mark Sangster		x	x
Mark Simons			
Mark Williams		x	
Marlene Espinoza	x	x	x
Marta Gaglia		x	x
Martha Nelson			x
Martin Blaser	x	x	x

Martin Linster		x	
Mary Allen Staat	x	x	
Masato Hatta (UW)			
Mathew Esona			
Matt Frieman	x	x	x
Maureen McGargill	x	x	x
Mehul Suttar			
Melissa Rolfes			
Melissa Uccellini	x	x	
Mercy Prabhudas			x
Michael Bryan			
Michael Chan			
Michael Martin			
Mike Cooper			
Mike Holbrook	x	x	x
Mindy Davis			
Missy			
Monica McNeal		x	x
Nat Moorman			
Nasia Safdar		x	
Natalie Thornburg			
newmanlm			
Nidia Trovao			x
Noffisat Oki			
Octavio Ramilo	x		x
Oluwasanmi Adenaiye	x	x	
Pamela McKenzie	x	x	x
Patrice Becker	x		
Paul McCray	x	x	x
Paul Jacob Bueno de Mesquita	x		
Paul Thomas			
Peter Daszak			
Peter Halfmann			x
Peter Myler			
Peter Palese		x	x
Phuong Nguyen-Contant			x
Punam Mathur	x	x	x
Qifang Bi			
Rachel Graham			
Rafael Medina		x	
Ralph Baric			
Randall Tressler			
Raul Andino			
Rebecca Dutch		x	
Reed Johnson	x		x

Reed Shabman	x	x	
Richard Rothman			
Richard Sciotti			
Richard Webby	x		
Rick Bushman			
Robert Bruno			x
Robert Johnson		x	x
Robert Schwartz	x		
Rogier van Doorn			x
Ron Fouchier			x
Rudra Goudavet			
Russell Ray		x	x
Ryan Langlois			
Ryan Ranallo	x	x	x
Sabra Klein	x		
Sander Herfst			
Sanjay Jain		x	x
Sanmi Adenaiye			
Samantha Loeber			
Sara Cherry	x	x	x
Sara Woodson			x
Scott Hensley			x
Scott Strome	x	x	x
Sean Whelan		x	
Seema Lakdawala			
Shahida Baqar	x	x	
Sharon Saydah			
Shelby O'Connor			x
Sheldon Tai	x	x	x
Shiho Chiba		x	x
Simon Anthony			
Sing Sing	x		
Sook Ho			
Sonnie Kim	x	x	x
Stacey Schultz-Cherry	x	x	
Stacy Ferguson	x	x	
Stanley Perlman		x	
Stephen Tompkins			
Steve Smiley			
Steve Tsang			
Sue Cammarata		x	x
Surender Khurana		x	x
Susan Gerber			
Susan Weiss		x	
Teresa Hauguel	x		

Thames P	x	x	x
Theresa Fitzgerald			
Thomas Friedrich	x		x
Tim Burgess		x	
Timothy Sheahan			
Tristan			
Troy Sutton	x	x	x
Tom Fabrizio	x		
Tori Baxter			
Vanessa Merino			
Vernon Musale			
Vineet Menachery			
Viviana Simon			
Walt Orenstein		x	x
Weina Sun			
Wesley C Van Voorhis	x	x	x
William Karesh			
William Kilembe			
William Florence			
William Morgenlander			
Willy Valdivia			
Wiriya Rutvisuttinunt	x		x
Wolfgang Leitner			
Xizhi Guo			
Yoshihiro Kawaoka			

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/99380423092?pwd= **552.136**
Importance:	Normal
Subject:	Canceled: SIG U19 Monthly Meeting
Start Time:	Thur 3/25/2021 12:30:00 PM (UTC-05:00)
End Time:	Thur 3/25/2021 1:30:00 PM (UTC-05:00)
Required Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande
Optional Attendees:	Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Due to Systems annual meeting earlier this week, we are cancelling this call.

To: Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; qingtan@wustl.edu[qingtan@wustl.edu]
From: Mcdermott, Jason E[Jason.McDermott@pnnl.gov]
Sent: Thur 5/13/2021 12:10:30 PM (UTC-05:00)
Subject: Re: final official acceptance!

Wahooo!!!

Great job Emilie and team –

Jason

Jason McDermott, Ph.D.
Lead, Systems Biology Team
Pacific Northwest National Laboratory, MSIN: J4-18
902 Battelle Boulevard PO Box 999
Richland, Washington 99352
Phone: 509-372-4360
Fax : 509-371-6946
Email: Jason.McDermott@pnnl.gov

From: "Purvine, Emilie" <Emilie.Purvine@pnnl.gov>
Date: Thursday, May 13, 2021 at 10:06 AM
To: "Feng, Song" <song.feng@pnnl.gov>, "Heath, Emily Jane Finnigan" <eheath3@illinois.edu>, "Jefferson, Brett A" <brett.jefferson@pnnl.gov>, "Joslyn, Cliff A" <Cliff.Joslyn@pnnl.gov>, "Kvinge, Henry J" <henry.kvinge@pnnl.gov>, "Mitchell, Hugh D" <Hugh.Mitchell@pnnl.gov>, "Praggastis, Brenda" <Brenda.Praggastis@pnnl.gov>, Amie Eisfeld <amie.eisfeld@wisc.edu>, "Sims, Amy C" <amy.sims@pnnl.gov>, "Thackray, Larissa" <lthackray@wustl.edu>, "shufang.fan@wisc.edu" <shufang.fan@wisc.edu>, KEVIN B WALTERS <kevin.walters@wisc.edu>, Peter Halfmann <peter.halfmann@wisc.edu>, "danielle.westhoffsmith@wisc.edu" <danielle.westhoffsmith@wisc.edu>, "vimenach@utmb.edu" <vimenach@utmb.edu>, "sheahan@email.unc.edu" <sheahan@email.unc.edu>, "adam_cockrell@unc.edu" <adam_cockrell@unc.edu>, "jacob.kocher@unc.edu" <jacob.kocher@unc.edu>, "Stratton, Kelly G" <kelly.stratton@pnnl.gov>, "Heller, Natalie C" <natalie.heller@pnnl.gov>, "Bramer, Lisa M" <Lisa.Bramer@pnnl.gov>, "Diamond, Michael" <mdiamond@wustl.edu>, Ralph Baric <rbaric@email.unc.edu>, "Waters, Katrina M" <Katrina.Waters@pnnl.gov>, YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>, "jason.mcdermott@pnnl.gov" <Jason.McDermott@pnnl.gov>, "qingtan@wustl.edu" <qingtan@wustl.edu>
Subject: final official acceptance!

Hi all,

Over the past two weeks I worked with the BMC Bioinformatics editorial system to get the right headings and order of sections. I just received the final official acceptance! From the journal email:

“I am pleased to inform you that your manuscript "Hypergraph Models of Biological Networks to Identify Genes Critical to Pathogenic Viral Response" (BINF-D-20-01029R3) has been accepted for publication in BMC Bioinformatics.”

Thank you all for the work to carry out the experiments, gather and process data, and complete the hypergraph analysis. I think we can now officially list this one as “In Press” :).

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Data Science and Analytics Group

Pacific Northwest National Laboratory
PNNL/Battelle Suite 500
1100 Dexter Ave. N
Seattle, WA 98109
Phone: 206-528-3461

To: Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Cockrell, Adam[adam_cockrell@unc.edu]; Kocher, Jacob Frederick[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
From: Baric, Ralph S[rbaric@email.unc.edu]
Sent: Thur 5/13/2021 12:37:50 PM (UTC-05:00)
Subject: RE: final official acceptance!

Awesome news

From: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Sent: Thursday, May 13, 2021 1:06 PM
To: Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; vimenach@utmb.edu; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Cockrell, Adam <adam_cockrell@unc.edu>; Kocher, Jacob Frederick <jacob.kocher@unc.edu>; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Baric, Ralph S <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>; qingtan@wustl.edu
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Thank you all for the work to carry out the experiments, gather and process data, and complete the hypergraph analysis. I think we can now officially list this one as “In Press” :).

Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Data Science and Analytics Group

Pacific Northwest National Laboratory
PNNL/Battelle Suite 500
1100 Dexter Ave. N
Seattle, WA 98109
Phone: 206-528-3461

To: Baric, Ralph S[rbaric@email.unc.edu]; Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Cockrell, Adam[adam_cockrell@unc.edu]; Kocher, Jacob Frederick[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
Cc: Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]
From: Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]
Sent: Thur 5/13/2021 7:08:18 PM (UTC-05:00)
Subject: RE: final official acceptance!

Woot woot woot.

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Thursday, May 13, 2021 10:38 AM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>; Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; vimenach@utmb.edu; Sheahan, Timothy Patrick <sheahan@email.unc.edu>; Cockrell, Adam <adam_cockrell@unc.edu>; Kocher, Jacob Frederick <jacob.kocher@unc.edu>; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>; qingtan@wustl.edu
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Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Data Science and Analytics Group

Pacific Northwest National Laboratory
PNNL/Battelle Suite 500
1100 Dexter Ave. N
Seattle, WA 98109
Phone: 206-528-3461

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Location: https://zoom.us/j/99380423092?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting-Canceled

Start Time: Thur 4/22/2021 12:30:00 PM (UTC-05:00)

End Time: Thur 4/22/2021 1:30:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Today's call is canceled due to scheduling conflicts. We will resume calls in May.

Join Zoom Meeting
https://zoom.us/j/99380423092?pwd= **552.136**

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833 548 0276 US Toll-free
833 548 0282 US Toll-free
877 853 5257 US Toll-free
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Join by H.323
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162.255.36.11 (US East)
Meeting ID: 993 8042 3092
Passcode: **552.136**

To: Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
From: Purvine, Emilie[Emilie.Purvine@pnnl.gov]
Sent: Thur 5/13/2021 12:06:03 PM (UTC-05:00)
Subject: final official acceptance!

Hi all,

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“I am pleased to inform you that your manuscript "Hypergraph Models of Biological Networks to Identify Genes Critical to Pathogenic Viral Response" (BINF-D-20-01029R3) has been accepted for publication in BMC Bioinformatics.”

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Senior Data Scientist and Mathematician
Data Science and Analytics Group

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Phone: 206-528-3461

To: Purvine, Emilie[Emilie.Purvine@pnnl.gov]; Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
From: Jefferson, Brett A[brett.jefferson@pnnl.gov]
Sent: Thur 5/13/2021 12:10:11 PM (UTC-05:00)
Subject: RE: final official acceptance!

Awesome! Thank you for all your hard work on this!!!

From: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Sent: Thursday, May 13, 2021 1:06 PM
To: Feng, Song <song.feng@pnnl.gov>; Heath, Emily Jane Finnigan <eheath3@illinois.edu>; Jefferson, Brett A <brett.jefferson@pnnl.gov>; Joslyn, Cliff A <Cliff.Joslyn@pnnl.gov>; Kvinge, Henry J <henry.kvinge@pnnl.gov>; Mitchell, Hugh D <Hugh.Mitchell@pnnl.gov>; Praggastis, Brenda <Brenda.Praggastis@pnnl.gov>; Amie Eisfeld <amie.eisfeld@wisc.edu>; Sims, Amy C <amy.sims@pnnl.gov>; Thackray, Larissa <lthackray@wustl.edu>; shufang.fan@wisc.edu; KEVIN B WALTERS <kevin.walters@wisc.edu>; Peter Halfmann <peter.halfmann@wisc.edu>; danielle.westhoffsmith@wisc.edu; vimenach@utmb.edu; sheahan@email.unc.edu; adam_cockrell@unc.edu; jacob.kocher@unc.edu; Stratton, Kelly G <kelly.stratton@pnnl.gov>; Heller, Natalie C <natalie.heller@pnnl.gov>; Bramer, Lisa M <Lisa.Bramer@pnnl.gov>; Diamond, Michael <mdiamond@wustl.edu>; Ralph Baric <rbaric@email.unc.edu>; Waters, Katrina M <Katrina.Waters@pnnl.gov>; YOSHIHIRO KAWAOKA <yoshihiro.kawaoka@wisc.edu>; Mcdermott, Jason E <Jason.McDermott@pnnl.gov>; qingtan@wustl.edu
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1100 Dexter Ave. N
Seattle, WA 98109
Phone: 206-528-3461

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Michael Davis; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Location: https://zoom.us/j/99380423092?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 5/27/2021 12:30:00 PM (UTC-05:00)

End Time: Thur 5/27/2021 1:30:00 PM (UTC-05:00)

Required Attendees: Michael Davis; Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Due to family illness, May's call is cancelled. Have a wonderful Memorial Day weekend.

Join Zoom Meeting
https://zoom.us/j/99380423092?pwd= **552.136**

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162.255.36.11 (US East)
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From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Thur 5/27/2021 8:45:24 AM (UTC-05:00)
Subject: SIG U19 call cancelled

Hi Everyone,
I just sent a cancellation for today's call from my outlook calendar. I hope you all received it.

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

To: Feng, Song[song.feng@pnnl.gov]; Heath, Emily Jane Finnigan[eheath3@illinois.edu]; Jefferson, Brett A[brett.jefferson@pnnl.gov]; Joslyn, Cliff A[Cliff.Joslyn@pnnl.gov]; Kvinge, Henry J[henry.kvinge@pnnl.gov]; Mitchell, Hugh D[Hugh.Mitchell@pnnl.gov]; Praggastis, Brenda[Brenda.Praggastis@pnnl.gov]; Amie Eisfeld[amie.eisfeld@wisc.edu]; Sims, Amy C[amy.sims@pnnl.gov]; Thackray, Larissa[lthackray@wustl.edu]; shufang.fan@wisc.edu[shufang.fan@wisc.edu]; KEVIN B WALTERS[kevin.walters@wisc.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; danielle.westhoffsmith@wisc.edu[danielle.westhoffsmith@wisc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; sheahan@email.unc.edu[sheahan@email.unc.edu]; adam_cockrell@unc.edu[adam_cockrell@unc.edu]; jacob.kocher@unc.edu[jacob.kocher@unc.edu]; Stratton, Kelly G[kelly.stratton@pnnl.gov]; Heller, Natalie C[natalie.heller@pnnl.gov]; Bramer, Lisa M[Lisa.Bramer@pnnl.gov]; Diamond, Michael[mdiamond@wustl.edu]; Ralph Baric[rbaric@email.unc.edu]; Waters, Katrina M[Katrina.Waters@pnnl.gov]; YOSHIHIRO KAWAOKA[yoshihiro.kawaoka@wisc.edu]; Mcdermott, Jason E[Jason.McDermott@pnnl.gov]; qingtan@wustl.edu[qingtan@wustl.edu]
From: Purvine, Emilie[Emilie.Purvine@pnnl.gov]
Sent: Tue 6/1/2021 11:26:11 AM (UTC-05:00)
Subject: FW: Your article published in BMC Bioinformatics is now online

Hello all,

See below for our final published paper! Thanks again to you all!

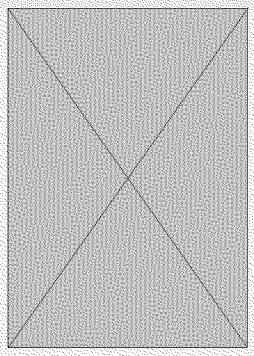
Emilie Purvine, Ph.D.
Senior Data Scientist and Mathematician
Pacific Northwest National Laboratory
Phone: 206-528-3461

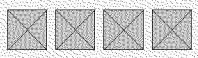
From: Springer <SpringerAlerts@springeronline.com>
Sent: Monday, May 31, 2021 3:28 PM
To: Purvine, Emilie <Emilie.Purvine@pnnl.gov>
Subject: Your article published in BMC Bioinformatics is now online

Publication of your article 2021-06-01

Dear Author,

We are pleased to inform you that your open access article has now been published:





BMC Bioinformatics

Hypergraph models of biological networks to identify genes critical to pathogenic viral response

Song Feng, Emily Heath, Brett Jefferson, Cliff Joslyn, Henry Kvinge, Hugh D. Mitchell, Brenda Praggastis, Amie J. Eisfeld, Amy C. Sims, Larissa B. Thackray, Shufang Fan, Kevin B. Walters, Peter J. Halfmann, Danielle Westhoff-Smith, Qing Tan, Vineet D. Menachery, Timothy P. Sheahan, Adam S. Cockrell, Jacob F. Kocher, Kelly G. Stratton, Natalie C. Heller, Lisa M. Bramer, Michael S. Diamond, Ralph S. Baric, Katrina M. Waters, Yoshihiro Kawaoka, Jason E. McDermott, Emilie Purvine

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Location:	https://zoom.us/j/95848751377?pwd= **552.136**
Importance:	Normal
Subject:	Canceled: SIG U19 Monthly Meeting
Start Time:	Thur 11/12/2020 1:30:00 PM (UTC-05:00)
End Time:	Thur 11/12/2020 2:30:00 PM (UTC-05:00)
Required Attendees:	Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; mtferris; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Michael Davis
Optional Attendees:	Michael J Gale; Renee Ireton; Graham PhD, Jessica B

The November call is cancelled due to a scheduling conflict.

Join Zoom Meeting
https://zoom.us/j/95848751377?pwd= **552.136**

Meeting ID: 958 4875 1377
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+1 669 900 6833 US (San Jose)
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+1 346 248 7799 US (Houston)
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833 548 0282 US Toll-free
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162.255.37.11 (US West)
162.255.36.11 (US East)
Meeting ID: 958 4875 1377
Passcode: **552.136**

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; mtferris[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]; Michael Davis[madphd@uw.edu]
Cc: Michael J Gale[mgale@uw.edu]; Renee Ireton[rireton@uw.edu]
From: Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]
Sent: Wed 10/14/2020 2:16:46 AM (UTC-05:00)
Subject: AW: SIG U19 Monthly Meeting
limma_DEG_subset2_severe_mod_low_thresh_131020.xlsx
DEGs_Human_MG_SYD_141020.pdf

Dear all,
I thought that you might find this useful for your candidate gene analysis. Mark mention it a few times during our presentation at the NIAID meeting.
Enclosed is a list of differentially expressed genes from a comparison of patients with severe to moderate influenza disease. You can use it directly to check your candidate genes to see whether they are regulated in severely infected patients. The list contains differentially expressed genes with a fold change abs>0.5849 (log2 of 1.5) and an adj.p-value<0.01.
If you have any questions concerning the list or particular genes, do not hesitate to contact me.
With best regards,
Klaus

ProbeID	PrimaryAcces	RefSeqAccessi	GenbankAcce	UniGeneID	EntrezGeneID	GeneSymbol
A_23_P25986	NM_020406	NM_020406	NM_020406	Hs.232165	57126	CD177
A_24_P18125	NM_006418	NM_006418	NM_006418	Hs.508113	10562	OLFM4
A_33_P33508	NM_020415	NM_020415	NM_020415	Hs.283091	56729	RETN
A_23_P20676	NM_005143	NM_005143	NM_005143	Hs.513711	3240	HP
A_23_P11922	NM_020415	NM_020415	NM_020415	Hs.283091	56729	RETN
A_23_P33056	NM_174918	NM_174918	NM_174918	Hs.709539	199675	MCEMP1
A_23_P32608	NM_001925	NM_001925	NM_001925	Hs.591391	1669	DEFA4
A_23_P13096	NM_001972	NM_001972	NM_001972	Hs.99863	1991	ELANE
A_23_P14117	NM_000250	NM_000250	NM_000250	Hs.458272	4353	MPO
A_33_P32892	NM_020995	NM_020995	NM_020995	Hs.655361	3250	HPR
A_23_P16943	NM_005564	NM_005564	NM_005564	Hs.204238	3934	LCN2
A_33_P33857	NM_005621	NM_005621	NM_005621	Hs.19413	6283	S100A12
A_33_P33199	NM_0012444	NM_0012444	NM_0012444	Hs.440934	383	ARG1
A_23_P16684	NM_002343	NM_002343	NM_002343	Hs.529517	4057	LTF
A_23_P31816	NM_005217	NM_005217	NM_005217	Hs.654448	1668	DEFA3
A_33_P33523	NM_0012444	NM_0012444	NM_0012444	Hs.440934	383	ARG1
A_23_P38024	NM_001816	NM_001816	NM_001816	Hs.41	1088	CEACAM8
A_23_P14038	NM_001911	NM_001911	NM_001911	Hs.421724	1511	CTSG
A_23_P74001	NM_005621	NM_005621	NM_005621	Hs.19413	6283	S100A12
A_33_P33995	NM_004666	NM_004666	NM_004666	Hs.12114	8876	VNN1
A_23_P13178	NM_001725	NM_001725	NM_001725	Hs.529019	671	BPI
A_23_P40174	NM_004994	NM_004994	NM_004994	Hs.297413	4318	MMP9
A_24_P63019	NM_004633	NM_004633	NM_004633	Hs.25333	7850	IL1R2
A_23_P67847	NM_024572	NM_024572	NM_024572	Hs.468058	79623	GALNT14
A_24_P19047	NM_003064	NM_003064	NM_003064	Hs.517070	6590	SLPI
A_32_P20835	NM_153046	NM_153046	NM_153046	Hs.21454	122402	TDRD9
A_23_P4096	NM_000717	NM_000717	NM_000717	Hs.89485	762	CA4
A_23_P58266	NM_005980	NM_005980	NM_005980	Hs.2962	6286	S100P
A_23_P12171	NM_005139	NM_005139	NM_005139	Hs.480042	306	ANXA3
A_23_P20874	NM_005091	NM_005091	NM_005091	Hs.137583	8993	PGLYRP1
A_23_P12808	NM_002206	NM_002206	NM_002206	Hs.524484	3679	ITGA7
A_33_P32360	NM_016509	NM_016509	NM_016509	Hs.409794	51266	CLEC1B
A_23_P25155	NM_020370	NM_020370	NM_020370	Hs.306199	53831	GPR84
A_33_P32704	NM_030810	NM_030810	NM_030810	Hs.150837	81567	TXNDC5
A_33_P32116	NM_003855	NM_003855	NM_003855	Hs.469521	8809	IL18R1
A_23_P20705	NM_003955	NM_003955	NM_003955	Hs.527973	9021	SOCS3
A_23_P13295	NM_004181	NM_004181	NM_004181	Hs.518731	7345	UCHL1
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A_23_P12286	NM_0010015	NM_0010015	NM_0010015	Hs.164060	2887	GRB10
A_23_P83110	NM_018249	NM_018249	NM_018249	Hs.269560	55755	CDK5RAP2
A_23_P57709	NM_013363	NM_013363	NM_013363	Hs.8944	26577	PCOLCE2
A_33_P33329	NM_016509	NM_016509	NM_016509	Hs.409794	51266	CLEC1B
A_33_P32518	NM_003855	NM_003855	NM_003855	Hs.469521	8809	IL18R1
A_24_P23526	NM_0010015	NM_0010015	NM_0010015	Hs.164060	2887	GRB10
A_23_P64372	NM_001062	NM_001062	NM_001062	Hs.2012	6947	TCN1
A_23_P39309	NM_003226	NM_003226	NM_003226	Hs.82961	7033	TFF3
A_24_P35361	NM_000478	NM_000478	NM_000478	Hs.75431	249	ALPL

A_23_P84596	NM_016459	NM_016459	NM_016459	Hs.409563	51237	MZB1
A_33_P32793	NM_001700	NM_001700	NM_001700	Hs.72885	566	AZU1
A_23_P16949	NM_000607	NM_000607	NM_000607	Hs.522356	5004	ORM1
A_23_P68601	NM_003650	NM_003650	NM_003650	Hs.143212	8530	CST7
A_23_P25360	NM_001721	NM_001721	NM_001721	Hs.495731	660	BMX
A_23_P60248	NM_003329	NM_003329	NM_003329	Hs.435136	7295	TXN
A_23_P24493	NM_002424	NM_002424	NM_002424	Hs.161839	4317	MMP8
A_33_P32576	NM_0010054	NM_0010054	NM_0010054	Hs.706618	333932	HIST2H3A
A_23_P23221	NM_001924	NM_001924	NM_001924	Hs.80409	1647	GADD45A
A_33_P32360	NM_016509	NM_016509	NM_016509	Hs.409794	51266	CLEC1B
A_23_P13178	NM_001725	NM_001725	NM_001725	Hs.529019	671	BPI
A_23_P14234	NM_002777	NM_002777	NM_002777	Hs.928	5657	PRTN3
A_24_P20856	NM_003855	NM_003855	NM_003855	Hs.469521	8809	IL18R1
A_33_P33081	NM_003878	NM_003878	NM_003878	Hs.78619	8836	GGH
A_23_P16716	NM_144646	NM_144646	NM_144646	Hs.643431	3512	IGJ
A_23_P29422	NM_004130	NM_004130	NM_004130	Hs.477892	2992	GYG1
A_23_P38451	NM_004130	NM_004130	NM_004130	Hs.477892	2992	GYG1
A_23_P25950	NM_032412	NM_032412	NM_032412	Hs.529798	84418	CYSTM1
A_24_P38573	NM_152672	NM_152672	NM_152672	Hs.630585	200931	SLC51A
A_23_P30694	NM_153615	NM_153615	NM_153615	Hs.658997	266747	RGL4
A_33_P33890	NM_018249	NM_018249	NM_018249	Hs.269560	55755	CDK5RAP2
A_23_P9485	NM_000608	NM_000608	NM_000608	Hs.719954	5005	ORM2
A_33_P33014	NM_019037	NM_019037	NM_019037	Hs.632041	54512	EXOSC4
A_23_P16145	NM_0010397	NM_0010397	NM_0010397	Hs.24309	55301	OLAH
A_23_P68851	NM_0010395	NM_0010395	NM_0010395	Hs.229335	83999	KREMEN1
A_23_P10604	NM_0010372	NM_0010372	NM_0010372	Hs.99272	116173	CMTM5
A_33_P33343	NM_003226	NM_003226	NM_003226	Hs.82961	7033	TFF3
A_23_P31671	NM_006294	NM_006294	NM_006294	Hs.131255	7381	UQCRB
A_23_P13019	NM_006907	NM_006907	NM_006907	Hs.163451	5831	PYCR1
A_33_P33167	NM_080759	NM_080759	NM_080759	Hs.129452	1602	DACH1
A_23_P52207	NM_012342	NM_012342	NM_012342	Hs.533336	25805	BAMBI
A_23_P31338	NM_003358	NM_003358	NM_003358	Hs.304249	7357	UGCG
A_23_P57856	NM_0011308	NM_0011308	NM_0011308	Hs.478588	604	BCL6
A_23_P17018	NM_017570	NM_017570	NM_017570	Hs.305882	26873	OPLAH
A_23_P12244	NM_005319	NM_005319	NM_005319	Hs.7644	3006	HIST1H1C
A_23_P12627	NM_003465	NM_003465	NM_003465	Hs.201688	1118	CHIT1
A_23_P33860	NM_0010116	NM_0010116	NM_0010116	Hs.436913	79145	CHCHD7
A_33_P37434	NR_073407	NR_073407	NR_073407	Hs.627154	449491	DEFA8P
A_24_P32032	NM_006713	NM_006713	NM_006713	Hs.229641	10923	SUB1
A_22_P00013	NR_033909	NR_033909	NR_033909	Hs.730362	643332	ECRP
A_33_P32903	NM_000104	NM_000104	NM_000104	Hs.154654	1545	CYP1B1
A_23_P35127	NM_0012874	NM_0012874	NM_0012874	Hs.488240	7378	UPP1
A_23_P15163	NM_002934	NM_002934	NM_002934	Hs.728	6036	RNASE2
A_23_P11881	NM_0010122	NM_0010122	NM_0010122	Hs.744872	332	BIRC5
A_23_P65757	NM_004701	NM_004701	NM_004701	Hs.194698	9133	CCNB2
A_23_P21844	NM_002483	NM_002483	NM_002483	Hs.466814	4680	CEACAM6
A_23_P38061	NM_006045	NM_006045	NM_006045	Hs.649234	10079	ATP9A
A_23_P16015	NM_003039	NM_003039	NM_003039	Hs.530003	6518	SLC2A5

A_23_P85903	NM_003268	NM_003268	NM_003268	Hs.604542	7100	TLR5
A_24_P26125	NM_004566	NM_004566	NM_004566	Hs.195471	5209	PFKFB3
A_33_P33602	NM_003509	NM_003509	NM_003509	Hs.534035	8329	HIST1H2AI
A_24_P14621	NM_021063	NM_021063	NM_021063	Hs.591797	3017	HIST1H2BD
A_32_P10825	NM_017565	NM_017565	NM_017565	Hs.268874	54757	FAM20A
A_23_P32057	NM_002928	NM_002928	NM_002928	Hs.413297	6004	RGS16
A_24_P29753	NM_181801	NM_181801	NM_181801	Hs.93002	11065	UBE2C
A_23_P10465	NM_080668	NM_080668	NM_080668	Hs.434886	113130	CDCA5
A_23_P11104	NM_003525	NM_003525	NM_003525	Hs.553506	8346	HIST1H2BI
A_33_P3232C	NM_020406	NM_020406	NM_020406	Hs.232165	57126	CD177
A_33_P33879	NM_001805	NM_001805	NM_001805	Hs.558308	1053	CEBPE
A_23_P29005	NM_022136	NM_022136	NM_022136	Hs.473341	64092	SAMSN1
A_23_P58953	NM_000904	NM_000904	NM_000904	Hs.533050	4835	NQO2
A_24_P3783	NM_003521	NM_003521	NM_003521	Hs.182432	8342	HIST1H2BM
A_23_P39629	NR_034094	NR_034094	NR_034094	Hs.246769	100129827	MRVI1-AS1
A_23_P12159	NM_002704	NM_002704	NM_002704	Hs.2164	5473	PPBP
A_21_P00001	NM_021064	NM_021064	NM_021064	Hs.51011	8969	HIST1H2AG
A_23_P20962	NM_000104	NM_000104	NM_000104	Hs.154654	1545	CYP1B1
A_23_P1663C	NM_000071	NM_000071	NM_000071	Hs.533013	875	CBS
A_33_P33885	NM_003465	NM_003465	NM_003465	Hs.201688	1118	CHIT1
A_23_P12897	NM_006399	NM_006399	NM_006399	Hs.509964	10538	BATF
A_33_P3229C	NM_080593	NM_080593	NM_080593	Hs.437275	85236	HIST1H2BK
A_23_P36621	NM_003524	NM_003524	NM_003524	Hs.247815	8345	HIST1H2BH
A_23_P21731	NM_004114	NM_004114	NM_004114	Hs.6540	2258	FGF13
A_21_P00006	NR_033839	NR_033839	NR_033839	Hs.585206	399972	ST3GAL4-AS1
A_23_P8013	NM_003519	NM_003519	NM_003519	Hs.137594	8340	HIST1H2BL
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A_23_P85783	NM_006623	NM_006623	NM_006623	Hs.487296	26227	PHGDH
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A_23_P99253	NM_004664	NM_004664	NM_004664	Hs.144333	8825	LIN7A
A_23_P12082	NM_016327	NM_016327	NM_016327	Hs.731656	51733	UPB1
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A_24_P30299	NM_007100	NM_007100	NM_007100	Hs.85539	521	ATP5I
A_23_P4348C	NM_002964	NM_002964	NM_002964	Hs.416073	6279	S100A8
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A_23_P10447	NM_0010072	NM_0010072	NM_0010072	Hs.178170	51207	DUSP13
A_23_P16799	NM_003518	NM_003518	NM_003518	Hs.591809	8339	HIST1H2BG
A_24_P97342	NM_021935	NM_021935	NM_021935	Hs.528665	60675	PROK2

A_21_P00141	BC010926	NA	BC010926	NA	8365	HIST1H4H
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A_23_P15576	NM_002129	NM_002129	NM_002129	Hs.434953	3148	HMGB2
A_32_P54137	NM_006004	NM_006004	NM_006004	Hs.481571	7388	UQCRH
A_24_P29524	NM_032467	NM_032467	NM_032467	Hs.332422	444	ASPH
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A_23_P48676	NM_002863	NM_002863	NM_002863	Hs.282417	5836	PYGL
A_23_P14605	NM_001695	NM_001695	NM_001695	Hs.86905	528	ATP6V1C1
A_23_P7636	NM_004219	NM_004219	NM_004219	Hs.350966	9232	PTTG1
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A_23_P21033	NM_014181	NM_014181	NM_014181	Hs.372208	29094	LGALSL
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A_23_P39537	NM_003539	NM_003539	NM_003539	Hs.248179	8360	HIST1H4D
A_23_P41114	NM_005213	NM_005213	NM_005213	Hs.518198	1475	CSTA
A_24_P65373	NM_000419	NM_000419	NM_000419	Hs.411312	3674	ITGA2B
A_24_P18518	NM_174920	NM_174920	NM_174920	Hs.567769	201191	SAMD14
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A_33_P34135	NM_0012571	NM_0012571	NM_0012571	Hs.109760	4709	NDUFB3
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A_23_P11548	NM_014176	NM_014176	NM_014176	Hs.5199	29089	UBE2T
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A_23_P95130	NM_207113	NM_207113	NM_207113	Hs.446021	84255	SLC37A3
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A_24_P31865	NM_000212	NM_000212	NM_000212	Hs.218040	3690	ITGB3
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A_33_P32998	NM_0012975	NM_0012975	NM_0012975	Hs.481571	7388	UQCRH
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A_33_P33817	NM_178174	NM_178174	NM_178174	Hs.117331	340205	TREML1
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A_23_P30247	NM_014465	NM_014465	NM_014465	Hs.129742	27284	SULT1B1
A_23_P16700	NM_014373	NM_014373	NM_014373	Hs.231320	26996	GPR160
A_32_P22179	NM_003514	NM_003514	NM_003514	Hs.134999	8336	HIST1H2AM
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A_23_P47565	NM_005566	NM_005566	NM_005566	Hs.2795	3939	LDHA
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A_23_P78209	NM_002359	NM_002359	NM_002359	Hs.744113	4097	MAFG
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A_23_P74609	NM_015714	NM_015714	NM_015714	Hs.432132	50486	G0S2
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A_23_P20605	NM_003981	NM_003981	NM_003981	Hs.366401	9055	PRC1
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A_24_P64653	NM_152637	NM_152637	NM_152637	Hs.51483	196410	METTL7B
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A_23_P13850	NM_001786	NM_001786	NM_001786	Hs.732435	983	CDK1
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A_24_P29707	NM_020531	NM_020531	NM_020531	Hs.472330	57136	APMAP
A_33_P32715	NM_032546	NM_032546	NM_032546	Hs.516036	57159	TRIM54
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A_24_P22050	NM_017817	NM_017817	NM_017817	Hs.743563	55647	RAB20
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A_23_P10210	NM_006000	NM_006000	NM_006000	Hs.75318	7277	TUBA4A
A_23_P13769	NM_003005	NM_003005	NM_003005	Hs.73800	6403	SELP
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A_23_P16523	NM_004864	NM_004864	NM_004864	Hs.616962	9518	GDF15
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A_33_P32878	NM_003536	NM_003536	NM_003536	Hs.591778	8357	HIST1H3H
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A_33_P32750	NM_0011600	NM_0011600	NM_0011600	Hs.337040	256435	ST6GALNAC3
A_24_P18837	NM_000574	NM_000574	NM_000574	Hs.126517	1604	CD55
A_23_P51085	NM_020675	NM_020675	NM_020675	Hs.421956	57405	SPC25
A_23_P42897	NM_004668	NM_004668	NM_004668	Hs.122785	8972	MGAM
A_23_P30799	NM_021018	NM_021018	NM_021018	Hs.247814	8968	HIST1H3F
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A_23_P7976	NM_005321	NM_005321	NM_005321	Hs.248133	3008	HIST1H1E
A_23_P11021	NM_001995	NM_001995	NM_001995	Hs.406678	2180	ACSL1
A_23_P13364	NM_005013	NM_005013	NM_005013	Hs.654599	4925	NUCB2
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A_24_P24494	NM_018349	NM_018349	NM_018349	Hs.33368	55784	MCTP2
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A_23_P16689	NM_016306	NM_016306	NM_016306	Hs.317192	51726	DNAJB11
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A_33_P32449	NM_0010798	NM_0010798	NM_0010798	Hs.78888	1622	DBI
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A_23_P63343	NM_021995	NM_021995	NM_021995	Hs.715862	10911	UTS2
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A_23_P11824	NM_016095	NM_016095	NM_016095	Hs.433180	51659	GINS2
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A_23_P20639	NM_0010401	NM_0010401	NM_0010401	Hs.15159	51192	CKLF
A_23_P21591	NM_001831	NM_001831	NM_001831	Hs.436657	1191	CLU
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A_23_P11226	NM_0010179	NM_0010179	NM_0010179	Hs.534196	2790	GNG10
A_33_P33504	NM_016359	NM_016359	NM_016359	Hs.615092	51203	NUSAP1
A_23_P35954	NM_003540	NM_003540	NM_003540	Hs.247816	8361	HIST1H4F
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A_23_P12188	NM_031916	NM_031916	NM_031916	Hs.381089	83853	ROPN1L
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A_24_P34309	NM_000791	NM_000791	NM_000791	Hs.648635	1719	DHFR
A_24_P38081	NM_004117	NM_004117	NM_004117	Hs.407190	2289	FKBP5
A_23_P21140	NM_0010395	NM_0010395	NM_0010395	Hs.229335	83999	KREMEN1
A_32_P14867	NM_006938	NM_006938	NM_006938	Hs.464734	6632	SNRPD1
A_24_P37982	NM_030926	NM_030926	NM_030926	Hs.111577	81618	ITM2C
A_23_P16115	NM_014317	NM_014317	NM_014317	Hs.558468	23590	PDSS1
A_23_P72503	NM_007246	NM_007246	NM_007246	Hs.388668	11275	KLHL2
A_23_P15406	NM_006000	NM_006000	NM_006000	Hs.75318	7277	TUBA4A
A_23_P40108	NM_001853	NM_001853	NM_001853	Hs.716639	1299	COL9A3
A_24_P55148	NM_021058	NM_021058	NM_021058	Hs.656567	8970	HIST1H2BJ
A_33_P33442	NM_003538	NM_003538	NM_003538	Hs.248178	8359	HIST1H4A
A_33_P33191	NM_175710	NM_175710	NM_175710	Hs.655194	1379	CR1L
A_23_P25918	NM_013943	NM_013943	NM_013943	Hs.440544	25932	CLIC4
A_33_P33920	NM_004881	NM_004881	NM_004881	Hs.50649	9540	TP53I3
A_21_P00137	NM_021029	NM_021029	NM_021029	Hs.432485	6173	RPL36A
A_24_P67306	NM_001444	NM_001444	NM_001444	Hs.408061	2171	FABP5
A_33_P32726	ENST000003(	NA	NA	NA	2207	FCER1G
A_23_P39168	NM_0011711	NM_0011711	NM_0011711	Hs.728837	100131801	PET100
A_23_P81212	NM_016067	NM_016067	NM_016067	Hs.436161	51023	MRPS18C
A_23_P16915	NM_012413	NM_012413	NM_012413	Hs.79033	25797	QPCT
A_23_P13279	NM_006010	NM_006010	NM_006010	Hs.436446	7873	MANF
A_23_P88740	NM_018455	NM_018455	NM_018455	Hs.726537	55839	CENPN
A_23_P33046	NM_144686	NM_144686	NM_144686	Hs.355126	147798	TMC4
A_23_P16997	NM_020747	NM_020747	NM_020747	Hs.266616	57507	ZNF608
A_23_P5392	NM_004881	NM_004881	NM_004881	Hs.50649	9540	TP53I3
A_23_P26254	NM_016013	NM_016013	NM_016013	Hs.106529	51103	NDUFAF1
A_32_P22877	NM_174907	NM_174907	NM_174907	Hs.431092	151987	PPP4R2
A_23_P13899	NM_002046	NM_002046	NM_002046	Hs.544577	2597	GAPDH
A_24_P30348	NM_006834	NM_006834	NM_006834	Hs.287714	10981	RAB32
A_33_P33665	NM_0011305	NM_0011305	NM_0011305	Hs.613729	55790	CSGALNACT1
A_24_P18105	NM_006278	NM_006278	NM_006278	Hs.591947	6484	ST3GAL4
A_23_P32170	NM_004049	NM_004049	NM_004049	Hs.227817	597	BCL2A1
A_33_P32767	NM_0010109	NM_0010109	NM_0010109	Hs.396530	3082	HGF

A_23_P81859	NM_080596	NM_080596	NM_080596	Hs.352225	85235	HIST1H2AH
A_33_P32122	NM_007351	NM_007351	NM_007351	Hs.268107	22915	MMRN1
A_23_P97932	NM_012228	NM_012228	NM_012228	Hs.461420	22921	MSRB2
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A_33_P33878	ENST000004	XR_244383	XR_244383	Hs.208912	79019	CENPM
A_24_P16640	NM_003544	NM_003544	NM_003544	Hs.143080	8366	HIST1H4B
A_33_P34017	NM_005304	NM_005304	NM_005304	Hs.248055	2865	FFAR3
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A_23_P11806	NM_181641	NM_181641	NM_181641	Hs.15159	51192	CKLF
A_23_P20823	NM_052844	NM_052844	NM_052844	Hs.495240	89891	WDR34
A_24_P23727	NM_000675	NM_000675	NM_000675	Hs.197029	135	ADORA2A
A_21_P00008	NR_038974	NR_038974	NR_038974	Hs.709795	100288432	IL10RB-AS1
A_23_P39931	NM_003494	NM_003494	NM_003494	Hs.252180	8291	DYSF
A_24_P48539	NM_003830	NM_003830	NM_003830	Hs.310333	8778	SIGLEC5
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A_33_P33935	NM_0012520	NM_0012520	NM_0012520	Hs.279257	5110	PCMT1
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A_33_P34232	NM_0012844	NM_0012844	NM_0012844	Hs.475502	55287	TMEM40
A_23_P21760	NM_021029	NM_021029	NM_021029	Hs.432485	6173	RPL36A
A_23_P42257	NM_003897	NM_003897	NM_003897	Hs.76095	8870	IER3
A_23_P13966	NM_006931	NM_006931	NM_006931	Hs.419240	6515	SLC2A3
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A_24_P10388	NM_004508	NM_004508	NM_004508	Hs.283652	3422	IDI1
A_33_P32472	NM_022746	NM_022746	NM_022746	Hs.497816	64757	MARC1
A_33_P33963	NM_000877	NM_000877	NM_000877	Hs.701982	3554	IL1R1
A_24_P22830	NM_006890	NM_006890	NM_006890	Hs.74466	1087	CEACAM7
A_23_P88731	NM_002875	NM_002875	NM_002875	Hs.631709	5888	RAD51
A_23_P21371	NM_014402	NM_014402	NM_014402	Hs.146602	27089	UQCRQ
A_23_P80048	NR_119376	NR_119376	NR_119376	Hs.72222	80307	FER1L4
A_33_P33348	NM_0012655	NM_0012655	NM_0012655	Hs.37062	3640	INSL3
A_24_P23973	NM_004776	NM_004776	NM_004776	Hs.370487	9334	B4GALT5
A_24_P29001	NM_014463	NM_014463	NM_014463	Hs.111632	27258	LSM3
A_23_P37655	NM_022468	NM_022468	NM_022468	Hs.654979	64386	MMP25
A_23_P20886	NM_004877	NM_004877	NM_004877	Hs.5210	9535	GMFG
A_24_P33562	NM_003486	NM_003486	NM_003486	Hs.513797	8140	SLC7A5
A_23_P16540	NM_016047	NM_016047	NM_016047	Hs.177861	51639	SF3B6
A_23_P54477	NM_018648	NM_018648	NM_018648	Hs.14317	55505	NOP10
A_24_P41499	NM_018407	NM_018407	NM_018407	Hs.492314	55353	LAPTM4B
A_33_P33636	NM_0010988	NM_0010988	NM_0010988	Hs.709417	641649	TMEM91
A_22_P00024	NM_0011361	NM_0011361	NM_0011361	Hs.515351	57655	GRAMD1A
A_24_P56130	NM_079423	NM_079423	NM_079423	Hs.632717	4637	MYL6
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A_23_P25620	NM_014945	NM_014945	NM_014945	Hs.49688	22885	ABLIM3
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A_24_P14506	NM_183416	NM_183416	NM_183416	Hs.97858	23095	KIF1B
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A_33_P33284	NM_0012048	NM_0012048	NM_0012048	Hs.656657	55129	ANO10
A_23_P36317	NM_003511	NM_003511	NM_003511	Hs.233568	8332	HIST1H2AL
A_33_P38496	M30627	NA	M30627	Hs.523560	3324	HSP90AA2P
A_33_P32615	NM_0010044	NM_0010044	NM_0010044	Hs.519404	340120	ANKRD34B
A_23_P57199	NM_178311	NM_178311	NM_178311	Hs.355394	92086	GGTLC1
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A_24_P64167	NM_000962	NM_000962	NM_000962	Hs.201978	5742	PTGS1
A_21_P00135	NR_110439	NR_110439	NA	Hs.153412	100506365	OTUD6B-AS1
A_33_P33238	NM_004260	NM_004260	NM_004260	Hs.31442	9401	RECQL4
A_23_P61398	NM_0010018	NM_0010018	NM_0010018	Hs.530381	415116	PIM3
A_23_P37103	NM_002531	NM_002531	NM_002531	Hs.590869	4923	NTSR1
A_24_P41570	NM_002106	NM_002106	NM_002106	Hs.119192	3015	H2AFZ
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A_23_P41728	NM_000875	NM_000875	NM_000875	Hs.643120	3480	IGF1R
A_22_P00003	NM_020747	NM_020747	NM_020747	Hs.266616	57507	ZNF608
A_23_P12758	NM_006169	NM_006169	NM_006169	Hs.503911	4837	NNMT
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A_23_P21144	NM_016733	NM_016733	NM_016733	Hs.474596	3985	LIMK2
A_23_P375	NM_018101	NM_018101	NM_018101	Hs.524571	55143	CDCA8
A_23_P11983	NM_021209	NM_021209	NM_021209	Hs.574741	58484	NLRC4
A_21_P00142	ENST000003	XR_247499	XR_247499	Hs.737229	399716	DKFZp667F07
A_24_P16096	NM_0012583	NM_0012583	NM_0012583	Hs.554791	9537	TP53I11
A_23_P32145	NM_173791	NM_173791	NM_173791	Hs.501149	118987	PDZD8
A_23_P5903	NM_016354	NM_016354	NM_016354	Hs.235782	28231	SLCO4A1
A_23_P94932	NM_015702	NM_015702	NM_015702	Hs.5324	27249	MMADHC
A_33_P34049	NM_003536	NM_003536	NM_003536	Hs.591778	8357	HIST1H3H
A_23_P43130	NM_152421	NM_152421	NM_152421	Hs.741305	138311	FAM69B
A_23_P68610	NM_012112	NM_012112	NM_012112	Hs.244580	22974	TPX2
A_33_P33825	NR_001445	NR_001445	NR_001445	Hs.224866	125050	RN7SK
A_23_P12794	NM_001124	NM_001124	NM_001124	Hs.441047	133	ADM
A_32_P96719	NM_024745	NM_024745	NM_024745	Hs.123253	79801	SHCBP1
A_33_P32118	NM_0010018	NM_0010018	NM_0010018	Hs.149261	861	RUNX1
A_33_P34614	NM_0010838	NM_0010838	NM_0010838	Hs.661752	51206	GP6
A_33_P33408	NM_032587	NM_032587	NM_032587	Hs.200242	84674	CARD6
A_23_P21784	NM_002928	NM_002928	NM_002928	Hs.413297	6004	RGS16
A_23_P15090	NM_018099	NM_018099	NM_018099	Hs.728955	55711	FAR2
A_23_P401	NM_016343	NM_016343	NM_016343	Hs.497741	1063	CENPF
A_23_P50101	NM_000494	NM_000494	NM_000494	Hs.117938	1308	COL17A1
A_23_P67980	NM_003709	NM_003709	NM_003709	Hs.59908	8609	KLF7
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A_33_P34089	NM_0012828	NM_0012828	NM_0012828	Hs.632765	91227	GGTLC2
A_23_P32270	NM_0010795	NM_0010795	NM_0010795	Hs.446357	283635	FAM177A1
A_23_P66719	NM_144683	NM_144683	NM_144683	Hs.631760	147015	DHRS13
A_23_P20128	NM_015074	NM_015074	NM_015074	Hs.97858	23095	KIF1B
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A_32_P17366	NM_003296	NM_003296	NM_003296	Hs.2042	7180	CRISP2

A_23_P1782	NM_002231	NM_002231	NM_002231	Hs.527778	3732	CD82
A_33_P32845	NM_016653	NM_016653	NM_016653	Hs.444451	51776	ZAK
A_33_P33464	ENST0000062	NA	AK311046	Hs.710305	4671	NAIP
A_24_P37317	NM_004580	NM_004580	NM_004580	Hs.654978	5873	RAB27A
A_23_P20601	NM_0010180	NM_0010180	NM_0010180	Hs.133892	7168	TPM1
A_33_P32511	NM_0012565	NM_0012565	NM_0012565	Hs.202	706	TSPO
A_21_P00118	NM_207366	NM_207366	NA	Hs.453629	346288	Sep-14
A_23_P77859	NM_203411	NM_203411	NM_203411	Hs.389669	92162	TMEM88
A_23_P49376	NM_000078	NM_000078	NM_000078	Hs.89538	1071	CETP
A_24_P59667	NM_000215	NM_000215	NM_000215	Hs.515247	3718	JAK3
A_24_P21784	NM_003510	NM_003510	NM_003510	Hs.734717	8330	HIST1H2AK
A_24_P20873	NM_003495	NM_003495	NM_003495	Hs.248172	8294	HIST1H4I
A_23_P71727	NM_001827	NM_001827	NM_001827	Hs.83758	1164	CKS2
A_23_P42198	NM_003534	NM_003534	NM_003534	Hs.247813	8355	HIST1H3G
A_24_P10794	NM_024598	NM_024598	NM_024598	Hs.408702	79650	USB1
A_33_P33431	NM_002072	NM_002072	NM_002072	Hs.269782	2776	GNAQ
A_24_P85449	NR_003491	NR_003491	NR_003491	Hs.517502	440823	MIAT
A_23_P93431	NM_016108	NM_016108	NM_016108	Hs.567501	51390	AIG1
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A_33_P32983	NM_0012066	NM_0012066	NM_0012066	Hs.136309	51100	SH3GLB1
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A_33_P33845	NM_213636	NM_213636	NM_213636	Hs.533040	9260	PDLIM7
A_23_P14999	NM_020992	NM_020992	NM_020992	Hs.368525	9124	PDLIM1
A_33_P34154	NM_005346	NM_005346	NM_005346	Hs.719966	3304	HSPA1B
A_24_P14121	NM_198194	NM_198194	NM_198194	Hs.253903	2040	STOM
A_23_P12200	NM_033211	NM_033211	NM_033211	Hs.482976	90355	C5orf30
A_33_P33691	NM_002254	NM_002254	NM_002254	Hs.21611	3797	KIF3C
A_23_P14189	NM_0010804	NM_0010804	NM_0010804	Hs.532872	147699	PPM1N
A_23_P92842	NM_0010335	NM_0010335	NM_0010335	Hs.432984	51128	SAR1B
A_23_P12616	NM_002249	NM_002249	NM_002249	Hs.490765	3782	KCNN3
A_21_P00003	NR_003004	NR_003004	NR_003004	Hs.676951	677770	SCARNA22
A_23_P20031	NM_017779	NM_017779	NM_017779	Hs.445098	55635	DEPDC1
A_23_P38795	NM_002029	NM_002029	NM_002029	Hs.753	2357	FPR1
A_23_P32368	NM_003543	NM_003543	NM_003543	Hs.591790	8365	HIST1H4H
A_19_P00321	ENST000005C	NA	NA	NA	285550	FAM200B
A_23_P76364	NM_001769	NM_001769	NM_001769	Hs.114286	928	CD9
A_22_P00009	NM_018349	NM_018349	NM_018349	Hs.33368	55784	MCTP2
A_23_P47527	NM_014206	NM_014206	NM_014206	Hs.437779	746	TMEM258
A_23_P20920	NM_001238	NM_001238	NM_001238	Hs.244723	898	CCNE1
A_23_P32577	NM_080759	NM_080759	NM_080759	Hs.129452	1602	DACH1
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A_33_P32205	NM_024954	NM_024954	NM_024954	Hs.500724	80019	UBTD1
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A_23_P13703	NM_003662	NM_003662	NM_003662	Hs.495728	8544	PIR
A_24_P20604	NM_001151	NM_001151	NM_001151	Hs.246506	291	SLC25A4
A_23_P16046	NM_003115	NM_003115	NM_003115	Hs.492859	6675	UAP1
A_23_P20622	NM_020821	NM_020821	NM_020821	Hs.511668	54832	VPS13C
A_23_P20252	NM_0010034	NM_0010034	NM_0010034	Hs.438236	3983	ABLIM1

A_33_P33876	NM_198081	NM_198081	NM_198081	Hs.486109	256380	SCML4
A_33_P33291	NM_0011308	NM_0011308	NM_0011308	Hs.202672	1786	DNMT1
A_22_P00017	NM_0010302	NM_0010302	NM_0010302	Hs.632188	6693	SPN
A_23_P20258	NM_018330	NM_018330	NM_018330	Hs.501140	57698	KIAA1598
A_23_P39294	NM_002445	NM_002445	NM_002445	Hs.147635	4481	MSR1
A_23_P36561	NM_004557	NM_004557	NM_004557	Hs.436100	4855	NOTCH4
A_23_P88222	NM_138790	NM_138790	NM_138790	Hs.407101	122618	PLD4
A_23_P49674	NM_173728	NM_173728	NM_173728	Hs.443109	22899	ARHGEF15
A_23_P12121	NM_003656	NM_003656	NM_003656	Hs.434875	8536	CAMK1
A_23_P27606	NM_004843	NM_004843	NM_004843	Hs.132781	9466	IL27RA
A_33_P34142	NM_0011707	NM_0011707	NM_0011707	Hs.105134	55796	MBNL3
A_23_P10697	NM_006640	NM_006640	NM_006640	Hs.440932	10801	Sep-09
A_33_P35702	NR_077215	NR_077215	NR_077215	Hs.676500	644962	TNRC18P1
A_23_P17345	NM_005461	NM_005461	NM_005461	Hs.169487	9935	MAFB
A_23_P10196	NM_006887	NM_006887	NM_006887	Hs.503093	678	ZFP36L2
A_23_P43544	NM_032087	NM_032087	NM_032087	Hs.368160	56108	PCDHGA7
A_33_P32745	NM_0012918	NM_0012918	NM_0012918	Hs.183125	51348	KLRF1
A_33_P33997	ENST0000057	NA	NA	NA	2038	EPB42
A_23_P20492	NM_016248	NM_016248	NM_016248	Hs.105105	11215	AKAP11
A_32_P23255	NR_036502	NR_036502	NR_036502	Hs.13262	439949	PRKCQ-AS1
A_24_P82630	NM_015295	NM_015295	NM_015295	Hs.8118	23347	SMCHD1
A_23_P35420	NM_152348	NM_152348	NM_152348	Hs.234572	124997	WDR81
A_23_P11557	NM_198149	NM_198149	NM_198149	Hs.632471	149345	SHISA4
A_33_P32137	NM_014205	NM_014205	NM_014205	Hs.121025	741	ZNHIT2
A_23_P86504	NM_024541	NM_024541	NM_024541	Hs.16004	79591	C10orf76
A_23_P16506	NM_198969	NM_198969	NM_198969	Hs.515053	166	AES
A_23_P15496	NM_015672	NM_015672	NM_015672	Hs.115429	85376	RIMBP3
A_23_P88278	NM_020366	NM_020366	NM_020366	Hs.126035	57096	RPGRIP1
A_33_P32652	NM_020775	NM_020775	NM_020775	Hs.708190	57535	KIAA1324
A_33_P32812	NM_005226	NM_005226	NM_005226	Hs.585118	1903	S1PR3
A_23_P39377	NM_000953	NM_000953	NM_000953	Hs.306831	5729	PTGDR
A_33_P33680	NM_0010401	NM_0010401	NM_0010401	Hs.334637	84329	HVCN1
A_23_P40468	NM_178348	NM_178348	NM_178348	Hs.534645	353131	LCE1A
A_23_P13485	NM_003974	NM_003974	NM_003974	Hs.71215	9046	DOK2
A_22_P00006	NR_046783	NR_046783	NR_046783	Hs.738190	100874295	KCND3-IT1
A_23_P84344	NM_021805	NM_021805	NM_021805	Hs.501624	59307	SIGIRR
A_24_P30183	NM_007232	NM_007232	NM_007232	Hs.251399	11255	HRH3
A_23_P30192	ENST000003E	NA	HV963900	NA	4512	COX1
A_22_P00024	NR_026914	NR_026914	NR_026914	Hs.706954	85001	MGC16275
A_23_P42369	NM_006454	NM_006454	NM_006454	Hs.655020	10608	MXD4
A_23_P11579	NM_0010019	NM_0010019	NM_0010019	Hs.643512	59338	PLEKHA1
A_23_P42663	NM_001620	NM_001620	NM_001620	Hs.502756	79026	AHNAK
A_24_P27582	NM_033419	NM_033419	NM_033419	Hs.462971	93210	PGAP3
A_33_P35771	ENST000005E	NA	BC033227	Hs.620382	10607	TBL3
A_23_P20211	NR_046310	NR_046310	NR_046310	Hs.500512	84333	PCGF5
A_23_P13657	NM_003896	NM_003896	NM_003896	Hs.415117	8869	ST3GAL5
A_33_P32405	NM_138444	NM_138444	NM_138444	Hs.644125	115207	KCTD12
A_21_P00124	NM_014831	NM_014831	NA	Hs.170999	9881	TRANK1

A_33_P33866	NM_005060	NM_005060	NM_005060	Hs.256022	6097	RORC
A_32_P14850	ENST0000042	XM_0052562	XM_0052562	Hs.513695	440348	NPIPB15
A_33_P37241	NM_198440	NM_198440	NM_198440	Hs.593679	91319	DERL3
A_33_P32351	NM_152345	NM_152345	NM_152345	Hs.662164	124930	ANKRD13B
A_23_P14804	NM_000958	NM_000958	NM_000958	Hs.199248	5734	PTGER4
A_23_P14445	NM_001221	NM_001221	NM_001221	Hs.144114	817	CAMK2D
A_33_P32506	NM_000074	NM_000074	NM_000074	Hs.592244	959	CD40LG
A_23_P37994	NM_0010804	NM_0010804	NM_0010804	Hs.525536	440193	CCDC88C
A_24_P41560	NM_002939	NM_002939	NM_002939	Hs.530687	6050	RNH1
A_33_P38839	NR_036442	NR_036442	NR_036442	Hs.71912	64788	LMF1
A_22_P00003	NR_120496	NR_120496	NR_120496	Hs.738690	100132159	CALML3-AS1
A_23_P40638	NM_153350	NM_153350	NM_153350	Hs.513244	146330	FBXL16
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A_33_P32839	NM_016101	NM_016101	NM_016101	Hs.585728	51388	NIP7
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A_33_P33969	NM_004331	NM_004331	NM_004331	Hs.131226	665	BNIP3L
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A_23_P12290	NM_015570	NM_015570	NM_015570	Hs.21631	26053	AUTS2
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A_23_P50214	NM_002037	NM_002037	NM_002037	Hs.390567	2534	FYN
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A_22_P00002	NM_0011008	NM_0011008	NM_0011008	Hs.658684	123775	C16orf46
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A_24_P12528	NM_0010150	NM_0010150	NM_0010150	Hs.438782	10014	HDAC5
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A_33_P32398	NM_017758	NM_017758	NM_017758	Hs.744130	54890	ALKBH5
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A_24_P37496	NR_040584	NR_040584	NR_040584	Hs.666638	442582	STAG3L2
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A_24_P32277	NM_003225	NM_003225	NM_003225	Hs.162807	7031	TFF1
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A_24_P39616	NM_001335	NM_001335	NM_001335	Hs.416848	1521	CTSW
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A_23_P70688	NM_004271	NM_004271	NM_004271	Hs.653138	9450	LY86
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A_23_P25030	NM_001837	NM_001837	NM_001837	Hs.506190	1232	CCR3
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A_23_P25700	NM_006200	NM_006200	NM_006200	Hs.368542	5125	PCSK5
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A_33_P34158	AK090476	NA	AK090476	NA	197358	NLRC3
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A_23_P42824	NM_145755	NM_145755	NM_145755	Hs.443935	199223	TTC21A
A_33_P33209	NM_206833	NM_206833	NM_206833	Hs.657978	404217	CTXN1
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A_32_P20647	NM_178457	NM_178457	NM_178457	Hs.473204	128611	ZNF831
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A_21_P00147	NM_0012829	NM_0012829	NM_0012829	Hs.292026	9470	EIF4E2
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A_23_P44505	NM_003597	NM_003597	NM_003597	Hs.12229	8462	KLF11
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A_33_P34061	NM_002262	NM_002262	NM_002262	Hs.562457	3824	KLRD1
A_23_P15621	NM_002104	NM_002104	NM_002104	Hs.277937	3003	GZMK
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A_24_P97374	NM_005442	NM_005442	NM_005442	Hs.591663	8320	EOMES
A_24_P28295	NM_0012437	NM_0012437	NM_0012437	Hs.744937	9910	RABGAP1L
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A_33_P33783	NM_013237	NM_013237	NM_013237	Hs.744904	27166	PRELID1
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A_32_P84369	NR_038353	NR_038353	NR_038353	Hs.652193	653316	FAM153C
A_23_P25435	NM_006647	NM_006647	NM_006647	Hs.495554	10811	NOXA1
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A_23_P10336	NM_005356	NM_005356	NM_005356	Hs.470627	3932	LCK
A_23_P33174	NM_001772	NM_001772	NM_001772	Hs.83731	945	CD33
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A_23_P65651	NM_004184	NM_004184	NM_004184	Hs.497599	7453	WARS
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A_23_P37375	NM_004755	NM_004755	NM_004755	Hs.510225	9252	RPS6KA5
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A_23_P14665	NM_004323	NM_004323	NM_004323	Hs.377484	573	BAG1
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A_32_P10186	NM_0012915	NM_0012915	NM_0012915	Hs.536474	113277	TMEM106A
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A_23_P50678	NM_139355	NM_139355	NM_139355	Hs.631845	4145	MATK
A_24_P76854	NM_0011233	NM_0011233	NM_0011233	Hs.528921	81872	KRTAP2-1
A_33_P32209	NM_005160	NM_005160	NM_005160	Hs.657494	157	ADRBK2
A_32_P16669	NM_020733	NM_020733	NM_020733	Hs.477420	57493	HEG1
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A_24_P68079	NM_014831	NM_014831	NM_014831	Hs.170999	9881	TRANK1
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A_23_P41674	NM_000733	NM_000733	NM_000733	Hs.3003	916	CD3E
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A_33_P32704	NR_002780	NR_002780	NR_002780	Hs.434111	123346	HIGD2B
A_24_P27245	ENST0000057	XM_0052566	XM_0052566	Hs.462080	388325	SCIMP
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A_33_P33517	NM_024070	NM_024070	NM_024070	Hs.729356	79037	PVRIG
A_23_P14042	NM_016337	NM_016337	NM_016337	Hs.125867	51466	EVL
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A_22_P00025	NM_0012429	NM_0012429	NM_0012429	Hs.56729	4046	LSP1
A_33_P32217	NM_0010316	NM_0010316	NM_0010316	Hs.170019	864	RUNX3
A_33_P32210	NM_173059	NM_173059	NM_173059	Hs.307004	7455	ZAN
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A_33_P32972	NM_0010424	NM_0010424	NM_0010424	Hs.437365	27163	NAAA
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A_23_P1473	NM_005041	NM_005041	NM_005041	Hs.2200	5551	PRF1
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A_23_P34339	NM_001838	NM_001838	NM_001838	Hs.370036	1236	CCR7
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A_23_P11253	NM_0010352	NM_0010352	NM_0010352	Hs.535972	399665	FAM102A
A_21_P0014C	XM_0034034	XM_0034034	XM_0034034	NA	164714	TTLL8
A_23_P31674	NM_0010252	NM_0010252	NM_0010252	Hs.654836	7106	TSPAN4
A_24_P38248	ENST000005	XM_0067227	XM_0067227	Hs.363138	376497	SLC27A1
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A_23_P43451	NM_0010401	NM_0010401	NM_0010401	Hs.159142	3955	LFNG
A_23_P31187	NM_006725	NM_006725	NM_006725	Hs.744366	923	CD6
A_23_P40449	NM_002185	NM_002185	NM_002185	Hs.591742	3575	IL7R
A_24_P40373	NM_015481	NM_015481	NM_015481	Hs.505653	25946	ZNF385A
A_33_P32314	NM_006669	NM_006669	NM_006669	Hs.667388	10859	LILRB1
A_33_P33792	NM_207103	NM_207103	NM_207103	Hs.462080	388325	SCIMP
A_33_P33935	NM_0011647	NM_0011647	NM_0011647	Hs.77542	5724	PTAFR
A_33_P32935	NM_004210	NM_004210	NM_004210	Hs.594708	9148	NEURL1
A_24_P20630	NM_016269	NM_016269	NM_016269	Hs.743478	51176	LEF1
A_33_P33838	NM_016381	NM_016381	NM_016381	Hs.707026	11277	TREX1
A_33_P32187	ENST000003	NA	NA	NA	79144	PPDPF
A_23_P80382	NM_015366	NM_015366	NM_015366	Hs.102336	55615	PRR5
A_23_P27424	NM_133460	NM_133460	NM_133460	Hs.660728	147686	ZNF418
A_33_P33321	NM_0011438	NM_0011438	NM_0011438	Hs.405607	162466	PHOSPHO1
A_32_P15944	NM_015075	NM_015075	NM_015075	Hs.496138	23096	IQSEC2
A_33_P32149	NM_014767	NM_014767	NM_014767	Hs.523009	9806	SPOCK2
A_23_P15104	NM_002259	NM_002259	NM_002259	Hs.512576	3821	KLRC1
A_33_P32841	NM_0012437	NM_0012437	NM_0012437	Hs.525134	55624	POMGNT1
A_23_P12858	NM_152710	NM_152710	NM_152710	Hs.386698	219793	TBATA
A_23_P42588	NM_018384	NM_018384	NM_018384	Hs.647079	55340	GIMAP5
A_22_P00017	NR_033387	NR_033387	NR_033387	Hs.568831	642394	ADARB2-AS1
A_24_P37639	NM_015103	NM_015103	NM_015103	Hs.301685	23129	PLXND1
A_23_P85240	NM_016562	NM_016562	NM_016562	Hs.659215	51284	TLR7
A_24_P91519	NM_153045	NM_153045	NM_153045	Hs.522357	203197	C9orf91
A_23_P25816	NM_001302	NM_001302	NM_001302	Hs.412311	1325	CORT
A_23_P41232	NM_000579	NM_000579	NM_000579	Hs.450802	1234	CCR5
A_33_P33153	NM_175068	NM_175068	NM_175068	Hs.55410	319101	KRT73
A_33_P33575	NM_006598	NM_006598	NM_006598	Hs.172613	10723	SLC12A7
A_33_P33835	XM_0052615	XM_0052615	XM_0052615	Hs.505601	266629	SEC14L3
A_33_P32156	NM_153370	NM_153370	NM_153370	Hs.25391	221476	PI16
A_33_P33562	NM_0011659	NM_0011659	NM_0011659	Hs.728838	10948	STARD3
A_23_P15146	NM_0010126	NM_0010126	NM_0010126	Hs.943	9235	IL32
A_24_P91371	NM_145236	NM_145236	NM_145236	Hs.299329	93010	B3GNT7
A_24_P11968	NM_052843	NM_052843	NM_052843	Hs.656999	84033	OBSCN
A_33_P32989	NM_014207	NM_014207	NM_014207	Hs.58685	921	CD5
A_33_P33663	NM_0010244	NM_0010244	NM_0010244	Hs.97837	388228	SBK1
A_24_P36612	NM_024722	NM_024722	NM_024722	Hs.110298	79777	ACBD4

A_32_P11428	NM_0010795	NM_0010795	NM_0010795	Hs.604950	22807	IKZF2
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A_33_P33989	NM_017585	NM_017585	NM_017585	Hs.244378	11182	SLC2A6
A_32_P15896	NM_016523	NM_016523	NM_016523	Hs.183125	51348	KLRF1
A_24_P94529	NM_016079	NM_016079	NM_016079	Hs.591582	51652	CHMP3
A_24_P94339	NM_001620	NM_001620	NM_001620	Hs.502756	79026	AHNAK
A_23_P15337	NM_032855	NM_032855	NM_032855	Hs.631617	84941	HSH2D
A_23_P20573	NM_138576	NM_138576	NM_138576	Hs.709690	64919	BCL11B
A_23_P19510	NM_0011988	NM_0011988	NM_0011988	Hs.731563	3120	HLA-DQB2
A_33_P32898	NM_001804	NM_001804	NM_001804	Hs.1545	1044	CDX1
A_22_P00006	NR_002724	NR_002724	NA	Hs.733579	8512	MBL1P
A_22_P00008	NR_026971	NR_026971	NR_026971	Hs.592432	144571	A2M-AS1
A_33_P33237	NM_0012824	NM_0012824	NM_0012824	Hs.730678	10123	ARL4C
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A_33_P33419	NM_173808	NM_173808	NM_173808	Hs.146542	257194	NEGR1
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A_23_P21738	NM_003916	NM_003916	NM_003916	Hs.121592	8905	AP1S2
A_33_P33316	NM_0011456	NM_0011456	NM_0011456	Hs.239370	26086	GPSM1
A_21_P00005	NR_028483	NR_028483	NR_028483	Hs.632761	646023	ADORA2A-AS1
A_23_P43412	NM_018437	NM_018437	NM_018437	Hs.176626	55363	HEMGN
A_23_P42306	NM_006120	NM_006120	NM_006120	Hs.728759	3108	HLA-DMA
A_33_P33709	ENST000003	NA	NA	NA	3912	LAMB1
A_23_P14155	NM_013351	NM_013351	NM_013351	Hs.272409	30009	TBX21
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A_22_P00018	NR_024166	NR_024166	NR_024166	Hs.669490	81854	ZNF205-AS1
A_32_P44836	NR_049729	NR_049729	NR_049729	Hs.656564	339201	ASB16-AS1
A_33_P34743	NM_198277	NM_198277	NM_198277	Hs.352661	219855	SLC37A2
A_33_P34096	NM_005775	NM_005775	NM_005775	Hs.528572	10174	SORBS3
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A_23_P14150	NM_182906	NM_182906	NM_182906	Hs.54403	10462	CLEC10A
A_23_P25188	NM_147130	NM_147130	NM_147130	Hs.509513	259197	NCR3
A_33_P32474	NM_181624	NM_181624	NM_181624	Hs.553688	337963	KRTAP23-1
A_23_P2705	NM_005767	NM_005767	NM_005767	Hs.123464	10161	LPAR6
A_32_P20996	NM_000246	NM_000246	NM_000246	Hs.701991	4261	CIITA
A_23_P98565	NM_032597	NM_032597	NM_032597	Hs.709736	84689	MS4A14
A_22_P00011	ENST0000032	NA	AF086044	Hs.439682	5027	P2RX7
A_33_P32574	NM_018973	NM_018973	NM_018973	Hs.110477	54344	DPM3
A_33_P33019	NM_018571	NM_018571	NM_018571	Hs.652338	55437	STRADB
A_23_P87329	NM_024662	NM_024662	NM_024662	Hs.577281	55226	NAT10
A_22_P00007	NR_038287	NR_038287	NR_038287	Hs.654878	100507064	TEX26-AS1
A_23_P43157	NM_0010804	NM_0010804	NM_0010804	Hs.445898	4603	MYBL1
A_33_P32260	NM_207103	NM_207103	NM_207103	Hs.462080	388325	SCIMP
A_23_P64898	NM_005810	NM_005810	NM_005810	Hs.558446	10219	KLRG1
A_23_P20784	NM_0010248	NM_0010248	NM_0010248	Hs.654583	5914	RARA
A_24_P38352	NM_015589	NM_015589	NM_015589	Hs.98259	23034	SAMD4A
A_33_P33782	NM_0010016	NM_0010016	NM_0010016	Hs.526712	400935	IL17REL
A_33_P33817	NM_003253	NM_003253	NM_003253	Hs.517228	7074	TIAM1

A_33_P38189	NM_152486	NM_152486	NM_152486	Hs.335293	148398	SAMD11
A_23_P12684	NM_148965	NM_148965	NM_148965	Hs.462529	8718	TNFRSF25
A_23_P21485	NM_017933	NM_017933	NM_017933	Hs.745038	55022	PID1
A_23_P12982	NM_139280	NM_139280	NM_139280	Hs.514151	94103	ORMDL3
A_23_P83098	NM_000689	NM_000689	NM_000689	Hs.76392	216	ALDH1A1
A_33_P3358C	NM_181449	NM_181449	NM_181449	Hs.158954	342510	CD300E
A_33_P32809	NR_026971	NR_026971	NR_026971	Hs.592432	144571	A2M-AS1
A_23_P8452	NM_0010401	NM_0010401	NM_0010401	Hs.159142	3955	LFNG
A_23_P50043	NM_052813	NM_052813	NM_052813	Hs.694071	64170	CARD9
A_24_P50245	NM_006120	NM_006120	NM_006120	Hs.728759	3108	HLA-DMA
A_23_P2097C	NM_006056	NM_006056	NM_006056	Hs.471619	10316	NMUR1
A_23_P99642	NM_0011261	NM_0011261	NM_0011261	Hs.513147	9056	SLC7A7
A_23_P17045	NM_001900	NM_001900	NM_001900	Hs.121489	1473	CST5
A_22_P00000	NM_198576	NM_198576	NM_198576	Hs.273330	375790	AGRN
A_33_P33639	NM_0012842	NM_0012842	NM_0012842	Hs.196955	343413	FCRL6
A_24_P64407	NM_005519	NM_005519	NM_005519	Hs.444756	3167	HMX2
A_23_P34676	NM_198053	NM_198053	NM_198053	Hs.156445	919	CD247
A_24_P38439	NM_133452	NM_133452	NM_133452	Hs.744952	125950	RAVER1
A_32_P23086	NM_024519	NM_024519	NM_024519	Hs.152717	79567	FAM65A
A_24_P24203	NR_002184	NR_002184	NR_002184	Hs.534041	91695	RRP7B
A_33_P34166	NM_022834	NM_022834	NM_022834	Hs.449009	64856	VWA1
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A_22_P00008	NR_002798	NR_002798	NR_002798	Hs.636624	256236	NAPSB
A_23_P14142	NM_016428	NM_016428	NM_016428	Hs.130719	51225	ABI3
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A_24_P28883	NR_001435	NR_001435	NR_001435	Hs.665450	3116	HLA-DPB2
A_23_P1397C	NM_001946	NM_001946	NM_001946	Hs.298654	1848	DUSP6
A_23_P13768	NM_015441	NM_015441	NM_015441	Hs.507515	25903	OLFML2B
A_23_P98402	NM_0010404	NM_0010404	NM_0010404	Hs.712144	51092	SIDT2
A_23_P12339	NM_004519	NM_004519	NM_004519	Hs.374023	3786	KCNQ3
A_33_P33391	ENST0000051	NA	CA416988	Hs.584839	9533	POLR1C
A_23_P36024	NM_138768	NM_138768	NM_138768	Hs.523848	26579	MYEOV
A_23_P90679	NM_018571	NM_018571	NM_018571	Hs.652338	55437	STRADB
A_23_P82929	NM_002514	NM_002514	NM_002514	Hs.235935	4856	NOV
A_33_P33366	NM_004669	NM_004669	NM_004669	Hs.64746	9022	CLIC3
A_23_P39453	NM_203304	NM_203304	NM_203304	Hs.436495	399664	MEX3D
A_33_P34204	NM_0011615	NM_0011615	NM_0011615	Hs.671729	401387	LRRD1
A_33_P33946	NM_006339	NM_006339	NM_006339	Hs.406534	10362	HMG20B
A_23_P70095	NM_0010251	NM_0010251	NM_0010251	Hs.436568	972	CD74
A_23_P35114	NM_053282	NM_053282	NM_053282	Hs.350581	117157	SH2D1B
A_33_P32282	NM_000099	NM_000099	NM_000099	Hs.304682	1471	CST3
A_33_P33387	NM_004977	NM_004977	NM_004977	Hs.467146	3748	KCNC3
A_23_P49254	NM_005331	NM_005331	NM_005331	Hs.247921	3049	HBQ1
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A_33_P33312	ENST000003	NA	NA	NA	10146	G3BP1
A_33_P32434	NM_019858	NM_019858	NM_019858	Hs.631654	27239	GPR162
A_33_P33758	NR_002712	NR_002712	NR_002712	Hs.647858	3580	CXCR2P1
A_33_P33235	NM_000394	NM_000394	NM_000394	Hs.184085	1409	CRYAA

A_33_P3323(	ENST0000037	NA	NA	NA	4878	NPPA
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A_22_P00008	NR_002798	NR_002798	NR_002798	Hs.636624	256236	NAPSB
A_32_P73837	NR_026961	NR_026961	NR_026961	Hs.592159	284837	AATBC
A_24_P25615	NM_0011463	NM_0011463	NM_0011463	Hs.712041	390010	NKX1-2
A_23_P10866	NM_006302	NM_006302	NM_006302	Hs.516119	7841	MOGS
A_24_P37047	NM_021983	NM_021983	NM_021983	Hs.696211	3126	HLA-DRB4
A_24_P29559	NM_032023	NM_032023	NM_032023	Hs.522895	83937	RASSF4
A_21_P00146	NR_120438	NR_120438	NR_120438	NA	26628	OR7E47P
A_24_P2030(	NM_000878	NM_000878	NM_000878	Hs.474787	3560	IL2RB
A_33_P32826	NM_0012566	NM_0012566	NM_0012566	Hs.372640	441476	C9orf173
A_23_P13704	NM_022567	NM_022567	NM_022567	Hs.302019	60506	NYX
A_23_P20995	NM_006433	NM_006433	NM_006433	Hs.105806	10578	GNLY
A_33_P33494	NR_001552	NR_001552	NR_001552	Hs.522848	252948	TTTY16
A_33_P34242	NM_0012439	NM_0012439	NM_0012439	Hs.409934	3119	HLA-DQB1
A_33_P33144	NM_0011633	NM_0011633	NM_0011633	Hs.657225	64839	FBXL17
A_22_P00002	NR_033339	NR_033339	NR_033339	Hs.561314	92070	CTBP1-AS2
A_33_P33643	ENST000005(	NA	BC040551	NA	146183	OTOA
A_23_P53081	NM_020896	NM_020896	NM_020896	Hs.436166	114879	OSBPL5
A_23_P1546(	NM_018837	NM_018837	NM_018837	Hs.162016	55959	SULF2
A_33_P38777	AI821758	NA	AI821758	Hs.369680	140768	SMCR2
A_23_P15923	NM_005293	NM_005293	NM_005293	Hs.188859	2843	GPR20
A_33_P33647	NM_006039	NM_006039	NM_006039	Hs.7835	9902	MRC2
A_23_P13434	NM_019029	NM_019029	NM_019029	Hs.233389	54504	CPVL
A_23_P32854	NM_014211	NM_014211	NM_014211	Hs.26225	2568	GABRP
A_23_P20075	NM_013389	NM_013389	NM_013389	Hs.567486	29881	NPC1L1
A_19_P00812	NR_034160	NR_034160	NR_034160	Hs.662365	100499227	USP2-AS1
A_33_P32352	NM_032213	NM_032213	NM_032213	Hs.269990	84173	ELMOD3
A_33_P32122	NM_0010393	NM_0010393	NM_0010393	Hs.744920	219972	MPEG1
A_23_P52986	NM_152718	NM_152718	NM_152718	Hs.60640	220001	VWCE
A_33_P33804	NM_022049	NM_022049	NM_022049	Hs.170053	54112	GPR88
A_33_P38355	NM_0012070	NM_0012070	NM_0012070	Hs.147381	5452	POU2F2
A_33_P33839	NM_022555	NM_022555	NM_022555	Hs.696211	3125	HLA-DRB3
A_23_P5028(	NM_178013	NM_178013	NM_178013	Hs.432401	145270	PRIMA1
A_33_P32716	NM_002121	NM_002121	NM_002121	Hs.485130	3115	HLA-DPB1
A_24_P16644	NM_002121	NM_002121	NM_002121	Hs.485130	3115	HLA-DPB1
A_23_P8108	NM_0012439	NM_0012439	NM_0012439	Hs.409934	3119	HLA-DQB1
A_32_P87697	NM_019111	NM_019111	NM_019111	Hs.520048	3122	HLA-DRA
A_33_P3332(	NM_006682	NM_006682	NM_006682	Hs.520989	10875	FGL2
A_24_P76671	NM_0011423	NM_0011423	NM_0011423	Hs.197143	1240	CMKLR1
A_33_P32886	NM_018951	NM_018951	NM_018951	Hs.110637	3206	HOXA10
A_33_P33295	NM_0011050	NM_0011050	NM_0011050	Hs.247186	64319	FBRS
A_22_P00007	NM_0012439	NM_0012439	NM_0012439	Hs.409934	3119	HLA-DQB1
A_33_P32716	NM_002121	NM_002121	NM_002121	Hs.485130	3115	HLA-DPB1
A_24_P16907	NM_182623	NM_182623	NM_182623	Hs.126825	348487	FAM131C
A_33_P32155	NM_018125	NM_018125	NM_018125	Hs.443460	55160	ARHGEF10L
A_33_P33372	NR_033266	NR_033266	NR_033266	Hs.572592	375690	WASH5P
A_23_P30199	NM_173083	NM_173083	NM_173083	Hs.120817	286826	LIN9

A_33_P32981	NM_000954	NM_000954	NM_000954	Hs.446429	5730	PTGDS
A_24_P70888	NM_012401	NM_012401	NM_012401	Hs.3989	23654	PLXNB2
A_23_P23839	NM_0010174	NM_0010174	NM_0010174	Hs.497402	59352	LGR6
A_33_P33592	NM_0012566	NM_0012566	NM_0012566	Hs.372640	441476	C9orf173
A_32_P51634	NM_182608	NM_182608	NM_182608	Hs.433492	341405	ANKRD33
A_33_P33060	NM_0010330	NM_0010330	NM_0010330	Hs.437922	4610	MYCL
A_33_P34242	NM_002123	NM_002123	NM_002123	Hs.409934	3119	HLA-DQB1
A_33_P32221	NM_0010052	NM_0010052	NM_0010052	Hs.592123	6720	SREBF1
A_23_P45099	NM_002125	NM_002125	NM_002125	Hs.534322	3127	HLA-DRB5
A_23_P11676	NM_002289	NM_002289	NM_002289	Hs.72938	3906	LALBA
A_21_P00022	ENST000005	NA	NA	Hs.48589	7771	ZNF112
A_33_P34057	ENST000003	NA	BC050721	Hs.509017	9731	CEP104
A_33_P33359	NM_182961	NM_182961	NM_182961	Hs.12967	23345	SYNE1
A_33_P33426	NM_021170	NM_021170	NM_021170	Hs.154029	57801	HES4
A_33_P32965	NM_013318	NM_013318	NM_013318	Hs.743955	84726	PRRC2B
A_32_P35196	NM_002118	NM_002118	NM_002118	Hs.351279	3109	HLA-DMB
A_33_P33576	NM_198699	NM_198699	NM_198699	Hs.297526	386685	KRTAP10-12
A_24_P34323	NM_002124	NM_002124	NM_002124	Hs.696211	3123	HLA-DRB1
A_33_P32342	NM_0012425	NM_0012425	NM_0012425	Hs.347270	3113	HLA-DPA1
A_33_P34054	NM_152899	NM_152899	NM_152899	Hs.741750	259307	IL4I1
A_33_P33033	ENST000006	NA	NA	NA	644353	ZCCHC18
A_23_P25479	NM_025227	NM_025227	NM_025227	Hs.257045	80341	BPIFB2
A_23_P12153	NM_012445	NM_012445	NM_012445	Hs.635350	10417	SPON2
A_33_P32626	NM_0012822	NM_0012822	NM_0012822	Hs.170310	51816	CECR1
A_23_P13668	NM_0012439	NM_0012439	NM_0012439	Hs.409934	3119	HLA-DQB1
A_22_P00014	NR_046654	NR_046654	NR_046654	NA	100874007	VIPR1-AS1
A_23_P40037	NM_0010771	NM_0010771	NM_0010771	Hs.160954	151306	GPBAR1
A_23_P11738	NM_138344	NM_138344	NM_138344	Hs.525550	90050	FAM181A
A_33_P32797	ENST000006	NA	NA	NA	10139	ARFRP1
A_23_P25876	NM_002121	NM_002121	NM_002121	Hs.485130	3115	HLA-DPB1
A_24_P15356	NM_0010393	NM_0010393	NM_0010393	Hs.744920	219972	MPEG1
A_23_P30913	NM_033554	NM_033554	NM_033554	Hs.347270	3113	HLA-DPA1
A_23_P20628	NM_201525	NM_201525	NM_201525	Hs.513633	9289	GPR56
A_23_P13213	NM_0012864	NM_0012864	NM_0012864	Hs.236572	54058	C21orf58
A_22_P00007	NR_126467	NR_126467	NR_126467	Hs.633621	102724826	ZNF337-AS1
A_33_P32164	NM_0011637	NM_0011637	NM_0011637	Hs.390171	1302	COL11A2
A_21_P00109	NR_111968	NR_111968	NA	Hs.615912	414212	GLUD1P7
A_19_P00322	ENST000005	NA	AK307375	Hs.369632	55769	ZNF83
A_33_P33520	NM_021201	NM_021201	NM_021201	Hs.530735	58475	MS4A7
A_23_P40756	NM_001337	NM_001337	NM_001337	Hs.78913	1524	CX3CR1
A_33_P37999	NM_018125	NM_018125	NM_018125	Hs.443460	55160	ARHGEF10L
A_21_P00027	NR_109996	NR_109996	NR_109996	Hs.634259	100506637	PRKAR2A-AS1
A_23_P15632	NM_000358	NM_000358	NM_000358	Hs.369397	7045	TGFBI
A_23_P11079	NM_005211	NM_005211	NM_005211	Hs.586219	1436	CSF1R
A_23_P12090	NM_006498	NM_006498	NM_006498	Hs.531776	3957	LGALS2
A_23_P42812	NM_000076	NM_000076	NM_000076	Hs.106070	1028	CDKN1C

GeneName	EnsemblID	Description	SystematicNa	logFC	P.Value	adj.P.Val
CD177 molec	ENST0000061	Homo sapiens	NM_020406	3.54347827	4.62E-13	2.99E-10
olfactomedin	ENST0000021	Homo sapiens	NM_006418	2.43039741	1.74E-07	7.33E-06
resistin	ENST0000022	Homo sapiens	NM_020415	2.32249341	2.98E-11	8.41E-09
haptoglobin	ENST0000056	Homo sapiens	NM_005143	2.225845	8.07E-11	1.73E-08
resistin	ENST0000022	Homo sapiens	NM_020415	2.17897115	6.52E-11	1.44E-08
mast cell-expr	ENST0000033	Homo sapiens	NM_174918	2.16739084	7.92E-15	2.24E-11
defensin, alph	ENST0000029	Homo sapiens	NM_001925	1.98882097	5.56E-05	0.00071495
elastase, neut	ENST0000026	Homo sapiens	NM_001972	1.9845666	1.06E-06	3.02E-05
myeloperoxid	ENST0000022	Homo sapiens	NM_000250	1.98286272	2.66E-09	2.55E-07
haptoglobin-r	ENST0000035	Homo sapiens	NM_020995	1.98038426	1.44E-10	2.71E-08
lipocalin 2	ENST0000037	Homo sapiens	NM_005564	1.93869422	2.29E-07	9.03E-06
S100 calcium	ENST0000036	Homo sapiens	NM_005621	1.89208612	2.11E-13	1.93E-10
arginase 1	ENST0000035	Homo sapiens	NM_0012444	1.87995816	3.46E-08	2.06E-06
lactotransferr	ENST0000042	Homo sapiens	NM_002343	1.8658587	1.15E-05	0.00020574
defensin, alph	ENST0000061	Homo sapiens	NM_005217	1.86351408	8.53E-07	2.53E-05
arginase 1	ENST0000035	Homo sapiens	NM_0012444	1.86220289	4.72E-08	2.64E-06
carcinoembry	ENST0000024	Homo sapiens	NM_001816	1.85973793	2.66E-06	6.50E-05
cathepsin G	ENST0000021	Homo sapiens	NM_001911	1.85523329	6.15E-05	0.00077261
S100 calcium	ENST0000036	Homo sapiens	NM_005621	1.82015258	9.37E-14	1.04E-10
vanin 1	ENST0000036	Homo sapiens	NM_004666	1.76104247	2.06E-10	3.49E-08
bactericidal/p	ENST0000026	Homo sapiens	NM_001725	1.74607892	4.21E-08	2.41E-06
matrix metall	ENST0000037	Homo sapiens	NM_004994	1.68475347	1.09E-08	8.32E-07
interleukin 1 r	ENST0000045	Homo sapiens	NM_004633	1.65272339	4.02E-07	1.42E-05
polypeptide N	ENST0000034	Homo sapiens	NM_024572	1.64327304	1.44E-10	2.71E-08
secretory leuk	ENST0000033	Homo sapiens	NM_003064	1.58578026	1.77E-07	7.47E-06
tudor domain	ENST0000055	Homo sapiens	NM_153046	1.58162724	2.84E-14	5.15E-11
carbonic anhy	ENST000003C	Homo sapiens	NM_000717	1.55183245	1.64E-10	2.95E-08
S100 calcium	ENST0000029	Homo sapiens	NM_005980	1.51559106	5.77E-07	1.89E-05
annexin A3	ENST000005C	Homo sapiens	NM_005139	1.5047062	1.03E-09	1.21E-07
peptidoglycar	ENST000000C	Homo sapiens	NM_005091	1.47436833	3.48E-07	1.26E-05
integrin, alpha	ENST0000045	Homo sapiens	NM_002206	1.43774962	2.36E-11	7.06E-09
C-type lectin d	ENST0000034	Homo sapiens	NM_016509	1.42577082	3.86E-09	3.53E-07
G protein-cou	ENST0000055	Homo sapiens	NM_020370	1.4094826	7.49E-10	9.11E-08
thioredoxin d	ENST0000043	Homo sapiens	NM_030810	1.40790448	0.000411	0.00341926
interleukin 18	ENST0000033	Homo sapiens	NM_003855	1.39276321	6.97E-08	3.59E-06
suppressor of	ENST0000033	Homo sapiens	NM_003955	1.37602	9.70E-10	1.15E-07
ubiquitin carb	ENST0000047	Homo sapiens	NM_004181	1.37168628	2.67E-09	2.56E-07
CD24 molecul	ENST000006C	Homo sapiens	NM_013230	1.3708844	4.26E-06	9.30E-05
growth factor	ENST000004C	Homo sapiens	NM_0010015	1.36885903	2.73E-07	1.04E-05
CDK5 regulato	ENST0000048	Homo sapiens	NM_018249	1.36550888	6.11E-11	1.37E-08
procollagen C	ENST0000047	Homo sapiens	NM_013363	1.35540572	2.27E-08	1.45E-06
C-type lectin d	ENST0000034	Homo sapiens	NM_016509	1.34941268	3.30E-09	3.05E-07
interleukin 18	ENST0000041	Homo sapiens	NM_003855	1.34556218	5.30E-08	2.87E-06
growth factor	ENST000004C	Homo sapiens	NM_0010015	1.3395837	4.13E-09	3.66E-07
transcobalam	ENST0000025	Homo sapiens	NM_001062	1.33765429	2.21E-07	8.79E-06
trefoil factor 3	ENST0000029	Homo sapiens	NM_003226	1.33617716	7.35E-07	2.27E-05
alkaline phosp	ENST0000037	Homo sapiens	NM_000478	1.3324678	7.29E-08	3.71E-06

marginal zone	ENST000005C	Homo sapiens	NM_016459	1.32352741	0.00061356	0.00472454
azurocidin 1	ENST0000062	Homo sapiens	NM_001700	1.32023218	0.00023956	0.00223844
orosomucoid	ENST0000047	Homo sapiens	NM_000607	1.31320795	4.11E-06	9.03E-05
cystatin F (leu	ENST0000048	Homo sapiens	NM_003650	1.31092573	5.67E-10	7.52E-08
BMX non-rece	ENST0000034	Homo sapiens	NM_001721	1.30641795	3.34E-10	4.89E-08
thioredoxin	ENST0000048	Homo sapiens	NM_003329	1.30273027	1.22E-19	3.77E-15
matrix metall	ENST0000052	Homo sapiens	NM_002424	1.30229301	1.42E-07	6.26E-06
histone cluste	ENST0000036	Homo sapiens	NM_0010054	1.29989154	6.40E-07	2.04E-05
growth arrest	ENST0000037	Homo sapiens	NM_001924	1.2972038	3.91E-10	5.67E-08
C-type lectin d	ENST0000034	Homo sapiens	NM_016509	1.29417154	4.13E-09	3.66E-07
bactericidal/p	ENST0000048	Homo sapiens	NM_001725	1.29298292	1.62E-07	6.94E-06
proteinase 3	ENST0000023	Homo sapiens	NM_002777	1.28634445	1.48E-06	3.97E-05
interleukin 18	ENST000004C	Homo sapiens	NM_003855	1.28125146	7.40E-07	2.28E-05
gamma-glutar	ENST0000026	Homo sapiens	NM_003878	1.26902224	1.03E-11	3.56E-09
immunoglobu	ENST0000054	Homo sapiens	NM_144646	1.25737546	0.0004028	0.00336827
glycogenin 1	ENST0000029	Homo sapiens	NM_004130	1.22796723	2.61E-13	2.08E-10
glycogenin 1	ENST0000034	Homo sapiens	NM_004130	1.22340903	9.79E-11	1.99E-08
cysteine-rich t	ENST0000026	Homo sapiens	NM_032412	1.223337	9.15E-09	7.20E-07
solute carrier	ENST0000047	Homo sapiens	NM_152672	1.21766596	3.46E-08	2.06E-06
ral guanine nu	ENST0000061	Homo sapiens	NM_153615	1.19216488	2.29E-08	1.46E-06
CDK5 regulato	ENST0000048	Homo sapiens	NM_018249	1.19035126	2.98E-10	4.49E-08
orosomucoid	ENST0000043	Homo sapiens	NM_000608	1.17591213	1.15E-05	0.00020627
exosome com	ENST0000031	Homo sapiens	NM_019037	1.1749967	3.64E-12	1.55E-09
oleoyl-ACP hy	ENST0000037	Homo sapiens	NM_0010397	1.17306489	3.21E-06	7.51E-05
kringle contai	ENST000004C	Homo sapiens	NM_0010395	1.16910302	2.34E-07	9.20E-06
CKLF-like MAF	ENST0000055	Homo sapiens	NM_0010372	1.16454825	5.96E-07	1.93E-05
trefoil factor 3	ENST0000051	Homo sapiens	NM_003226	1.16153438	2.44E-07	9.48E-06
ubiquinol-cyt	ENST0000052	Homo sapiens	NM_006294	1.15876809	4.40E-09	3.84E-07
pyrroline-5-ca	ENST0000061	Homo sapiens	NM_006907	1.14830008	1.52E-08	1.06E-06
dachshund fa	ENST0000061	Homo sapiens	NM_080759	1.14491636	4.85E-11	1.17E-08
BMP and activ	ENST0000037	Homo sapiens	NM_012342	1.14337352	4.78E-10	6.56E-08
UDP-glucose d	ENST0000047	Homo sapiens	NM_003358	1.14070407	8.16E-09	6.54E-07
B-cell CLL/lym	ENST0000041	Homo sapiens	NM_0011308	1.13913851	3.01E-10	4.49E-08
5-oxoprolinas	ENST0000061	Homo sapiens	NM_017570	1.13467896	6.27E-08	3.31E-06
histone cluste	ENST0000034	Homo sapiens	NM_005319	1.1337454	3.07E-10	4.56E-08
chitinase 1 (ch	ENST0000048	Homo sapiens	NM_003465	1.13303801	4.89E-07	1.66E-05
coiled-coil-he	ENST0000052	Homo sapiens	NM_0010116	1.12954454	2.57E-15	1.14E-11
defensin, alph	ENST0000045	Homo sapiens	NR_073407	1.12772456	0.00021615	0.00205693
SUB1 homolo	ENST0000051	Homo sapiens	NM_006713	1.11782893	7.42E-10	9.09E-08
ribonuclease,	NA	Homo sapiens	NR_033909	1.11695874	4.84E-09	4.17E-07
cytochrome P	ENST0000061	Homo sapiens	NM_000104	1.11399623	2.85E-08	1.77E-06
uridine phosp	ENST0000041	Homo sapiens	NM_0012874	1.10791133	1.56E-10	2.86E-08
ribonuclease,	ENST000003C	Homo sapiens	NM_002934	1.1036837	1.14E-07	5.23E-06
baculoviral IA	ENST000003C	Homo sapiens	NM_0010122	1.10350917	1.05E-06	3.01E-05
cyclin B2	ENST0000062	Homo sapiens	NM_004701	1.0914833	1.81E-06	4.69E-05
carcinoembry	ENST0000019	Homo sapiens	NM_002483	1.08391297	0.00018671	0.00183644
ATPase, class I	ENST0000033	Homo sapiens	NM_006045	1.06598031	2.30E-09	2.28E-07
solute carrier	ENST0000037	Homo sapiens	NM_003039	1.06438751	6.13E-06	0.00012536

toll-like recep	ENST0000036	Homo sapiens	NM_003268	1.06382075	3.09E-10	4.57E-08
6-phosphofru	ENST0000037	Homo sapiens	NM_004566	1.05842482	1.06E-07	4.98E-06
histone cluste	ENST0000035	Homo sapiens	NM_003509	1.05060645	2.37E-10	3.88E-08
histone cluste	ENST0000037	Homo sapiens	NM_021063	1.04570646	2.59E-13	2.08E-10
family with se	ENST0000037	Homo sapiens	NM_017565	1.0439375	3.98E-05	0.00055072
regulator of G	ENST0000036	Homo sapiens	NM_002928	1.04103299	1.73E-12	8.52E-10
ubiquitin-con	ENST0000061	Homo sapiens	NM_181801	1.03973123	1.82E-10	3.18E-08
cell division c	ENST0000027	Homo sapiens	NM_080668	1.03544211	4.26E-07	1.49E-05
histone cluste	ENST0000037	Homo sapiens	NM_003525	1.03515103	1.46E-13	1.46E-10
CD177 molec	ENST0000061	Homo sapiens	NM_020406	1.03327697	4.14E-08	2.38E-06
CCAAT/enhan	ENST000002C	Homo sapiens	NM_001805	1.03201563	4.06E-06	8.94E-05
SAM domain,	ENST0000061	Homo sapiens	NM_022136	1.02717483	2.59E-07	9.99E-06
NAD(P)H dehy	ENST0000042	Homo sapiens	NM_000904	1.02700293	3.28E-10	4.83E-08
histone cluste	ENST0000062	Homo sapiens	NM_003521	1.02602514	5.10E-12	1.93E-09
MRVI1 antiser	NA	Homo sapiens	NR_034094	1.01861713	3.16E-11	8.67E-09
pro-platelet b	ENST0000029	Homo sapiens	NM_002704	1.01795162	2.83E-05	0.00042022
histone cluste	ENST0000035	Homo sapiens	NM_021064	1.01160961	6.56E-08	3.44E-06
cytochrome P	ENST0000061	Homo sapiens	NM_000104	1.0106387	2.90E-06	6.92E-05
cystathionine	ENST0000061	Homo sapiens	NM_000071	1.00863393	1.42E-05	0.00024348
chitinase 1 (cl	ENST0000049	Homo sapiens	NM_003465	1.00732939	3.64E-07	1.31E-05
basic leucine z	ENST0000028	Homo sapiens	NM_006399	1.00436327	5.79E-14	7.52E-11
histone cluste	ENST0000035	Homo sapiens	NM_080593	0.99305121	1.12E-13	1.20E-10
histone cluste	NA	Homo sapiens	NM_003524	0.99149742	3.56E-13	2.51E-10
fibroblast gro	ENST0000044	Homo sapiens	NM_004114	0.9889459	2.33E-07	9.17E-06
ST3GAL4 antis	NA	Homo sapiens	NR_033839	0.98890591	1.07E-07	4.98E-06
histone cluste	ENST0000037	Homo sapiens	NM_003519	0.98432036	3.77E-13	2.55E-10
histone cluste	NA	Homo sapiens	NM_080593	0.98266692	5.51E-12	2.04E-09
phosphoglyce	ENST0000036	Homo sapiens	NM_006623	0.98227765	4.13E-09	3.66E-07
histone cluste	ENST0000061	Homo sapiens	NM_021062	0.97498688	1.75E-13	1.64E-10
dimethylargin	ENST0000037	Homo sapiens	NM_013974	0.9744418	6.59E-10	8.39E-08
histone cluste	NA	Homo sapiens	NM_003527	0.96676731	8.90E-13	5.02E-10
7-dehydrocho	ENST0000035	Homo sapiens	NM_001360	0.96635192	1.57E-10	2.86E-08
uridine phosp	ENST0000045	Homo sapiens	NM_0012874	0.96519587	5.20E-11	1.21E-08
lysosomal pro	ENST0000061	Homo sapiens	NM_018407	0.96409203	4.09E-10	5.82E-08
BCL2-related p	ENST0000026	Homo sapiens	NM_004049	0.96150239	1.22E-06	3.39E-05
Fc fragment of	ENST0000061	Homo sapiens	NM_133271	0.96025396	3.01E-10	4.49E-08
myosin, light c	ENST0000034	Homo sapiens	NM_181526	0.96004862	8.49E-05	0.00098769
copine V	ENST0000024	Homo sapiens	NM_020939	0.95709164	6.28E-07	2.01E-05
lin-7 homolog	ENST0000026	Homo sapiens	NM_004664	0.95705252	3.04E-11	8.41E-09
ureidopropion	ENST0000032	Homo sapiens	NM_016327	0.9568816	3.59E-11	9.52E-09
phosphoglucc	ENST0000049	Homo sapiens	NM_002631	0.95455322	2.48E-10	3.94E-08
small integral	ENST0000044	Homo sapiens	NM_0011637	0.95263545	0.00090343	0.00643012
ATP synthase,	ENST0000051	Homo sapiens	NM_007100	0.95231854	7.26E-11	1.58E-08
S100 calcium	ENST0000036	Homo sapiens	NM_002964	0.95086778	1.02E-08	7.89E-07
histone cluste	ENST0000033	Homo sapiens	NM_005322	0.94958394	2.50E-06	6.14E-05
dual specificit	ENST000006C	Homo sapiens	NM_0010072	0.9493468	1.02E-05	0.00018696
histone cluste	ENST0000054	Homo sapiens	NM_003518	0.94110663	6.32E-14	7.63E-11
prokineticin 2	ENST0000035	Homo sapiens	NM_021935	0.94097042	2.38E-05	0.0003686

histone cluste	NA	Homo sapiens	BC010926	0.93644602	3.20E-07	1.19E-05
complement (	ENST000004(	Homo sapiens	NM_000651	0.93447841	5.43E-10	7.30E-08
high mobility	ENST0000051	Homo sapiens	NM_002129	0.93330309	1.13E-07	5.19E-06
ubiquinol-cyt	ENST0000048	Homo sapiens	NM_006004	0.93043375	4.84E-11	1.17E-08
aspartate beta	ENST0000051	Homo sapiens	NM_032467	0.9260049	2.28E-06	5.69E-05
CYP1B1 antise	NA	Homo sapiens	NR_027252	0.92406269	1.98E-07	8.11E-06
phosphorylas	ENST0000021	Homo sapiens	NM_002863	0.91984636	6.05E-08	3.22E-06
ATPase, H+ tra	ENST0000051	Homo sapiens	NM_001695	0.91949127	7.17E-11	1.58E-08
pituitary tum	ENST0000052	Homo sapiens	NM_004219	0.91840077	7.47E-07	2.29E-05
ankyrin repeat	ENST0000055	Homo sapiens	NM_152326	0.91773447	0.00018323	0.00180967
lectin, galactc	ENST0000023	Homo sapiens	NM_014181	0.91754638	3.86E-09	3.53E-07
glycoprotein I	ENST000003(	Homo sapiens	NM_000407	0.91533184	4.03E-05	0.00055587
HRAS-like sup	ENST0000025	Homo sapiens	NM_017878	0.91529398	2.65E-05	0.00040035
interleukin-1	ENST000002(	Homo sapiens	NM_007199	0.91504084	8.91E-08	4.35E-06
histone cluste	NA	Homo sapiens	NM_003539	0.91214672	1.37E-09	1.50E-07
cystatin A (ste	ENST000002(	Homo sapiens	NM_005213	0.91177421	5.61E-08	3.00E-06
integrin, alpha	ENST000002(	Homo sapiens	NM_000419	0.90569901	1.89E-05	0.0003079
sterile alpha m	ENST000005(	Homo sapiens	NM_174920	0.90023946	2.18E-07	8.71E-06
histone cluste	ENST0000062	Homo sapiens	NM_003537	0.89600735	2.41E-07	9.38E-06
SPOC domain	ENST0000047	Homo sapiens	NM_144569	0.89444267	1.70E-05	0.00028287
G protein-cou	ENST000005(	Homo sapiens	NM_170776	0.89415486	1.17E-06	3.28E-05
serpin peptida	ENST000004(	Homo sapiens	NM_030666	0.89371567	1.00E-07	4.78E-06
NOP2/Sun do	ENST0000038	Homo sapiens	NM_024677	0.89181989	1.56E-07	6.71E-06
hydroxy-delta	ENST000002(	Homo sapiens	NM_0011427	0.88728489	8.73E-11	1.82E-08
C-type lectin d	ENST0000038	Homo sapiens	NM_080387	0.88607277	9.70E-06	0.00018041
cyclin B1	ENST0000025	Homo sapiens	NM_031966	0.88507565	8.80E-07	2.59E-05
mitochondria	ENST0000039	Homo sapiens	NM_020409	0.88472021	5.73E-11	1.32E-08
NADH dehydr	ENST0000037	Homo sapiens	NM_004552	0.88054442	1.32E-09	1.47E-07
NADH dehydr	ENST0000043	Homo sapiens	NM_0012571	0.87723968	8.42E-13	4.84E-10
tumor necrosi	ENST0000005	Homo sapiens	NM_001192	0.8770331	0.00054923	0.00432032
mitogen-activ	ENST0000047	Homo sapiens	NM_139013	0.87246844	2.32E-09	2.29E-07
folate recepto	ENST0000062	Homo sapiens	NM_000804	0.87173574	0.000671	0.00508358
ATP-binding c	ENST0000044	Homo sapiens	NM_005689	0.86746706	8.93E-15	2.31E-11
uncharacteriz	ENST0000043	NA	ENST0000043	0.86664252	8.41E-09	6.69E-07
family with se	ENST0000037	Homo sapiens	NR_027421	0.86579051	1.36E-07	6.06E-06
NADH dehydr	ENST0000037	Homo sapiens	NM_004541	0.85998934	4.01E-12	1.62E-09
high mobility	ENST0000039	Homo sapiens	NR_002165	0.85709051	7.60E-09	6.18E-07
Fc fragment of	ENST0000046	Homo sapiens	NM_0010179	0.85679089	4.66E-05	0.00062475
ubiquitin-con	ENST000003(	Homo sapiens	NM_014176	0.85649494	1.14E-07	5.26E-06
ring finger pro	NA	Homo sapiens	BC016958	0.85586495	1.38E-06	3.77E-05
6-phosphofru	ENST000003(	Homo sapiens	NM_0010180	0.85571187	5.77E-05	0.00073681
solute carrier	ENST0000043	Homo sapiens	NM_0012862	0.84978914	7.27E-09	5.95E-07
solute carrier	ENST0000047	Homo sapiens	NM_207113	0.84950587	2.46E-07	9.55E-06
v-myb avian m	ENST0000039	Homo sapiens	NM_002466	0.84734541	1.58E-09	1.69E-07
v-maf avian m	ENST0000039	Homo sapiens	NM_032711	0.84542419	6.28E-16	3.90E-12
SEC11 homol	ENST0000029	Homo sapiens	NM_033280	0.84421743	0.00028965	0.00260305
arachidonate	ENST0000061	Homo sapiens	NM_001629	0.84332861	1.36E-08	9.71E-07
aspartate beta	ENST0000054	Homo sapiens	NM_004318	0.84092732	1.22E-06	3.38E-05

integrin, beta	ENST0000055	Homo sapiens	NM_000212	0.8357383	0.00039991	0.0033504
histone cluste	ENST0000039	Homo sapiens	NM_003526	0.83537276	1.67E-12	8.35E-10
ubiquinol-cyt	ENST0000049	Homo sapiens	NM_0012975	0.83505537	6.68E-09	5.50E-07
family with se	ENST0000049	Homo sapiens	NM_198552	0.83455286	5.18E-10	7.03E-08
triggering rec	ENST0000043	Homo sapiens	NM_178174	0.83437002	0.00025168	0.00232654
monoamine o	ENST0000033	Homo sapiens	NM_0012704	0.83402823	0.00099542	0.00694305
Opa interactir	ENST0000022	Homo sapiens	NM_007280	0.83335121	3.11E-07	1.17E-05
leucine-rich al	ENST000003C	Homo sapiens	NM_052972	0.83118659	7.79E-07	2.37E-05
thymidine kin	ENST000003C	Homo sapiens	NM_003258	0.82897892	0.00015936	0.00161554
flotillin 1	ENST0000037	Homo sapiens	NM_005803	0.82763824	2.40E-11	7.10E-09
tyrosylproteir	ENST000004C	Homo sapiens	NM_0010085	0.82733641	2.41E-16	2.87E-12
ring finger prc	ENST0000039	Homo sapiens	NM_031297	0.82681972	4.16E-06	9.13E-05
caspase recrui	ENST0000037	Homo sapiens	NM_0010072	0.82497554	4.07E-07	1.44E-05
aquaporin 10	ENST0000048	Homo sapiens	NM_080429	0.82474631	0.00078877	0.0057756
thymidylate s	ENST0000058	Homo sapiens	NM_001071	0.82450607	0.00024829	0.0023014
kinesin family	ENST0000037	Homo sapiens	NM_006845	0.82435069	1.08E-05	0.00019668
sulfotransfera	ENST0000031	Homo sapiens	NM_014465	0.82234386	2.46E-09	2.40E-07
G protein-cou	ENST0000035	Homo sapiens	NM_014373	0.81751538	7.46E-07	2.29E-05
histone cluste	NA	Homo sapiens	NM_003514	0.81716853	4.41E-08	2.50E-06
BCL2-interact	ENST0000021	Homo sapiens	NM_001197	0.81600188	6.26E-13	3.88E-10
lactate dehyd	ENST0000037	Homo sapiens	NM_005566	0.81520748	3.98E-09	3.61E-07
hexokinase 3 (	ENST0000029	Homo sapiens	NM_002115	0.81507044	3.87E-07	1.38E-05
v-maf avian m	ENST0000035	Homo sapiens	NM_002359	0.81375061	2.85E-13	2.11E-10
Fc fragment of	ENST0000035	Homo sapiens	NM_002000	0.81040353	4.91E-07	1.66E-05
G0/G1 switch	ENST0000036	Homo sapiens	NM_015714	0.80917838	0.00056955	0.0044508
phosphoserin	ENST0000039	Homo sapiens	NM_004577	0.8089447	1.91E-05	0.00030991
peroxisomal t	ENST0000046	Homo sapiens	NM_018441	0.80741807	7.74E-12	2.76E-09
protein regula	ENST0000036	Homo sapiens	NM_003981	0.80409796	1.76E-08	1.18E-06
solute carrier	ENST0000046	Homo sapiens	NM_052961	0.80358247	7.65E-08	3.86E-06
methyltransfe	ENST0000061	Homo sapiens	NM_152637	0.80327679	1.13E-09	1.29E-07
BUB1 mitotic	ENST000003C	Homo sapiens	NM_004336	0.8031445	4.70E-07	1.61E-05
cyclin-depend	ENST0000044	Homo sapiens	NM_001786	0.80209925	8.22E-09	6.58E-07
prostaglandin	ENST0000022	Homo sapiens	NM_000962	0.8016514	2.43E-06	6.01E-05
serglycin	ENST0000046	Homo sapiens	NM_002727	0.79959803	6.38E-09	5.28E-07
Holliday junct	ENST0000043	Homo sapiens	NM_018410	0.79956417	1.51E-06	4.04E-05
solute carrier	ENST0000048	Homo sapiens	NM_006931	0.79955787	2.10E-08	1.36E-06
crystallin, mu	ENST0000021	Homo sapiens	NM_001888	0.79906182	3.27E-05	0.00047357
signal-induce	ENST000003C	Homo sapiens	NM_020808	0.79808398	3.90E-06	8.68E-05
syndecan 1	ENST0000038	Homo sapiens	NM_0010069	0.79715673	6.57E-07	2.08E-05
cytoskeleton-a	ENST0000037	Homo sapiens	NM_006825	0.7924803	4.29E-08	2.45E-06
histone cluste	NA	Homo sapiens	NM_003522	0.78897568	1.28E-08	9.23E-07
phosphoserin	ENST0000037	Homo sapiens	NM_058179	0.78682333	3.15E-07	1.17E-05
glycoprotein I	ENST0000043	Homo sapiens	NM_000407	0.7862127	0.00026571	0.00242869
COX17 cytoch	ENST0000046	Homo sapiens	NM_005694	0.78562625	3.80E-11	1.00E-08
zinc finger anc	ENST0000039	Homo sapiens	NM_014383	0.78543933	3.39E-05	0.00048638
solute carrier	ENST0000061	Homo sapiens	NM_020689	0.78406121	4.19E-07	1.47E-05
Fc fragment of	ENST0000057	Homo sapiens	NM_0012449	0.7837164	0.0001208	0.00129941
fatty acid binc	ENST0000052	Homo sapiens	NM_001444	0.78265139	1.82E-08	1.21E-06

adipocyte pla	ENST0000021	Homo sapiens	NM_020531	0.78165906	1.71E-07	7.23E-06
tripartite mot	ENST0000038	Homo sapiens	NM_032546	0.78137156	3.82E-07	1.36E-05
centromere p	ENST0000036	Homo sapiens	NM_0010125	0.78135037	2.05E-08	1.34E-06
chloride intra	ENST0000042	Homo sapiens	NM_013943	0.78086692	2.43E-12	1.16E-09
RAB20, memb	ENST0000026	Homo sapiens	NM_017817	0.77969711	4.50E-08	2.55E-06
KIAA0101	ENST000003C	Homo sapiens	NM_014736	0.77889095	0.00021045	0.00201209
inhibin, beta A	ENST0000044	Homo sapiens	NM_002192	0.77828657	1.66E-05	0.00027659
tubulin, alpha	ENST0000048	Homo sapiens	NM_006000	0.77795775	2.59E-09	2.50E-07
selectin P (gra	ENST0000046	Homo sapiens	NM_003005	0.77494427	2.78E-06	6.69E-05
ribosomal pro	ENST0000049	Homo sapiens	NM_0010996	0.77472879	5.62E-05	0.00072102
growth differe	ENST0000025	Homo sapiens	NM_004864	0.77453391	2.02E-05	0.00032286
ArfGAP with F	ENST000004C	Homo sapiens	NM_0011351	0.77448525	2.53E-08	1.59E-06
ACN9 homolo	ENST0000047	Homo sapiens	NM_020186	0.77413456	1.10E-08	8.35E-07
oncostatin M	ENST0000021	Homo sapiens	NM_020530	0.77367001	7.05E-05	0.00086318
sperm associa	ENST0000058	Homo sapiens	NM_006461	0.77305111	4.99E-07	1.68E-05
SRSF protein k	ENST0000037	Homo sapiens	NM_003137	0.7699544	3.19E-07	1.18E-05
histone cluste	ENST0000061	Homo sapiens	NM_003546	0.76907485	5.44E-12	2.03E-09
mitogen-activ	ENST0000059	Homo sapiens	NM_002758	0.76870362	1.43E-06	3.85E-05
arachidonate	ENST0000025	Homo sapiens	NM_000697	0.76861268	5.02E-05	0.0006617
histone acetyl	ENST0000049	Homo sapiens	NM_003642	0.76789793	1.82E-08	1.22E-06
EGF-like-doma	ENST000003C	Homo sapiens	NM_201446	0.76766527	3.51E-07	1.27E-05
histone cluste	ENST0000036	Homo sapiens	NM_003536	0.76755308	1.52E-11	4.92E-09
chromatin lic	ENST000003C	Homo sapiens	NM_030928	0.76732337	6.96E-06	0.00013882
ZW10 interact	ENST0000048	Homo sapiens	NM_032997	0.76725391	1.13E-05	0.00020358
gamma-glutar	ENST0000032	Homo sapiens	NM_0010997	0.76696558	1.73E-05	0.00028679
histone cluste	ENST0000061	Homo sapiens	NM_003539	0.76545939	6.68E-09	5.50E-07
chromosome	ENST0000062	Homo sapiens	NM_0011703	0.76460252	9.31E-11	1.91E-08
selectin P (gra	ENST0000026	Homo sapiens	NM_003005	0.76124507	5.18E-08	2.82E-06
RAB guanine n	ENST0000043	Homo sapiens	NM_014504	0.76118885	1.97E-10	3.35E-08
histone cluste	ENST000006C	Homo sapiens	NM_0010408	0.76096134	4.33E-06	9.41E-05
chromosome	ENST0000034	Homo sapiens	NM_207417	0.76094366	5.25E-05	0.00068598
ST6 (alpha-N-a	ENST0000062	Homo sapiens	NM_0011600	0.75951385	1.44E-08	1.01E-06
CD55 molecul	ENST0000048	Homo sapiens	NM_000574	0.75815363	1.94E-07	8.00E-06
SPC25, NDC80	ENST0000061	Homo sapiens	NM_020675	0.75689888	8.31E-08	4.13E-06
maltase-gluco	ENST0000062	Homo sapiens	NM_004668	0.75545956	7.39E-06	0.00014582
histone cluste	ENST0000061	Homo sapiens	NM_021018	0.75325585	1.62E-10	2.92E-08
cell division c	ENST0000052	Homo sapiens	NM_152562	0.7523208	9.02E-07	2.64E-05
histone cluste	ENST000003C	Homo sapiens	NM_005321	0.75040131	3.54E-07	1.28E-05
acyl-CoA synth	ENST0000028	Homo sapiens	NM_001995	0.75022491	5.47E-06	0.00011446
nucleobindin	ENST0000053	Homo sapiens	NM_005013	0.74957635	2.01E-07	8.17E-06
caspase recrui	ENST0000052	Homo sapiens	NM_0010175	0.74911471	6.96E-08	3.59E-06
geminin, DNA	ENST0000062	Homo sapiens	NM_015895	0.74892495	3.34E-07	1.22E-05
adenylate cycl	ENST000004C	Homo sapiens	NM_004036	0.7488722	2.33E-05	0.00036266
growth arrest	ENST0000025	Homo sapiens	NM_006705	0.74862913	5.42E-08	2.93E-06
leucine-rich si	ENST0000031	Homo sapiens	NM_182597	0.74806333	1.48E-06	3.97E-05
tropomyosin 4	ENST0000052	Homo sapiens	NM_003290	0.74781815	3.94E-12	1.62E-09
interleukin 4 r	ENST0000017	Homo sapiens	NM_000418	0.74699353	4.41E-06	9.54E-05
small nuclear	ENST000003C	Homo sapiens	NM_006938	0.74619667	3.79E-08	2.22E-06

protein-L-isoa	ENST0000048	Homo sapiens	NM_005389	0.7434955	5.81E-14	7.52E-11
ATP synthase,	ENST000004C	Homo sapiens	NM_0010037	0.7408222	4.56E-10	6.35E-08
carcinoembry	ENST000004C	Homo sapiens	NM_0011848	0.74081317	5.80E-05	0.00073971
PDS5 cohesin	ENST000003C	Homo sapiens	NM_0011003	0.74013469	2.81E-08	1.75E-06
lipoma HMGI(	ENST0000037	Homo sapiens	NM_005780	0.73971112	3.11E-09	2.94E-07
hepatocyte gr	ENST0000042	Homo sapiens	NM_0010109	0.73864809	2.46E-07	9.55E-06
lymphocyte a	ENST0000038	Homo sapiens	NM_0010036	0.73803872	0.00031315	0.00276687
brain abunda	ENST0000032	Homo sapiens	NM_006317	0.73516374	1.41E-06	3.82E-05
protein-L-isoa	ENST000003E	Homo sapiens	NM_005389	0.73411888	1.73E-13	1.64E-10
lactate dehyd	ENST0000039	Homo sapiens	NM_005566	0.7341154	1.07E-08	8.21E-07
5',3'-nucleotic	ENST0000061	Homo sapiens	NM_020201	0.73405084	0.00020865	0.00199974
multiple C2 d	ENST0000045	Homo sapiens	NM_018349	0.73404143	1.47E-08	1.03E-06
tubulin, gamn	ENST0000025	Homo sapiens	NM_001070	0.73360606	2.95E-08	1.82E-06
FK506 bindin	ENST0000061	Homo sapiens	NM_054014	0.7297361	1.39E-07	6.15E-06
endothelial P/	ENST000004E	Homo sapiens	NM_001430	0.72804731	2.30E-06	5.72E-05
chromobox h	ENST0000048	Homo sapiens	NM_016587	0.727812	7.95E-10	9.56E-08
B-cell CLL/lym	ENST000001E	Homo sapiens	NM_005178	0.72690877	3.23E-06	7.55E-05
coagulation fa	ENST0000025	Homo sapiens	NM_000505	0.72669539	1.62E-09	1.72E-07
leukocyte imn	ENST0000044	Homo sapiens	NM_181879	0.72628226	1.30E-05	0.00022693
peptidyl argin	ENST0000037	Homo sapiens	NM_012387	0.72533306	2.37E-06	5.88E-05
fatty acid binc	ENST0000048	Homo sapiens	NM_001444	0.72475727	1.33E-09	1.48E-07
diphthamide l	ENST000004E	Homo sapiens	NM_206831	0.72351471	1.07E-14	2.54E-11
histone cluste	ENST0000035	Homo sapiens	NM_003530	0.72341752	8.54E-10	1.02E-07
tumor proteir	ENST0000053	Homo sapiens	NM_0012583	0.72284878	3.73E-08	2.20E-06
S100 calcium	ENST000003E	Homo sapiens	NM_002965	0.72284799	3.44E-08	2.06E-06
calcium chan	ENST000003E	Homo sapiens	NM_0012052	0.72258851	1.53E-05	0.00025879
thromboxane	ENST0000037	Homo sapiens	NM_001060	0.7195467	8.05E-05	0.00094697
DnaJ (Hsp40) l	ENST0000049	Homo sapiens	NM_016306	0.71739439	1.03E-07	4.87E-06
FOS-like antig	ENST000002E	Homo sapiens	NM_005253	0.71507158	6.31E-08	3.33E-06
5,10-metheny	ENST0000047	Homo sapiens	NM_006441	0.71460037	7.91E-07	2.40E-05
transient rece	ENST0000062	Homo sapiens	NM_003307	0.71416289	1.26E-08	9.14E-07
histone cluste	ENST0000037	Homo sapiens	NM_003542	0.71157667	0.0001615	0.00163514
myosin, light	ENST0000054	Homo sapiens	NM_0011996	0.71001511	4.01E-10	5.76E-08
diazepam binc	ENST000004C	Homo sapiens	NM_0010798	0.70613849	1.23E-08	8.98E-07
MAX dimeriza	ENST0000042	Homo sapiens	NM_0011429	0.7054731	4.06E-09	3.66E-07
urotensin 2	ENST0000005	Homo sapiens	NM_021995	0.70278723	0.00121888	0.00812259
histone cluste	ENST0000035	Homo sapiens	NM_003514	0.7019322	1.75E-08	1.18E-06
GINS complex	ENST0000025	Homo sapiens	NM_016095	0.70068223	9.38E-06	0.00017589
trophinin assc	ENST0000025	Homo sapiens	NM_005480	0.69881556	3.00E-08	1.83E-06
peptidyl argin	ENST0000037	Homo sapiens	NM_007365	0.69686284	1.12E-05	0.00020271
multiple C2 d	ENST0000045	Homo sapiens	NM_018349	0.69661658	4.43E-08	2.51E-06
CD63 molecul	ENST0000055	Homo sapiens	NM_0012573	0.69650462	3.13E-09	2.95E-07
X inactive spe	ENST0000044	Homo sapiens	NR_001564	0.69649488	0.00142947	0.00923549
C-type lectin c	ENST0000029	Homo sapiens	NM_080387	0.69642441	0.00104073	0.00719124
Fc fragment of	ENST0000048	Fc fragment of	ENST0000048	0.69427444	0.00011254	0.00123189
6-phosphofru	ENST0000048	Homo sapiens	NM_004566	0.69422283	1.15E-06	3.24E-05
maltase-gluco	NA	PREDICTED: H	XM_0067161	0.69329967	2.77E-05	0.00041386
proline-serine	ENST0000058	Homo sapiens	NM_024430	0.69319085	4.85E-07	1.65E-05

chemokine-lik	ENST0000052	Homo sapiens	NM_0010401	0.69276229	1.80E-11	5.71E-09
clusterin	ENST000004C	Homo sapiens	NM_001831	0.6920241	3.31E-05	0.00047694
desmocollin 2	ENST0000025	Homo sapiens	NM_024422	0.69136905	0.00019549	0.00190526
histone cluste	NA	Homo sapiens	NM_003546	0.69120706	5.86E-05	0.00074385
small nuclear	ENST0000042	Homo sapiens	NM_003096	0.69024819	3.48E-05	0.00049515
immediate ea	ENST0000037	Homo sapiens	NM_003897	0.6893228	7.19E-10	8.89E-08
LIM domain ki	ENST0000046	Homo sapiens	NM_0010318	0.68859797	5.22E-06	0.00010967
guanine nucle	ENST0000037	Homo sapiens	NM_0010179	0.68786664	0.00021591	0.00205522
nucleolar and	ENST0000041	Homo sapiens	NM_016359	0.68759567	6.89E-07	2.17E-05
histone cluste	ENST0000024	Homo sapiens	NM_003540	0.68736903	2.53E-08	1.59E-06
histone cluste	ENST0000061	Homo sapiens	NM_003513	0.68721614	1.91E-09	1.99E-07
rhophilin assc	ENST000005C	Homo sapiens	NM_031916	0.68663868	2.74E-06	6.65E-05
carcinoembry	ENST000004C	Homo sapiens	NM_001712	0.68614012	0.00109742	0.00750111
ChaC glutathi	ENST0000061	Homo sapiens	NM_024111	0.68613458	4.05E-10	5.79E-08
histone cluste	NA	Homo sapiens	NM_021052	0.68590475	1.97E-07	8.08E-06
dihydrofolate	ENST0000051	Homo sapiens	NM_000791	0.68347103	8.25E-11	1.75E-08
FK506 bindin	ENST0000035	Homo sapiens	NM_004117	0.68344432	0.00130537	0.00857682
kringle contai	ENST000004C	Homo sapiens	NM_0010395	0.68335857	9.53E-07	2.77E-05
small nuclear	ENST000004C	Homo sapiens	NM_006938	0.68290708	4.02E-09	3.64E-07
integral memb	ENST0000032	Homo sapiens	NM_030926	0.68272148	9.29E-05	0.00106018
prenyl (decap	ENST0000047	Homo sapiens	NM_014317	0.68112964	2.27E-09	2.27E-07
kelch-like fam	ENST0000022	Homo sapiens	NM_007246	0.68070911	0.0003087	0.00273861
tubulin, alpha	ENST0000024	Homo sapiens	NM_006000	0.68047338	8.28E-10	9.92E-08
collagen, type	ENST0000046	Homo sapiens	NM_001853	0.67946087	0.00029833	0.00266484
histone cluste	ENST0000033	Homo sapiens	NM_021058	0.6789052	3.48E-09	3.21E-07
histone cluste	NA	Homo sapiens	NM_003538	0.67744086	4.86E-08	2.70E-06
complement (	ENST000005C	Homo sapiens	NM_175710	0.67733126	2.30E-07	9.07E-06
chloride intra	ENST0000048	Homo sapiens	NM_013943	0.67732607	4.71E-10	6.49E-08
tumor protein	ENST0000023	Homo sapiens	NM_004881	0.67731922	4.42E-06	9.55E-05
ribosomal pro	ENST0000037	Homo sapiens	NM_021029	0.67657297	9.02E-06	0.00017029
fatty acid binc	ENST0000043	Homo sapiens	NM_001444	0.6765095	2.40E-10	3.89E-08
Fc fragment of	ENST0000036	Fc fragment of	ENST0000036	0.67612603	8.07E-05	0.00094834
PET100 homo	ENST000006C	Homo sapiens	NM_0011711	0.6758909	1.21E-07	5.52E-06
mitochondria	ENST0000051	Homo sapiens	NM_016067	0.67555108	7.70E-09	6.24E-07
glutaminyl-pe	ENST0000046	Homo sapiens	NM_012413	0.67533846	2.08E-06	5.26E-05
mesencephali	ENST0000047	Homo sapiens	NM_006010	0.67517048	4.67E-05	0.00062475
centromere pr	ENST0000029	Homo sapiens	NM_018455	0.67514649	1.12E-08	8.40E-07
transmembra	ENST0000061	Homo sapiens	NM_144686	0.67340254	1.08E-07	5.02E-06
zinc finger pro	ENST000005C	Homo sapiens	NM_020747	0.67287029	2.75E-06	6.66E-05
tumor protein	ENST0000023	Homo sapiens	NM_004881	0.67203174	9.66E-07	2.80E-05
NADH dehydr	ENST0000055	Homo sapiens	NM_016013	0.6700521	3.96E-14	6.15E-11
protein phosp	ENST0000047	Homo sapiens	NM_174907	0.66964921	8.28E-13	4.84E-10
glyceraldehyd	ENST0000047	Homo sapiens	NM_002046	0.66957239	2.14E-09	2.16E-07
RAB32, memb	ENST0000036	Homo sapiens	NM_006834	0.66869426	9.31E-09	7.30E-07
chondroitin su	ENST0000039	Homo sapiens	NM_0011305	0.66859255	2.46E-05	0.00037733
ST3 beta-galac	ENST0000053	Homo sapiens	NM_006278	0.66731302	9.47E-06	0.00017697
BCL2-related p	ENST0000048	Homo sapiens	NM_004049	0.66145099	4.04E-07	1.43E-05
hepatocyte gr	ENST0000045	Homo sapiens	NM_0010109	0.66122484	1.04E-07	4.90E-06

histone cluste	NA	Homo sapiens	NM_080596	0.6608041	9.60E-07	2.79E-05
multimerin 1	ENST0000026	Homo sapiens	NM_007351	0.65973158	1.39E-05	0.00023895
methionine su	ENST0000046	Homo sapiens	NM_012228	0.65971277	2.35E-08	1.50E-06
uncharacteriz	ENST0000039	PREDICTED: H	ENST0000039	0.65951214	8.87E-06	0.00016805
centromere pı	ENST000004C	centromere pı	ENST000004C	0.65926999	0.00117418	0.00789536
histone cluste	ENST0000037	Homo sapiens	NM_003544	0.65920103	2.54E-05	0.00038738
free fatty acid	ENST0000059	Homo sapiens	NM_005304	0.65916557	0.00042935	0.00354792
mitochondria	ENST0000022	Homo sapiens	NM_016497	0.65826189	7.55E-07	2.31E-05
chemokine-lik	ENST0000052	Homo sapiens	NM_181641	0.65806128	3.85E-11	1.00E-08
WD repeat do	ENST0000037	Homo sapiens	NM_052844	0.65775248	7.37E-07	2.27E-05
adenosine A2a	ENST0000035	Homo sapiens	NM_000675	0.65620997	4.59E-10	6.37E-08
IL10RB antise	NA	Homo sapiens	NR_038974	0.65588552	7.61E-09	6.18E-07
dysferlin	ENST0000041	Homo sapiens	NM_003494	0.65523691	9.46E-06	0.00017688
sialic acid bin	ENST0000057	Homo sapiens	NM_003830	0.65517823	3.56E-07	1.29E-05
histone cluste	ENST0000034	Homo sapiens	NM_021065	0.65423165	8.04E-06	0.0001554
androgen-indı	ENST0000027	Homo sapiens	NM_016108	0.6532605	1.26E-08	9.14E-07
protein-L-isoa	ENST0000046	Homo sapiens	NM_0012520	0.65292915	5.07E-13	3.21E-10
Bloom syndro	ENST0000055	Homo sapiens	NM_000057	0.6526139	1.99E-09	2.03E-07
transmembra	ENST0000043	Homo sapiens	NM_0012844	0.65227009	2.26E-07	8.94E-06
ribosomal prc	ENST0000037	Homo sapiens	NM_021029	0.65187421	5.76E-05	0.00073596
immediate ea	ENST0000037	Homo sapiens	NM_003897	0.65163098	1.15E-08	8.53E-07
solute carrier	ENST0000047	Homo sapiens	NM_006931	0.65085912	5.19E-08	2.82E-06
E2F transcript	ENST0000034	Homo sapiens	NM_005225	0.65059599	6.47E-07	2.05E-05
growth arrest	ENST0000061	Homo sapiens	NM_152236	0.65045314	0.00040583	0.00338633
isopentenyl-d	ENST0000038	Homo sapiens	NM_004508	0.64960159	5.60E-06	0.00011646
mitochondria	ENST0000036	Homo sapiens	NM_022746	0.64954017	7.29E-05	0.00088249
interleukin 1 r	ENST0000041	Homo sapiens	NM_000877	0.64931186	2.89E-06	6.92E-05
carcinoembry	ENST000000C	Homo sapiens	NM_006890	0.64896684	0.00076149	0.00561948
RAD51 recom	ENST0000052	Homo sapiens	NM_002875	0.64785666	2.59E-05	0.00039361
ubiquinol-cyt	ENST0000037	Homo sapiens	NM_014402	0.64739861	3.64E-05	0.00051303
fer-1-like fami	ENST0000061	Homo sapiens	NR_119376	0.64687756	3.70E-06	8.35E-05
insulin-like 3 (	ENST0000031	Homo sapiens	NM_0012655	0.64516061	5.15E-08	2.82E-06
UDP-Gal:beta	ENST0000037	Homo sapiens	NM_004776	0.64511686	7.52E-06	0.00014767
LSM3 homolo	ENST000003C	Homo sapiens	NM_014463	0.64474603	2.33E-05	0.00036298
matrix metall	ENST0000033	Homo sapiens	NM_022468	0.64442984	0.00013742	0.00143725
glia maturatic	ENST000006C	Homo sapiens	NM_004877	0.64397078	1.34E-08	9.65E-07
solute carrier	ENST0000026	Homo sapiens	NM_003486	0.64345461	7.36E-05	0.00088872
splicing factor	ENST0000023	Homo sapiens	NM_016047	0.64269749	2.47E-09	2.40E-07
NOP10 ribonu	ENST0000032	Homo sapiens	NM_018648	0.64250792	2.37E-11	7.06E-09
lysosomal pro	ENST0000052	Homo sapiens	NM_018407	0.64249203	3.93E-09	3.58E-07
transmembra	ENST0000053	Homo sapiens	NM_0010988	0.64237505	3.28E-08	1.98E-06
GRAM domair	ENST0000059	Homo sapiens	NM_0011361	0.64202538	4.06E-12	1.62E-09
myosin, light	ENST0000055	Homo sapiens	NM_079423	0.64052756	7.05E-07	2.20E-05
P450 (cytochr	ENST0000041	Homo sapiens	NM_000941	0.64010725	3.14E-07	1.17E-05
histone cluste	ENST000006C	Homo sapiens	NM_003512	0.6396168	2.64E-05	0.00039915
actin binding	ENST000005C	Homo sapiens	NM_014945	0.6388187	4.25E-05	0.00058093
heat shock 10	ENST0000046	heat shock 10	ENST0000046	0.638434	4.42E-05	0.000598
DNA-damage r	ENST0000025	Homo sapiens	NM_018370	0.63832295	3.69E-07	1.33E-05

kinesin family	ENST0000037	Homo sapiens	NM_183416	0.63829231	4.61E-08	2.59E-06
v-myb avian m	ENST0000034	Homo sapiens	NM_005375	0.63776045	0.00101619	0.00706038
anoctamin 10	ENST0000035	Homo sapiens	NM_0012048	0.63641882	1.21E-07	5.51E-06
histone cluste	NA	Homo sapiens	NM_003511	0.63565889	1.70E-07	7.19E-06
heat shock pr	NA	Human heat sl	M30627	0.63536514	1.97E-06	5.03E-05
ankyrin repeat	ENST0000033	Homo sapiens	NM_0010044	0.63531061	0.00027786	0.00251244
gamma-glutar	ENST0000033	Homo sapiens	NM_178311	0.63244884	5.96E-08	3.17E-06
small nuclear	ENST0000042	Homo sapiens	NM_003096	0.63225669	0.00010868	0.00120067
prostaglandin	ENST0000054	Homo sapiens	NM_000962	0.63200215	4.84E-05	0.00064269
OTUD6B antis	NA	Homo sapiens	NR_110439	0.63066409	9.24E-09	7.26E-07
RecQ protein-	ENST0000061	Homo sapiens	NM_004260	0.63059473	9.18E-05	0.00105127
Pim-3 proto-c	ENST000003(	Homo sapiens	NM_0010018	0.62983418	1.03E-07	4.86E-06
neurotensin r	ENST0000037	Homo sapiens	NM_002531	0.62887343	0.00027283	0.00247995
H2A histone fa	ENST0000052	Homo sapiens	NM_002106	0.62886863	5.12E-11	1.21E-08
glutaminyl-pe	ENST000004(	Homo sapiens	NM_012413	0.6283791	1.15E-05	0.00020627
insulin-like gr	ENST000002(	Homo sapiens	NM_000875	0.62741848	5.44E-05	0.00070494
zinc finger pro	ENST000005(	Homo sapiens	NM_020747	0.62716226	2.34E-06	5.83E-05
nicotinamide	ENST0000029	Homo sapiens	NM_006169	0.62688428	1.18E-05	0.00021056
mitochondria	ENST0000047	Homo sapiens	NM_022746	0.62683729	6.88E-06	0.0001375
LIM domain ki	ENST0000033	Homo sapiens	NM_016733	0.62544436	0.00010073	0.00112848
cell division c	ENST0000032	Homo sapiens	NM_018101	0.62484193	1.17E-06	3.28E-05
NLR family, CA	ENST000004(	Homo sapiens	NM_021209	0.62389968	3.87E-05	0.0005382
uncharacteriz	ENST0000039	PREDICTED: H	ENST0000039	0.62382376	1.14E-06	3.22E-05
tumor protein	ENST0000053	Homo sapiens	NM_0012583	0.62374104	6.07E-11	1.37E-08
PDZ domain c	ENST0000033	Homo sapiens	NM_173791	0.62321081	1.97E-07	8.08E-06
solute carrier	ENST0000046	Homo sapiens	NM_016354	0.62265962	1.34E-09	1.48E-07
methylmaloni	ENST0000042	Homo sapiens	NM_015702	0.61997905	4.00E-10	5.76E-08
histone cluste	ENST000003(	Homo sapiens	NM_003536	0.61970444	0.00010589	0.00117528
family with se	ENST0000061	Homo sapiens	NM_152421	0.61942874	1.14E-05	0.00020543
TPX2, microtu	ENST0000034	Homo sapiens	NM_012112	0.61940781	8.57E-07	2.54E-05
RNA, 7SK smal	NA	Homo sapiens	NR_001445	0.61848422	3.79E-06	8.50E-05
adrenomedull	ENST0000052	Homo sapiens	NM_001124	0.61826267	0.00045565	0.00372098
SHC SH2-dom	ENST000003(	Homo sapiens	NM_024745	0.61823926	2.38E-07	9.32E-06
runt-related t	ENST0000048	Homo sapiens	NM_0010018	0.61822538	4.12E-06	9.06E-05
glycoprotein V	ENST0000031	Homo sapiens	NM_0010838	0.61804338	9.96E-05	0.00111821
caspase recrui	ENST0000025	Homo sapiens	NM_032587	0.61789121	5.97E-09	4.96E-07
regulator of G	ENST000003(	Homo sapiens	NM_002928	0.6175697	5.46E-10	7.30E-08
fatty acyl CoA	ENST0000018	Homo sapiens	NM_018099	0.61732198	6.09E-06	0.00012479
centromere pr	ENST000003(	Homo sapiens	NM_016343	0.61515472	5.55E-05	0.0007144
collagen, type	ENST0000043	Homo sapiens	NM_000494	0.61360112	4.04E-05	0.0005575
Kruppel-like fa	ENST000003(	Homo sapiens	NM_003709	0.6124996	1.16E-07	5.32E-06
Fc receptor-lik	ENST000003(	Fc receptor-lik	ENST000003(	0.61140388	0.0002588	0.0023789
gamma-glutar	ENST0000061	Homo sapiens	NM_0012828	0.61104959	2.33E-07	9.16E-06
family with se	ENST0000055	Homo sapiens	NM_0010795	0.60999056	1.22E-10	2.39E-08
dehydrogenas	ENST0000039	Homo sapiens	NM_144683	0.60895047	3.21E-05	0.00046751
kinesin family	ENST0000062	Homo sapiens	NM_015074	0.60756387	5.69E-06	0.00011806
nerve growth	ENST0000037	Homo sapiens	NM_014380	0.60746098	0.00110807	0.00755891
cysteine-rich s	ENST0000033	Homo sapiens	NM_003296	0.606453	0.00092875	0.00655914

CD82 molecul	ENST0000022	Homo sapiens	NM_002231	0.60645096	1.61E-06	4.27E-05
sterile alpha m	ENST000004C	Homo sapiens	NM_016653	0.60557192	3.59E-06	8.16E-05
NLR family, ap	ENST0000062	NLR family, ap	ENST0000062	0.60517086	7.43E-05	0.00089311
RAB27A, mem	ENST0000033	Homo sapiens	NM_004580	0.60401177	2.17E-07	8.70E-06
tropomyosin	ENST0000055	Homo sapiens	NM_0010180	0.6038985	5.41E-05	0.00070182
translocator p	ENST0000032	Homo sapiens	NM_0012565	0.60364155	2.79E-05	0.00041585
septin 14	ENST0000038	Homo sapiens	NM_207366	0.60288696	9.25E-05	0.00105753
transmembra	ENST000003C	Homo sapiens	NM_203411	0.60141529	2.84E-06	6.82E-05
cholesteryl est	ENST0000037	Homo sapiens	NM_000078	0.60113543	1.02E-07	4.85E-06
Janus kinase 3	ENST0000045	Homo sapiens	NM_000215	0.6009826	4.68E-07	1.60E-05
histone cluste	ENST0000061	Homo sapiens	NM_003510	0.60071201	1.22E-07	5.56E-06
histone cluste	ENST0000061	Homo sapiens	NM_003495	0.60065853	3.99E-07	1.42E-05
CDC28 protei	ENST0000031	Homo sapiens	NM_001827	0.60043674	0.00014515	0.00150493
histone cluste	ENST0000061	Homo sapiens	NM_003534	0.59959054	2.98E-10	4.49E-08
U6 snRNA bio	ENST000005E	Homo sapiens	NM_024598	0.59905168	1.40E-07	6.16E-06
guanine nucle	ENST0000028	Homo sapiens	NM_002072	0.59868245	4.36E-08	2.48E-06
myocardial in	ENST0000061	Homo sapiens	NR_003491	0.59865135	0.00049612	0.00397508
androgen-ind	ENST0000035	Homo sapiens	NM_016108	0.59850123	4.06E-07	1.44E-05
KIAA0125	ENST0000061	Homo sapiens	NR_026800	0.59833176	0.00051988	0.00412816
SH3-domain G	ENST0000061	Homo sapiens	NM_0012066	0.59740895	3.71E-06	8.35E-05
small nuclear	ENST0000042	Homo sapiens	NM_003096	0.59713326	0.00013972	0.00145687
PDZ and LIM d	ENST0000035	Homo sapiens	NM_213636	0.59494603	1.43E-07	6.26E-06
PDZ and LIM d	ENST0000049	Homo sapiens	NM_020992	0.59455977	2.11E-05	0.00033533
heat shock 70	ENST0000054	Homo sapiens	NM_005346	0.59436879	0.00019231	0.00187881
stomatin	ENST0000028	Homo sapiens	NM_198194	0.59409863	0.00052618	0.00417077
chromosome	ENST0000051	Homo sapiens	NM_033211	0.59353225	0.00132806	0.00869097
kinesin family	NA	Homo sapiens	NM_002254	0.59339354	1.24E-08	9.02E-07
protein phosp	ENST000004C	Homo sapiens	NM_0010804	0.59202031	1.11E-05	0.00020107
secretion asso	ENST000005C	Homo sapiens	NM_0010335	0.59159654	2.88E-07	1.09E-05
potassium cha	ENST0000061	Homo sapiens	NM_002249	0.59094606	1.39E-06	3.78E-05
small Cajal bo	NA	Homo sapiens	NR_003004	0.59073623	0.00035071	0.00302397
DEP domain c	ENST0000048	Homo sapiens	NM_017779	0.59071491	1.57E-07	6.75E-06
formyl peptid	ENST0000059	Homo sapiens	NM_002029	0.59025059	6.27E-06	0.00012788
histone cluste	ENST0000037	Homo sapiens	NM_003543	0.58965365	1.14E-06	3.20E-05
family with se	ENST000005C	family with se	ENST000005C	0.58961071	2.75E-10	4.29E-08
CD9 molecule	ENST0000054	Homo sapiens	NM_001769	0.58923051	8.23E-05	0.00096339
multiple C2 d	ENST0000035	Homo sapiens	NM_018349	0.58909006	1.78E-06	4.62E-05
transmembra	ENST0000054	Homo sapiens	NM_014206	0.58881977	8.70E-08	4.27E-06
cyclin E1	ENST0000057	Homo sapiens	NM_001238	0.58877528	6.78E-06	0.00013604
dachshund fa	ENST0000061	Homo sapiens	NM_080759	0.58867639	1.58E-05	0.00026501
histone cluste	ENST0000037	histone cluste	ENST0000037	0.58837703	2.41E-05	0.00037157
ubiquitin don	ENST0000037	Homo sapiens	NM_024954	0.58794452	7.90E-08	3.95E-06
endothelin co	NA	Homo sapiens	NR_028501	0.58738193	7.74E-07	2.36E-05
pirin (iron-bi	ENST0000038	Homo sapiens	NM_003662	0.58626751	3.23E-09	3.02E-07
solute carrier	ENST0000049	Homo sapiens	NM_001151	0.58561741	0.0007308	0.00543317
UDP-N-acetyl	ENST0000036	Homo sapiens	NM_003115	0.58535649	1.31E-06	3.60E-05
vacuolar prot	ENST000005E	Homo sapiens	NM_020821	-0.5852773	5.60E-07	1.85E-05
actin binding	ENST0000036	Homo sapiens	NM_0010034	-0.5856433	0.00015244	0.00156021

sex comb on r	ENST000003(	Homo sapiens	NM_198081	-0.5877289	2.87E-05	0.00042432
DNA (cytosine	ENST000005	Homo sapiens	NM_0011308	-0.5882951	5.65E-07	1.86E-05
sialophorin	ENST000003(	Homo sapiens	NM_0010302	-0.5888443	7.03E-08	3.60E-06
KIAA1598	ENST000004	Homo sapiens	NM_018330	-0.5893615	1.05E-05	0.00019255
macrophage s	ENST000003	Homo sapiens	NM_002445	-0.5902999	1.17E-06	3.29E-05
notch 4	ENST000004	Homo sapiens	NM_004557	-0.5905581	3.84E-08	2.25E-06
phospholipas	ENST000003	Homo sapiens	NM_138790	-0.5914406	2.78E-10	4.31E-08
Rho guanine r	ENST000004	Homo sapiens	NM_173728	-0.5916462	7.16E-07	2.23E-05
calcium/calm	ENST000003	Homo sapiens	NM_003656	-0.5918259	7.28E-08	3.71E-06
interleukin 27	ENST000002(	Homo sapiens	NM_004843	-0.5933179	1.78E-07	7.50E-06
muscleblind-l	ENST000004(	Homo sapiens	NM_0011707	-0.5940242	0.00054037	0.00426466
septin 9	ENST000003	Homo sapiens	NM_006640	-0.594068	6.21E-07	1.99E-05
TNRC18P1	NA	Homo sapiens	NR_077215	-0.5941249	0.00016226	0.00164017
v-maf avian m	ENST000003	Homo sapiens	NM_005461	-0.5943299	0.00019113	0.00187101
ZFP36 ring fin	ENST000002	Homo sapiens	NM_006887	-0.5948656	7.26E-06	0.00014365
protocadherir	ENST000006	Homo sapiens	NM_032087	-0.5949998	0.00156698	0.00991768
killer cell lecti	ENST000005	Homo sapiens	NM_0012918	-0.5953352	3.69E-06	8.33E-05
erythrocyte m	ENST000005	erythrocyte m	ENST000005	-0.5968791	0.0001492	0.00153406
A kinase (PRKA	ENST000000	Homo sapiens	NM_016248	-0.5979555	1.50E-08	1.05E-06
PRKCQ antiser	ENST000004	Homo sapiens	NR_036502	-0.5982553	5.11E-05	0.0006709
structural mai	ENST000003	Homo sapiens	NM_015295	-0.5983567	9.82E-06	0.00018196
WD repeat do	ENST000006	Homo sapiens	NM_152348	-0.5989746	5.16E-11	1.21E-08
shisa family m	ENST000003(	Homo sapiens	NM_198149	-0.5989754	5.53E-05	0.00071196
zinc finger, HI	ENST000003	Homo sapiens	NM_014205	-0.5997475	0.00042121	0.00348934
chromosome	ENST000003	Homo sapiens	NM_024541	-0.6003538	6.06E-07	1.96E-05
amino-termin	ENST000005	Homo sapiens	NM_198969	-0.6005627	2.35E-05	0.00036473
RIMS binding	ENST000004	Homo sapiens	NM_015672	-0.6012109	1.10E-08	8.33E-07
retinitis pigm	ENST000004(	Homo sapiens	NM_020366	-0.6031765	1.03E-06	2.96E-05
KIAA1324	ENST000005	Homo sapiens	NM_020775	-0.6039464	0.00105409	0.00726416
sphingosine-1	ENST000003	Homo sapiens	NM_005226	-0.6057141	7.46E-05	0.00089445
prostaglandin	ENST000003(	Homo sapiens	NM_000953	-0.6069227	1.80E-07	7.55E-06
hydrogen volt	ENST000003	Homo sapiens	NM_0010401	-0.607994	3.54E-07	1.28E-05
late cornified	ENST000003	Homo sapiens	NM_178348	-0.6079984	0.00034274	0.00296677
docking prote	ENST000005	Homo sapiens	NM_003974	-0.6085284	1.80E-08	1.21E-06
KCND3 intron	NA	Homo sapiens	NR_046783	-0.6088555	0.00047896	0.00387265
single immun	ENST000005	Homo sapiens	NM_021805	-0.6106415	4.88E-07	1.66E-05
histamine rec	ENST000003	Homo sapiens	NM_007232	-0.611757	0.00155657	0.0098712
cytochrome c	ENST000003(	mitochondria	ENST000003(	-0.6118285	1.43E-06	3.85E-05
uncharacteriz	NA	Homo sapiens	NR_026914	-0.6122879	1.04E-08	7.97E-07
MAX dimeriza	ENST000005	Homo sapiens	NM_006454	-0.612389	2.13E-09	2.16E-07
pleckstrin hor	ENST000003	Homo sapiens	NM_0010019	-0.6133151	5.76E-05	0.00073605
AHNAK nuclec	ENST000003	Homo sapiens	NM_001620	-0.6135832	7.22E-06	0.00014303
post-GPI attac	ENST000006	Homo sapiens	NM_033419	-0.614198	1.92E-10	3.30E-08
transducin (b	ENST000005(	transducin (b	ENST000005(	-0.6142818	0.00109858	0.00750743
polycomb gro	ENST000004	Homo sapiens	NR_046310	-0.6150613	0.00149755	0.00958779
ST3 beta-galac	ENST000004(	Homo sapiens	NM_003896	-0.6152644	3.36E-07	1.23E-05
potassium cha	ENST000003	Homo sapiens	NM_138444	-0.6159948	0.00024966	0.00230994
tetratricopep	ENST000004	Homo sapiens	NM_014831	-0.6165473	0.00011111	0.00122051

RAR-related o	ENST0000035	Homo sapiens	NM_005060	-0.6172868	1.57E-06	4.18E-05
nuclear pore c	ENST0000042	nuclear pore c	ENST0000042	-0.6175949	5.45E-09	4.60E-07
derlin 3	ENST0000061	Homo sapiens	NM_198440	-0.6181566	9.14E-06	0.00017214
ankyrin repeat	ENST0000061	Homo sapiens	NM_152345	-0.6191315	0.00078038	0.00572769
prostaglandin	ENST000003C	Homo sapiens	NM_000958	-0.6194541	1.35E-05	0.00023362
calcium/calm	ENST000005C	Homo sapiens	NM_001221	-0.6210807	2.77E-13	2.11E-10
CD40 ligand	ENST0000037	Homo sapiens	NM_000074	-0.6217302	0.00042668	0.00352894
coiled-coil do	ENST0000038	Homo sapiens	NM_0010804	-0.6222198	1.34E-08	9.65E-07
ribonuclease/	ENST0000052	Homo sapiens	NM_002939	-0.6236698	5.24E-07	1.75E-05
lipase matura	ENST0000056	Homo sapiens	NR_036442	-0.6244155	5.38E-05	0.0006992
CALML3 antis	NA	Homo sapiens	NR_120496	-0.6247302	0.00107945	0.00739462
F-box and leu	ENST0000032	Homo sapiens	NM_153350	-0.6260845	4.68E-05	0.00062594
agrin	ENST0000046	Homo sapiens	NM_198576	-0.6275429	1.16E-06	3.26E-05
single strande	ENST0000027	Homo sapiens	NM_032627	-0.6277179	7.83E-07	2.38E-05
NIP7, nucleol	ENST0000025	Homo sapiens	NM_016101	-0.628758	0.0013446	0.00877508
IKAROS family	ENST0000062	Homo sapiens	NM_0012845	-0.6288132	0.00034519	0.00298362
negative regul	ENST0000032	Homo sapiens	NM_198565	-0.6288558	2.32E-10	3.85E-08
BCL2/adenovi	ENST0000062	Homo sapiens	NM_004331	-0.6301904	0.00052397	0.00415429
inositol polyp	ENST0000026	Homo sapiens	NM_003866	-0.630418	9.27E-07	2.70E-05
autism suscep	ENST0000061	Homo sapiens	NM_015570	-0.6304957	2.41E-05	0.0003713
interferon reg	ENST0000026	Homo sapiens	NM_002163	-0.6309132	5.86E-07	1.91E-05
sterile alpha m	ENST0000043	Homo sapiens	NM_0010173	-0.6311827	7.46E-05	0.00089456
serine dehydr	ENST000004C	Homo sapiens	NM_138432	-0.6321089	5.69E-05	0.00072832
asialoglycopr	ENST0000061	Homo sapiens	NM_001671	-0.6327557	0.00030966	0.00274352
plexin B2	ENST0000061	Homo sapiens	NM_012401	-0.6332427	2.94E-08	1.81E-06
transgelin	ENST0000039	Homo sapiens	NM_0010015	-0.633375	1.53E-09	1.64E-07
FYN proto-on	ENST0000036	Homo sapiens	NM_002037	-0.6374782	5.78E-07	1.89E-05
killer cell lecti	ENST000003C	Homo sapiens	NM_013431	-0.6390721	2.33E-05	0.00036266
dendritic cell-	ENST0000053	Homo sapiens	NM_130848	-0.640174	1.30E-13	1.35E-10
TraB domain c	ENST0000033	Homo sapiens	NM_0012770	-0.6402827	0.00010419	0.0011605
SH2 domain c	ENST0000039	Homo sapiens	NM_003975	-0.640477	0.00012708	0.00135101
chromosome	ENST0000037	Homo sapiens	NM_0011008	-0.6412106	5.99E-05	0.00075587
CD7 molecule	ENST0000031	Homo sapiens	NM_006137	-0.6413523	2.56E-06	6.26E-05
Kruppel-like f	ENST0000037	Homo sapiens	NM_007249	-0.6426459	7.65E-06	0.00014946
human immu	ENST0000037	Homo sapiens	NM_024503	-0.6437018	5.36E-05	0.00069735
ephrin-A1	ENST0000046	Homo sapiens	NM_004428	-0.6469042	0.0011856	0.00796524
histone deace	ENST0000022	Homo sapiens	NM_0010150	-0.6478979	0.00010408	0.0011605
spectrin repea	ENST0000055	Homo sapiens	NM_182914	-0.6483146	2.45E-08	1.55E-06
solute carrier	ENST0000048	Homo sapiens	NM_0012902	-0.6489712	3.53E-05	0.00050007
uncoupling pr	ENST0000031	Homo sapiens	NM_003355	-0.6492378	1.02E-07	4.83E-06
transmembra	ENST0000035	Homo sapiens	NM_182526	-0.6499684	0.00024779	0.00229805
AlkB family m	ENST0000039	Homo sapiens	NM_017758	-0.6500729	0.00076662	0.00564943
sushi, nidoger	ENST000004C	Homo sapiens	NM_0010804	-0.6515058	0.00101236	0.0070375
napsin A aspa	ENST0000059	Homo sapiens	NM_004851	-0.6526001	7.87E-07	2.39E-05
stromal antig	ENST0000042	Homo sapiens	NR_040584	-0.6543302	0.00030743	0.00273205
adaptor-relate	ENST0000054	Homo sapiens	NM_003916	-0.6554851	5.94E-09	4.95E-07
trefoil factor 1	ENST0000029	Homo sapiens	NM_003225	-0.6557134	0.00053956	0.00426031
NK2 homeobo	ENST0000062	Homo sapiens	NM_145285	-0.656934	0.00076894	0.00566384

RAS guanyl rel	ENST0000053	Homo sapiens	NM_005739	-0.6591001	5.31E-05	0.00069291
pleckstrin hor	ENST000006C	Homo sapiens	NM_016274	-0.6596692	3.30E-07	1.21E-05
cathepsin W	ENST000003C	Homo sapiens	NM_001335	-0.6598587	0.00013671	0.00143207
complement (	ENST0000029	Homo sapiens	NM_000063	-0.6606966	0.00011697	0.0012691
lymphocyte a	ENST0000037	Homo sapiens	NM_004271	-0.6609682	7.22E-07	2.24E-05
CAP-GLY dom	ENST0000032	Homo sapiens	NM_024692	-0.6609998	2.04E-06	5.19E-05
GTPase, IMAP	ENST000003C	Homo sapiens	NM_130759	-0.6618981	1.57E-08	1.08E-06
chemokine (C	ENST0000035	Homo sapiens	NM_001837	-0.6627264	0.00027596	0.00250108
sterile alpha m	ENST0000055	Homo sapiens	NM_015589	-0.6640706	2.33E-05	0.00036246
homolog of ra	ENST0000061	Homo sapiens	NM_0010808	-0.6671203	3.52E-06	8.05E-05
WD repeat do	ENST0000058	Homo sapiens	NM_024100	-0.667354	0.00150937	0.00964156
unc-51 like au	ENST0000039	Homo sapiens	NM_014683	-0.6686467	3.15E-14	5.15E-11
proprotein co	ENST0000037	Homo sapiens	NM_006200	-0.6688132	2.16E-07	8.68E-06
transmembra	ENST0000039	Homo sapiens	NM_052932	-0.6690738	0.00100416	0.00699149
SCO-spondin	ENST0000048	Homo sapiens	NM_198455	-0.6701571	0.00120963	0.00808297
NLR family, CA	NA	Homo sapiens	AK090476	-0.6710645	0.00012545	0.00133869
purinergic rec	ENST0000034	Homo sapiens	NM_170683	-0.6713289	0.00026685	0.00243773
tetratricopep	ENST0000044	Homo sapiens	NM_145755	-0.673273	0.00092329	0.00653849
cortexin 1	ENST0000031	Homo sapiens	NM_206833	-0.6742449	0.00031644	0.00278731
solute carrier	ENST0000033	Homo sapiens	NM_0010397	-0.6747793	0.001438	0.00927924
zinc finger prc	ENST0000037	Homo sapiens	NM_178457	-0.6763502	3.48E-07	1.26E-05
ATH1, acid tre	ENST0000047	Homo sapiens	NM_025092	-0.6769973	1.21E-06	3.37E-05
kelch domain	ENST0000039	Homo sapiens	NM_138433	-0.67958	8.23E-05	0.00096339
eukaryotic tra	NA	Homo sapiens	NM_0012829	-0.6799308	0.00113753	0.0077175
olfactory rece	ENST000003C	Homo sapiens	NM_013939	-0.6803743	0.00037359	0.00318849
Kruppel-like fa	ENST0000053	Homo sapiens	NM_003597	-0.6818549	1.51E-09	1.63E-07
interleukin 1C	ENST0000022	Homo sapiens	NM_001558	-0.6821004	2.04E-07	8.27E-06
metastasis sup	ENST0000052	Homo sapiens	NM_014751	-0.6850558	1.94E-09	2.00E-07
transketolase-	ENST0000036	Homo sapiens	NM_012253	-0.6854987	1.86E-05	0.00030419
GTPase, IMAP	ENST0000025	Homo sapiens	NM_018326	-0.6862625	7.79E-08	3.92E-06
F-box and leuc	ENST0000033	Homo sapiens	NM_0010997	-0.6863854	0.00116448	0.00785565
killer cell lecti	ENST0000034	Homo sapiens	NM_002262	-0.6866676	3.21E-05	0.00046751
granzyme K (gr	ENST0000023	Homo sapiens	NM_002104	-0.6881096	0.00076791	0.00565758
mannosidase,	ENST0000026	Homo sapiens	NM_020379	-0.6884706	4.42E-07	1.54E-05
eomesodermi	ENST0000044	Homo sapiens	NM_005442	-0.6893754	2.89E-05	0.0004272
RAB GTPase ac	ENST0000036	Homo sapiens	NM_0012437	-0.6898145	9.80E-10	1.15E-07
integrin, alpha	NA	Homo sapiens	NM_000885	-0.6910353	3.66E-06	8.29E-05
leucine rich re	ENST0000037	Homo sapiens	NM_0010136	-0.6919571	0.00099564	0.00694305
Fc receptor-lik	ENST0000048	Fc receptor-lik	ENST0000048	-0.6930214	1.93E-05	0.0003119
runt-related tr	ENST000003C	Homo sapiens	NM_0010316	-0.6932845	2.90E-05	0.00042864
PRELI domain	ENST0000056	Homo sapiens	NM_013237	-0.6934914	1.15E-06	3.23E-05
brain-enriche	ENST0000044	Homo sapiens	NM_0011595	-0.6950978	2.59E-05	0.00039361
family with se	ENST000005C	Homo sapiens	NR_038353	-0.6952724	1.41E-05	0.00024266
NADPH oxidas	ENST0000039	Homo sapiens	NM_006647	-0.6960727	7.64E-15	2.24E-11
ATPase, class V	ENST0000055	Homo sapiens	NM_024490	-0.6961731	1.71E-06	4.46E-05
secretoglobin	ENST0000051	Homo sapiens	NM_052863	-0.6962979	0.00022179	0.00209966
Ras and Rab in	ENST0000031	Homo sapiens	NM_004292	-0.6965659	9.80E-06	0.00018185
coiled-coil do	ENST0000039	Homo sapiens	NM_017918	-0.6971111	7.04E-10	8.73E-08

Rab9 effector	ENST0000037	Rab9 effector	ENST0000037	-0.6983977	1.94E-07	8.00E-06
PQ loop repea	ENST0000044	Homo sapiens	NM_152391	-0.6988942	1.44E-09	1.57E-07
keratin 72, ty	ENST0000035	Homo sapiens	NM_080747	-0.6995037	0.00012601	0.00134427
NLR family, C/	ENST0000061	Homo sapiens	NM_178844	-0.6995119	9.36E-06	0.00017583
cathepsin S	ENST000006C	Homo sapiens	NM_004079	-0.6999082	1.43E-08	1.01E-06
LCK proto-on	ENST0000046	Homo sapiens	NM_005356	-0.7005307	5.55E-05	0.00071451
CD33 molecul	ENST0000042	Homo sapiens	NM_001772	-0.7014538	2.09E-06	5.29E-05
CD79a molecu	ENST0000022	Homo sapiens	NM_001783	-0.7016081	0.00055609	0.00436213
tryptophanyl-	ENST0000055	Homo sapiens	NM_004184	-0.7029102	0.00065675	0.00499514
T cell receptor	NA	Homo sapiens	BC027954	-0.7032245	2.42E-10	3.89E-08
ribosomal prc	ENST0000026	Homo sapiens	NM_004755	-0.7044634	1.37E-08	9.82E-07
erythrocyte m	ENST0000054	Homo sapiens	NM_012307	-0.7046824	2.46E-10	3.93E-08
zinc finger anc	ENST0000039	Homo sapiens	NM_024784	-0.7065867	0.00032828	0.00286719
protease, seri	ENST0000057	Homo sapiens	NM_173502	-0.7078715	3.53E-05	0.00050007
phospholipas	ENST0000053	Homo sapiens	NM_005084	-0.7092551	2.84E-08	1.77E-06
envoplakin	ENST000003C	Homo sapiens	NM_001988	-0.7099847	0.00027149	0.00247285
hyaluronan ar	ENST0000055	Homo sapiens	NM_178232	-0.7134646	3.98E-05	0.00055072
BCL2-associat	ENST0000037	Homo sapiens	NM_004323	-0.7140019	0.00017105	0.00171142
lethal giant la	ENST0000057	Homo sapiens	NM_0010318	-0.7155938	9.46E-06	0.00017691
transgelin	ENST0000039	Homo sapiens	NM_0010015	-0.7162077	2.97E-09	2.82E-07
granzyme M (l	ENST0000026	Homo sapiens	NM_005317	-0.7163402	2.84E-07	1.08E-05
adenylate kin	ENST0000037	Homo sapiens	NM_000476	-0.7164528	0.00054613	0.00429923
lipase, hormo	ENST0000024	Homo sapiens	NM_005357	-0.7165537	1.90E-05	0.00030889
TCR gamma al	ENST0000061	Homo sapiens	NM_0010037	-0.717621	0.00020135	0.00195043
transmembra	NA	Homo sapiens	NM_0012915	-0.7176857	2.90E-10	4.42E-08
keratin 7, type	ENST0000033	Homo sapiens	NM_005556	-0.7179286	7.21E-05	0.00087522
chimerin 2	ENST0000043	Homo sapiens	NM_0012930	-0.720257	1.06E-07	4.98E-06
CD52 molecul	ENST0000037	Homo sapiens	NM_001803	-0.7209184	0.00037432	0.00319116
tubulin polym	ENST0000056	Homo sapiens	NM_016140	-0.721498	1.11E-09	1.27E-07
hydrogen volt	ENST0000035	Homo sapiens	NM_0010401	-0.7220375	1.62E-09	1.72E-07
glypican 4	ENST0000037	Homo sapiens	NM_001448	-0.7226516	0.00080398	0.00585795
mab-21-like 2	ENST0000031	Homo sapiens	NM_006439	-0.7254962	0.00019164	0.0018742
megakaryocyt	ENST0000061	Homo sapiens	NM_139355	-0.7257319	4.33E-09	3.80E-07
keratin associ	ENST0000039	Homo sapiens	NM_0011233	-0.7273333	0.00102609	0.00711388
adrenergic, be	ENST0000032	Homo sapiens	NM_005160	-0.7277898	4.13E-09	3.66E-07
heart develop	ENST0000031	Homo sapiens	NM_020733	-0.7282466	5.00E-07	1.68E-05
calcium chan	ENST0000035	Homo sapiens	NM_145814	-0.728924	0.00018909	0.00185569
Ras and Rab in	ENST0000025	Homo sapiens	NM_018993	-0.7297222	3.45E-05	0.00049283
aldehyde deh	ENST0000026	Homo sapiens	NM_000690	-0.7312012	7.98E-05	0.0009394
transcription	ENST0000052	Homo sapiens	NM_003202	-0.7315363	0.0001232	0.0013192
achaete-scute	ENST0000033	Homo sapiens	NM_005170	-0.7324234	5.05E-08	2.77E-06
cytochrome b	ENST0000058	Homo sapiens	NM_0010179	-0.7327653	1.63E-07	6.97E-06
macrophage r	ENST0000049	Homo sapiens	NM_006770	-0.7340191	0.00041071	0.00341788
N-acylethanol	ENST0000051	Homo sapiens	NM_0010424	-0.7348968	6.66E-10	8.43E-08
src kinase assc	ENST0000057	Homo sapiens	NM_003726	-0.7350565	2.50E-05	0.00038193
forkhead box	ENST0000037	Homo sapiens	NM_003923	-0.7359252	0.00130135	0.00855473
casein kinase	ENST0000061	Homo sapiens	NM_001319	-0.7359403	1.33E-05	0.00023219
Fc fragment o	ENST0000036	Homo sapiens	NM_002001	-0.736716	0.00094867	0.00667401

sphingomyeli	ENST0000021	Homo sapiens	NM_018667	-0.7368744	0.00032937	0.0028751
NEL-like 2 (chi	ENST0000043	Homo sapiens	NM_006159	-0.7380494	1.63E-06	4.30E-05
utrophin	ENST000003(	Homo sapiens	NM_007124	-0.7404867	7.79E-10	9.40E-08
olfactory rece	ENST000003(	Homo sapiens	NM_0010044	-0.7422163	0.00116599	0.0078558
limb bud and	ENST0000039	Homo sapiens	NM_030915	-0.742638	4.83E-07	1.65E-05
napsin A aspar	ENST0000059	Homo sapiens	NM_004851	-0.7438567	3.52E-07	1.28E-05
interleukin 32	ENST0000052	Homo sapiens	NM_0010126	-0.7450103	6.26E-06	0.00012774
fibroblast gro	ENST0000025	Homo sapiens	NM_031950	-0.7484264	0.00017312	0.00172741
tetratricopep	ENST0000042	Homo sapiens	NM_014831	-0.7488608	3.99E-06	8.83E-05
kelch domain	ENST0000039	Homo sapiens	NM_138433	-0.7499499	0.00014963	0.00153697
CD244 molec	ENST000003(	Homo sapiens	NM_016382	-0.7500199	4.34E-08	2.47E-06
leucine rich re	ENST000003(	Homo sapiens	NM_018334	-0.7505435	2.36E-05	0.00036625
KIAA1324	ENST000003(	Homo sapiens	NM_020775	-0.7528584	6.07E-05	0.00076417
ubiquitin spe	ENST0000033	Homo sapiens	NM_201402	-0.7529085	0.00053885	0.00425871
killer cell lecti	ENST0000053	Homo sapiens	NM_002262	-0.7530509	1.36E-05	0.00023535
zeta-chain (TC	ENST0000045	Homo sapiens	NM_001079	-0.7537277	8.66E-06	0.00016468
family with se	ENST0000039	Homo sapiens	NM_173511	-0.7540708	1.18E-08	8.75E-07
vasohibin 1	ENST000001(	Homo sapiens	NM_014909	-0.7540926	0.00026472	0.00242114
chromosome	ENST0000025	Homo sapiens	NM_024093	-0.7553878	1.97E-05	0.0003166
GTPase, IMAP	ENST0000061	Homo sapiens	NM_024711	-0.7560296	3.01E-11	8.41E-09
complement c	ENST0000037	Homo sapiens	NM_015991	-0.7580255	0.00071137	0.00531549
interferon reg	ENST0000047	Homo sapiens	NM_0010986	-0.7581334	0.00068799	0.00517442
ATPase, H+ tra	ENST000003(	Homo sapiens	NM_130463	-0.7593545	0.00044028	0.00361836
chemokine-lik	ENST0000055	Homo sapiens	NM_004072	-0.7610433	1.24E-09	1.39E-07
raftlin, lipid ra	ENST0000033	Homo sapiens	NM_015150	-0.7612522	1.07E-08	8.18E-07
CD3e molecul	ENST0000053	Homo sapiens	NM_000733	-0.7619586	5.59E-08	3.00E-06
keratin 81, typ	ENST0000032	Homo sapiens	NM_002281	-0.7639031	1.85E-06	4.78E-05
CD4 molecule	ENST0000001	Homo sapiens	NM_000616	-0.7649276	8.61E-08	4.24E-06
G protein-cou	ENST0000053	Homo sapiens	NM_003485	-0.7653248	1.29E-06	3.54E-05
HIG1 hypoxia	ENST0000031	Homo sapiens	NR_002780	-0.7656841	0.00019691	0.00191614
SLP adaptor a	ENST0000057	SLP adaptor a	ENST0000057	-0.7701435	5.77E-06	0.00011911
lysophospholi	ENST0000037	Homo sapiens	NM_007260	-0.771443	0.00079365	0.00579903
killer cell imm	ENST0000062	Homo sapiens	NM_002255	-0.7746202	0.00020238	0.00195711
CD2 molecule	ENST000003(	Homo sapiens	NM_001767	-0.7749807	4.06E-05	0.00055948
family with se	ENST000003(	Homo sapiens	NM_0010109	-0.7776068	5.16E-05	0.0006768
poliovirus rec	ENST0000045	Homo sapiens	NM_024070	-0.7803634	2.81E-05	0.00041852
Enah/Vasp-lik	ENST0000055	Homo sapiens	NM_016337	-0.781052	1.56E-06	4.16E-05
GTPase, IMAP	ENST000003(	Homo sapiens	NM_175571	-0.7812471	2.17E-09	2.18E-07
lymphocyte-s	NA	Homo sapiens	NM_0012429	-0.7812974	0.00028793	0.00259135
runt-related t	ENST0000033	Homo sapiens	NM_0010316	-0.781804	1.21E-05	0.00021374
zonadhesin (g	ENST0000054	Homo sapiens	NM_173059	-0.7831972	0.00021588	0.00205522
spectrin, alph	ENST0000037	Homo sapiens	NM_0011304	-0.7836033	3.85E-06	8.57E-05
dual specificit	ENST0000033	Homo sapiens	NM_004420	-0.786533	0.00021333	0.00203467
N-acylethanol	ENST000005(	Homo sapiens	NM_0010424	-0.7865515	1.40E-07	6.18E-06
RAR-related o	ENST0000044	Homo sapiens	NM_134260	-0.7867627	4.23E-07	1.49E-05
folate recepto	ENST0000029	Homo sapiens	NM_000803	-0.7876738	2.58E-15	1.14E-11
BCL2-associat	ENST0000037	Homo sapiens	NM_0011724	-0.7887278	6.37E-05	0.00079481
purinergic rec	ENST0000026	Homo sapiens	NM_002562	-0.7907393	1.03E-07	4.87E-06

v-maf avian m	ENST0000037	Homo sapiens	NM_005461	-0.7912932	1.31E-05	0.0002281
ZFP41 zinc fin	ENST0000033	Homo sapiens	NM_173832	-0.7923297	4.87E-06	0.00010345
perforin 1 (po	ENST0000044	Homo sapiens	NM_005041	-0.7950449	7.11E-05	0.00086786
BCL2-associat	ENST0000046	Homo sapiens	NM_0011724	-0.7955873	0.00016456	0.00165747
chemokine (C	ENST0000024	Homo sapiens	NM_001838	-0.7956351	0.0001716	0.00171455
ring finger prc	ENST0000021	Homo sapiens	NM_017831	-0.7957855	4.31E-11	1.07E-08
family with se	ENST000003C	Homo sapiens	NM_0010352	-0.7987324	1.49E-05	0.00025339
tubulin tyrosi	NA	PREDICTED: H	XM_0034034	-0.7989133	0.00092803	0.00655802
tetraspanin 4	ENST0000046	Homo sapiens	NM_0010252	-0.8011591	1.54E-12	7.83E-10
solute carrier	ENST0000059	solute carrier	ENST0000059	-0.8049469	9.80E-08	4.69E-06
TOB1 antisens	NA	Homo sapiens	NR_038458	-0.8068337	0.00024334	0.00226971
LFNG O-fucosy	ENST0000035	Homo sapiens	NM_0010401	-0.8077943	2.76E-06	6.67E-05
CD6 molecule	ENST0000034	Homo sapiens	NM_006725	-0.8080382	1.86E-05	0.00030362
interleukin 7 r	ENST000003C	Homo sapiens	NM_002185	-0.8096447	5.66E-05	0.00072571
zinc finger prc	ENST0000054	Homo sapiens	NM_015481	-0.8097809	4.00E-12	1.62E-09
leukocyte imr	ENST0000042	Homo sapiens	NM_006669	-0.8097854	1.23E-05	0.00021682
SLP adaptor a	ENST0000057	Homo sapiens	NM_207103	-0.8115988	1.09E-09	1.26E-07
platelet-activa	ENST0000053	Homo sapiens	NM_0011647	-0.8133388	6.01E-05	0.0007577
neuralized E3	ENST0000036	Homo sapiens	NM_004210	-0.8142063	8.26E-08	4.11E-06
lymphoid enh	ENST000005C	Homo sapiens	NM_016269	-0.8146452	3.74E-05	0.00052407
three prime re	ENST0000044	Homo sapiens	NM_016381	-0.8199667	2.39E-05	0.00036904
pancreatic prc	ENST0000037	pancreatic prc	ENST0000037	-0.82238	0.00024516	0.00227919
proline rich 5	ENST0000043	Homo sapiens	NM_015366	-0.8226467	0.00013868	0.00144848
zinc finger prc	ENST0000059	Homo sapiens	NM_133460	-0.8232387	0.0005965	0.00462071
phosphatase,	ENST0000041	Homo sapiens	NM_0011438	-0.8249149	0.00033129	0.00288866
IQ motif and S	ENST0000037	Homo sapiens	NM_015075	-0.8253761	0.00012665	0.00134875
sparc/osteone	ENST0000037	Homo sapiens	NM_014767	-0.825429	5.08E-06	0.00010694
killer cell lecti	ENST0000054	Homo sapiens	NM_002259	-0.8273998	2.75E-06	6.66E-05
protein O-link	ENST0000037	Homo sapiens	NM_0012437	-0.8279861	9.08E-05	0.00104241
thymus, brain	ENST0000045	Homo sapiens	NM_152710	-0.8281633	7.37E-05	0.00088905
GTPase, IMAP	ENST0000047	Homo sapiens	NM_018384	-0.8290567	2.42E-10	3.89E-08
ADARB2 antis	NA	Homo sapiens	NR_033387	-0.8310757	0.0001152	0.00125582
plexin D1	ENST0000051	Homo sapiens	NM_015103	-0.8312951	2.26E-08	1.45E-06
toll-like recep	ENST0000038	Homo sapiens	NM_016562	-0.8326803	2.77E-06	6.69E-05
chromosome	ENST0000037	Homo sapiens	NM_153045	-0.8328558	3.99E-07	1.42E-05
cortistatin	ENST0000037	Homo sapiens	NM_001302	-0.8353128	0.00045916	0.00373979
chemokine (C	ENST0000029	Homo sapiens	NM_000579	-0.8356942	5.97E-07	1.94E-05
keratin 73, ty	ENST000003C	Homo sapiens	NM_175068	-0.8372994	0.00089961	0.00641195
solute carrier	ENST0000061	Homo sapiens	NM_006598	-0.8373239	1.96E-06	5.02E-05
SEC14-like 3 (S	NA	PREDICTED: H	XM_0052615	-0.8376035	0.00033848	0.0029378
peptidase inhi	ENST0000061	Homo sapiens	NM_153370	-0.8377885	2.60E-08	1.63E-06
StAR-related li	ENST0000058	Homo sapiens	NM_0011659	-0.8407558	3.47E-05	0.0004941
interleukin 32	ENST0000052	Homo sapiens	NM_0010126	-0.8446587	5.00E-06	0.00010547
UDP-GlcNAc:b	ENST0000059	Homo sapiens	NM_145236	-0.8462668	0.0005396	0.00426031
obscurin, cytc	ENST0000028	Homo sapiens	NM_052843	-0.8463704	3.43E-05	0.00049053
CD5 molecule	ENST0000034	Homo sapiens	NM_014207	-0.8505964	4.33E-06	9.42E-05
SH3 domain b	ENST0000034	Homo sapiens	NM_0010244	-0.8516559	2.28E-06	5.70E-05
acyl-CoA bind	ENST0000059	Homo sapiens	NM_024722	-0.8554202	0.00070611	0.00528894

IKAROS family	ENST0000045	Homo sapiens	NM_0010795	-0.8579042	4.40E-09	3.84E-07
MAM domain	ENST0000037	MAM domain	ENST0000037	-0.8640087	0.00016393	0.00165321
solute carrier	ENST0000048	Homo sapiens	NM_017585	-0.8647207	7.11E-07	2.21E-05
killer cell lecti	ENST0000061	Homo sapiens	NM_016523	-0.8653046	1.25E-07	5.64E-06
charged multi	ENST0000026	Homo sapiens	NM_016079	-0.8654055	0.00015821	0.0016068
AHNAK nuclec	ENST0000037	Homo sapiens	NM_001620	-0.8698748	2.65E-07	1.02E-05
hematopoieti	ENST0000061	Homo sapiens	NM_032855	-0.8717554	1.08E-06	3.08E-05
B-cell CLL/lym	ENST0000034	Homo sapiens	NM_138576	-0.8732096	1.26E-07	5.66E-06
major histoco	ENST0000041	Homo sapiens	NM_0011988	-0.8747309	1.78E-07	7.48E-06
caudal type h	ENST0000023	Homo sapiens	NM_001804	-0.8764015	0.00073388	0.00545088
mannose-binc	ENST0000048	Homo sapiens	NR_002724	-0.8779967	0.00015012	0.00154001
A2M antisense	NA	Homo sapiens	NR_026971	-0.8782049	8.13E-06	0.00015655
ADP-ribosylat	ENST0000039	Homo sapiens	NM_0012824	-0.8785979	1.24E-07	5.61E-06
RNA, 5.8S ribc	NA	Homo sapiens	NR_003285	-0.8804692	6.43E-06	0.00013063
neuronal grov	ENST000003C	Homo sapiens	NM_173808	-0.8818452	0.000184	0.00181556
cathepsin O	ENST0000043	Homo sapiens	NM_001334	-0.8826157	1.84E-11	5.77E-09
siah E3 ubiqui	ENST0000056	siah E3 ubiqui	ENST0000056	-0.8832127	0.00032613	0.00285244
adaptor-relate	ENST0000032	Homo sapiens	NM_003916	-0.8883842	1.66E-09	1.75E-07
G-protein sign	ENST0000039	Homo sapiens	NM_0011456	-0.8885398	0.0008119	0.0059012
ADORA2A anti	NA	Homo sapiens	NR_028483	-0.8886622	5.25E-05	0.000686
hemogen	ENST0000061	Homo sapiens	NM_018437	-0.8909767	0.00013091	0.00138411
major histoco	ENST0000046	Homo sapiens	NM_006120	-0.8913561	4.86E-11	1.17E-08
laminin, beta	ENST0000039	laminin, beta	ENST0000039	-0.8919138	0.00019702	0.00191659
T-box 21	ENST0000017	Homo sapiens	NM_013351	-0.8941216	1.45E-05	0.00024861
prostate canc	ENST0000059	Homo sapiens	NR_040109	-0.8941726	0.00036078	0.00310047
ZNF205 antise	NA	Homo sapiens	NR_024166	-0.9006877	3.93E-05	0.00054472
ASB16 antisen	NA	Homo sapiens	NR_049729	-0.9019913	0.00015353	0.00156933
solute carrier	ENST0000052	Homo sapiens	NM_198277	-0.9039866	1.63E-08	1.11E-06
sorbin and SH	ENST0000024	Homo sapiens	NM_005775	-0.9098712	5.70E-06	0.00011806
serine/arginin	ENST0000034	Homo sapiens	NM_054016	-0.9134792	0.00024427	0.00227501
C-type lectin c	ENST0000057	Homo sapiens	NM_182906	-0.913802	5.05E-10	6.90E-08
natural cytotc	ENST0000037	Homo sapiens	NM_147130	-0.9146282	5.00E-06	0.00010547
keratin associ	ENST0000033	Homo sapiens	NM_181624	-0.9167837	0.00055664	0.00436439
lysophosphati	ENST0000034	Homo sapiens	NM_005767	-0.9168567	1.69E-09	1.77E-07
class II, major	ENST0000061	Homo sapiens	NM_000246	-0.9179856	1.01E-11	3.52E-09
membrane-sp	ENST0000052	Homo sapiens	NM_032597	-0.9185863	7.38E-10	9.09E-08
purinergic rec	ENST0000032	purinergic rec	ENST0000032	-0.9194948	9.95E-09	7.73E-07
dolichyl-phos	ENST0000034	Homo sapiens	NM_018973	-0.9196178	5.88E-06	0.00012107
STE20-related	ENST0000039	Homo sapiens	NM_018571	-0.9208628	0.00047343	0.00383388
N-acetyltransf	ENST0000053	Homo sapiens	NM_024662	-0.9238812	6.35E-05	0.00079279
TEX26 antisen	NA	Homo sapiens	NR_038287	-0.9281491	0.00040865	0.00340525
v-myb avian m	ENST0000052	Homo sapiens	NM_0010804	-0.9292749	1.04E-06	2.98E-05
SLP adaptor a	ENST0000057	Homo sapiens	NM_207103	-0.9294219	6.41E-10	8.25E-08
killer cell lecti	ENST0000053	Homo sapiens	NM_005810	-0.9324201	4.39E-05	0.00059442
retinoic acid r	ENST0000061	Homo sapiens	NM_0010248	-0.93489	0.00069426	0.00521274
sterile alpha m	ENST0000055	Homo sapiens	NM_015589	-0.935534	6.60E-06	0.00013332
interleukin 17	ENST0000034	Homo sapiens	NM_0010016	-0.9399216	0.0001862	0.00183262
T-cell lympho	ENST0000054	Homo sapiens	NM_003253	-0.9429646	9.69E-11	1.98E-08

sterile alpha n	ENST0000034	Homo sapiens	NM_152486	-0.9433666	8.85E-05	0.00102278
tumor necrosi	ENST0000051	Homo sapiens	NM_148965	-0.9445517	1.65E-06	4.34E-05
phosphotyros	ENST000003	Homo sapiens	NM_017933	-0.945362	2.32E-13	2.00E-10
ORMDL sphin	ENST0000057	Homo sapiens	NM_139280	-0.9456297	1.35E-05	0.00023371
aldehyde deh	ENST000002	Homo sapiens	NM_000689	-0.9456902	1.10E-10	2.18E-08
CD300e mole	ENST000003	Homo sapiens	NM_181449	-0.9459956	1.43E-09	1.56E-07
A2M antisens	NA	Homo sapiens	NR_026971	-0.9472808	4.30E-07	1.50E-05
LFNG O-fucos	ENST0000061	Homo sapiens	NM_0010401	-0.9550521	2.48E-09	2.40E-07
caspase recrui	ENST0000048	Homo sapiens	NM_052813	-0.9550832	4.46E-11	1.10E-08
major histoco	ENST0000041	Homo sapiens	NM_006120	-0.9560468	2.77E-12	1.27E-09
neuromedin U	ENST000003C	Homo sapiens	NM_006056	-0.95606	6.72E-08	3.50E-06
solute carrier	ENST0000055	Homo sapiens	NM_0011261	-0.9564708	4.10E-09	3.66E-07
cystatin D	ENST000003C	Homo sapiens	NM_001900	-0.9612767	4.06E-09	3.66E-07
agrin	ENST000004E	Homo sapiens	NM_198576	-0.9636802	0.00010276	0.00114792
Fc receptor-lil	ENST0000032	Homo sapiens	NM_0012842	-0.969503	1.11E-05	0.00020187
H6 family hon	ENST0000033	Homo sapiens	NM_005519	-0.9703418	0.00011078	0.00121964
CD247 molecu	ENST0000048	Homo sapiens	NM_198053	-0.9716818	2.19E-07	8.74E-06
ribonucleopro	ENST0000061	Homo sapiens	NM_133452	-0.9720492	0.00099347	0.00693575
family with se	ENST0000042	Homo sapiens	NM_024519	-0.9734603	7.61E-06	0.00014864
ribosomal RNA	ENST0000045	Homo sapiens	NR_002184	-0.9764283	2.05E-05	0.00032686
von Willebran	ENST0000033	Homo sapiens	NM_022834	-0.9814999	0.00076435	0.00563404
HGF activator	ENST0000038	Homo sapiens	NM_0012974	-0.9918966	9.64E-05	0.00109122
napsin B aspar	ENST0000053	Homo sapiens	NR_002798	-0.9950177	3.88E-08	2.27E-06
ABI family, me	ENST0000041	Homo sapiens	NM_016428	-1.000869	3.06E-12	1.35E-09
LINGO1 antise	NA	Homo sapiens	NR_045123	-1.0083258	0.00030831	0.00273594
major histoco	ENST000004E	Homo sapiens	NR_001435	-1.0097	2.13E-11	6.62E-09
dual specificit	ENST0000027	Homo sapiens	NM_001946	-1.0100087	1.61E-10	2.92E-08
olfactomedin-	ENST000002	Homo sapiens	NM_015441	-1.0108326	7.43E-05	0.00089322
SID1 transmer	ENST0000062	Homo sapiens	NM_0010404	-1.0120722	2.35E-11	7.06E-09
potassium cha	ENST0000051	Homo sapiens	NM_004519	-1.0166426	0.00075867	0.00560152
polymerase (R	ENST0000051	polymerase (R	ENST0000051	-1.0173138	0.00013363	0.00140522
myeloma over	ENST0000053	Homo sapiens	NM_138768	-1.02341	7.93E-05	0.00093504
STE20-related	ENST0000041	Homo sapiens	NM_018571	-1.0236229	0.00027005	0.00246115
nephroblastor	ENST0000025	Homo sapiens	NM_002514	-1.0289866	5.49E-07	1.82E-05
chloride intra	NA	Homo sapiens	NM_004669	-1.0290707	8.70E-07	2.57E-05
mex-3 RNA bir	ENST000004C	Homo sapiens	NM_203304	-1.0312934	8.81E-05	0.00101988
leucine-rich re	ENST0000043	Homo sapiens	NM_0011615	-1.0339263	2.81E-07	1.07E-05
high mobility	ENST0000061	Homo sapiens	NM_006339	-1.0341078	0.00016388	0.00165321
CD74 molecul	ENST0000052	Homo sapiens	NM_0010251	-1.043362	3.59E-11	9.52E-09
SH2 domain c	ENST000003E	Homo sapiens	NM_053282	-1.0466324	2.77E-07	1.05E-05
cystatin C	ENST000003	Homo sapiens	NM_000099	-1.0510165	6.22E-10	8.07E-08
potassium cha	ENST0000047	Homo sapiens	NM_004977	-1.0523915	0.00011796	0.00127584
hemoglobin, t	ENST0000019	Homo sapiens	NM_005331	-1.0586485	2.39E-05	0.00036964
coiled-coil do	ENST0000047	Homo sapiens	NM_0010317	-1.0638768	1.41E-05	0.00024262
GTPase activat	ENST000003	GTPase activat	ENST000003	-1.0733426	0.00046267	0.00376047
G protein-cou	ENST0000031	Homo sapiens	NM_019858	-1.0741075	1.41E-09	1.54E-07
chemokine (C-	ENST0000043	Homo sapiens	NR_002712	-1.0743737	2.68E-05	0.0004034
crystallin, alp	ENST000002	Homo sapiens	NM_000394	-1.0835498	0.00010849	0.001199

natriuretic pe	ENST0000037	natriuretic pe	ENST0000037	-1.0863415	0.00022899	0.0021566
acyl-CoA syntl	ENST0000056	Homo sapiens	NM_017888	-1.0910149	7.56E-05	0.00090176
napsin B aspar	ENST0000056	Homo sapiens	NR_002798	-1.0942767	2.97E-08	1.82E-06
uncharacteriz	NA	Homo sapiens	NR_026961	-1.0960095	2.23E-13	1.98E-10
NK1 homeobc	NA	Homo sapiens	NM_0011463	-1.096256	3.83E-05	0.00053388
mannosyl-olig	ENST0000046	Homo sapiens	NM_006302	-1.1032199	3.27E-06	7.60E-05
major histoco	ENST0000061	Homo sapiens	NM_021983	-1.103826	6.38E-07	2.03E-05
Ras associatio	ENST0000048	Homo sapiens	NM_032023	-1.1044125	6.53E-13	3.97E-10
olfactory rece	NA	Homo sapiens	NR_120438	-1.1050879	4.29E-05	0.00058469
interleukin 2 r	ENST0000021	Homo sapiens	NM_000878	-1.1055086	1.54E-08	1.07E-06
chromosome	ENST0000038	Homo sapiens	NM_0012566	-1.1059341	0.0001647	0.00165776
nyctalopin	ENST0000037	Homo sapiens	NM_022567	-1.1082074	0.00028836	0.00259446
granulysin	ENST0000048	Homo sapiens	NM_006433	-1.1107762	5.75E-05	0.00073466
testis-specific	ENST0000043	Homo sapiens	NR_001552	-1.1109744	0.0002653	0.00242573
major histoco	ENST0000039	Homo sapiens	NM_0012439	-1.1113721	3.34E-07	1.22E-05
F-box and leuc	ENST0000061	Homo sapiens	NM_0011633	-1.1113903	1.36E-05	0.00023569
CTBP1 antisen	NA	Homo sapiens	NR_033339	-1.114316	1.55E-05	0.00026178
otoancorin	ENST0000056	otoancorin [S	ENST0000056	-1.1166027	0.00011705	0.0012691
oxysterol binc	ENST0000038	Homo sapiens	NM_020896	-1.1175662	3.72E-12	1.56E-09
sulfatase 2	ENST0000046	Homo sapiens	NM_018837	-1.1191218	3.89E-07	1.39E-05
Smith-Magenis	NA	ag52h12.x5 G	AI821758	-1.1261715	0.00010927	0.00120586
G protein-cou	ENST0000037	Homo sapiens	NM_005293	-1.1292608	2.03E-08	1.33E-06
mannose rece	ENST0000058	Homo sapiens	NM_006039	-1.1454802	3.21E-05	0.00046751
carboxypeptic	ENST0000061	Homo sapiens	NM_019029	-1.1604005	4.72E-08	2.64E-06
gamma-aminc	ENST0000051	Homo sapiens	NM_014211	-1.1708054	9.46E-05	0.00107581
NPC1-like 1	ENST0000054	Homo sapiens	NM_013389	-1.1781348	0.00021548	0.00205237
USP2 antisens	NA	Homo sapiens	NR_034160	-1.1787005	0.00030536	0.00271828
ELMO/CED-12	ENST0000048	Homo sapiens	NM_032213	-1.1947056	6.38E-06	0.00012983
macrophage e	ENST0000036	Homo sapiens	NM_0010393	-1.1947985	3.06E-14	5.15E-11
von Willebran	ENST0000033	Homo sapiens	NM_152718	-1.2111913	2.66E-05	0.00040221
G protein-cou	ENST0000031	Homo sapiens	NM_022049	-1.2212699	0.00014738	0.00152099
POU class 2 hc	ENST0000052	Homo sapiens	NM_0012070	-1.2266529	1.56E-05	0.00026293
major histoco	ENST0000041	Homo sapiens	NM_022555	-1.2272143	1.30E-11	4.35E-09
proline rich m	ENST0000047	Homo sapiens	NM_178013	-1.2282586	4.48E-05	0.00060432
major histoco	ENST000004C	Homo sapiens	NM_002121	-1.2293264	3.47E-12	1.51E-09
major histoco	ENST000004C	Homo sapiens	NM_002121	-1.2416325	4.56E-12	1.77E-09
major histoco	ENST0000047	Homo sapiens	NM_0012439	-1.2424373	2.25E-11	6.92E-09
major histoco	ENST0000061	Homo sapiens	NM_019111	-1.2446559	2.51E-12	1.18E-09
fibrinogen-lik	ENST0000024	Homo sapiens	NM_006682	-1.2470591	2.84E-10	4.37E-08
chemokine-lik	ENST0000031	Homo sapiens	NM_0011423	-1.2505884	8.96E-11	1.85E-08
homeobox A1	ENST0000061	Homo sapiens	NM_018951	-1.2564168	8.64E-06	0.00016433
fibrosin	ENST0000054	Homo sapiens	NM_0011050	-1.2567916	1.72E-05	0.00028476
major histoco	ENST0000046	Homo sapiens	NM_0012439	-1.2588891	8.72E-09	6.89E-07
major histoco	ENST0000047	Homo sapiens	NM_002121	-1.2596356	9.93E-13	5.50E-10
family with se	ENST0000037	Homo sapiens	NM_182623	-1.2709757	8.12E-06	0.00015643
Rho guanine n	ENST0000037	Homo sapiens	NM_018125	-1.2743587	3.63E-16	2.87E-12
WAS protein f	ENST000006C	Homo sapiens	NR_033266	-1.2768674	0.00040309	0.0033698
lin-9 DREAM M	ENST0000032	Homo sapiens	NM_173083	-1.2790498	0.0001151	0.00125543

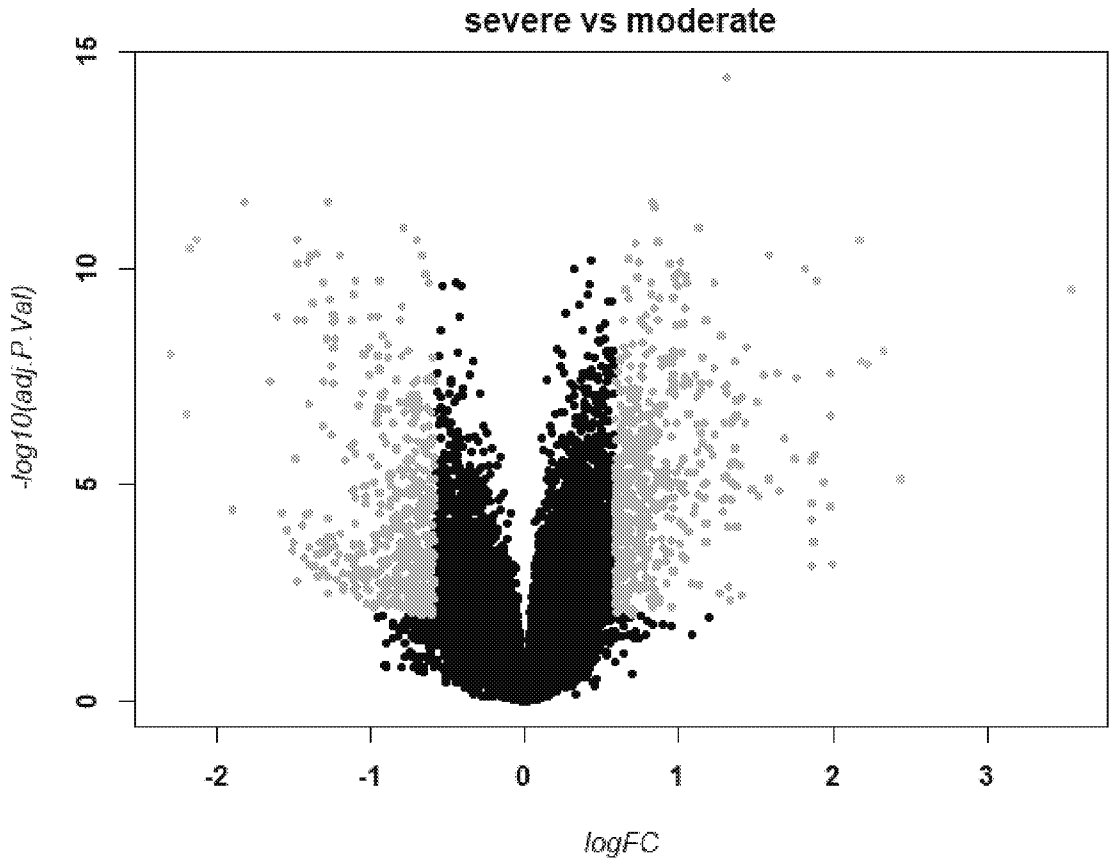
prostaglandin	ENST0000044	Homo sapiens	NM_000954	-1.2804765	2.47E-06	6.10E-05
plexin B2	ENST0000046	Homo sapiens	NM_012401	-1.283273	1.28E-11	4.35E-09
leucine-rich re	ENST0000048	Homo sapiens	NM_0010174	-1.2842199	2.27E-05	0.00035447
chromosome	ENST0000062	Homo sapiens	NM_0012566	-1.2873769	1.45E-05	0.00024833
ankyrin repeat	ENST0000054	Homo sapiens	NM_182608	-1.2912433	1.25E-05	0.00021962
v-myc avian m	NA	Homo sapiens	NM_0010330	-1.3036846	2.81E-13	2.11E-10
major histoco	ENST0000048	Homo sapiens	NM_002123	-1.3041479	2.60E-10	4.12E-08
sterol regulato	ENST0000057	Homo sapiens	NM_0010052	-1.3060042	7.55E-05	0.00090176
major histoco	ENST0000037	Homo sapiens	NM_002125	-1.3082059	5.14E-09	4.37E-07
lactalbumin, a	ENST000003C	Homo sapiens	NM_002289	-1.3085484	1.14E-05	0.00020472
zinc finger pro	ENST0000059	zinc finger pro	ENST0000059	-1.3173591	2.34E-05	0.00036434
centrosomal p	ENST0000037	centrosomal p	ENST0000037	-1.317534	2.40E-05	0.00037033
spectrin repea	ENST0000036	Homo sapiens	NM_182961	-1.3267215	1.17E-05	0.00020899
hes family bHI	ENST000003C	Homo sapiens	NM_021170	-1.3395031	0.00011624	0.00126341
proline-rich c	ENST000004C	Homo sapiens	NM_013318	-1.3409059	2.59E-05	0.0003938
major histoco	ENST0000046	Homo sapiens	NM_002118	-1.3514981	2.19E-14	4.53E-11
keratin associa	ENST0000061	Homo sapiens	NM_198699	-1.3636096	6.09E-05	0.00076547
major histoco	ENST0000042	Homo sapiens	NM_002124	-1.3750554	1.19E-12	6.27E-10
major histoco	ENST0000046	Homo sapiens	NM_0012425	-1.3908004	3.07E-14	5.15E-11
interleukin 4 i	ENST0000059	Homo sapiens	NM_152899	-1.3926836	1.23E-09	1.39E-07
zinc finger, CC	ENST000006C	zinc finger, CC	ENST000006C	-1.3943304	1.69E-05	0.00028103
BPI fold conta	ENST0000017	Homo sapiens	NM_025227	-1.3950244	5.18E-05	0.00067886
spondin 2, ext	ENST0000061	Homo sapiens	NM_012445	-1.3950567	1.66E-06	4.36E-05
cat eye syndro	ENST0000026	Homo sapiens	NM_0012822	-1.410666	5.43E-14	7.52E-11
major histoco	ENST0000048	Homo sapiens	NM_0012439	-1.4160871	1.94E-06	4.99E-05
VIPR1 antisen	NA	Homo sapiens	NR_046654	-1.4253198	3.24E-05	0.00047121
G protein-cou	ENST0000052	Homo sapiens	NM_0010771	-1.4333402	4.20E-12	1.65E-09
family with se	ENST0000061	Homo sapiens	NM_138344	-1.4473445	4.01E-06	8.88E-05
ADP-ribosylat	ENST0000061	ADP-ribosylat	ENST0000061	-1.469774	0.00016277	0.00164424
major histoco	ENST0000039	Homo sapiens	NM_002121	-1.4748137	3.58E-12	1.54E-09
macrophage e	ENST0000036	Homo sapiens	NM_0010393	-1.4753544	5.97E-15	2.24E-11
major histoco	ENST0000051	Homo sapiens	NM_033554	-1.4789378	6.39E-14	7.63E-11
G protein-cou	ENST0000038	Homo sapiens	NM_201525	-1.4871782	4.53E-08	2.55E-06
chromosome	ENST0000041	Homo sapiens	NM_0012864	-1.495579	1.15E-05	0.00020627
ZNF337 antise	NA	Homo sapiens	NR_126467	-1.4991434	1.19E-05	0.00021167
collagen, type	ENST0000038	Homo sapiens	NM_0011637	-1.5115875	2.11E-05	0.00033434
glutamate deh	NA	Homo sapiens	NR_111968	-1.5453668	5.54E-06	0.00011568
zinc finger pro	ENST0000059	zinc finger pro	ENST0000059	-1.5757308	1.69E-06	4.43E-05
membrane-sp	ENST0000035	Homo sapiens	NM_021201	-1.6080282	2.89E-12	1.30E-09
chemokine (C-	ENST0000054	Homo sapiens	NM_001337	-1.656473	2.71E-10	4.26E-08
Rho guanine n	ENST0000016	Homo sapiens	NM_018125	-1.8186919	3.70E-16	2.87E-12
PRKAR2A anti	NA	Homo sapiens	NR_109996	-1.8929197	1.39E-06	3.77E-05
transforming g	ENST000005C	Homo sapiens	NM_000358	-2.1303995	7.85E-15	2.24E-11
colony stimul	ENST0000028	Homo sapiens	NM_005211	-2.1693844	1.53E-14	3.38E-11
lectin, galactc	ENST0000021	Homo sapiens	NM_006498	-2.1962076	2.44E-09	2.39E-07
cyclin-depend	ENST0000061	Homo sapiens	NM_000076	-2.2907348	3.91E-11	1.00E-08

DEGs subset2

```
> lim.FC; lim.P
[1] 0.5849625
[1] 0.01
```

```
> dim(y5)
[1] 1005  125
> dim(up1)
[1] 525 125
> dim(down1)
[1] 480 125
```

```
# Add colored points:
with(subset(y2, abs(logFC)>lim.FC & adj.P.Val<lim.P),
     points(logFC, -log10(adj.P.Val), pch=20, col="orange"))
with(subset(y2, adj.P.Val<0.001 & abs(logFC)>2),
     points(logFC, -log10(adj.P.Val), pch=20, col="green"))
```



To SIG consortium:
limma_DEG_subset2_severe_mod_low_thresh_131020.xlsx

From:	Baric, Toni C[antoinette_baric@med.unc.edu]
Attendees:	Gralinski, Lisa E; Menachery, Vineet; Baric, Ralph S; Ralph Baric
Location:	https://zoom.us/j/91896758073?pwd= **552.136**
Importance:	Normal
Subject:	Call to discuss SIG Annual Meeting
Start Time:	Sun 10/4/2020 7:30:00 AM (UTC-05:00)
End Time:	Sun 10/4/2020 8:00:00 AM (UTC-05:00)
Required Attendees:	Baric, Toni C; Gralinski, Lisa E; Menachery, Vineet; Baric, Ralph S
Optional Attendees:	Ralph Baric

Antoinette Baric is inviting you to a scheduled Zoom meeting.

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From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

Location: https://www.zoomgov.com/j/1611090134?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV2 Variant Testing Discussion

Start Time: Thur 1/28/2021 7:00:00 AM (UTC-06:00)

End Time: Thur 1/28/2021 8:00:00 AM (UTC-06:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

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From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: Third Webinar for Systems Immunology Program

Start Time: Thur 4/1/2021 12:00:00 PM (UTC-06:00)

End Time: Thur 4/1/2021 1:00:00 PM (UTC-06:00)

Required Attendees: Liu, Joy (NIH/NIAID) [E]; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 10:01 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Leitner, Wolfgang (NIH/NIAID) [E]; Diercks, Alan; Bruce Beutler
Subject: Third Webinar for Systems Immunology Program
When: Thursday, April 1, 2021 2:00 PM-3:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

According to your availability, our third webinar will be held from 2:00 to 3:00 PM EDT on April 1st. **Richard Ulevitch's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

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From: Liu, Joy (NIH/NIAID) [E][liujoy@niaid.nih.gov]

Attendees: Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

Location: Zoom meeting

Importance: Normal

Subject: FW: First Webinar for Systems Immunology Program

Start Time: Wed 3/17/2021 1:00:00 PM (UTC-06:00)

End Time: Wed 3/17/2021 2:00:00 PM (UTC-06:00)

Required Attendees: Liu, Joy (NIH/NIAID) [E]; Baric, Ralph S; Cornett, Cathy; Gralinski, Lisa E; Heise, Mark T; JACKIE V. BERHORST (jdao@uw.edu); Jennifer M. Lund; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Ferris, Martin Thomas; Menachery, Vineet; mgale@u.washington.edu; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shannon McWeeney; Suthar, Mehul S. (mehul.s.suthar@emory.edu)

-----Original Appointment-----
From: Liu, Joy (NIH/NIAID) [E] <liujoy@niaid.nih.gov>
Sent: Tuesday, February 16, 2021 9:51 AM
To: Liu, Joy (NIH/NIAID) [E]; Arlene Sharpe; Jonathan Kagan; Baric, Ralph S; Heise, Mark T; Ulevitch, Richard; Diercks, Alan; Bruce Beutler; Leitner, Wolfgang (NIH/NIAID) [E]
Subject: First Webinar for Systems Immunology Program
When: Wednesday, March 17, 2021 3:00 PM-4:00 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Zoom meeting

Dear All,

Thank you for your responses. I have set up the dates and times for our webinar according to your availability. The first webinar will be held from 3:00 to 4:00 PM EDT on March 17th. **Arlene Sharpe's group will give us a 45-min presentation. We will have 15 minutes for Q&A after that. Ideally, the topic would be COVID-19 related. Please forward the invitation to the laboratories in your group**. Please use the following information to access the meeting. Please let me know if you have any questions.

Best regards,
Joy Liu

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Passcode: **552.136**

From: Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]

Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Ho, David D.

Location: https://nih.zoomgov.com/j/1619922848?pwd=bzUxRXErSFJ6STNSZklpYXU4cWNIdz09

Importance: Normal

Subject: Leah Vincent (NIAID)'s Zoom Meeting

Start Time: Fri 4/30/2021 7:30:00 AM (UTC-05:00)

End Time: Fri 4/30/2021 8:30:00 AM (UTC-05:00)

Required Attendees: Vincent, Leah (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Ho, David D.

Good morning,
Please use this link for today's meeting only. Apologies for issues this morning.

Leah

Leah Vincent (NIAID) is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
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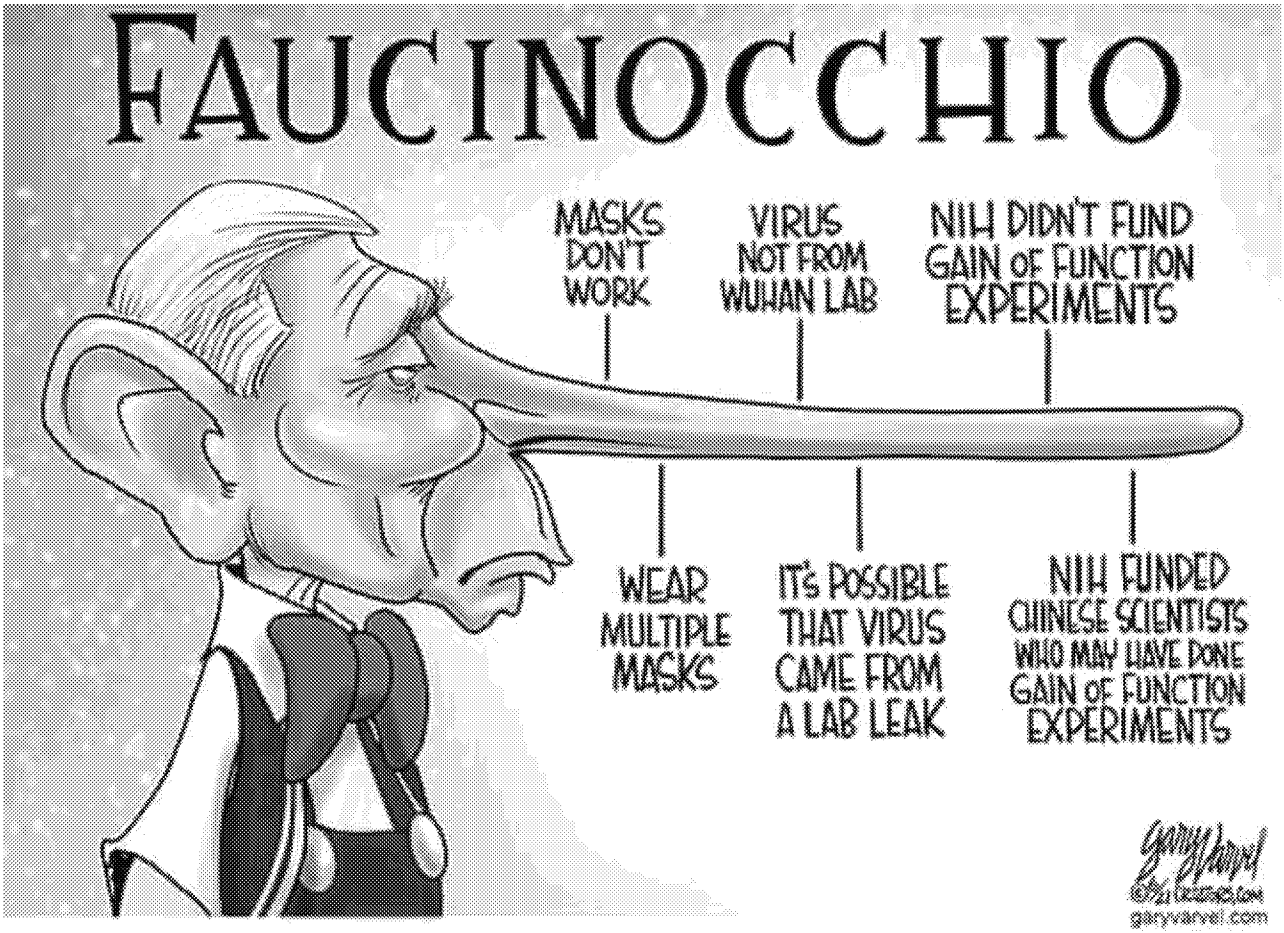
From: Vinu Arumugham [vaccine.safety@aol.com]
Sent: 6/7/2021 2:24:28 AM
To: kanchanmvk@yahoo.com; ushamvk@yahoo.co.in; mike.agogliati@wfsb.com; fox2newsdesk@foxtv.com; wjbkwebteam@foxtv.com; [wjbkwebteam@foxtv.com]; sanjay.mishra@Vanderbilt.Edu; kienym@who.int; Pasi.Penttinen@ecdc.europa.eu; sbaldwin@idri.org; friedem@who.int; angela.shen@hhs.gov; Bruce.Gellin@sabin.org; cww@austin.utexas.edu; henaorestrepoa@who.int; www.felix@konpotey-ahulu.com; olin0012@umn.edu; sinabavari@comcast.net; maryam.keshtkar@jhmi.edu; corey.casper@idri.org; theiland@immunomix.com; ProjanSJ@medimmune.com; schleiss@umn.edu; mail@wired.com; submit@wired.com; megan_molteni@wired.com; Claire-Anne.Siegrist@medecine.unige.ch; tyagi@ebi.ac.uk; Nick.Furnham@lshtm.ac.uk; betsy.mckay@wsj.com; kris.maher@wsj.com; conall.jones@wsj.com; brianna.abbott@wsj.com; Christopher.Weaver@wsj.com; jared.hopkins@wsj.com; Peter.Loftus@dowjones.com; jon.kamp@wsj.com; Holman.Jenkins@wsj.com; sarah.toy@wsj.com; moderator@wsj.com; susan.pulliam@wsj.com; drew.hinshaw@wsj.com; JEREMY.PAGE@WSJ.COM; jonathan.rockoff@wsj.com; mccormick.john@wsj.com; constantine.panagiotatos@dowjones.com; t.sanfilippo@dowjones.com; James.Freeman@wsj.com; newley.purnell@wsj.com; dschui@cuhk.edu.hk; wpchnwr@who.int; wpchnmedia@who.int; wprocom@who.int; mediainquiries@who.int; 13698665@qq.com; lifang@umn.edu; LDu@nybc.org; kyyuen@hku.hk; mark.woolhouse@ed.ac.uk; Christopher.Whitty@lshtm.ac.uk; Menachery, Vineet [vimenach@UTMB.EDU]; jiwei_yunlong@126.com; Jennifer.Layden@Illinois.gov; rothe@lrz.uni-muenchen.de; zhangyongzhen@shphc.org.cn; sanchak@gmail.com; badrishanthi@hotmail.com; gmaclaren@iinet.net.au; ljli@zju.edu.cn; sunguibo@126.com; suoban@simm.ac.cn; wiv@wh.iov.cn; yqi@implad.ac.cn; kalisvar_marimuthu@ncid.sg; oon_tek_ng@ncid.sg; Linfa.wang@csiro.au; zlshi@wh.iov.cn; ahong22@wustl.edu; andley@wustl.edu; apte@wustl.edu; arlee@wustl.edu; bassnett@wustl.edu; bhorade@wustl.edu; brian.s.clark@wustl.edu; brosenthal@wustl.edu; chenshiming@wustl.edu; couchS@wustl.edu; custer@wustl.edu; demetruliasa@wustl.edu; eric.harris@wustl.edu; erin.sieck@wustl.edu; ferguson@wustl.edu; harocopos@wustl.edu; hoekel@wustl.edu; huangandrew@wustl.edu; jlmorgan@wustl.edu; jones.j.k@wustl.edu; julia.pulliam@wustl.edu; kass@wustl.edu; kdohrman@wustl.edu; kefalov@wustl.edu; kerschensteinerd@wustl.edu; lhassman@wustl.edu; lueder@wustl.edu; lukasiewicz@wustl.edu; maamarir@wustl.edu; mae@wustl.edu; margaret.reynolds@wustl.edu; margolist@wustl.edu; markbarlow@wustl.edu; mblatt@wustl.edu; migneco@wustl.edu; montanac@wustl.edu; mortonsmith@wustl.edu; nathantuttle@wustl.edu; nicklasa@wustl.edu; njamin@email.wustl.edu; obrienm@wustl.edu; piggottk@wustl.edu; p.ruzycki@wustl.edu; prwillia@wustl.edu; rajagopalr@wustl.edu; rallo@wustl.edu; raopk@wustl.edu; ravi@wustl.edu; sarahgore@wustl.edu; shepherd@wustl.edu; sheybaniar@wustl.edu; shiels@wustl.edu; siegfried@wustl.edu; smith.robert.e@wustl.edu; sotof@wustl.edu; steskaJ@wustl.edu; stunkell@wustl.edu; tsai@wustl.edu; tychsen@wustl.edu; vanstaverng@wustl.edu; vollmanD@wustl.edu; wieder@wustl.edu; kmpruss@wustl.edu; katharine.m.lee@wustl.edu; david.szymkowski@xencor.com; virgil.schijns@wur.nl; valerijus.ostapenko@vuoi.lt; agata.mlynska@vuoi.lt; vita.pasukoniene@vuoi.lt; adas@arbata.lt; strioga@gmail.com; marius.strioga@vuoi.lt; media.relations@roche.com; murthy.aditya@gene.com; joshua.wallach@yale.edu; alexander.egilman@yale.edu; margaret.e.mccarthy@yale.edu; jennifer.miller@nyumc.org; steven.woloshin@dartmouth.edu; lisa.schwartz@dartmouth.edu; joseph.ross@yale.edu; karen.peart@yale.edu; lacevedo@jbrpt.org; johan.neyts@kuleuven.be; kai.dallmeier@kuleuven.be; hendrikjan.thibaut@kuleuven.be; manjunath.k@zyduscadila.com; rajeshbahekar@zyduscadila.com; ashokd.jaiswal@zyduscadila.com; kevinkumarkansagra@zyduscadila.com; poonamgiri@zyduscadila.com; mukul.jain@zyduscadila.com; abhijitchatterjee@zyduscadila.com; amitjoharapurkar@zyduscadila.com; nuggehally.srinivas@zyduscadila.com; sameeragarwal@zyduscadila.com; Deven.Parmar@zyduscadila.com; maulikr.patel@zyduscadila.com; jainebrownell@yahoo.com; dougmcmahon@hotmail.com; terijeffers@gmail.com; tneeno@allergyalaska.com; nojojain@yahoo.com; pierresakali@aol.com; cmawer@taais.org; oleag@aol.com; allergyasthmacare@gmail.com; kshaw@texallergy.com; Lumrymd@att.net; segurat@mwaac.com; katzcats@msn.com; osaaisecretary@gmail.com; larissa_and_justin@msn.com; gwickern@gmail.com; andrew.smithmd@utahallergies.com; nicole@nwasthma.com; pchristi@u.washington.edu; kevin.dooms@gmail.com; kkvolkman@gmail.com; pearl.b.scott@kp.org; naveena.bobba@gmail.com; email.csaai@gmail.com; sbonillamd@gmail.com; sgierer@kumc.edu; dakotaallergy@mac.com; laallergysociety@gmail.com; marilyn@usc.edu; timandleah@hotmail.com; dinovids@hotmail.com; michael.h.land@kp.org; wsaai.email@gmail.com; amywsmd@gmail.com; tmiller@sacent.com; avtwang@gmail.com; andojrr001@hawaii.rr.com; sm4@medicine.wisc.edu; tguastella@outlook.com; bmcclimon@mahealthcare.com; lbethea@allergyasthmadoc.net; nnakhtar@aol.com; stuartabramson@shannonhealth.org; teepstein@allergypartners.com; drmlvand@aol.com; dredara@yahoo.com; rcorriel.md@gmail.com; bgchandr@optonline.net; jmfactor@comcast.net; jaydry@gmail.com; wanda.phipatanakul@childrens.harvard.edu; andrewcmd@aol.com; dbcoyle3@yahoo.com; hkm@buffalo.edu; mkatlan@nycap.rr.com; eweis@aair.info; tprince@allergyasc.com; kellybmd@yahoo.com;

	kuriakose@hudsonallergy.com; bnovick@prohealthcare.com; rtg2112@gmail.com; setti5@aol.com; aricci3640@msn.com; todd.green@chp.edu; henochmd@burkemed.net; mwydila@comcast.net; shlakhani@hotmail.com; metroallergy@gmail.com; hotto@familyallergy.com; leigh.kerns@uhhospitals.org; jennbullock@yahoo.com; jennygentner@gmail.com; mprema11@gmail.com; Magee.Defelice@nemours.org; petrovaa@upmc.edu; jalvasimpson@verizon.net; wsoong@alabamaallergy.com; specsoc@aol.com; wdavidson@lungmds.com; john@eaallergy.com; jlieber1@uthsc.edu; sbl246@aol.com; tomlupoli@gmail.com; fsu_md@yahoo.com; faais@aol.com; dr.thomaschacko@gmail.com; ksheerin@atlantaallergy.com
Subject:	Contaminated vaccines killed 3.5 million; It's a US funded Chinese lab virus; Regulation failure: Formal FDA petitions/lawsuit to withdraw ALL vaccines

Government "scientists", "top virologists", "top medical journals", Big Tech social media, mainstream media, "fact-check" criminals, 77 mad Nobel "scientists", colluded, conspired, lied and censored to cover up the lab origin of the SARS-CoV-2 virus. Only the incredibly stupid would still believe that these same lying criminals are magically telling us the truth about vaccine dangers.

Now that the SARS-CoV-2 cover up has failed spectacularly, the criminals at Facebook have graciously decided to allow people to have discussions on the matter.

Fauci wrote in 2012 that the benefits of gain-of-function (GOF) experiments outweigh the risk. He killed 3.5 million people in 15 months by funding a sloppy lab in China performing GOF research, which created the SARS-CoV-2 virus. This mass murderer pushes killer quackccines lying again that the benefits outweigh the risks. He maimed and killed millions more. This mass murderer is the Chief Medical Adviser to POTUS.



Vaccines killed 3.5 million in 15 months

3.5 million people died of COVID-19 disease because they were injured by quackccines such as the flu shot, Tdap, etc. Dirty quackccines contaminated with proteins that are similar to SARS-CoV-2 proteins, induced allergy against the SARS-CoV-2 virus.

Severe COVID-19 is therefore a severe allergic reaction suffered upon infection. Predicted in Jan 2020, confirmed in Aug 2020:

"Some cytokines not associated with antiviral responses, such as IL-5, which aids defence against parasitic worms and is released during **allergic reactions**, were, surprisingly, upregulated as people developed severe disease."

COVID-19 poses a riddle for the immune system
https://www.nature.com/articles/d41586-020-02379-1

OTC antihistamines famotidine/cetirizine could have prevented all these deaths. Corrupted criminals in the medical establishment, actively suppressed use of these proven, cheap medicines, killed millions while pushing for new, unnecessary, lucrative SARS-CoV-2 quackccines. These quackccines have maimed and killed thousands. At least 4000 deaths have been reported to VAERS. Clueless FDA does not understand a thing about modmRNA quackccines but they have magically determined that these deaths are unrelated to the quackccines?

https://www.foxnews.com/opinion/tucker-carlson-how-many-americans-have-died-after-taking-the-covid-vaccine

My email to Fauci/Collins/Redfield sent **Feb 1 2020** on using antihistamines to treat COVID-19 (see pg. 97-98 of FOIA doc. below):

https://www.judicialwatch.org/wp-content/uploads/2021/02/DCNF-v-HHS-Nov-2020-00149.pdf

The biggest lie ever told: "the doctor has determined the benefits outweigh the risks"

After billions and decades wasted on "research", doctors (make that quacks) admit they are clueless about the root cause of food allergy, autism, asthma, leukemia, countless autoimmune disorders or even COVID-19 severity. All immunological disorders. Even vaccinologists admit they are clueless about the immunological mechanisms involved in how vaccines work/fail/hurt the body. But these quacks have magically determined that immunological interventions - vaccines are safe? The benefits outweigh the risks? Who are they trying to fool?

Corrupt Pharma criminals hiding behind liability protection for their vaccines, tells you EVERYTHING you need to know about vaccine safety. If vaccines were safe, why can't these criminals put their money where their mouth is? Instead these organized criminals have raked in billions for their killer quackccines.

Why are the anti-vaxxers winning, and how do you stop them in their tracks?

https://www.quora.com/Why-are-the-anti-vaxxers-winning-and-how-do-you-stop-them-in-their-tracks/answer/Vinu-Arumugham

How do I argue against anti vaxxers?

https://www.quora.com/How-do-I-argue-against-anti-vaxxers/answers/131896199

Allogeneic and xenogeneic antigens in vaccines/biologics cause the explosion of autoimmune diseases

One protein contaminating the AstraZeneca and Janssen vaccines causes the autoimmune disease that leads to clotting in the brain. The German team found almost 2000 such contaminating proteins in the AstraZeneca vaccine. The Janssen vaccine is manufactured using human embryonic retinal cells (PER.C6) while the AstraZeneca vaccine used human embryonic kidney cells. So they can be expected to have the same contamination profile. This autoimmune clotting problem is just the first of 2000 more to come.

Towards Understanding ChAdOx1 nCov-19 Vaccine-induced Immune Thrombotic Thrombocytopenia (VITT)

https://assets.researchsquare.com/files/rs-440461/v1/8eabf306-6fd4-4a89-a7a3-8f4d06c89a55.pdf

"In this regard, we identied (sic) an array of cell-culture derived human proteins in the vaccine, potentially predisposing to immune reactions against these antigens. If such proteins express a structures (sic), e.g. by a genetic polymorphism not found in the corresponding endogenous protein of the vaccinated individual, **a possible strong alloimmune response (with potential for autoreactivity) in a susceptible vaccine recipient should be considered**"

https://assets.researchsquare.com/files/rs-440461/v1/dadfb0d76a7a31650e518d70.pdf

"This proteome analysis revealed a surprisingly large number of proteins of 1856 – 1939 proteins per LOT"

These are just the latest quackccine induced autoimmune diseases.

5 to 7% of blood donors have detectable PF4–heparin antibodies induced by quackccines.

It's a US funded, Chinese lab virus

"Top virologists" are lying criminals. How can you trust them to create safe vaccines?

http://thebulletin.org/2021/05/the-origin-of-covid-did-people-or-nature-open-pandoras-box-at-wuhan/

Root cause of COVID-19? Biotechnology's dirty secret: Contamination. Bioinformatics evidence demonstrates that SARS-CoV-2 was created in a laboratory, unlikely to be a bioweapon but most likely a result of sloppy experiments

https://doi.org/10.5281/zenodo.3766462

Fauci Emails: How Top Public Health Officials Spun Tangled Web of Lies Around COVID Origin, Treatments

https://childrenshealthdefense.org/defender/fauci-emails-top-public-health-officials-lies-covid-origin-treatments/

Bell's palsy observed in mRNA vaccine trials but not in the real world? Means VAERS reports undercount 12X or trials were cooked.

From the clinical trials, it was obvious that the mRNA quackccines cause Bell's palsy. There was only a 1 in 7000 chance that the trial outcome was a result of random chance. Looking at Bell's palsy cases reported to the VAERS, it means either only 8% of adverse events are being captured in VAERS or if VAERS is representing reality then the trials were cooked. It is unlikely that both vendors would have observed spikes in Bell's palsy cases in the trial.

Assume SARS-CoV-2 vaccines DO NOT cause Bell's palsy

40,000 cases of Bell's palsy occur in the US per year. So 40,000 cases for 330,000,000 person-years. 40,000/12=3333 cases for 330,000,000 person-months.

Due to CDC mandated reporting to VAERS, assume all cases of Bell's palsy occurring within a month of the SARS-CoV-2 vaccine administration are reported. That is 260,000,000 person-months.

So for 260M doses administered, we have 260*3333/330 = 2626 background cases unrelated to the vaccine, are expected in VAERS.

With only ~1500 reports, it means they are only reporting 1500*100/2626 = 57%, at best.

Assume SARS-CoV-2 vaccines cause Bell's palsy at the same rate observed in the trial

There were 7 times more cases in the vaccine arms than the placebo arms.

So the number of Bell's palsy cases expected in the VAERS is 2626*7= 18382. This suggests reporting rate may be as low as 1500*100/18382=~8%. Closer to Harvard Pilgrim 2010 VAERS study.

Possible conclusions from above

Even under CDC mandated VAERS reporting, only ~8% of adverse events are being reported.

OR

VAERS reporting is closer to ~57% but vaccine batch/lot characteristics used during Phase 3 trial were not representative of what is being administered to the general public. This invalidates trial and EUA.

However, if this is true, it is unlikely that batch/lot deviation will happen to both vendors - Pfizer and Moderna, by random chance.

Raises the possibility that Pfizer/Moderna may have carefully selected batch/lot with desirable characteristics for trial use? For example, 30% of the modmRNA is truncated/modified in the vaccine. They could have screened for batch/lots that have say 10% truncation/modification to improve efficacy observed in the trial? Then the spike in Bell's palsy cases observed only in the trials may be the smoking gun showing the trials were cooked ...

Ethics of vaccine refusal

https://jme.bmj.com/content/early/2021/02/25/medethics-2020-107026

"In practical terms, mandatory vaccination amounts to discrimination against healthy, innate biological characteristics, which goes against the established ethical norms and is also defeasible a priori."

Universities mandating COVID-19 quackccines is an admission of their abject failure

If universities succeeded in imparting thinking skills to students, why can students not be trusted to make the right decision regarding the vaccines? Why is a mandate needed? This shows that our universities are an abject failure. Alternately, the universities are lying about the "safety and efficacy" of the vaccines hence they expect vaccine refusal.

Referring to investigational quackccines under EUA as "safe and effective" violates 21 U.S.C. § 360bbb-3.

FDA/NIH employees refuse to eat their own dog food. Only 50-60% of FDA/NIH employees are vaccinated.

https://www.rev.com/blog/transcripts/dr-fauci-cdc-director-testify-before-senate-on-covid-19-guidelines-transcript

Perhaps they learned the lessons I taught them. Dirty quackccines cause autism, autoimmune diseases and allergies:

https://list.nih.gov/cgi-bin/wa.exe?A2=IMMUNI-L;65e1e89d.1811

Please add your comment on petition calling for **revocation of EUA** for these unnecessary and unsafe quackccines:

Citizen Petition from Scientific Advisory Board on behalf of Children's Health Defense

https://www.regulations.gov/document/FDA-2021-P-0460-0001

TRO - Motion for Temporary Restraining Order Against Use of COVID Vaccine in Children

https://www.americasfrontlinedoctors.org/files/tro-motion-for-temporary-restraining-order-against-use-of-covid-vaccine-in-children

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Significant Under-Reporting of Quadrivalent Human Papillomavirus Vaccine-Associated Adverse Events in the United States: Time for Change?

https://cf5e727d-d02d-4d71-89ff-9fe2d3ad957f.filesusr.com/ugd/adf864_2dede593f4a04e64ab6c0c45bc14d450.pdf

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Oregon Health Authority Condemned by Scientists For Scrubbing Report on Wireless Hazards in Schools

http://washingtonspectator.org/oregon-health-authority-forbes/

In a quackccine, anything goes. Vaccine regulation is an oxymoron thus turning them into quackccines.

Aluminum content in vaccines vary, wildly exceeding levels documented in package insert or fall significantly below documented levels. So these quackccines are neither safe nor effective.

https://www.regulations.gov/document/FDA-2021-P-0433-0001

The measurement and full statistical analysis including Bayesian methods of the aluminium content of infant vaccines

https://www.sciencedirect.com/science/article/pii/S0946672X21000523

https://www.regulations.gov/comment/FDA-2021-P-0433-0040

Regulators fail to regulate vaccine content, mislead and thus invalidate all vaccine trials and studies

There are three points to be raised here.

No regulation/control of vaccine ingredients

Prof. Exley and his team have done excellent work revealing the lack of control/regulation of aluminum content in the vaccines (Shardlow et al. 2021). This problem of course is not limited to aluminum. There are no controls or specifications for thousands of other ingredients either. Egg protein content has been shown to vary a 100-fold in the influenza vaccines (Goldis et al. 2010). Bovine casein varied 2-fold in just 8 samples of the DTap/Tdap vaccines (Kattan et al. 2011). Yeast protein content among the Hep B vaccines vary 5-fold per the

package insert itself. I describe the details in my comments (two of them) posted in the Annals of Internal Medicine (please see comments section).

https://www.acpjournals.org/doi/10.7326/m18-2101

All vaccine safety, efficacy trials/studies are therefore invalid and must be withdrawn

This invalidates all vaccine trials and epidemiological studies because no one characterized/controlled the products that were the subject of these studies. We don't know if the results of such studies apply to vaccines with high or low levels of any of the ingredients. All these studies must therefore be withdrawn. The Pandemrix vaccines made in Europe contained more H1N1 nucleoprotein compared to Arepanrix made by the same vendor in Canada. Pandemrix caused way more cases of narcolepsy compared to Arepanrix. We have many examples of vaccine studies done in Denmark that are then interpreted as being applicable anywhere in the world. The above information shows that notion is absurd.

As many as 7 times the number of Bell's palsy cases were observed in the vaccine arms of the Phase III clinical trials of the Pfizer and Moderna modmRNA SARS-CoV-2 vaccines (Ozonoff et al. 2021), compared to the placebo arms. However, now the CDC claims no excess Bell's palsy cases are being observed in the general population. This is evidence that the product used in the trials were not representative of what is being administered to the public. This invalidates the trial and the emergency use authorization (EUA) that relied on that trial.

Regulatory agencies repeatedly mislead the public regarding vaccine content and the damage they cause

The FDA/CDC, UK's MHRA and EMA have continued to repeatedly mislead the public regarding vaccine content.

Human protein contamination of vaccines

One protein contaminating the AstraZeneca and Janssen vaccines causes the autoimmune disease that leads to clotting in the brain (Arumugham 2021). The German team found almost 2000 such contaminating proteins in the AstraZeneca vaccine. The Janssen vaccine is manufactured using human embryonic retinal cells (PER.C6) while the AstraZeneca vaccine used human embryonic kidney cells. So they can be expected to have the same contamination profile. This autoimmune clotting problem is therefore just the first of 2000 more to come.

Towards Understanding ChAdOx1 nCov-19 Vaccine-induced Immune Thrombotic Thrombocytopenia (VITT)

https://assets.researchsquare.com/files/rs-440461/v1/8eabf306-6fd4-4a89-a7a3-8f4d06c89a55.pdf

"In this regard, we identied (sic) an array of cell-culture derived human proteins in the vaccine, potentially predisposing to immune reactions against these antigens. If such proteins express a structures (sic), e.g. by a genetic polymorphism not found in the corresponding endogenous protein of the vaccinated individual, **a possible strong alloimmune response (with potential for autoreactivity) in a susceptible vaccine recipient should be considered**"

https://assets.researchsquare.com/files/rs-440461/v1/dadfb0d76a7a31650e518d70.pdf

"This proteome analysis revealed a **surprisingly** large number of proteins of 1856 – 1939 proteins per LOT"

So in the case of human protein contamination, a genetic polymorphism is needed for the immune system to recognize the antigen as a neoantigen, thus leading to autoimmune disease. But vaccines are contaminated with numerous plant/animal/fungal proteins (homologous xenogeneic antigens) that are similar to human proteins. Here no genetic polymorphism is needed as xenogeneic antigens already have numerous single amino acid residue differences compared to self antigens thus making them ideal neoantigens (Arumugham 2020a). In fact, oncologists use xenogeneic antigens in cancer vaccines to break immune tolerance and induce autoimmunity to treat cancer (Strioga et al. 2014). So the probability of vaccine induced autoimmune responses are much higher with xenogeneic antigens (Arumugham 2020a) than with human antigens in vaccines. VITT that was observed

so quickly with the AstraZeneca and Janssen vaccines shows that vaccine induced autoimmunity is extremely common. 5-7% of blood donors test positive for such vaccine induced anti-PF4 antibodies (Schultz et al. 2021).

The AstraZeneca vaccine package insert fails to document the 2000 proteins discovered above.

List of ingredients in the Janssen vaccine from the fact sheet for vaccination providers:

FACT SHEET FOR HEALTHCARE PROVIDERS ADMINISTERING VACCINE (VACCINATION PROVIDERS)

https://www.fda.gov/media/146304/download

"Each 0.5 mL dose of Janssen COVID-19 Vaccine is formulated to contain 5×10^{10} virus particles (VP) and the following inactive ingredients: citric acid monohydrate (0.14 mg), trisodium citrate dihydrate (2.02 mg), ethanol (2.04 mg), 2-hydroxypropyl-β-cyclodextrin (HBCD) (25.50 mg), polysorbate-80 (0.16 mg), sodium chloride (2.19 mg). **Each dose may also contain residual amounts of host cell proteins (≤0.15 mcg) and/or host cell DNA (≤3 ng).**"

But the fact sheet for recipients and care givers says:

FACT SHEET FOR RECIPIENTS AND CAREGIVERS

https://www.fda.gov/media/146305/download

"The Janssen COVID-19 Vaccine includes the following ingredients: recombinant, replication-incompetent adenovirus type 26 expressing the SARS-CoV-2 spike protein, citric acid monohydrate, trisodium citrate dihydrate, ethanol, 2-hydroxypropyl-β-cyclodextrin (HBCD), polysorbate-80, sodium chloride."

Why are the highlighted items missing from the list provided to the vaccine recipient? Why is the FDA misleading consumers?

Ovalbumin

Ovalbumin is the only egg protein listed for some influenza vaccines (CDC 2020). But 293 chicken proteins were identified in the influenza vaccine (Jacob et al. 2015).

Deoxycholate

Deoxycholate is listed as an ingredient in some vaccines (CDC 2020). Deoxycholate is derived from bovine gall bladders and is thus contaminated with bovine proteins (Jacob et al. 2015). The CDC fails to document those contaminants.

Casein

Bovine casein contaminates the DTaP/TdaP vaccines. Children with milk allergy react to the DTaP/Tdap shots. 8-18ng/ml of casein have been measured in the DTaP/TdaP vaccines (Kattan et al. 2011). The CDC fails to document that (CDC 2020).

Food proteins

Numerous food proteins contaminate vaccines per the National Academy of Medicine (2017).

Allergens in **Vaccines**, Medications, and Dietary Supplements

Physicians and patients with food allergy must consider potential **food allergen exposures in vaccines**, medications, and dietary supplement products (e.g., vitamins, probiotics), which are not regulated by labeling laws. Also, excipients (i.e., substances added to medications to improve various characteristics) may be **food or derived from foods** (Kelso, 2014). These include **milk proteins; soy derivatives; oils from sesame, peanut, fish or soy; and beef or fish gelatin.** The medications involved include **vaccines**; anesthetics; and oral, topical, and injected medications. With perhaps the exception of gelatin, reactions appear to be rare overall, likely because little residual protein is included in the final preparation of these items. The specific risk for each medication is not known.

Vaccines also may contain food allergens, such as egg protein or gelatin.

The FDA/CDC fail to document these contaminants. Polysorbate 80 used in many vaccines is derived from wheat/corn and is contaminated with wheat/corn proteins. The FDA/CDC fail to disclose that (Arumugham and Trushin 2019).

As a result, vaccines predictably cause the development of food allergies, asthma, autism, numerous autoimmune disorders, cancers (Arumugham 2020b) and the FDA/CDC deny it by ignoring the science and evidence.

All these vaccines must be immediately withdrawn. All these studies published based on these uncharacterized products must be immediately withdrawn. Safety specifications for vaccine ingredients based on safety research (not based just on vaccine maker's manufacturing capability) must be created and independently verified before these vaccines can be improved and reintroduced.

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Thanks,

Vinu

-------- Forwarded Message --------

Subject: Immunology Is Where Intuition Goes to Die; I predicted anti-helminth (IgE) immune response during COVID-19, back in Jan 2020

Date: Thu, 1 Oct 2020 17:38:15 -0700

From: vinu arumugham <igesynth@yahoo.com>

To: florian.krammer@mssm.edu <florian.krammer@mssm.edu>, cmetcalf@princeton.edu <cmetcalf@princeton.edu>, scrotty@ucsd.edu <scrotty@ucsd.edu>, cobey@uchicago.edu <cobey@uchicago.edu>, akiko.iwasaki@yale.edu <akiko.iwasaki@yale.edu>, df2396@columbia.edu <df2396@columbia.edu>, david.putrino@mountsinai.org <david.putrino@mountsinai.org>, taiawang@stanford.edu <taiawang@stanford.edu>, carolina.lucas@yale.edu <carolina.lucas@yale.edu>, patrick.wong@yale.edu <patrick.wong@yale.edu>, jon.klein@yale.edu <jon.klein@yale.edu>, trezende@mail.rockefeller.edu <trezende@mail.rockefeller.edu>, julio.silva@yale.edu <julio.silva@yale.edu>, maria.e.sundaram@emory.edu <maria.e.sundaram@emory.edu>, mallory.ellignson@yale.edu <mallory.ellignson@yale.edu>, tianyang.mao@yale.edu <tianyang.mao@yale.edu>, jieun.oh@yale.edu <jieun.oh@yale.edu>, benjamin.goldman-israelow@yale.edu <benjamin.goldman-israelow@yale.edu>, maria.tokuyama@yale.edu <maria.tokuyama@yale.edu>, peiwen.lu@yale.edu <peiwen.lu@yale.edu>, arvind.venkataraman@yale.edu <arvind.venkataraman@yale.edu>, annsea.park@yale.edu <annsea.park@yale.edu>, subhasis.mohanty@yale.edu <subhasis.mohanty@yale.edu>, haowei.wang@yale.edu <haowei.wang@yale.edu>, anne.wyllie@yale.edu <anne.wyllie@yale.edu>, chantal.vogels@yale.edu <chantal.vogels@yale.edu>, rebecca.earnest@yale.edu <rebecca.earnest@yale.edu>, sarah.lapidus@bulldogs.yale.edu <sarah.lapidus@bulldogs.yale.edu>, isabel.ott@yale.edu <isabel.ott@yale.edu>, adam.moore@yale.edu <adam.moore@yale.edu>, catherine.muenker@yale.edu <catherine.muenker@yale.edu>, john.fournier@yale.edu <john.fournier@yale.edu>, melissa.campbell@yale.edu <melissa.campbell@yale.edu>, camiodio@gmail.com <camiodio@gmail.com>, arnau.casanovas@yale.edu <arnau.casanovas@yale.edu>, roy.herbst@yale.edu <roy.herbst@yale.edu>, albert.shaw@yale.edu <albert.shaw@yale.edu>, ruslan.medzhitov@yale.edu <ruslan.medzhitov@yale.edu>, wade.schulz@yale.edu <wade.schulz@yale.edu>, nathan.grubaugh@yale.edu <nathan.grubaugh@yale.edu>, charles.delacruz@yale.edu <charles.delacruz@yale.edu>, shelli.farhadian@yale.edu <shelli.farhadian@yale.edu>, albert.ko@yale.edu <albert.ko@yale.edu>, saad.omer@yale.edu

<saad.omer@yale.edu>, jeffrey_goldberg@theatlantic.com <jeffrey_goldberg@theatlantic.com>, swati@theatlantic.com <swati@theatlantic.com>, janekim@theatlantic.com <janekim@theatlantic.com>, rrosen@theatlantic.com <rrosen@theatlantic.com>, vloeb@theatlantic.com <vloeb@theatlantic.com>, ross@theatlantic.com <ross@theatlantic.com>, swang@theatlantic.com <swang@theatlantic.com>, gwhite@theatlantic.com <gwhite@theatlantic.com>, pbisceglio@theatlantic.com <pbisceglio@theatlantic.com>, lenika@theatlantic.com <lenika@theatlantic.com>, shayes@theatlantic.com <shayes@theatlantic.com>, smahanta@theatlantic.com <smahanta@theatlantic.com>, caroline@theatlantic.com <caroline@theatlantic.com>, lola@theatlantic.com <lola@theatlantic.com>, afayyad@theatlantic.com <afayyad@theatlantic.com>, aneklason@theatlantic.com <aneklason@theatlantic.com>, yserhan@theatlantic.com <yserhan@theatlantic.com>, rosa@theatlantic.com <rosa@theatlantic.com>, letters@theatlantic.com <letters@theatlantic.com>, gmckenzie@citylab.com <gmckenzie@citylab.com>, emilyyoffe123@gmail.com <emilyyoffe123@gmail.com>, nflatow@citylab.com <nflatow@citylab.com>, jhamblin@theatlantic.com <jhamblin@theatlantic.com>, ed@theatlantic.com <ed@theatlantic.com>

CC: empoweredpatient@cnn.com <empoweredpatient@cnn.com>, munro.peter@abc.net.au <munro.peter@abc.net.au>, beth.mole@arstechnica.com <beth.mole@arstechnica.com>, news@axios.com <news@axios.com>, newswatch@bbc.co.uk <newswatch@bbc.co.uk>, edith.bracho.sanchez@gmail.com <edith.bracho.sanchez@gmail.com>, cnn@cnn.com <cnn@cnn.com>, news@coastnewsgroup.com <news@coastnewsgroup.com>, news@chron.com <news@chron.com>, letters@dailysignal.com <letters@dailysignal.com>, editor@dnews.com <editor@dnews.com>, newsroom@epochtimes.com <newsroom@epochtimes.com>, editorial@fatherly.com <editorial@fatherly.com>, myron.levin@fairwarning.org <myron.levin@fairwarning.org>, info@eyeonannapolis.net <info@eyeonannapolis.net>, thaelle@gmail.com <thaelle@gmail.com>, news@fox17online.com <news@fox17online.com>, science@theguardian.com <science@theguardian.com>, fullmeasurenews@gmail.com <fullmeasurenews@gmail.com>, allergy-immunology@healio.com <allergy-immunology@healio.com>, stories@healthline.com <stories@healthline.com>, newsdesk@irishtimes.com <newsdesk@irishtimes.com>, newsroom@idahostatesman.com <newsroom@idahostatesman.com>, KHN-tips@kff.org <KHN-tips@kff.org>, dhyde@kuow.org <dhyde@kuow.org>, info@thebureauinvestigates.com <info@thebureauinvestigates.com>, editor@thehill.com <editor@thehill.com>, letters@time.com <letters@time.com>, press@verywell.com <press@verywell.com>, lena.sun@washpost.com <lena.sun@washpost.com>, mike.agogliati@wfsb.com <mike.agogliati@wfsb.com>, submit@wired.com <submit@wired.com>, fox2newsdesk@foxtv.com <fox2newsdesk@foxtv.com>, betsy.mckay@wsj.com <betsy.mckay@wsj.com>, williamplooney@gmail.com <williamplooney@gmail.com>, investigate@ap.org <investigate@ap.org>, editor@bayareanewsgroup.com

<editor@bayareanewsgroup.com>, ashermullard@gmail.com <ashermullard@gmail.com>, editorial@bigissue.com <editorial@bigissue.com>, tips@buzzfeed.com <tips@buzzfeed.com>, stephen.colbert@cbs.com <stephen.colbert@cbs.com>, cfrederick@duluthnews.com <cfrederick@duluthnews.com>, scoops@huffpost.com <scoops@huffpost.com>, kotanews@kotatv.com <kotanews@kotatv.com>, news@ksby.com <news@ksby.com>, PRandhawa@KSDK.com <PRandhawa@KSDK.com>, newstips@latimes.com <newstips@latimes.com>, akrueger@mpr.org <akrueger@mpr.org>, editor@newatlas.com <editor@newatlas.com>, kanderson@observer-reporter.com <kanderson@observer-reporter.com>, news@politicshome.com <news@politicshome.com>, editors@sciam.com <editors@sciam.com>, jgoldsteinstreet@seattletimes.com <jgoldsteinstreet@seattletimes.com>, metro@sfchronicle.com <metro@sfchronicle.com>, editors@texasobserver.org <editors@texasobserver.org>, tips@rollingstone.com <tips@rollingstone.com>, info@the-scientist.com <info@the-scientist.com>, Blake.Montgomery@thedailybeast.com <Blake.Montgomery@thedailybeast.com>, sciencenetwork@ucsusa.org <sciencenetwork@ucsusa.org>, newsroom@waaytv.com <newsroom@waaytv.com>, newsroom@whyy.org <newsroom@whyy.org>, lrosenbaum@forbes.com <lrosenbaum@forbes.com>, felice.freyer@globe.com <felice.freyer@globe.com>, lgustus@sacbee.com<lgustus@sacbee.com>, deidre@acbio.org.za <deidre@acbio.org.za>, eva@i-sis.org.uk <eva@i-sis.org.uk>, jimmye@northsidesun.com <jimmye@northsidesun.com>, kbouffard@detroitnews.com <kbouffard@detroitnews.com>, tips@propublica.org <tips@propublica.org>, slivio@njadvancemedia.com <slivio@njadvancemedia.com>, peter.chianca@boston.com<peter.chianca@boston.com>, rowan@rowanjacobsen.com <rowan@rowanjacobsen.com>, thackerpd@gmail.com <thackerpd@gmail.com>

All,

Regarding:

Immunology Is Where Intuition Goes to Die
https://www.theatlantic.com/health/archive/2020/08/covid-19-immunity-is-the-pandemics-central-mystery/614956/

Says: "Normally, the immune system mobilizes different groups of cells and molecules when fighting three broad groups of pathogens: viruses and microbes that invade cells, bacteria and fungi that stay outside cells, and parasitic worms. Only the first of these programs should activate during a viral infection. But Iwasaki's team recently showed that all three activate in severe COVID-19 cases. "It seems completely random," she says. In the worst cases, "the immune system almost seems confused as to what it's supposed to be making.""

You refer to Iwasaki's paper:

Longitudinal analyses reveal immunological misfiring in severe COVID-19

https://www.nature.com/articles/s41586-020-2588-y

It says: "Moreover, severe COVID-19 was accompanied by an increase in multiple type 2 (anti-helminths) effectors, including interleukin-5 (IL-5), IL-13, immunoglobulin E and eosinophils."

I predicted the above in **Jan 2020** (please see forwarded email below) and explained **WHY** it occurs and how to treat it. Basically, vaccines contaminated with coronavirus-like proteins, program the immune system to attack those proteins as if they were parasitic worms/helminths (technically, immunoglobulin E or IgE mediated

sensitization). Upon SARS-CoV-2 infection, due to cross-reaction, part of the immune system recognizes the virus as a parasite thus resulting in an inappropriate and dangerous anti-parasite immune response. But it is important to recognize that allergy/anaphylaxis is an anti-parasite immune response. So we know how to treat it. Use antihistamines and mast cell stabilizers. That is why antihistamines work in COVID-19. **No clinical trials needed.**

Antihistamines May Help Calm COVID-19 Cytokine Storm

https://www.medscape.com/viewarticle/937178

We have known for years that the influenza vaccine causes the development of an anti-parasite (IgE) immune response against the influenza virus.

Long Term Persistence of IgE Anti-Influenza Virus Antibodies in Pediatric and Adult Serum Post Vaccination with Influenza Virus Vaccine
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3065793/

Seasonal split influenza vaccine induced IgE sensitization against influenza vaccine
https://pubmed.ncbi.nlm.nih.gov/26188254/

Influenza specific serum IgE is present in non-allergic subjects
https://pubmed.ncbi.nlm.nih.gov/16316424/

Highly increased levels of IgE antibodies to vaccine components in children with influenza vaccine–associated anaphylaxis
https://www.sciencedirect.com/science/article/pii/S0091674915010957

Severe influenza is caused by the same misdirected anti-parasite immune response we observe in COVID-19. I described the process in the BMJ back in 2018:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

So I was able quickly confirm that the same mechanism was occurring in COVID-19 when the SARS-CoV-2 proteome became available in Jan 2020.

The Atlantic says: "No one yet knows why this happens, and only in some people."

Now you do. Coronavirus-like protein contaminants by definition means no one knows which batch of vaccine contains how much. So it happens only in some people because it is a game of Russian roulette.

Please see details here:

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

It might seem intuitive to get a flu shot during the COVID-19 pandemic. But think again because Immunology Is Where Intuition Goes to Die.

Proteins that contaminate influenza vaccines have high homology to SARS-CoV-2 proteins thus increasing risk of severe COVID-19 disease and mortality
https://doi.org/10.5281/zenodo.3996984

The Atlantic says:

"For some diseases, like dengue, an antibody response to one infection can counterintuitively make the next infection more severe. So far, there's no evidence this happens with SARS-CoV-2, says Krammer,"

No, that is incorrect. As explained before, severe COVID-19 is in fact the "next infection". The "first infection" was the contaminated vaccine. So exactly as in dengue, the immune response that develops following first infection, results in severe disease the next time.

"Such immune overreactions also happen in extreme cases of influenza,"

We already covered that:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

Immunology Is Where Intuition Goes to Die, but there is a method to the madness. Unfortunately, as we can see, vaccinating without understanding the full immunological impact, is extremely dangerous.

Prof. Kounis' team and I, describe the common immunological mechanisms involved in cardiac injury in COVID-19, severe dengue infection and allergic reactions/anaphylaxis (Kounis syndrome). The medications for prevention/treatment include antihistamines such as famotidine/cetirizine.

The passepartout wayfares of Covid-19, Cytokine storm and Kounis syndrome

https://doi.org/10.5281/zenodo.3977923

Here's the bigger picture of the damage caused by contaminants, and non-target antigens in vaccines:

Vaccines and Biologics injury table based on mechanistic evidence – Feb 2020 Covering over 125 conditions
https://zenodo.org/record/3647593/files/vbitr2_final.pdf?download=1

Thanks,

Vinu

-------- Forwarded Message --------

Subject: Wuhan 2019-nCoV treatment; Vaccines induce autoimmunity: Epitope database evidence; Ebola vaccine will cause rice allergy epidemic
Date: Fri, 24 Jan 2020 17:42:02 -0800
From: vinu arumugham <igesynth@yahoo.com>
To: jay.slater@fda.hhs.gov <jay.slater@fda.hhs.gov>, jane.woo@fda.hhs.gov <jane.woo@fda.hhs.gov>, maureen.hess@fda.hhs.gov <maureen.hess@fda.hhs.gov>, Richard.Forshee@fda.hhs.gov <Richard.Forshee@fda.hhs.gov>, Mark.Walderhaug@fda.hhs.gov <Mark.Walderhaug@fda.hhs.gov>, CBER OCOD Consumer Account <cberocod@fda.hhs.gov>, Destefano, Frank (CDC/OID/NCEZID) <fxd1@cdc.gov>, isq8@cdc.gov <isq8@cdc.gov>, nar5@cdc.gov <nar5@cdc.gov>, hjn0@cdc.gov <hjn0@cdc.gov>, Secretary@HHS.gov <Secretary@HHS.gov>, CommissionerFDA@fda.hhs.gov <CommissionerFDA@fda.hhs.gov>, olx1@cdc.gov <olx1@cdc.gov>, directorsincoming@cdc.gov <directorsincoming@cdc.gov>, francis.collins@nih.gov <francis.collins@nih.gov>, mrolfes1@cdc.gov <mrolfes1@cdc.gov>, xzd2@cdc.gov <xzd2@cdc.gov>, acy9@cdc.gov <acy9@cdc.gov>, dbj0@cdc.gov <dbj0@cdc.gov>, jmk9@cdc.gov <jmk9@cdc.gov>, tft9@cdc.gov <tft9@cdc.gov>, gll9@cdc.gov <gll9@cdc.gov>, sharplessne@nih.hhs.gov <sharplessne@nih.hhs.gov>, tnc4@cdc.gov <tnc4@cdc.gov>, kok4@cdc.gov <kok4@cdc.gov>, rxl3@cdc.gov <rxl3@cdc.gov>, gbq7@cdc.gov <gbq7@cdc.gov>, fwf7@cdc.gov <fwf7@cdc.gov>, megan.mcseveney@fda.hhs.gov <megan.mcseveney@fda.hhs.gov>, afauci@niaid.nih.gov <afauci@niaid.nih.gov>, Emelia.Benjamin@bmc.org <Emelia.Benjamin@bmc.org>, mjessup@leducq.com <mjessup@leducq.com>, tavori@ohsu.edu <tavori@ohsu.edu>,

jessica.lilley@vanderbilt.edu <jessica.lilley@vanderbilt.edu>,
web@beasleyallen.com <web@beasleyallen.com>,
dr.flegg@bfwhospitals.nhs.uk <dr.flegg@bfwhospitals.nhs.uk>

IgE mediated sensitization to peptides that have homology to 2019-nCoV peptides may contribute to disease severity. In that case, antihistamines and other allergy treatments such as mast cell stabilizers may help reduce infection severity.

A BLASTP analysis of 2019-nCoV proteome against common vaccine antigens was performed. Preliminary results suggest that IgE mediated sensitization to common vaccine antigens can result in cross reactive immune responses to 2019-nCoV.

Please see details of the mechanisms here:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

https://www.quora.com/Why-was-the-flu-so-deadly-in-outbreaks-in-the-past-And-what-made-the-flu-become-less-deadly/answers/86456279

"Scientists" at the global vaccine safety summit spill the beans: There is no science behind vaccine safety claims, it's a fairy tale.

The party is over folks.

https://youtu.be/s2IujhTdCLE

ERVEBO Ebola vaccine will create a rice allergy epidemic, add to numerous autoimmune diseases, cancer and make Ebola disease even more severe. Design for safety and vaccine safety regulation remain abject failures. Incompetence or indifference?
https://doi.org/10.5281/zenodo.3595020

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

https://doi.org/10.5281/zenodo.3603480

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

Vinu Arumugham

Jan 2020

vinucubeacc@gmail.com

Lay summary

Proteins are a chain of amino acids. Proteins can have up to several hundred amino acids. Snippets of proteins (peptides), 7-15 amino acids in length are important in immunology. There are 20 types of amino acids. Each is assigned a letter (1 letter code).

Antibodies are proteins that can bind to peptides that have a specific amino acid sequence. Such a target peptide is known as an epitope.?? When an antibody binds to a peptide (which is part of a protein, which in turn may be part of a cell surface), it can trigger an immune attack on the cell. If the cell were a bacterium, the bacterium would be killed.

Humans (like all organisms) are made of numerous proteins (self proteins). So we have self-proteins, self-peptides and self-epitopes. In a healthy person, the body will not make antibodies that bind strongly to self-peptides (self-tolerance).

DNA is a chain of base-pairs. The DNA base-pair sequence determines the amino acid sequence in the protein produced. If there is a mutation that alters a single base-pair, the resulting protein will have a single amino acid that is altered. To prevent cancer, the immune system is capable of making antibodies against such altered peptides. Such antibodies can also weakly bind (cross react) to the unaltered normal peptide thus resulting in destruction of some healthy cells.

Say a normal protein has the following peptide (10 amino acids, each represented by its 1 letter code):

ALSTLVVNKI

Say DNA in a cell mutates due to a carcinogen exposure and it alters the protein thus resulting in this peptide with a single amino acid change:

ALSTLVV**S**KI

When the immune system makes antibodies targeted at ALSTLVV**S**KI (to attack the cell with the DNA mutation), the same antibodies can weakly bind to the normal ALSTLVVNKI peptide.

ALSTLVVNKI is an epitope associated with rheumatoid arthritis (RA).

So as a result of the immune system defending against cancer, the person can develop RA.

Now consider vaccines containing animal proteins. Animal proteins are very similar to human proteins, containing only occasional amino acid differences. An animal peptide could therefore have the ALSTLVV**S**KI sequence. Such a vaccine would fool the immune system into creating an anti-cancer immune response, creating antibodies targeted at ALSTLVV**S**KI. The result is vaccine induced RA.

Therefore one can predict that analyzing epitopes associated with autoimmune diseases, such single amino acid difference compared to animal peptides present in vaccines, would occur more frequently than can be expected merely by chance. The analysis confirms that this prediction is valid.

Abstract

The National Institute of Allergy and Infectious Diseases (NIAID) sponsors the Immune Epitope Data Base (IEDB). IEDB contains epitopes identified from the medical literature and organized by diseases and categories of diseases. All epitopes (23000+) associated with 82 autoimmune diseases in humans were analyzed.

The role of animal, plant, fungal proteins contained in vaccines in the etiology of autoimmune diseases have been described in humans and animals. BLASTP was used to analyze IEDB derived epitopes for sequence alignment to animal, plant, fungal (APF) proteins present in vaccines and biologics. Specifically, the search was performed against bovine, chicken, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes.

The results show that 57% of epitopes differed by exactly one amino acid residue from an APF peptide. 78% of the epitopes differed by up to two amino acid residues from an APF peptide. The rest of the epitopes were either identical or differed by more than two amino acid residues.

A majority of IEDB epitopes analyzed were 9-mer peptides. Comparing randomly selected 9-mer human peptides with APF proteomes, the probability of single amino acid residue difference (SAARD) outcomes was derived. This was used to estimate the probability that actual IEDB SAARD alignments to APF peptides were

merely a chance outcome. The estimates show that the probability that the observed IEDB alignments to APF being merely a chance outcome are vanishingly small. So the results make it absolutely clear that APF proteins in vaccines cause all these autoimmune diseases.

Introduction

Vaccines contain thousands of residual animal, plant and fungal (APF) proteins from the manufacturing process (1???6)???. 293 chicken proteins were identified in the influenza vaccine (7)???, for example. Actin and vimentin proteins were detected in the Priorix Tetra vaccine (8)???. Immunization with homologous xenogeneic antigens resulting in autoimmune diseases has been known for at least 40 years (9)???. Vaccines that contain bovine proteins caused autoimmunity in dogs (10)???. We previously described the immunological mechanism involved in autoimmunity induction by immunization with homologous xenogeneic antigens (11)???.

Cancer cells have minor differences when compared to healthy cells. Due to mutation of the DNA encoding the proteins, cancer cells can display altered proteins on their surface. Healthy cancer defense mechanisms include immune responses directed at such altered proteins. Therefore an immune response directed against cancer cells always carries a risk of cross reactive immune responses against healthy cells displaying the unaltered protein. Therefore, cancer induced autoimmune responses are a consequence of normal, healthy immune system behavior.

Animal proteins have minor differences compared to human proteins. Peptides that are identical between humans and animals are unlikely to cause any problem due to strong self tolerance. However, peptides with one amino acid residue difference produce the strongest cross reactive immune responses (11)???. They are ideally suited to induce autoimmune diseases. Injecting animal proteins results in anti-cancer immune responses because the immune system perceives animal proteins as altered human proteins. Adjuvants in the vaccine boost this anti-cancer immune response. This artificial anti-cancer response directed at thousands of APF proteins in vaccines or biologics, therefore cross react and cause numerous autoimmune disorders.

For this reason, one can predict that single amino acid residue difference (SAARD) between autoimmune disease related epitopes in the IEDB and homologous APF peptides in vaccines, would occur at a higher probability than by mere chance. We perform a BLASTP analysis to verify.

Methods

Basic local alignment search tool for proteins (BLASTP) (12)???, Universal Protein Resource (UniProt)(13)??? and the Immune Epitope Database (IEDB) (14)??? were used for bioinformatics analysis.

Specifically, the BLASTP sequence alignment of IEDB peptides was performed against bovine, chick, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes. Vaccines and biologics contain residual proteins from all these organism due to media used to grow viruses or bacteria, recombinant cells/organisms used for protein expression or as excipients.

Results

57% of IEDB peptides have a SAARD and 78% have up to two amino acid differences compared to animal, fungal or plant peptides present in vaccines.

Discussion

Could this result be a chance occurrence?

A majority of IEDB epitopes analyzed were 9-mer peptides. Five thousand 9-mer peptides were chosen at random from the human proteome. BLASTP was run using these peptides to compare against each

organism???s proteome or a subset. This provides us the probability that randomly selected human peptides have an alignment providing a SAARD compared to peptides from these organisms. These are listed in table 1 under ??? Random SAARD alignment???. Given this, we can compute the probability of the actual SAARD alignment to IEDB epitopes, occurring by chance. This is listed in table 1 under ???Estimated probability of actual SAARD outcome occurring just by chance???.

For a simple coin toss example, we would perform the calculation as follows:

Computing probability of say a 7 heads, 3 tails outcome of 10 trials of a fair coin:

Probability = (0.5^7) x (0.5^3) x 10! / (7! x 3!)

Where:

0.5 is the probability of a head or tail outcome of a fair coin.

For an unfair coin, say probability of head outcome = 0.4 and tail outcome 0.6, we would have:

Probability = (0.4^7) x (0.6^3) x 10! / (7! x 3!)

For the IEDB peptide probability analysis, the outcome is for 23192 trials (peptides).

The ???head outcome??? is the ???Random SAARD alignment ??? entries in table 1. The ???tail outcome??? probability is 1-???head outcome???.

Sample calculation for Chinese Hamster:

Probability = ((889/5000)^4574) x ((4111/5000)^18618) x 23192! / (4574! x 18618!)

Probability = 1.488e-15

Where: 889*100/5000 = 17.8% is the entry in Table 1 for Chinese Hamster. BLASTP analysis shows 889 SAARD out of 5000 peptides analyzed.

And, 4574*100/23192=19.7% is the IEDB entry in Table 1 for Chinese Hamster. BLASTP analysis shows 4574 SAARD out of 23192 peptides analyzed.

So the 1.488e-15 value is the probability that we will have exactly 4574 SAARD alignments out of 23192 peptides. The probability goes down for all values > 4574. Conservatively, applying the same probability as for 4574, to all values >4574, we can calculate the probability of the chance occurrence of 4574 or greater number of SAARD alignments as 1.488e15 * 18618 = 27e-12, entry in table.

The Gnome calculator was used to perform these calculations and the results were verified using the Qalculate! calculator and WolframAlpha (15)??? since spreadsheets are unable to perform these calculations.

Table 1

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
African green monkey (*Chlorocebus aethiops*)	26 (0.5)	420 (1.8)	~1.7e-96	Probability of this outcome occurring just by chance is vanishingly small. So these animal proteins in vaccines, caused these diseases.
Cow (*Bos taurus*)	936 (18.7)	4385 (18.9)	~1	There are two possibilities. (1) This outcome occurred just by chance. (2) The assumption that all cow proteins are

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
				present in the vaccines in equal amount is not true. We know that cow???s milk, bovine gelatin, bovine serum albumin are used in vaccines. So these proteins and proteins present in tissues in the vicinity, are included in vaccines but other cow proteins may not be present. This is the more likely explanation. Please see Cow???s milk entry below.
Cow???s Milk (*Bos taurus*)	0 (0)	12 (0.05)	0	Probability of this outcome occurring just by chance is 0. So these animal proteins in vaccines, caused these diseases.
Chinese Hamster (*Cricetulus griseus*)	889 (17.8)	4574 (19.7)	~27e-12	Probability of this outcome occurring just by chance is vanishingly small. So these animal proteins in vaccines, biologics caused these diseases.
Chicken (*Gallus gallus*)	536 (10.7)	3901 (16.8)	<1e-100	Probability of this outcome occurring just by chance is vanishingly small. So these animal proteins in vaccines, caused these diseases. Unlike bovine, porcine and murine proteins, since chicken egg or embryo is used for vaccine manufacture, all chicken proteins can be present in vaccines.
Guinea Pig (*Cavia porcellus*)	837 (16.7)	4439 (19.1)	~1e-18	Probability of this outcome occurring just by chance is vanishingly small. So these animal proteins in vaccines, caused these diseases.
Mice (*Mus musculus*)	940 (18.8)	4467 (19.3)	~1	There are two possibilities. (1) This outcome occurred just by chance. (2) The assumption that all mice proteins are present in biologics in equal amount is not true. We know that mice myeloma cells are used in biologics. So these proteins and proteins present in tissues in the vicinity, are present in biologics but other mice proteins may not be present. This is the more likely explanation.
Maize (*Zea mays*)	303 (6.1)	1667 (7.2)	~5e-9	Probability of this outcome occurring just by chance is vanishingly small. So these plant proteins in vaccines, caused these diseases.
Peanut (*Arachis*	223 (4.5)	1697 (7.3)	~79e-81	Probability of this outcome occurring just by chance is vanishingly small. So these

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
hypogaea)				plant proteins in vaccines, caused these diseases.
Yeast *(Saccharomyces cerevisiae)*	64 (1.3)	828 (3.6)	<1e-100	Probability of this outcome occurring just by chance is vanishingly small. So these fungal proteins in vaccines, biologics caused these diseases.
Sesame (*Sesamum indicum*)	155 (3.1)	1398 (6.0)	<1e-100	Probability of this outcome occurring just by chance is vanishingly small. So these plant proteins in vaccines, caused these diseases.
Soy (*Glycine max)*	215 (4.3)	1548 (6.7)	~86e-59	Probability of this outcome occurring just by chance is vanishingly small. So these plant proteins in vaccines, caused these diseases.
Pig (*Sus scrofa*)	963 (19.3)	4407 (19.0)	~1	There are two possibilities. (1) This outcome occurred just by chance. (2) The assumption that all porcine proteins are present in the vaccines in equal amount is not true. We know that porcine gelatin is used in vaccines. So these proteins and proteins present in tissues in the vicinity are included in vaccines but other porcine proteins may not be present. This is the more likely explanation.
Wheat (*Triticum aestivum*)	138 (2.8)	977 (4.2)	~18e-33	Probability of this outcome occurring just by chance is vanishingly small. So these plant proteins in vaccines, caused these diseases.

The calculations make it clear that the findings cannot be merely a chance outcome and that immunization against animal/plant/fungal antigens in the vaccines do cause these autoimmune diseases in the IEDB.

Conclusion

Vaccines containing animal, plant or fungal proteins are extremely dangerous and cause numerous autoimmune diseases and cancer (16???19)???. All non-target proteins in vaccines must be immediately removed using processes such affinity chromatography (20)???.

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From: Virologica Sinica [virosin@wh.iov.cn]
Sent: 7/25/2020 6:25:42 PM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: To Dr.Shi - Virologica Sinica, Volume 35, Special Issue on SARS-CoV-2 and COVID-19

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Dear Dr. Shi,

It is my pleasure to present you the Special Issue on SARS-CoV-2 and COVID-19 recently published in *Virologica Sinica*. This issue collectively includes original reports on virus characterization, clinical features, inflammatory responses, infection models, detection methods, drugs and treatments, etc., and we hope you will find this issue useful and informative.

Zheng-Li Shi, Ph.D.
Editor-in-Chief, *Virologica Sinica*

Browse the website www.virosin.org for more information

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Virologica Sinica is an academic journal which aims at presenting the cutting-edge research on viruses. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including research on animal, plant and microbe viruses. The journal welcomes articles on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related biotechniques. *Virologica Sinica*, the official journal of the Chinese Society for Microbiology, will serve as a platform for the communication and exchange of academic information and ideas in an international context.

The journal is indexed by: Science Citation Index (SCI), Journal Citation Reports (JCR), PubMed/Medline, Pubmed Central, Scopus, BIOSIS, Google Scholar.

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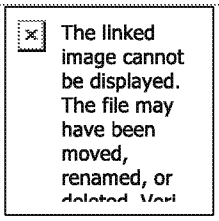


About the Special Issue on SARS-CoV-2 and COVID-19

Issue Editor: Prof. Zheng-Li Shi, Ph.D., Wuhan Institute of Virology, Chinese Academy of Sciences
The ongoing outbreak of Coronavirus Disease 2019 (COVID-19) has become a global public health emergency. The causative pathogen of COVID-19, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), hits the humankind so sudden and brings tremendous challenges to the world. In combating against the COVID-19 pandemic, *Virologica Sinica* delicates this focused issue to timely present the latest scientific progress. Original reports on virus characterization, clinical features, inflammatory responses, infection models, detection methods, drugs and treatments, etc. are collectively included in the issue. The cover depicts the SARS-CoV-2 virus particle, surrounded by human blood cells.

2020, Vol. 35, Issue 3

Perspective

Old Weapon for New Enemy: Drug Repurposing for Treatment of Newly Emerging Viral Diseases
Free Full Text (HTML) *Free* Full Text (PDF)
Deyin Guo

In December 2019, a dozen of patients with unusual pneumonia were hospitalized in Wuhan in central China, and the causative agent was identified as a new type of coronavirus (Zhu et al. 2020; Huang et al. 2020). The new virus was temporarily named as 2019 novel coronavirus (2019-nCoV) by the World Health Organization (WHO). As of January 29, 2020, 7736 confirmed cases of 2019-nCoV infection with 170 deaths were reported in China, and additional 77 cases in other 16 countries (National Health Commission of the People's Republic of China 2020; WHO 2020c). Since the emerging viruses are previously unknown pathogens, there are no specific and effective drugs available. Therefore, there is an urgent need for antiviral treatment in fighting the emerging viral diseases. However, the development of antiviral drugs is time- and resource-consuming, and thus repurposing of existing drugs to treat emerging viral diseases represents one of efficient strategies for drug development.

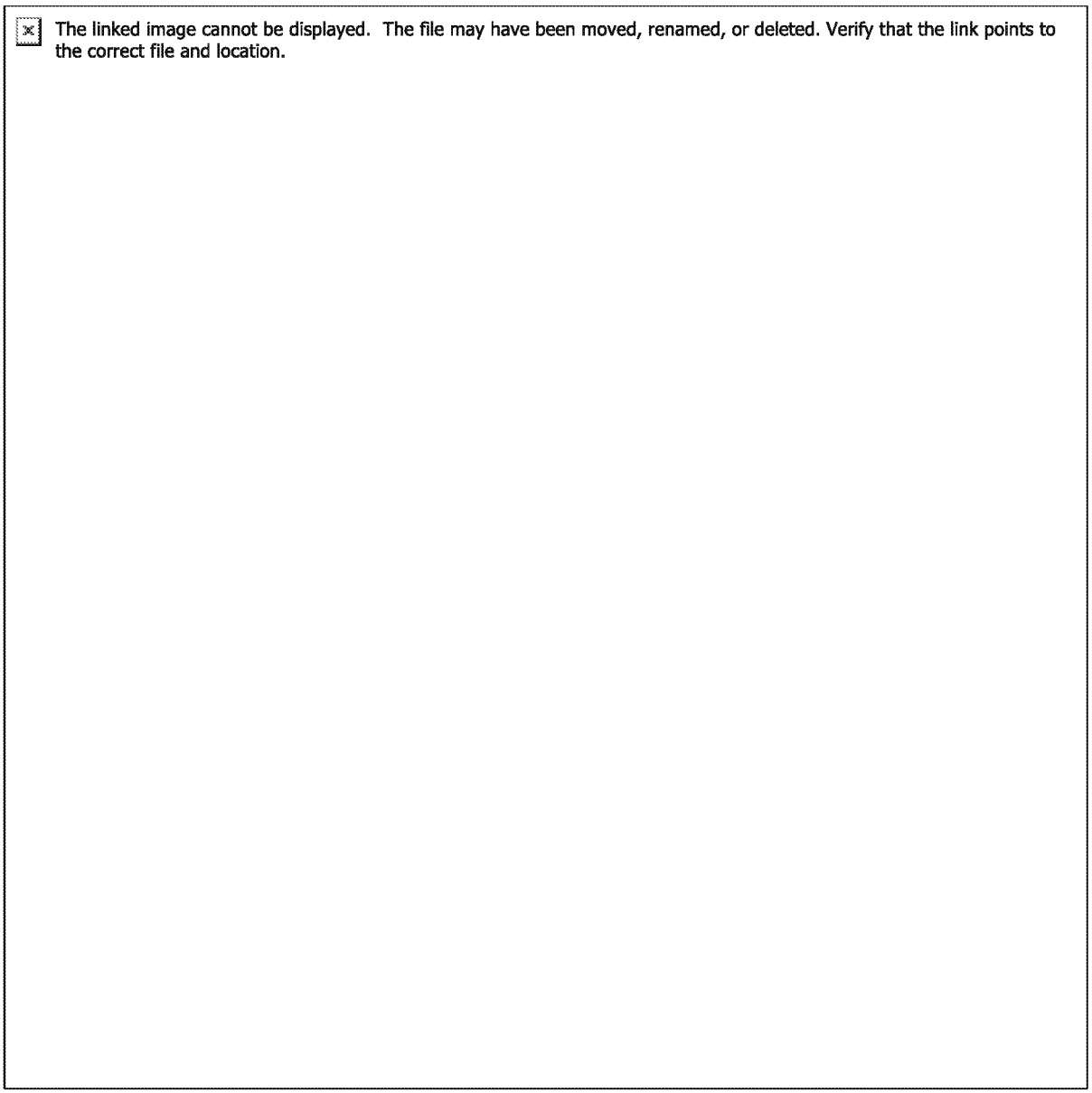
Perspective

Compensation of ACE2 Function for Possible Clinical Management of 2019-nCoV-Induced Acute Lung Injury

Free Full Text (HTML) *Free* Full Text (PDF)

Yuntao Wu

This perspective is intended to stimulate discussions about possible pathogenic mechanisms, based on the interaction of the virus with its receptor ACE2, so that rational therapies can be developed. Although ACE is regarded as the primary Ang II-converting enzyme, another enzyme, chymase, is also involved in converting Ang II in certain pathological conditions that may need attention (Fyhrquist and Saijonmaa 2008; Lindberg et al. 1997). In addition, coronavirus pathogenesis is a highly complex process (Lo et al. 2006), and much of the needed detail in host–pathogen interaction in 2019-nCoV infection awaits investigation. It also remains to be clinically tested whether some of these potential treatments, as proposed here, can be effective or beneficial in the management of 2019-nCoV-induced lung injury.



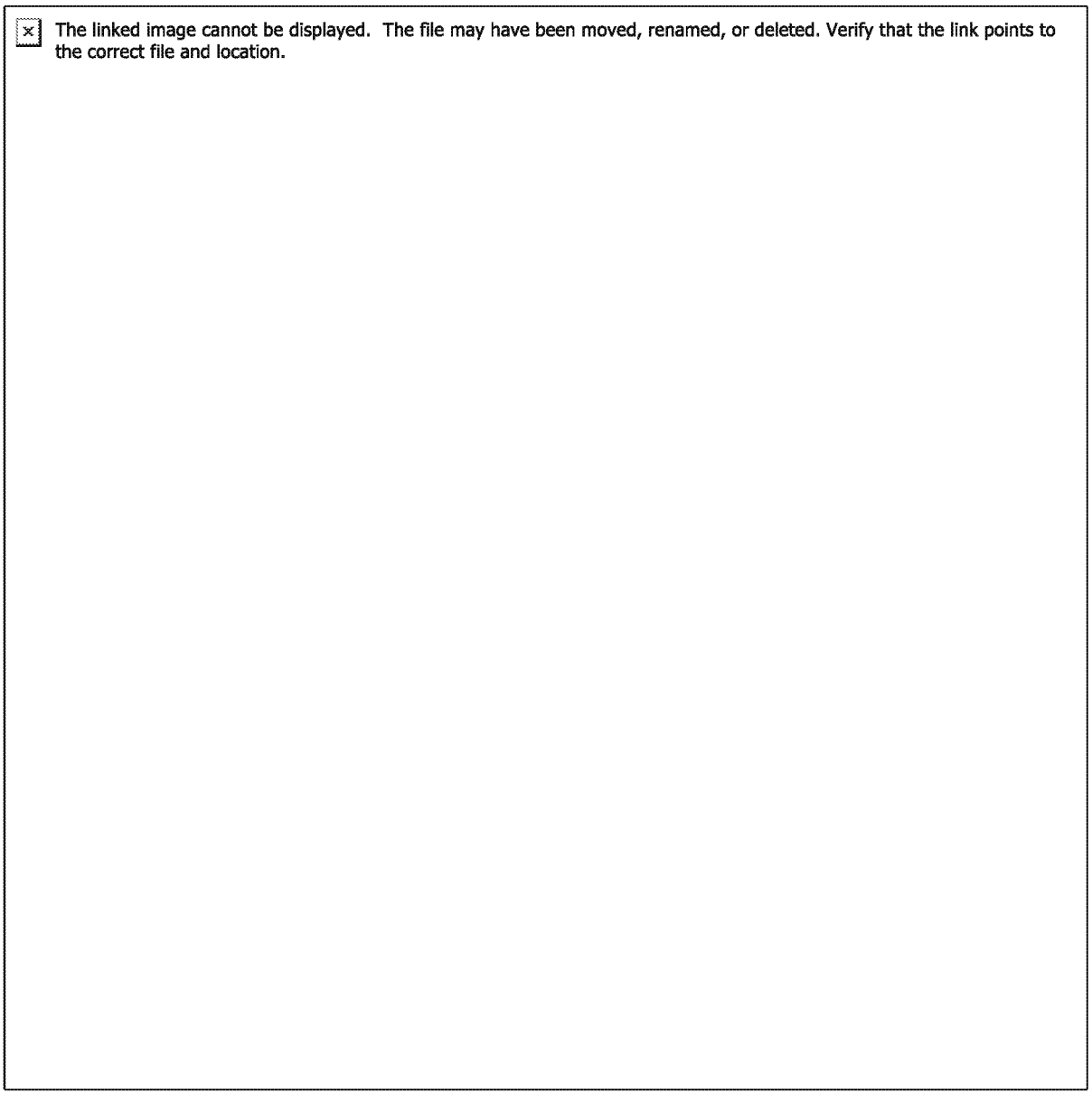
Perspective

mRNA Vaccines: Possible Tools to Combat SARS-CoV-2

Free Full Text (HTML) *Free* Full Text (PDF)

Changhua Yi, Yongxiang Yi, Junwei Li

Since December 2019, a novel coronavirus pneumonia outbreak has been reported in 212 countries and territories, with over 5, 000, 000 infections and over 300, 000 deaths on May 22, 2020. To date, except some repurposed drugs have been shown inhibitory effect on the so-called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), no drugs have been licensed to be effective and safe in treating COVID-19. Inspite of emergent need, no authorized vaccines have been approved for clinical use against this new virus currently. After the genetic map of SARS-CoV-2 was shared, scientists and biotech and vaccine companies promptly launched a race to pursue different types of vaccines to prevent illness from this novel virus. Among these vaccine projects, mRNA vaccines are showing a promising future with their feature of fast development.



Review

The First Disease X is Caused by a Highly Transmissible Acute Respiratory Syndrome Coronavirus

Free Full Text (HTML) *Free* Full Text (PDF)

Shibo Jiang, Zheng-Li Shi

Based on the announcement of the World Health Organization (WHO) in 2018, the Wuhan pneumonia caused by an unknown etiology should be recognized as the first Disease X. Later, the pathogen was identified to be a novel coronavirus denoted 2019-nCoV, which has 79.5% and 96% whole genome sequence identify to SARS-CoV and bat SARS-related coronavirus (SARSr-CoV-RaTG13), respectively, suggesting its potential bat origin. With high human-to-human transmission rate (R0), 2019-nCoV has quickly spread in China and other countries, resulting in 34, 953 confirmed cases and 725 deaths as of 8 February 2020, thus calling for urgent development of therapeutics and prophylactics. Here we suggest renaming 2019-nCoV as "transmissible acute respiratory syndrome coronavirus (TARS-CoV)" and briefly review the advancement of research and development of neutralizing antibodies and vaccines targeting the receptor-binding domain (RBD) and viral fusion inhibitors targeting the heptad repeat 1 (HR1) domain in spike protein of 2019-nCoV.

Review

Understanding SARS-CoV-2-Mediated Inflammatory Responses: From Mechanisms to Potential Therapeutic Tools

Free Full Text (HTML) *Free* Full Text (PDF)

Yajing Fu, Yuanxiong Cheng, Yuntao Wu

Currently there is no effective antiviral therapy for SARS-CoV-2 infection, which frequently leads to fatal inflammatory responses and acute lung injury. Here, we discuss the various mechanisms of SARS-CoV-mediated inflammation. We also assume that SARS-CoV-2 likely shares similar inflammatory responses. Potential therapeutic tools to reduce SARS-CoV-2-induced inflammatory responses include various methods to block FcR activation. In the absence of a proven clinical FcR blocker, the use of intravenous immunoglobulin to block FcR activation may be a viable option for the urgent treatment of pulmonary inflammation to prevent severe lung injury. Such treatment may also be combined with systemic anti-inflammatory drugs or corticosteroids. However, these strategies, as proposed here, remain to be clinically tested for effectiveness.

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Review

The Rapid Assessment and Early Warning Models for COVID-19

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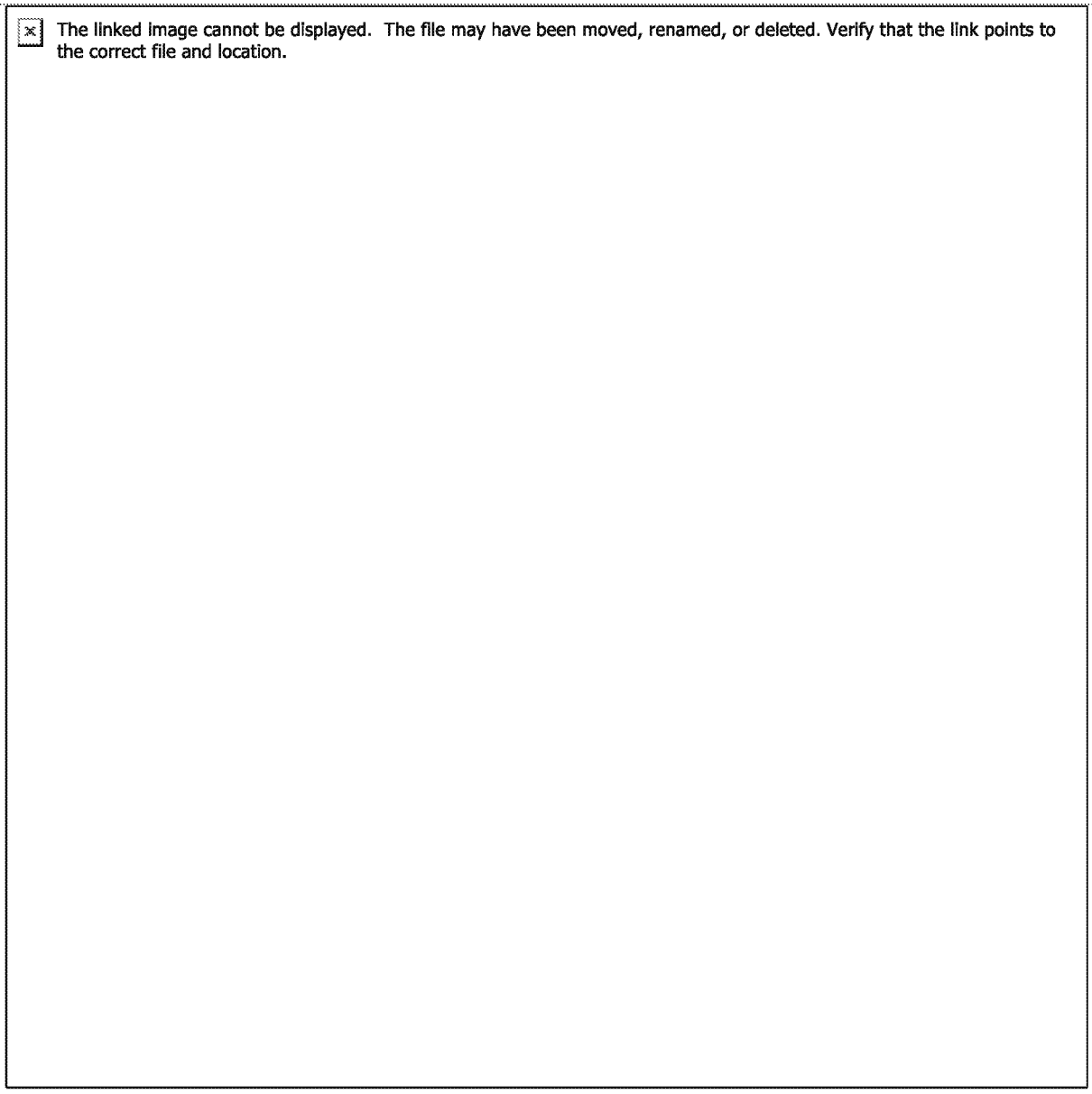
Zhihua Bai, Yue Gong, Xiaodong Tian, Ying Cao, Wenjun Liu, Jing Li

Human beings have experienced a serious public health event as the new pneumonia (COVID-19), caused by the severe acute respiratory syndrome coronavirus has killed more than 3000 people in China, most of them elderly or people with underlying chronic diseases or immunosuppressed states. Rapid assessment and early warning are essential for outbreak analysis in response to serious public health events. This paper reviews the current model analysis methods and conclusions from both micro and macro perspectives. The establishment of a comprehensive assessment model, and the use of model analysis prediction, is very efficient for the early warning of infectious diseases. This would significantly improve global surveillance capacity, particularly in developing regions, and improve basic training in infectious diseases and molecular epidemiology.



Review

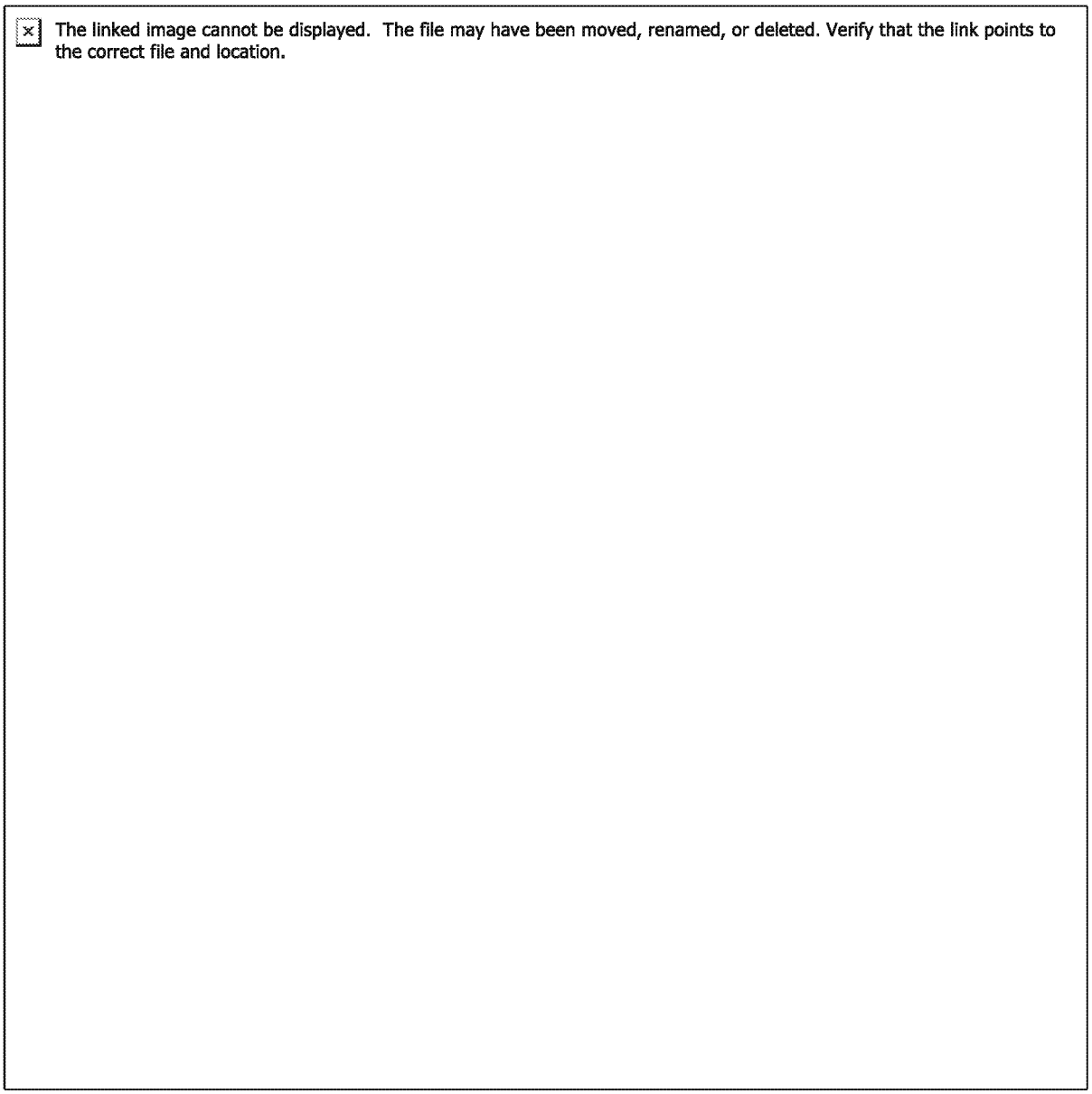
Conditionally Reprogrammed Human Normal Airway Epithelial Cells at ALI: A Physiological Model for Emerging Viruses

Free Full Text (HTML) *Free* Full Text (PDF)

Xuefeng Liu, Yuntao Wu, Lijun Rong

Cancer cell lines have been used widely in cancer biology, and as biological or functional cell systems in many biomedical research fields. These cells are usually defective for many normal activities or functions due to significant genetic and epigenetic changes. Normal primary cell yields and viability from any original tissue specimens are usually relatively low or highly variable. These normal cells cease after a few passages or population doublings due to very limited proliferative capacity. Animal models (ferret, mouse, etc.) are often used to study virus-host interaction. However, viruses usually need to be adapted to the animals by several passages due to tropism restrictions including viral receptors and intracellular restrictions. Here we summarize applications of conditionally reprogrammed cells (CRCs), long-term cultures of normal airway epithelial cells from human nose to lung generated by conditional cell reprogramming (CR) technology, as an ex vivo model in studies of emerging viruses. CR allows to robustly propagate cells from non-invasive or minimally invasive specimens, for example, nasal or endobronchial brushing. This process is rapid (2 days)

and conditional. The CRCs maintain their differentiation potential and lineage functions, and have been used for studies of adenovirus, rhinovirus, respiratory syncytial virus, influenza viruses, parvovirus, and SARS-CoV. The CRCs can be easily used for air-liquid interface (ALI) polarized 3D cultures, and these coupled CRC/ALI cultures mimic physiological conditions and are suitable for studies of viral entry including receptor binding and internalization, innate immune responses, viral replications, and drug discovery as an ex vivo model for emerging viruses.



Review

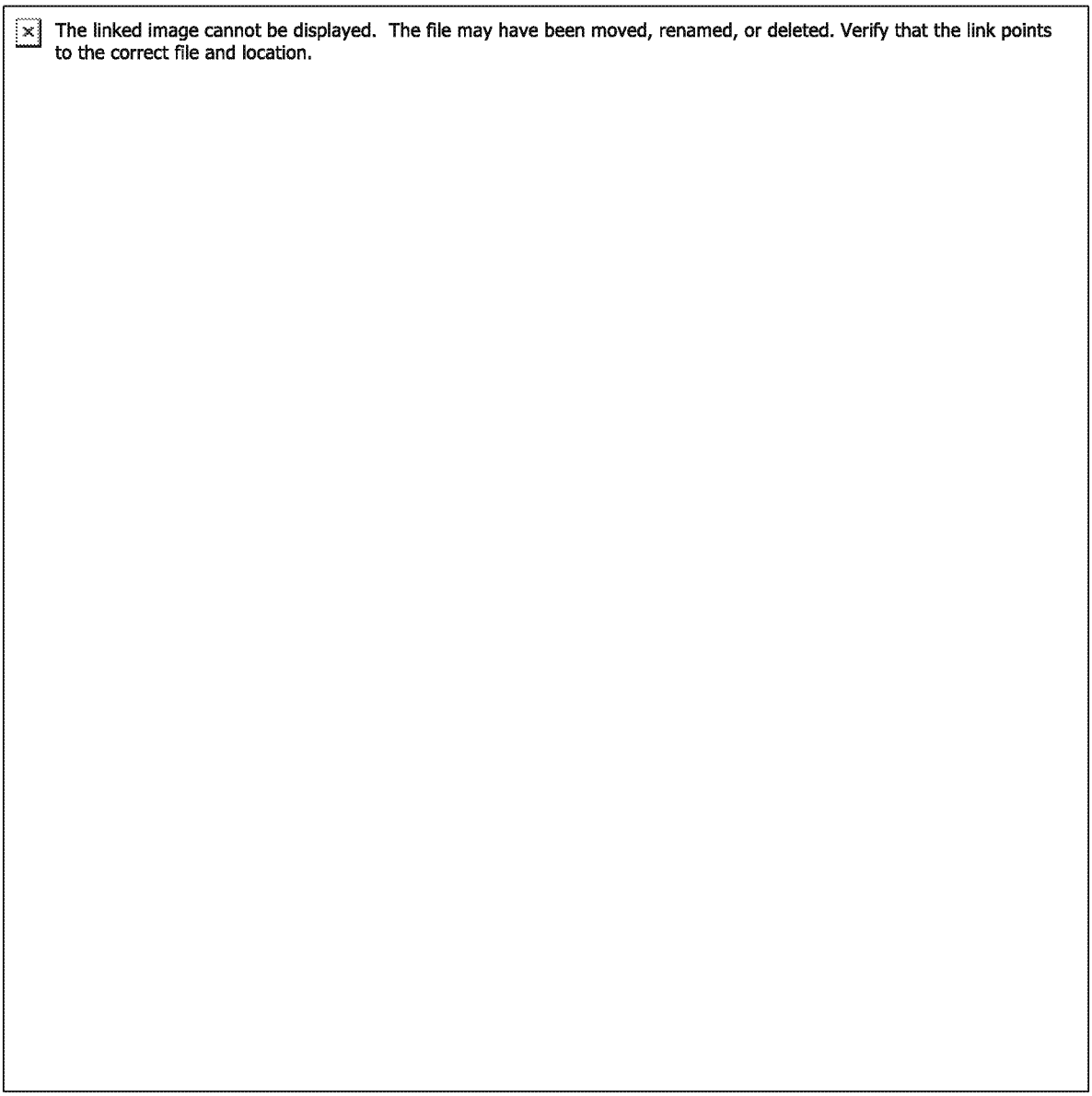
A Comprehensive Review of Animal Models for Coronaviruses: SARS-CoV-2, SARS-CoV, and MERS-CoV

Free Full Text (HTML) *Free* Full Text (PDF)

Ashutosh Singh, Rahul Soloman Singh, Phulen Sarma, Gitika Batra, Rupa Joshi, Hardeep Kaur, Amit Raj Sharma, Ajay Prakash, Bikash Medhi

The recent outbreak of coronavirus disease (COVID-19) caused by the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has already affected a large population of the world. SARS-CoV-2 belongs to the same family of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV). COVID-19 has a complex pathology involving severe acute

respiratory infection, hyper-immune response, and coagulopathy. At present, there is no therapeutic drug or vaccine approved for the disease. There is an urgent need for an ideal animal model that can reflect clinical symptoms and underlying etiopathogenesis similar to COVID-19 patients which can be further used for evaluation of underlying mechanisms, potential vaccines, and therapeutic strategies. The current review provides a paramount insight into the available animal models of SARS-CoV-2, SARS-CoV, and MERS-CoV for the management of the diseases.



Research Article

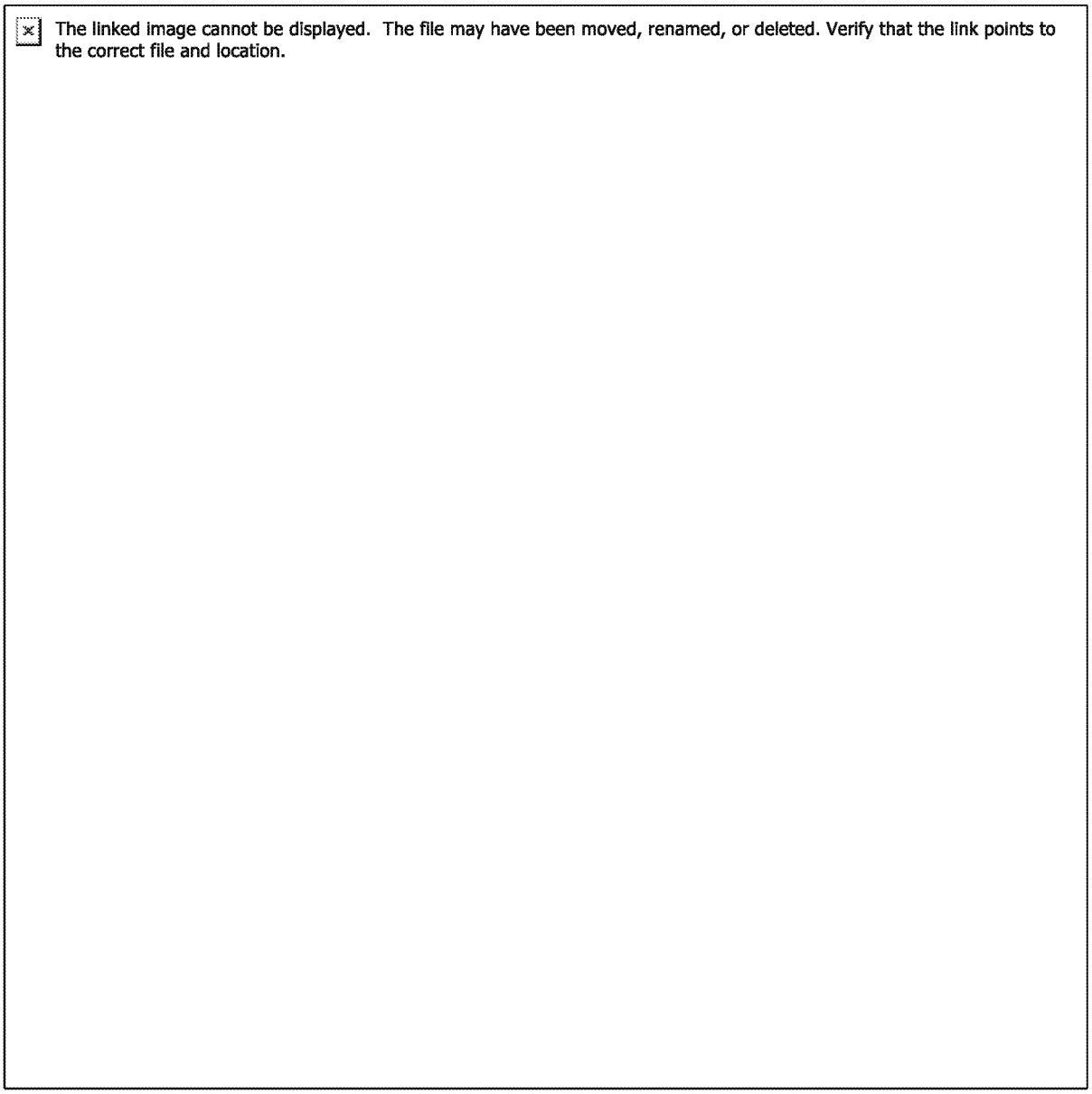
Clinical Manifestation and Laboratory Characteristics of SARS-CoV-2 Infection in Pregnant Women

Free Full Text (HTML) *Free* Full Text (PDF)

Chunchen Wu, Wenzhong Yang, Xiaoxue Wu, Tianzhu Zhang, Yaoyao Zhao, Wei Ren, Jianbo Xia

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic has become a major challenge to public health in China and other countries, considering its pathogenicity across all age groups. Pregnancy is a unique physiological condition, and is characterized by altered immunity and elevated hormone levels to actively tolerate the semi-allogeneic fetus, which undergoes a sudden and substantial fluctuation during the immediate postpartum period. Changes in clinical features, laboratory characteristics, and imaging features of pregnant women during the pre-partum and post-partum periods require further

elucidation. Here, we retrospectively analyzed the clinical features, laboratory characteristics, and imaging features of eight pregnant cases of SARS-CoV-2 infection during the pre-partum and post-partum periods. Our results showed that four of the eight pregnant women were asymptomatic before delivery but became symptomatic post-partum. Correspondingly, white blood cell (WBC) counts increased and lymphocyte (LYMPH) counts decreased. C-reactive protein (CRP) levels in the serum also increased to a higher level than those in general pregnancy. Therefore, it is imperative to closely monitor laboratory parameters including the WBC count, LYMPH count, and CRP, along with other imaging features in chest CT scans, to promptly prevent, diagnose, and treat a SARS-CoV-2 infection during pregnancy.



Research Article

Long Term Culture of Human Kidney Proximal Tubule Epithelial Cells Maintains Lineage Functions and Serves as an Ex vivo Model for Coronavirus Associated Kidney Injury

Free Full Text (HTML) *Free* Full Text (PDF)

Siyu Xia, Ming Wu, Si Chen, Tao Zhang, Lina Ye, Jun Liu, Hui Li

The mechanism of how SARS-CoV-2 causes severe multi-organ failure is largely unknown. Acute kidney injury (AKI) is one of the frequent organ damage in severe COVID-19 patients. Previous studies have shown that human renal tubule cells could be the potential host cells targeted by SARS-CoV-2. Traditional cancer

cell lines or immortalized cell lines are genetically and phenotypically different from host cells. Animal models are widely used, but often fail to reflect a physiological and pathogenic status because of species tropisms. There is an unmet need for normal human epithelial cells for disease modeling. In this study, we successfully established long term cultures of normal human kidney proximal tubule epithelial cells (KPTECs) in 2D and 3D culture systems using conditional reprogramming (CR) and organoids techniques. These cells had the ability to differentiate and repair DNA damage, and showed no transforming property. Importantly, the CR KPTECs maintained lineage function with expression of specific transporters ($SLC_{34}A_3$ and cubilin). They also expressed angiotensin-converting enzyme 2 (ACE2), a receptor for SARS-CoV and SARS-CoV-2. In contrast, cancer cell line did not express endogenous $SLC_{34}A_3$, cubilin and ACE2. Very interestingly, ACE2 expression was around twofold higher in 3D organoids culture compared to that in 2D CR culture condition. Pseudovirion assays demonstrated that SARS-CoV spike (S) protein was able to enter CR cells with luciferase reporter. This integrated 2D CR and 3D organoid cultures provide a physiological ex vivo model to study kidney functions, innate immune response of kidney cells to viruses, and a novel platform for drug discovery and safety evaluation.

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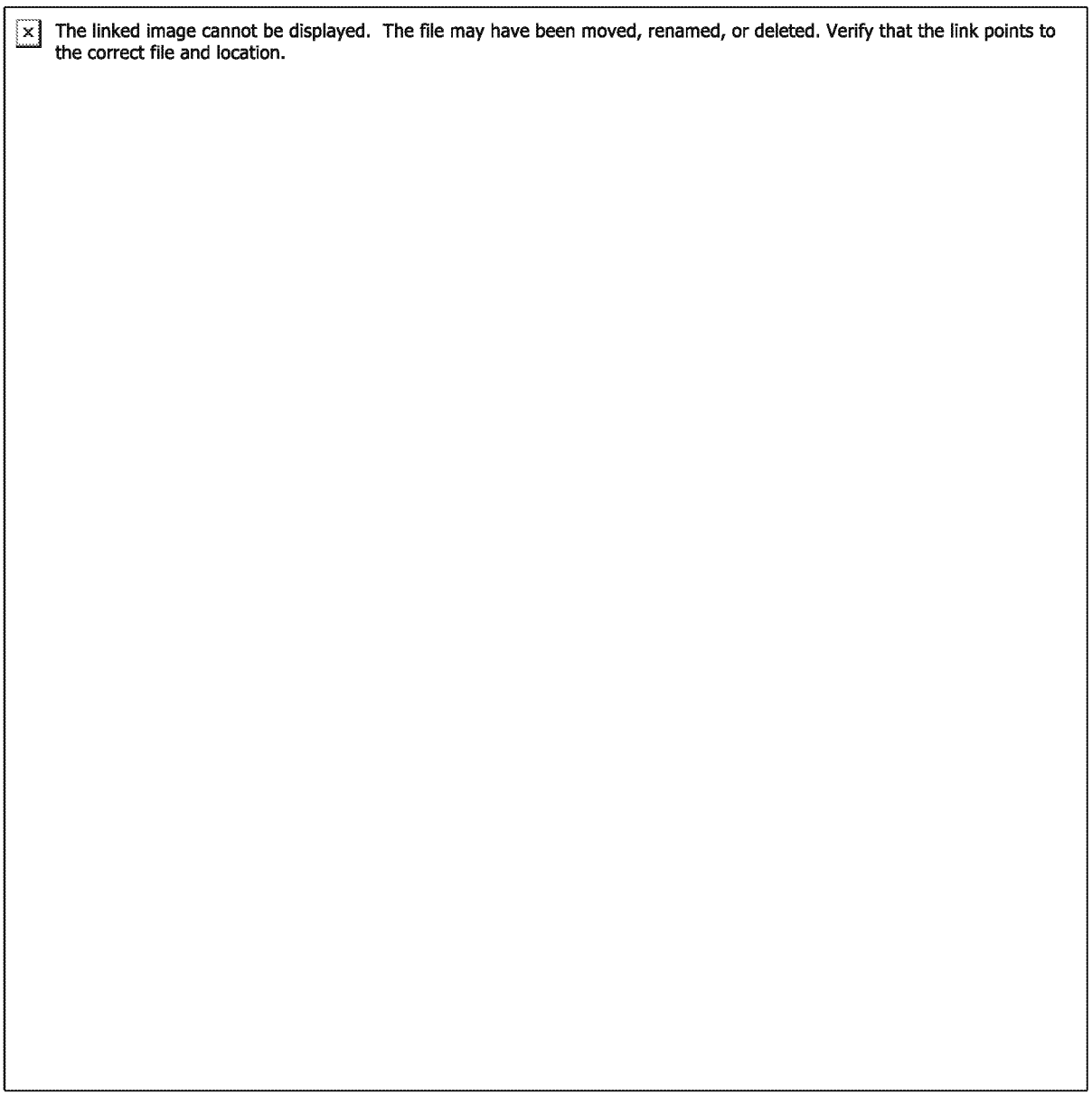
Research Article

SARS-Coronavirus-2 Nsp13 Possesses NTPase and RNA Helicase Activities That Can Be Inhibited by Bismuth Salts

Free Full Text (HTML) *Free* Full Text (PDF)

Ting Shu, Muhan Huang, Di Wu, Yujie Ren, Xueyi Zhang, Yang Han, Jingfang Mu, Ruibing Wang, Yang Qiu, Ding-Yu Zhang, Xi Zhou

The ongoing outbreak of Coronavirus Disease 2019 (COVID-19) has become a global public health emergency. SARS-coronavirus-2 (SARS-CoV-2), the causative pathogen of COVID-19, is a positive-sense single-stranded RNA virus belonging to the family Coronaviridae. For RNA viruses, virus-encoded RNA helicases have long been recognized to play pivotal roles during viral life cycles by facilitating the correct folding and replication of viral RNAs. Here, our studies show that SARS-CoV-2-encoded nonstructural protein 13 (nsp13) possesses the nucleoside triphosphate hydrolase (NTPase) and RNA helicase activities that can hydrolyze all types of NTPs and unwind RNA helices dependently of the presence of NTP, and further characterize the biochemical characteristics of these two enzymatic activities associated with SARS-CoV-2 nsp13. Moreover, we found that some bismuth salts could effectively inhibit both the NTPase and RNA helicase activities of SARS-CoV-2 nsp13 in a dose-dependent manner. Thus, our findings demonstrate the NTPase and helicase activities of SARS-CoV-2 nsp13, which may play an important role in SARS-CoV-2 replication and serve as a target for antivirals.



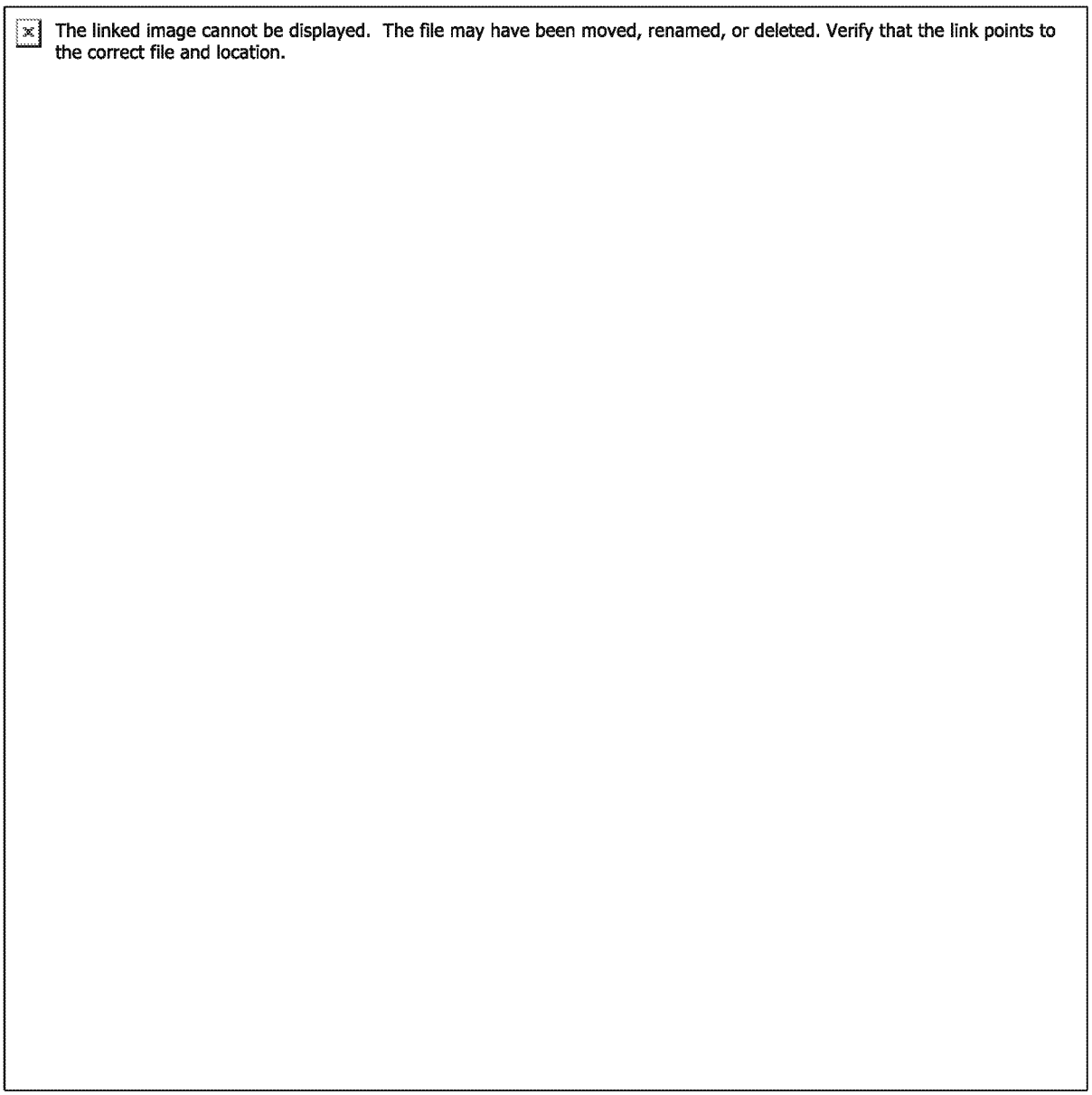
Letter

Clinical Features and Treatment of 2019-nCov Pneumonia Patients in Wuhan: Report of A Couple Cases

Free Full Text (HTML) *Free* Full Text (PDF)

Zhan Zhang, Xiaochen Li, Wei Zhang, Zheng-Li Shi, Zhishui Zheng, Tao Wang

Till January 20, 2020, the 2019-new coronavirus (2019-nCoV) has caused more than one hundred cases in Wuhan (WMHC 2020). During a retrospective study of recent pneumonia patients in our department, we found two patients who are likely being infected with the 2019-nCoV. During the hospitalization, those two patients were appropriately treated, and both were discharged within two weeks. Thus, we are reporting the clinical features and treatment regiment, and hope the information and experience can be shared.



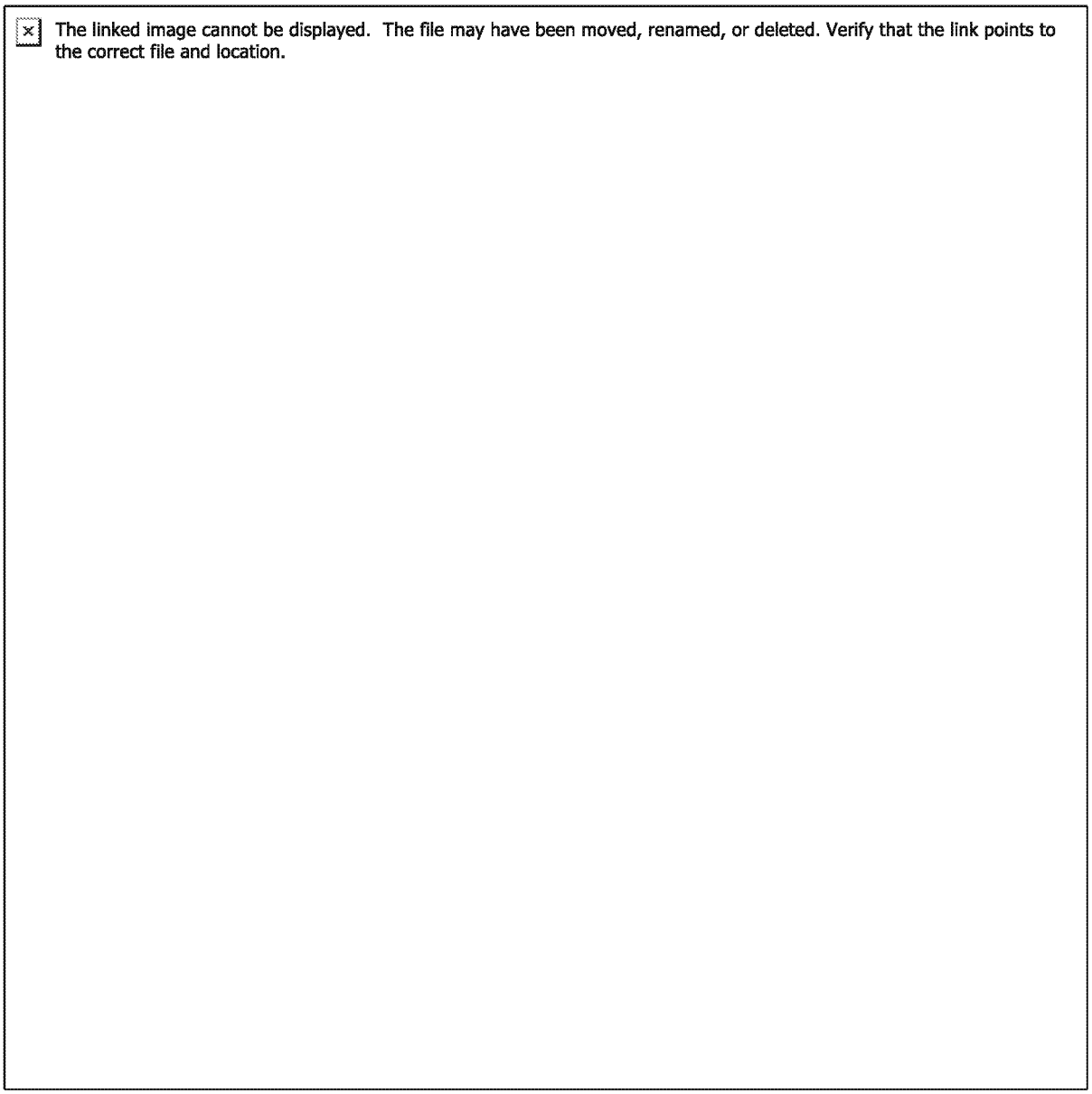
Letter

A Unique Protease Cleavage Site Predicted in the Spike Protein of the Novel Pneumonia Coronavirus (2019-nCoV) Potentially Related to Viral Transmissibility

Free Full Text (HTML) *Free* Full Text (PDF)

Qiong Wang, Ye Qiu, Jin-Yan Li, Zhi-Jian Zhou, Ce-Heng Liao, Xing-Yi Ge

In summary, our sequence analysis on the S protein of 2019-nCoV has predicted a novel furin cleavage site at S1/S2 linkage. The ubiquitous expression of furin in different organs and tissues may be a reason for the high transmissibility and pathogenicity of 2019-nCoV observed in the current epidemic. However, since our findings were mainly based on bioinformatic analysis, more laboratory studies on 2019-nCoV in cell and animal models are required to verify our speculations and to avoid any bias.



Letter

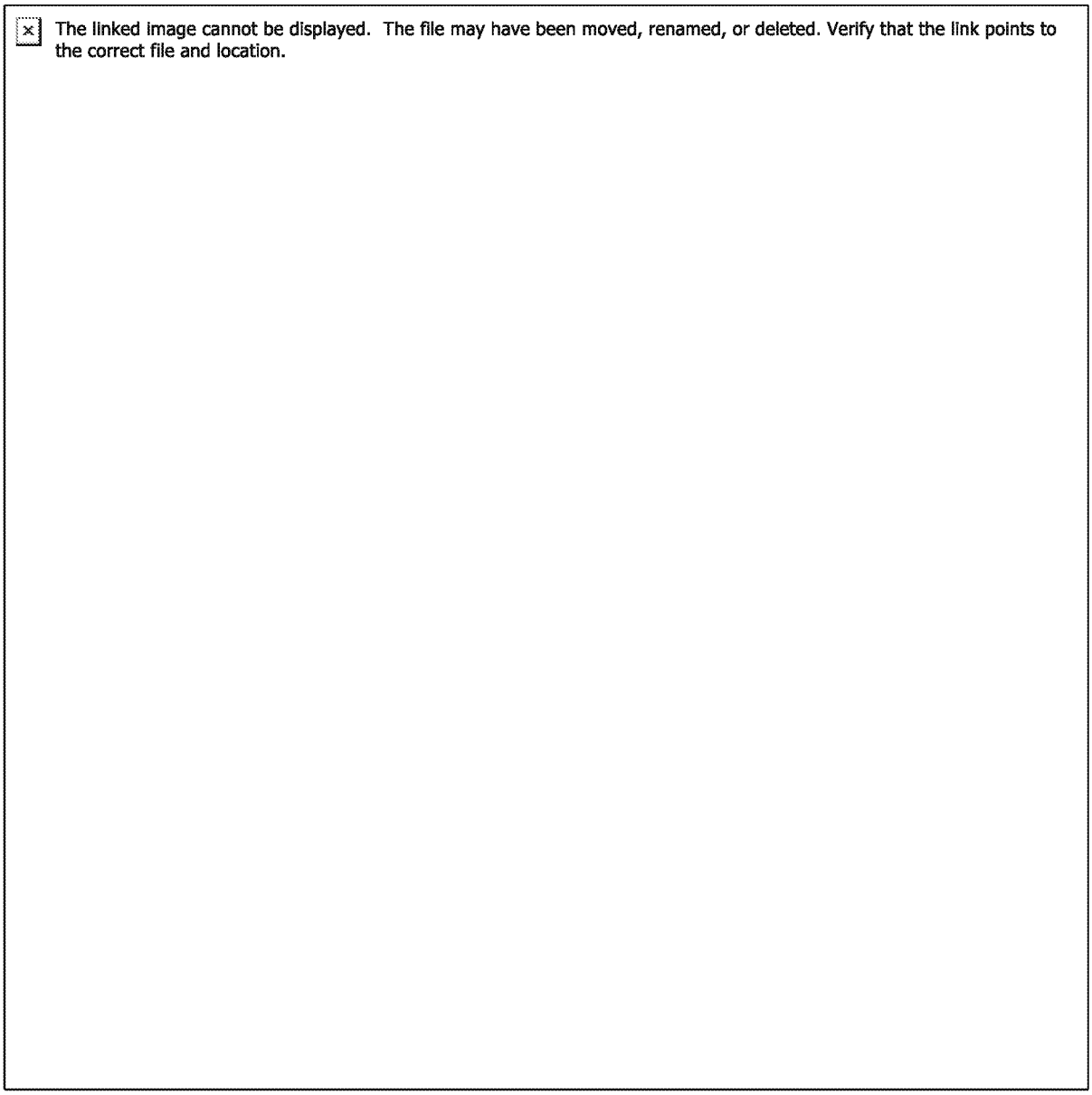
Inefficiency of Sera from Mice Treated with Pseudotyped SARS-CoV to Neutralize 2019-nCoV Infection

Free Full Text (HTML) *Free* Full Text (PDF)

Zezhong Liu, Shuai Xia, Xinling Wang, Qiaoshuai Lan, Wei Xu, Qian Wang, Shibo Jiang, Lu Lu

The novel coronavirus 2019-nCoV has caused the pandemic of Wuhan pneumonia recently, posing a serious threat to global public health, and thus calling for the development of therapeutics and prophylactics. Here we showed that high titer anti-SARS-CoV spike protein serum cannot effectively neutralize 2019-nCoV infection. Based on our previous research, we developed SARS pseudovirus (SARS-PsV) and MERS pseudovirus (MERS-PsV) as immunogens to immunize mice. We found sera from mice treated with SARS-CoV S protein

could potently cross-neutralize infection by SARS-CoV (50% neutralizing antibody titers, NT_{50} > 40, 000) and SARS-related coronavirus (NT_{50} > 7, 000), but weakly for 2019-nCoV infection NT_{50} < 100), implying that it may not be practical to treat 2019-nCoV infection with anti-SARS-CoV antibodies and that people with history of SARS-CoV infection many years ago may not be resistant to 2019-nCoV infection.



Letter

Development of a Novel Reverse Transcription Loop-Mediated Isothermal Amplification Method for Rapid Detection of SARS-CoV-2

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Renfei Lu, Xiuming Wu, Zhenzhou Wan, Yingxue Li, Lulu Zuo, Jianru Qin, Xia Jin, Chiyu Zhang

In conclusion, the novel visual RT-LAMP assay is a simple, rapid, and sensitive approach for detection of SARS-CoV-2, and it is ready for application in primary care and community hospitals or health care centers, and even patients' own houses in response to the current SARS-CoV-2 epidemic because the assay does not require sophisticated equipment and skilled personnel. Furthermore, it is also ready to be used in fields for screening samples from wild animals and environments to facilitate the identification of potential intermediate hosts that mediate the cross-species transmission of SARS-CoV-2 from bats to humans.

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Letter

Isolation and Growth Characteristics of SARS-CoV-2 in Vero Cell

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Pingping Yao, Yachun Zhang, Yisheng Sun, Yulin Gu, Fang Xu, Bo Su, Chen Chen, Hangjing Lu, Dehui Wang, Zhangnv Yang, Biao Niu, Jiancai Chen, Lixia Xie, Lei Chen, Yajing Zhang, Hui Wang, Yuying Zhao, Yue Guo, Juncheng Ruan, Zhiyong Zhu, Zhenfang Fu, Dayong Tian, Qi An, Jianmin Jiang, Hanping Zhu

The coronavirus disease 2019 (COVID-19) broke out in early December 2019 in Wuhan, China and escalated into a global pandemic. There is an urgent need to understand the biology of SARS-CoV-2. In this letter, we report the isolation and characterization of seven isolates of SARS-CoV-2. Results show that our viruses have 99% sequence identity with published virus sequences. In addition, all viruses grew well in Vero cells, and one of the viruses had a deletion mutation after short passage. These results shall facilitate the understanding of the characteristics of SARS-CoV-2 *in vitro*.

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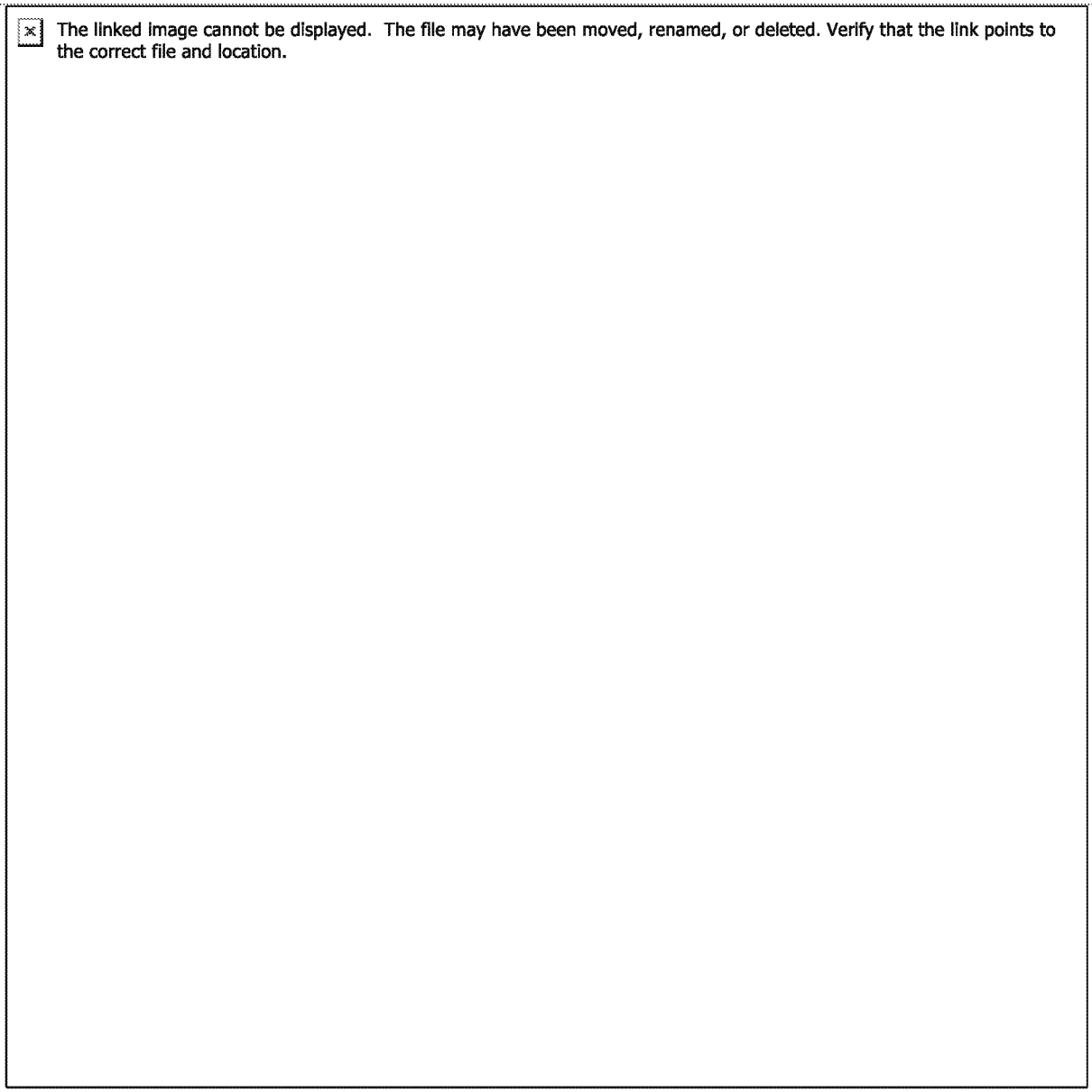
Letter

A DNA Aptamer Based Method for Detection of SARS-CoV-2 Nucleocapsid Protein

Free Full Text (HTML) *Free* Full Text (PDF)

Zhiqiang Chen, Qihan Wu, Jing Chen, Xiaohua Ni, Jianfeng Dai

Altogether, we have identified a novel method for the detection of SRAS-CoV-2 N protein using DNA based aptamers. Although the aptamers used in this study were designed based on an aptamer previously selected for SARS-CoV N protein, they bind to SRAS-CoV-2 N protein with a high affinity. Most importantly, SARS-CoV-2 N protein shares very low similarity (16%–38%) with N protein from other five known human coronaviruses except for SARS-CoV. Because there are no SARS-CoV cases reported since 2004, our aptamer-based method can be used as a supplementation to the current diagnosis of SARS-CoV-2.



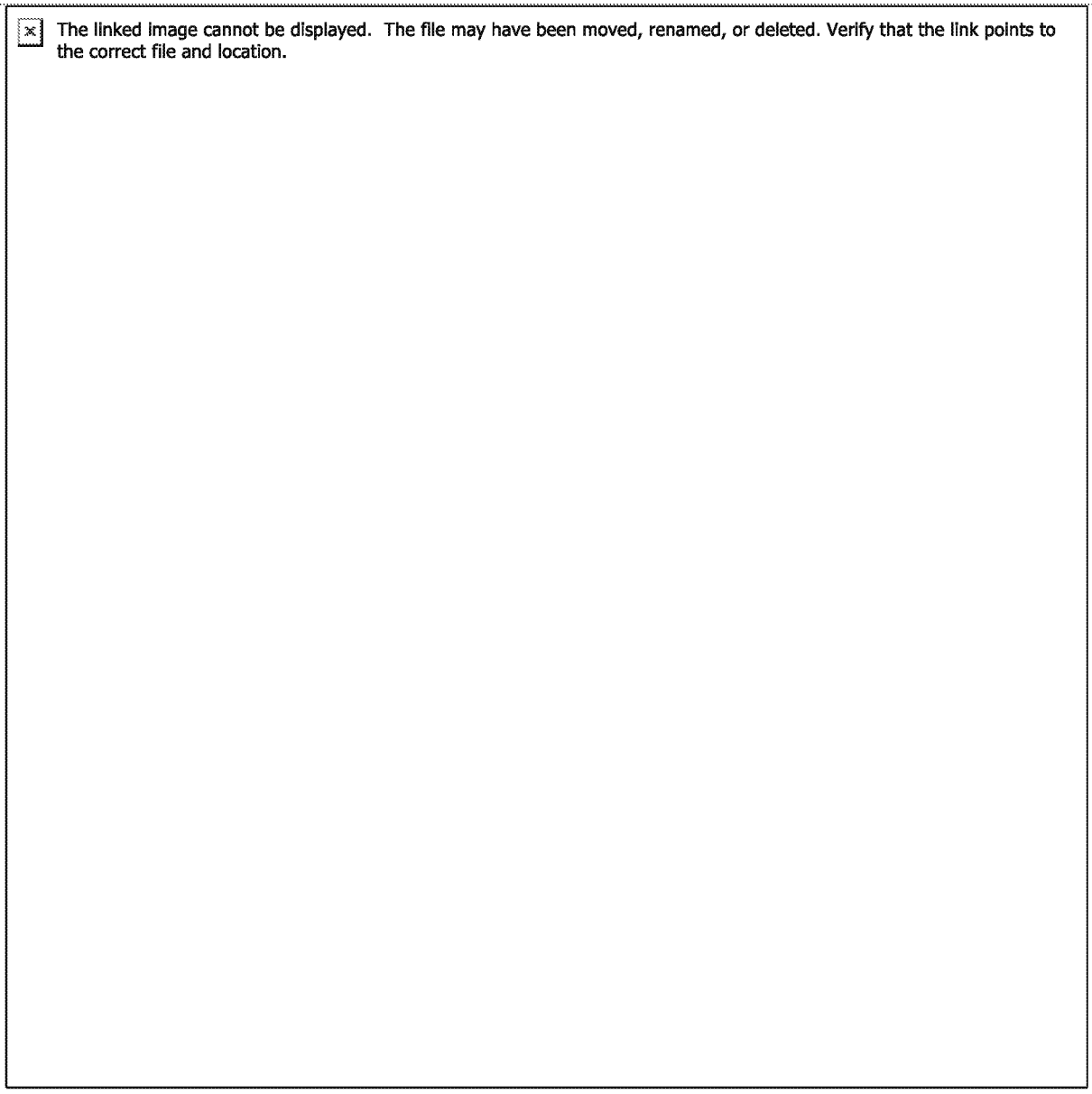
Letter

SARS-CoV-2 Does Not Replicate in Aedes Mosquito Cells nor Present in Field-Caught Mosquitoes from Wuhan

Free Full Text (HTML) *Free* Full Text (PDF)

Han Xia, Evans Atoni, Lu Zhao, Nanjie Ren, Doudou Huang, Rongjuan Pei, Zhen Chen, Jin Xiong, Raphael Nyaruaba, Shuqi Xiao, Bo Zhang, Zhiming Yuan

With the rapid spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and growing fear, people have become very concerned about whether this novel coronavirus could be transmitted by mosquitoes. We evaluate the infectivity of SARS-CoV-2 in *Aedes albopictus* and *Aedes aegypti* derived cell lines. The results indicated that SARS-CoV-2 could not replicate in both C6/36, Sf9 and Aag2 cells. Further, no SARS-CoV-2 RNA was detected in the field collected *Culex*, and *Anopheles* mosquitoes during the months of April and May in Wuhan in 2020. Our findings highlight the restricted replication of SARS-CoV-2 in mosquito cells and field-caught mosquitoes.



Letter

Computational Identification of Small Interfering RNA Targets in SARS-CoV-2

Free Full Text (HTML) *Free* Full Text (PDF)

Wei Chen, Pengmian Feng, Kewei Liu, Meng Wu, Hao Lin

With the epidemic of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) worldwide and in the absence of any effective vaccine, there is an urgent need to find a specific anti- SARS-CoV-2 agent. In this study, by analyzing the secondary structures of the SARS-CoV-2 genome (MN908947), several 21~25 base-long segments were obtained and selected as the potential targets of small interfering RNA duplexes. Moreover, it was also found that these targets are conserved among different strains. We hope the results will contribute to the pharmaceutical research and therapy of the SARS-CoV-2.

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To: Shi, Pei yong[peshi@UTMB.EDU]
From: yuxuejie@whu.edu.cn[yuxuejie@whu.edu.cn]
Sent: Wed 9/9/2020 6:38:48 AM (UTC-05:00)
Subject: Re: RE: Editoral board member

Pei-yong，
Thank you.
Xuejie

发自我的iPhone

---------- Original ----------
From: Shi, Pei yong <peshi@UTMB.EDU>
Date: Wed,Sep 9,2020 7:32 PM
To: 于学杰 <yuxuejie@whu.edu.cn>
Subject: Re: RE: Editoral board member

Hi Xuejie,
Thanks for the invitation. I will be happy to be on the editorial board and help the journal.
Hope all well on your side.
Best wishes,
Pei-Yong

Pei-Yong Shi, Ph.D.
John Sealy Distinguished Chair in Innovations in Molecular Biology
Vice Chair for Innovation and Commercialization
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch at Galveston
Phone: 409-772-6370

-----Original Message-----
From: 于学杰 <yuxuejie@whu.edu.cn>
Sent: Wednesday, September 9, 2020 6:16 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: Editoral board member

Hi Pei-yong,

I am writing to you to ask you to help me on a new journal, Infectious Medicine. I am the Editor-in-Chief for Infectious Medicine, a new journal on infectious diseases, which will be launched in the summer of 2021 by Tsinghua University and Tsinghua University Press. I hope you will be an editoral board member or an associate editor of the journal. I also hope you can recommend internationally well-known infectious disease and immunology experts and scholars to the jouranl to form an editorial board to participate in the peer review of manuscripts. With your outstanding academic status in the field of infectious diseases, I feel confident to make the journal successful!

Infectious Medicine is a comprehensive English-language journal in the field of infection and infectious diseases. It is dedicated to reporting on the intersection of emerging infectious diseases and animal-borne infectious diseases, and strives to become an integrated platform for One Health on studying human infectious diseases and animal infectious diseases. Our mission is to promote academic exchanges, advance scientific and technological progress, and improve the scientific level of infectious disease research. The scope of this journal includes all aspects of infectious diseases especially emerging infectious diseases, including but not limited to the following areas: (1) epidemiology, prevention and control of infectious diseases and nosocomial infections; (2) pathogenesis, immunology, diagnosis and

treatments of infection diseases; (3) Research and development of vaccines; (4) Public health policies and epidemic prevention measures for infectious diseases. The journal will have the following columns: Editorial, Original article, Commentary, Reviews, Short report & Case report, Research letter and Perspective. In order to increase the speed and breadth of dissemination, Infectious Medicine will adopt open access and ahead of print methods to publish, and all articles can be read for free online. Once the article is received, it will be retrieved, read and downloaded by readers worldwide as soon as possible.
The main responsibilities of the editorial board include:
1. Participate in the peer review of submissions; 2. Write manuscripts for the journal; 3. Recommend manuscripts to the journal; 4. When participating in international and domestic academic meetings, the editorial board members will actively publicize and recommend this journal to colleagues; 5. Provide feedback and suggestions for the development of the journal.

I know you are very busy and I promise there will not be too much work on you. I sincerely hope that you can accept my invitation. Please let me know whether you would like to be an associate editor or an editoral board memeber for the Infectious Medicine. Thank you.

Xuejie

于学杰
武汉大学健康学院
Xuejie Yu, M.D., Ph.D
Professor and Dean
School of Health Sciences
Wuhan University
Wuhan, China 430071
027-68759399

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 11/26/2020 8:27:51 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: Re: RE: paper-2020526
Attachments: GLP2R-20201126.docx; GLP2R 20201124.pptx

Pei-yong,

Here is the update draft of the paper. I would like invite you go through the MS.Thank you very much !

I am looking forward to hearing from you.

All mm regards,

Xinwen

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-05-27 20:29:20 (星期三)
收件人: "陈新文" <chenxw@wh.iov.cn>
抄送:
主题: RE: paper-2020526

Hi Xinwen,

I quickly went through the manuscript. Let's have a call to (i) go through the data and (ii) discuss the way forward. Please let me know when you have time to call.

Best,

- Pei-Yong

From: 陈新文 <chenxw@wh.iov.cn>
Sent: Tuesday, May 26, 2020 10:30 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: paper-2020526

佩勇，

附件是文章的结果。文章很初步，整体结构也需要大的调整。我想这是第一次请教，请你审核数据（文章的主体部分和图表），期待意见和建议，特别是：

1）需要补充的其他实验；

2）文章写作思路和整体布局

另外， 我们正在补充的数据包括：

1）GLP2R蛋白的ECL1结构域和E蛋白DIII直接相互作用证据（合成多肽，SPR分析），

2）缺陷小鼠感染实验（已经构建成功，正在繁殖）。

将在你意见和建议的基础上重新架构文章。

非常感谢！

祝好！

新文

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 5/26/2020 10:29:31 PM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: paper-2020526
Attachments: paper-2020526.docx; GLP2R.pptx

佩勇,

附件是文章的结果。文章很初步，整体结构也需要大的调整。我想这是第一次请教，请你审核数据（文章的主体部分和图表），期待意见和建议，特别是：

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2）缺陷小鼠感染实验（已经构建成功，正在繁殖）。

将在你意见和建议的基础上重新架构文章。

非常感谢！

祝好！

新文

From: 单超 [shanchao@wh.iov.cn]
Sent: 8/4/2020 9:17:57 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: Mailing address

Hi Pei-Yong,

Below is the mailing address.

Thanks,

Chao

Chao SHAN, Ph.D.
Wuhan Institute of Virology,
Chinese Academy of Sciences
No.44 Xiaohongshan, Wuhan,
430071, P. R. China
Cell: +86 18971463986

From: William Dowling [william.dowling@cepi.net]
Sent: 9/9/2020 8:49:00 AM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; Valentina Bernasconi [valentina.bernasconi@cepi.net]; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok [karin.bok@nih.gov]; dboyle@path.org; brooke.bozick@nih.gov; christian.brechot [christian.brechot@pasteur.fr]; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; Marco.Cavaleri [Marco.Cavaleri@ema.europa.eu]; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; Carolyn Clark [carolyn.clark@cepi.net]; kizzmekia.corbett@nih.gov; costaa@who.int; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/OID/NCEZID) [iad7@cdc.gov]; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; William Dowling [william.dowling@cepi.net]; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; barney.graham@nih.gov; ahgriff@bu.edu; d.goldblatt@ucl.ac.uk; Elwyn Griffiths [elwyn.griffiths@cepi.net]; gregory.d.gromowski.civ@mail.mil; GSELL, Pierre [gsellp@who.int]; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; henaorestrepoa@who.int; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; Johan Holst [johan.holst@cepi.net]; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; Cassandra.Kelly@finddx.org; Jacqueline.Kirchner@gatesfoundation.org; knezevici [knezevici@who.int]; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Phil Krause [philip.krause@fda.hhs.gov]; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; Arun Kumar [arun.kumar@cepi.net]; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey [janet.lathey@nih.gov]; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen Makar [Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; omorgan@who.int; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; perkinsm@who.int; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; lauriex@who.int; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan [moorthyv@who.int]; schendel@lji.org; Schmaljohn, Connie (NIH/NIAID) [E] [Connie.schmaljohn@nih.gov]; Barbara.Schnierle@pei.de; PScott@eidresearch.org; Shi, Pei yong [peshi@UTMB.EDU]; Ragini.Shivji@ema.europa.eu; Amy C. Shurtleff [amy.c.shurtleff@cepi.net]; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; swaminathans@who.int; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David Vaughn [David.Vaughn@gatesfoundation.org]; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; Solomon Abebe Yimer [solomon.yimer@cepi.net]; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn
Subject: FW: cell paper about very potent highly stable human domain
Attachments: 20Cell ab8 online published.pdf

Dear all
Here is the paper mentioned by Dimiter on our call today.
Thanks

Bill

From: Dimitrov, Dimiter Stanchev <mit666666@pitt.edu>
Sent: Wednesday, September 9, 2020 9:29 AM
To: William Dowling <william.dowling@cepi.net>
Subject: cell paper about very potent highly stable human domain

Hi Bill,

I put it on the chat in the last second, here it is
https://www.cell.com/cell/fulltext/S0092-8674(20)31148-X

also attached the file just in case.

It is human domain fused to Fc and every stable – for 3 months at 37C no change in activity.
Was thinking even could be used as reference reagent, you mentioned there is also another candidate.

Best
Mitko
(Dimiter Dimitrov)

From: William Dowling <william.dowling@cepi.net>
Sent: Tuesday, August 4, 2020 2:23 PM
To: galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; Valentina Bernasconi <valentina.bernasconi@cepi.net>; shinjini.bhatnagar@thsti.res.in; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; christian.brechot <christian.brechot@pasteur.fr>; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; Carolyn Clark <carolyn.clark@cepi.net>; kizzmekia.corbett@nih.gov; costaa@who.int; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/OID/NCEZID) <iad7@cdc.gov>; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; Dimitrov, Dimiter Stanchev <mit666666@pitt.edu>; William Dowling <william.dowling@cepi.net>; christian.drosten@charite.de; epstein@ecohealthalliance.org; Kari.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; barney.graham@nih.gov; ahgriff@bu.edu; Elwyn Griffiths <elwyn.griffiths@cepi.net>; gregory.d.gromowski.civ@mail.mil; GSELL, Pierre <gsellp@who.int>; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; henaorestrepoa@who.int; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; Johan Holst <johan.holst@cepi.net>; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; Cassandra.Kelly@finddx.org; Jacqueline.Kirchner@gatesfoundation.org; knezevici <knezevici@who.int>; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Phil Krause <philip.krause@fda.hhs.gov>; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; Arun Kumar <arun.kumar@cepi.net>; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey <janet.lathey@nih.gov>; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen Makar <Karen.Makar@gatesfoundation.org>; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; Mellors, John W <jwm1@pitt.edu>; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; kaitlyn.dambach@nih.gov; omorgan@who.int;

Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; perkinsm@who.int; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dsti.gov.uk; arimoin@g.ucla.edu; lauriex@who.int; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan <moorthyv@who.int>; schendel@lji.org; Schmaljohn, Connie (NIH/NIAID) [E] <Connie.schmaljohn@nih.gov>; Barbara.Schnierle@pei.de; PScott@eidresearch.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; Amy C. Shurtleff <amy.c.shurtleff@cepi.net>; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; swaminathans@who.int; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David Vaughn <David.Vaughn@gatesfoundation.org>; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; Solomon Abebe Yimer <solomon.yimer@cepi.net>; tiying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; PNorris@vitalant.org; Lisa@amicitiam.com; katie.doores@kcl.ac.uk; rolandsutter@gmail.com

Subject: [SPAM]WHO Viruses reagents and assays working group - No meeting this week

Hello all

There will be no meeting of WHO Viruses reagents and assays working group this week (Wed, Aug. 5). We will return next week on Aug 12 at 2:30 PM CET.

Thanks

Bill

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)

(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

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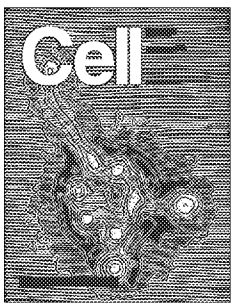

High potency of a bivalent human V_H domain in SARS-CoV-2 animal models

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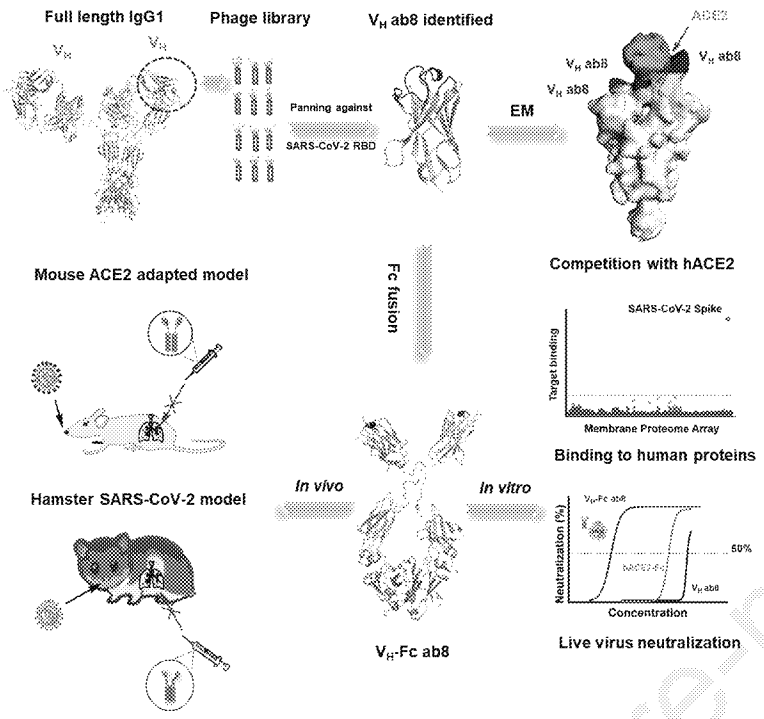

High potency of a bivalent human V_H domain in SARS-CoV-2 animal models

Wei Li[1*#], Alexandra Schäfer[2#], Swarali S. Kulkarni[3#], Xianglei Liu[1#], David R. Martinez[2#], Chuan Chen[1], Zehua Sun[1], Sarah R. Leist[2], Aleksandra Drelich[4], Liyong Zhang[1], Marcin L. Ura[5], Alison Berezuk[6], Sagar Chittori[6], Karoline Leopold[6], Dhiraj Mannar[6], Shanti S. Srivastava[6], Xing Zhu[6], Eric C. Peterson[5], Chien-Te Tseng[4], John W. Mellors[1,5], Darryl Falzarano[3], Sriram Subramaniam[6], Ralph S. Baric[2] and Dimiter S. Dimitrov[1,5,7*]

[1]Center for Antibody Therapeutics, Division of Infectious Diseases, Department of Medicine, University of Pittsburgh Medical School, 3550 Terrace Str, Pittsburgh, PA 15261, USA.

[2]Department of Epidemiology, University of North Carolina at Chapel Hill, 135 Dauer Drive, 3109 Michael Hooker Research Center Chapel Hill, NC 27599, USA.

[3]Vaccine and Infectious Disease Organization – International Vaccine Centre, and the Department of Veterinary Microbiology, University of Saskatchewan, 117 Veterinary Road, Saskatoon, SK S7N 5E3, Canada[4]Department of Microbiology & Immunology, Centers for Biodefense and Emerging Diseases, Galveston National Laboratory, 301 University Blvd, Galveston, Texas 77550, USA.

[5]Abound Bio, 1401 Forbes Ave, Pittsburgh, PA 15219, USA.

[6]Department of Biochemistry and Molecular Biology, University of British Columbia, Life Sciences Centre, 2350 Health Sciences Mall, Vancouver, BC Canada V6T 1Z3, Canada

[7]Lead Contact

Running title: Potent in vivo SARS-CoV-2 neutralization of by a human V_H

[#]Equal Contribution

[*]Corresponding Authors:

Wei Li, PhD and Dimiter S. Dimitrov, PhD, ScD

Center for Antibody Therapeutics

Division of Infectious Diseases, Department of Medicine, University of Pittsburgh Medical School

S845 and S843, Scaife Hall

3550 Terrace Street, Pittsburgh, PA 15261, USA

Tel: 412-383-4702, Fax: 412-383-7982

E-mails: liwei171@pitt.edu and mit666666@pitt.edu

Key words: Human V_H antibody domain, virus neutralization, electron microscopy, SARS-CoV-2, mouse and hamster models

Abstract

Novel COVID-19 therapeutics are urgently needed. We generated a phage-displayed human antibody V_H domain library from which we identified a high-affinity V_H binder ab8. Bivalent V_H, V_H-Fc ab8 bound with high avidity to membrane-associated S glycoprotein and to mutants found in patients. It potently neutralized mouse adapted SARS-CoV-2 in wild type mice at a dose as low as 2 mg/kg and exhibited high prophylactic and therapeutic efficacy in a hamster model of SARS-CoV-2 infection, possibly enhanced by its relatively small size. Electron microscopy combined with scanning mutagenesis identified ab8 interactions with all three S protomers and showed how ab8 neutralized the virus by directly interfering with ACE2 binding. V_H-Fc ab8 did not aggregate and did not bind to 5300 human membrane-associated proteins. The potent neutralization activity of V_H-Fc ab8 combined with good developability properties and cross-reactivity to SARS-CoV-2 mutants provide a strong rationale for its evaluation as a COVID-19 therapeutic.

Introduction

The global outbreak of a severe acute respiratory distress (SARS) coronavirus 2 (SARS-CoV-2) associated disease 2019 (COVID-19) requires rapid identification of therapeutics and vaccines. While many vaccines are in clinical development, the time to market can be relatively long and immunogenicity can be limited for high-risk groups (Amanat and Krammer, 2020). Alternatively and complementarily, antibodies can be used as safe and effective prophylactics and therapeutics (Pelegrin et al., 2015). Convalescent plasma from COVID-19 patients inhibited SARS-CoV-2 infection and alleviated symptoms of newly infected patients (Casadevall and Pirofski, 2020; Rojas et al., 2020) suggesting that potent neutralizing monoclonal antibodies (mAbs) may be even more effective.

SARS-CoV-2 genome shares more than 80% homology to the SARS-CoV (Li et al., 2020b). Similar to SARS-CoV, SARS-CoV-2 uses the spike (S) envelope glycoprotein to enter into host cells. The viral entry is initiated by the receptor binding domain (RBD) of the S protein binding to its receptor, angiotensin-converting enzyme 2 (ACE2), leading to conformational change of the S2 subunit and formation of six helical-bundle resulting in membrane fusion between viral and host cells (Jiang et al., 2020; Yan et al., 2020). The SARS-CoV RBD contains immune-dominant epitopes that can elicit neutralizing antibodies conferring protection to SARS-CoV infection (He et al., 2005). A recent bioinformatics study showed that SARS-CoV-2 RBD has several B cell epitopes (Grifoni et al., 2020). SARS-CoV-2 RBD based immunogens were able to elicit neutralizing sera in animals (Quinlan et al., 2020). Thus, SARS-CoV-2 RBD is a good target for developing potent neutralizing mAbs. We and others have identified such potent neutralizing human mAbs targeting the RBD of SARS-CoV (Zhu et al., 2007) and the middle east respiratory syndrome coronavirus (MERS-CoV) (Ying et al., 2014a). Recently, several groups have reported the isolation of potent neutralizing antibodies from convalescent human donors but all are in an Immunoglobulin G1 (IgG1) format with a molecular mass of about 150 kDa (Cao et al., 2020; Ju et al., 2020; Rogers et al., 2020; Shi et al., 2020; Zost et al., 2020).

Antibody domains and fragments such as Fab (fragment antigen binding, molecular weight of 50 kDa), scFv (singe-chain variable fragment, 30 kDa) and V_H (heavy chain variable domain, 15 kDa) are attractive antibody formats as candidate therapeutics (Nelson, 2010). For example, isotope labeled antibody fragments are more suitable for bio-imaging due to their better tissue penetration and faster clearance compared to full-size antibodies (Freise and Wu, 2015). Single antibody domains (sAbd), e.g., camelid V_HH (15 kDa) exhibit strong antigen binding and high stability (Harmsen and De Haard, 2007). We and others have demonstrated that human IgG1 heavy chain variable domain (V_H) can be engineered to achieve high stability and affinity to antigens (Nilvebrant et al., 2016), as exemplified by the V_H, m36.4, targeting the human immunodeficiency virus type 1 (HIV-1) envelope glycoprotein co-receptor binding site (Chen et al., 2008a). The V_H domains small size could improve therapeutic efficacy for infectious diseases, such as COVID-19 because of greater penetration to sites of infection. The conformation of the SARS-CoV-2 S trimer is dynamic with only one RBD in the "up" conformation presenting neutralizing epitopes while epitopes in the other two RBDs may be masked (Yan et al., 2020). Small V_Hs may achieve binding to the cryptic RBD epitopes during the dynamic "breathing" of the S trimer (Liu et al., 2020). In addition, V_Hs may have

an advantage for treatment of respiratory virus infections because V_HS could efficiently penetrate tissue, especially when using direct delivery through inhalation (Detalle et al., 2016).

To identify potent neutralizing V_HS against SARS-CoV-2, we panned our large (10^{11} clones) and diverse phage-displayed human V_H antibody library against recombinant RBD. Several V_H binders were isolated and screened for their affinities, ACE2 competition and stabilities. One of those V_HS, ab8, in an Fc (human IgG1, crystallizable fragment) fusion format, showed potent neutralization activity and specificity against SARS-CoV-2 both in vitro and in two animal models. To our knowledge, this is the first report for high potency of a human antibody domain (V_H) in two animal models of infection.

Results

Selection of a high-affinity V_H, ab8, and its conversion to a V_H-Fc

We generated a large phage-displayed human V_H library where heavy chain complementarity-determining regions (HCDR1, 2, 3s) were grafted into their cognate positions of a stable scaffold based on the germline V_H3-23 (**Figure S1A).** It was panned against recombinant RBD antigens with two different tags (avi-his and human IgG1 Fc tag) which were sequentially used to avoid phage enrichment to tags and related epitopes. The quality of the RBD used for panning was confirmed by ACE2 binding (**Figure S1B and C**). After three rounds of panning, a panel of V_H binders was obtained. Among the highest affinity binders, we selected one, V_H ab8, which did not aggregate during a six-days incubation at 37℃ as tested by dynamic light scattering (DLS) (**Figure S1D**). To increase the V_H ab8 avidity and extend its in vivo half-life, it was converted to a bivalent antibody domain by fusion to the human IgG1 Fc (V_H-Fc ab8) (**Figure S1E**).

High-avidity specific binding of V_H-Fc ab8 to RBD and cell surface associated native S protein

V_H ab8 bound to SARS-CoV-2 RBD and S1 with half-maximal binding concentrations (EC_{50}s) of 10 nM as measured by ELISA (**Figure 1A and D**) and an equilibrium dissociation constant (K_D) of 19 nM as measured by the biolayer interferometry (Blitz system) (**Figure 1B**). The relatively fast dissociation rate constant ($k_d = 4.1\times 10^{-3}$ S^{-1}) was significantly (23-fold) decreased by the conversion to a bivalent Fc fusion format ($k_d = 1.8\times 10^{-4}$ S^{-1}) (**Figure 1E)** resulting in high avidity. V_H-Fc ab8 bound to SARS-CoV-2 RBD and S1 subunit of S protein with EC_{50}s of 0.40 nM and 0.20 nM, respectively, and a K_D of 0.54 nM (**Figure 1E**). It specifically bound to 293T cells expressing S, but not to control 293T cells **(Figure 1C and Figure S2A)**. The binding of V_H-Fc ab8 was higher than that of IgG1 CR3022, an anti-SARS-CoV antibody cross-reactive with SARS-CoV-2 (Tian et al., 2020). The V_H-Fc ab8's half-maximal FACS measured binding concentration (FC_{50}) of 0.07 nM was higher than that of recombinant human ACE2-Fc (FC_{50} = 0.52 nM) (**Figure 1F**). These data demonstrate that ab8 selected by an isolated RBD can bind to cell surface associated native S trimer. The binding of V_H-Fc ab8 to the S protein was significantly improved compared to that of the V_H ab8 through avidity effect.

V_H-Fc ab8 and V_H ab8 outcompete human ACE2-Fc for binding to RBD

Competition with human ACE2 for binding to RBD is a surrogate indicator for antibody neutralization activity. V_H-Fc ab8 outcompeted human ACE2-Fc with a half-maximal inhibitory concentration (IC_{50}) of 1.0 nM **(Figure 2A)**. Note that the V_H-Fc ab8 was much more effective in outcompeting ACE2-Fc than V_H ab8, consistent with its enhanced binding. ACE2 can also block V_H ab8 for binding to RBD (**Figure S2B**) and cell surface associated S (**Figure S2C**). V_H-Fc ab8 also significantly decreased the kinetics of ACE2 binding as measured by Blitz (**Figure 2B**). V_H-Fc ab8 did not bind to the SARS-CoV RBD **(Figure 2C)** and did not compete with CR3022 for binding to RBD **(Figure 2D)**. The CR3022 epitope is located in a conserved region on the RBD core domain distal from the ACE2 binding interface, as seen in the crystal structure of the Fab CR3022-RBD complex (Yuan et al., 2020). These results indicate that the ab8 epitope may overlap with the ACE2 binding site on RBD.

V_H-Fc ab8 binds to SARS-CoV-2 RBD mutants found in patients; an alanine scanning mutation in the distal loop tip of the receptor binding motif (RBM) decreases its binding

Currently, nine prevalent RBD mutants were found in COVID-19 patients (Priyanka et al., 2020). Six of these mutations (F342L, N354D. N354D/D364Y, V367F, R408I, W436R) are located in the RBD core domain and three, K458R, G476S and V483A are in the receptor binding motif (RBM) (**Figure 3A**). V_H-Fc ab8 bound to all mutants similarly to wild type RBD as measured by ELISA (**Figure 3B**). To map the ab8 epitope, we also generated several mutations in non-conserved positions compared to SARS-CoV spanning the footprint of ACE2 on RBM (N439A, G446L, L455A, F456A, A475I, F486A, Q493A, Q498A, N501A, Y505A) (**Figure 3C**). Most of these mutants retained V_H-Fc ab8 binding except F486A, F456A and A475I **(Figure 3D and 3E)**. The F486A significantly decreased binding without affecting the overall RBD conformation (**Figure S2C and S2D**) indicating that F486 directly interacts with ab8. The F456A and A475I mutations decreased the binding by 15% and 40%, respectively, but they also affected the RBD conformation (**Figure S2C and S2D**). These results suggest that a portion of the V_H ab8 epitope could be in the RBM distal loop tip where the F486 is located at (**Figure 3F**).

Electron microscopic analysis of the SARS-CoV-2 S protein ectodomain bound to V_H ab8

To explore structural aspects of SARS-CoV-2 neutralization by V_H ab8, we performed negative stain electron microscopic analysis of the complex formed between the S protein ectodomain and V_H ab8 or soluble ACE2 (**Figure 4**). The density maps showed that both V_H ab8 and ACE2 were in a quaternary conformation in which two of the protomers in the trimer are in the "down" conformation with the third one in the "up" conformation (**Figures 4A and 4B**), similar to the quaternary conformation of the reported ACE2-bound S ectodomain (PDB ID: 6VYB) (Walls et al., 2020). One molecule of the V_H ab8 was observed bound to each RBD domain (**Figure 4A**). In the ACE2-S complex, one molecule of ACE2 was bound to the S protein trimer, straddling one "up" and one "down" RBD region **(Figure 4B)**. There appears to be a noticeable shift of the "up" RBD domain when it is bound to V_H ab8 (**Figure 4A**). This shift is not observed when ACE2 is bound to the trimer (**Figure 4B**). Superposition of the two density maps reveals that the binding site of V_H ab8 directly overlaps with the ACE2 one, precluding simultaneous occupancy on the S protein ectodomain **(Figure 4C).** We also found that when ACE2 was added subsequent to the

addition of V_H ab8, only the V_H ab8 bound state was observed, further confirming the ACE2 competition with V_H ab8. To better understand the spatial relationship between the site of V_H ab8 binding and that of ACE2 binding, we created a molecular model for ACE2 bound S trimer by aligning the RBD region of the crystal structure of SARS-CoV-2 RBD bound ACE2 (PDB ID: 6M0J) (Lan et al., 2020) to the "up" RBD region in the cryo-EM structure of the trimer (PDB ID: 6YVB) (Wrapp et al., 2020). Superposition of this chimeric structure with the density map of V_H ab8-bound S protein trimers reveals that the bound ACE2 has extensive overlap with the space occupied by bound V_H ab8 (**Figure 4D**). The direct spatial overlap between bound V_H ab8 and ACE2 provides a structural mechanism for the observed effect of ab8 on blocking ACE2 binding. The structural findings also showed that the RBM distal loop, which has F486 at its tip, is directly covered by the footprint of the bound V_H ab8, consistent with the epitope mapping results showing that F486 is a direct contacting residue for ab8.

Potent neutralization of SARS-CoV-2 by V_H-Fc ab8 in vitro

We used four different assays to evaluate V_H-Fc ab8 mediated inhibition of SARS-CoV-2 infection *in vitro*: a β-galactosidase (β-Gal) reporter gene-based quantitative cell-cell fusion assay (Xiao et al., 2003); an HIV-1 backbone-based SARS-CoV-2 pseudovirus assay (Zhao et al., 2013); and two different replication-competent virus neutralization assays (a luciferase reporter gene assay and a microneutralization (MN)-based assay) (Scobey et al., 2013; Yount et al., 2003). V_H-Fc ab8 inhibited cell-cell fusion much more potently than V_H ab8 **(Figure 5A)**. The inhibitory activity of V_H-Fc ab8 was also higher than that of ACE2-Fc. The control anti MERS-CoV antibody IgG1 m336 did not show any inhibitory activity. V_H-Fc ab8 neutralized pseudotyped SARS-CoV-2 virus (IC_{50} = 0.03 μg/ml) more potently than ACE2-Fc (IC_{50} = 0.40 μg/ml) and V_H ab8 (IC_{50} = 0.65 μg/ml) (**Figure 5B**). The pseudovirus neutralization IC_{50} for ACE2-Fc in our assay is comparable to the one reported by Changhai Lei *et al.* (0.03-0.1 μg/ml) (Lei et al., 2020). Interestingly, the maximum neutralization by V_H ab8 was only 50% compared to the 100% by V_H-Fc ab8 and ACE2-Fc, which was also observed for another antibody S309 (Pinto et al., 2020). The complete neutralization by V_H-Fc ab8/ACE2-Fc emphasizes the role of bivalency and related avidity in neutralization (Klasse and Sattentau, 2002). Furthermore, in the reporter gene assay V_H-Fc ab8 neutralized live SARS-CoV-2 with an IC_{50} of 0.04 μg/ml (**Figure 5C**), which is much lower than that for ACE2-Fc (IC_{50} of 6.1 μg/ml) and V_H ab8 (IC_{50} = 29 μg/ml). ACE2-Fc seemed to be much less potent against the live virus compared to the pseudovirus, which is also observed by others (IC_{50} = 12.6 μg/ml) (Case et al., 2020) and may relate to the S expression levels and RBD/S conformation on the virus surface. We also confirmed the high V_H-Fc ab8 live virus neutralization potency by a microneutralization (MN) assay-100% neutralization (NT_{100}) at 0.1 μg/ml (**Figure 5D**). The NT_{100} from the MN assay (0.1 μg/ml) was close to the IC_{100} (0.2 μg/ml) from the reporter gene assay suggesting consistency in the live virus neutralizing activity of V_H-Fc ab8 obtained with two independent assays at two different laboratories. These results suggest that V_H-Fc ab8 is a potent neutralizer of SARS-CoV-2, which correlates with its strong competition with ACE2 for binding to RBD.

High prophylactic efficacy of V_H-Fc ab8 in a mouse ACE2 adapted SARS-CoV-2 infection model

To evaluate the prophylactic efficacy of V_H-Fc ab8 *in vivo*, we used a recently developed mouse ACE2 adapted SARS-CoV-2 infection model, in which wild type BALB/c mice are challenged with SARS-CoV-2 carrying two

mutations Q498T/P499Y at the ACE2 binding interface in the RBD (Dinnon et al., 2020). It was shown that in this model, the aged BALB/c mice exhibited more clinically relevant phenotypes than those seen in hACE2 transgenic mice (Dinnon et al., 2020). Groups of 5 mice each were administered 36, 8, 2 mg/kg V_H-Fc ab8 prior to high titer (10^5 pfu) SARS-CoV-2 challenge followed by measurement of virus titer in lung tissue 2 days post infection. V_H-Fc ab8 effectively inhibited SARS-CoV-2 in the mouse lung tissue in a dose dependent manner (**Figure 6A**). There was complete neutralization of infectious virus at the highest dose of 36 mg/kg, and statistically significant reduction by 1000-fold at 8 mg/kg. Remarkably, even at the lowest dose of 2 mg/kg it significantly decreased virus titer by 10-fold (two tailed, unpaired *t* test, $p = 0.0075$). To exclude possible effects of residual ab8 on viral titration, we performed another experiment in which mouse lungs were perfused with 10 ml of PBS before harvesting for titration. The perfusion did not affect to any significant degree the infectious virus in the lungs **(Figure 6B)**. The V_H-Fc ab8 completely neutralized the virus in the lungs at 36 mg/kg and significantly reduced infectious virus at 8 mg/kg. V_H-Fc ab8 also reduced viral RNA in the lungs **(Figure 6C).** These results demonstrate the neutralization potency of V_H-Fc ab8 *in vivo*. They also suggest that the double mutations Q498T/P499Y on RBD did not influence V_H-Fc ab8 binding and contribute to the validation of the mouse adapted SARS-CoV-2 model for evaluation of neutralizing antibody efficacy.

V_H-Fc ab8 exhibited both prophylactic and therapeutic efficacy in a hamster model of SARS-CoV-2 infection

Recently hamsters were demonstrated to recapitulate clinical features of SARS-CoV-2 infection (Chan et al., 2020) (Imai et al., 2020). To evaluate the V_H-Fc ab8 efficacy in hamsters, it was intraperitoneally administered either 24 hours before (prophylaxis) or 6 hours after (therapy) intranasal 10^5 $TCID_{50}$ virus challenge. In the therapeutic group, the rationale for administration of the antibody six hours post viral infection is based on the replication cycle length of 5-6 hours after initial infection for SARS-CoV in VeroE6 cells (Keyaerts et al., 2005). Six hours after challenge with a high dose of 10^5 $TCID_{50}$, approximately the same number of susceptible cells could become infected and likely produce much more infectious virus, which would need to be neutralized by the antibody to prevent subsequent cycles of infection. Nasal washes and oral swab at 1, 3, 5 days post infection (dpi) and different lung lobes at 5 dpi were collected. V_H-Fc ab8 decreased viral RNA by 1.7 log in the lung when administered prophylactically. The lung viral RNA decrease in the therapeutic groups was slightly lower (by 1.2 log) (**Figure 6D**). Interestingly, the viral RNA load in the therapeutic groups was to some extent tissue location dependent (**Figure 6F**). The variation of the viral load in different lung lobes may relate to nonuniform antibody transport and viral spread inside the lung. Remarkably, V_H-Fc ab8 alleviated hamster pneumonia and reduced the viral antigen in the lung (H&E staining, **Figure 7A** and **C** and immunohistochemistry **Figure 7B** and **D**). The control hamsters exhibited severe interstitial pneumonia characterized by extensive inflammatory cell infiltration, presence of type II pneumocytes, alveolar septal thickening and alveolar hemorrhage. Both prophylactic and therapeutic treatment of V_H-Fc ab8 reduced the lesions of alveolar epithelial cells, focal hemorrhage and inflammatory cells infiltration. V_H-Fc ab8 also reduced the shedding from mucosal membranes including in nasal washes and oral swabs (**Figure S4**). The decrease in viral RNA in nasal washes and oral swabs were not as large as the decrease observed in the lung tissue, similar to a recent finding in hamsters (Imai et al., 2020). Overall, the

prophylactic treatment was more effective than the therapeutic treatment in decreasing viral load in nasal washes and oral swabs. Notably, prophylactic administration of V_H-Fc ab8 effectively reduced the infectious virus in the oral swab at 1 dpi, while the post-exposure treatment did not (**Figure S4C** and **G**). Interestingly, viral reduction (except the viral titer in the oral swab at 1 dpi) was more effective at 3 and 5 dpi compared to that at 1 dpi, likely due to the infection peak occurring before day 3 as reported in hamsters (Sia et al., 2020). A striking finding is that V_H-Fc ab8 given therapeutically at as low dose as 3 mg/kg can still decrease viral loads in the lung, nasal washes and oral swabs (**Figure S5**).

We measured the V_H-Fc ab8 concentrations at both doses (10 and 3 mg/kg) in the sera at 1 dpi and 5 dpi in the post-exposure treatment groups (**Figure S5C**). The higher dose (10 mg/kg) resulted in higher antibody concentration and better inhibitory activity than the lower dose (3 mg/kg). The relatively high concentration of V_H-Fc ab8 five days after administration also indicates good pharmacokinetics. Furthermore, we also compared the V_H-Fc ab8 concentration in both the sera and lung with that of IgG1 ab1, which has a similar affinity to SARS-CoV-2 and similar degree of competition with the receptor ACE2 as V_H-Fc ab8 (Li et al., 2020a). We found that the concentration of V_H-Fc ab8 in hamster sera is significantly higher than that of IgG1 ab1 at 1 and 5 dpi after post-exposure administration of the same dose of 10 mg/kg (**Figure 7E**), possibly indicating more effective delivery of V_H-Fc ab8 from the peritoneal cavity to the blood than that of IgG1 ab1. We also found that the V_H-Fc ab8 concentration in all hamster lung lobes was higher than that of the IgG1 ab1 (**Figure 7F**), suggesting that V_H-Fc ab8 appears to penetrate the lung tissue more effectively than IgG1 ab1. These results indicate that the in vivo delivery of V_H-Fc ab8 may be more effective than that of full-size antibodies in an IgG1 format.

V_H-Fc ab8 does not aggregate and does not bind to 5300 human membrane proteins

The V_H-Fc ab8 propensity for aggregation was measured at 37°C by dynamic light scattering (DLS), which detects particle size distributions in the nanometer range (Stetefeld et al., 2016). It displayed a single peak at 11.5 nm which is the size of a monomeric V_H-Fc protein **(Figure S6A)**. The absence of large-size peaks corresponding to large molecular weight species (aggregates) in solution, indicates that V_H-Fc ab8 is highly resistant to aggregation at high concentration (4 mg/ml) and relatively long times of incubation (6 days) at 37°C. The V_H-Fc ab8 propensity for aggregation was also evaluated by size exclusion chromatography (SEC), which showed that >96% of V_H-Fc ab8 was eluted in a peak at a position corresponding to a monomeric state with a molecular weight of 80 kDa (**Figure S6B)**.

Antibody nonspecificity and polyreactivity can be an obstacle for developing an antibody into a clinically useful therapeutic. Polyreactivity may not only cause off-target toxicities and interfere with normal cellular functions, but may also reduce antibody half□life (Chuang et al., 2015). To test for potential polyreactivity of V_H-Fc ab8, a Membrane Proteome Array (MPA) platform was used, in which 5,300 different human membrane protein clones were separately overexpressed in 293T cells in a matrix array achieving a high-throughput detection of binding by FACS. V_H-Fc ab8 did not bind to any of those proteins (**Figure S6C**), demonstrating its lack of polyreactivity and nonspecificity. Interestingly, we did not detect V_H-Fc ab8 binding to the human FcγRIA, which is probably due to the relatively low expression level of FcγRIA on HEK-293T cell surface without concomitant

expression of the common γ chain (Van Vugt et al., 1996). In addition, we found that V_H-Fc ab8 bound to the FcγRs much weaker than IgG1 (**Figure S7**), likely due to the different conformation in the lower hinge region for Fc fusion proteins compared to that of IgG1s (Ying et al., 2014b). For the Fc fusion proteins (even with the same hinge sequence as IgG1), binding to FcγRs may be different from that of IgG1, and can be affected by the fusion partners (Lagassé et al., 2019). The importance of antibody binding to FcγRs for therapeutic or prophylactic efficacy or toxicity in SARS-CoV-2 infection is unknown.

Discussion

Neutralizing mAbs are promising for prophylaxis and therapy of SARS-CoV-2 infections. Recently, many potent neutralizing antibodies from COVID19 patients were identified that neutralize pseudovirus with IC_{50}s ranging from 1 to 300 ng/ml, and replication-competent SARS-CoV-2 with IC_{50}s from 15 to 500 ng/ml (Cao et al., 2020; Ju et al., 2020; Rogers et al., 2020; Shi et al., 2020; Zost et al., 2020). By comparison, the V_H-Fcab8 reported here exhibited comparable or better neutralizing potency against SARS-CoV-2 pseudovirus and live virus (IC_{50}s of 30 ng/ml and 40 ng/ml respectively). Of note, IC_{50}s can vary widely between different assays and laboratories because there is no generally accepted standardized assay. In addition, there are many factors that contribute to potency and efficacy in vivo. Animal models are a more comprehensive and likely more reliable predictor of potential efficacy in humans than in vitro neutralization assays.

To our knowledge V_H-Fc ab8 is the first human antibody domain whose activity was validated in two animal models. In the mouse ACE2 adapted SARS-CoV-2 infection model, V_H-Fc ab8 significantly decreased infectious virus by 10-fold at 2 days post infection even at a very low dose of 2 mg/kg **(Figure 6A)**. It also exhibited both prophylactic and therapeutic efficacy in a hamster model. It not only reduced the viral load in the lung and alleviated pneumonia; but it also reduced shedding in the upper airway (nasal washes and oral swab), which could potentially reduce transmission of SARS-CoV-2. Impressively, V_H-Fc ab8 was active therapeutically even at 3 mg/kg. The finding that V_H-Fc ab8 persisted for 4 days post administration at significant levels indicates that the pharmacokinetics of V_H-Fc ab8 is comparable to that of a full size antibody; the half-lives of Fc fusion proteins were reported to vary from those of IgG1s and can range from hours to days (Unverdorben et al., 2016). The molecular weight of V_H-Fc ab8 (80 kDa) is half of that of full-size IgG1 which suggests an advantage in terms of smaller quantities needed to be produced compared to those for IgG1s to reach similar number of molecules and efficacy. In addition, it was shown that decreasing binder's size exponentially increases its diffusion through normal and tumor tissues (Jain, 1990). Thus, decreasing the size two-fold can increase diffusion through tissues by four-fold. We found that after administration at the same dose, the concentration of V_H-Fc ab8 was higher than that of IgG1 ab1 in both hamster sera and lung tissue. This result might suggest that the V_H-Fc ab8 diffusion from the peritoneal cavity to the blood and penetration of lung may be faster than that of IgG1 ab1. This may further explain its efficacy at low doses in animals. Although the low dose showed efficacy in the small animal models, it should be noted that in humans higher doses could be required to achieve comparable degree of efficacy. Another caveat is that in the

hamster post-exposure experiment, the V_H-Fc ab8 was administered at a time (six hours) when the first round of virus replication was likely completed (Keyaerts et al., 2005), but before the infection peak at 1-2 days (Sia et al., 2020). Because it inhibits infection of new cells, its administration at around the infection peak or after may not be as effective unless it also kills infected cells in vivo which is under investigation.

Recently antibody domains including human V_H and camelid V_HH were reported having varying neutralization potency (Chi et al., 2020; Sun et al., 2020; Wrapp et al., 2020; Wu et al., 2020a). Compared to those domains, V_H-Fc ab8 is unique in terms of potency, aggregation resistance and specificity. V_H-Fc ab8 exhibited good developability properties including stability at high concentrations and long incubation at 37°C, as well as absence or very low aggregation. In addition, V_H-Fc ab8 did not bind to the human cell line 293T even at high concentration (1 μM) which is about 1754-fold higher than its K_d indicating absence of non-specific binding to many membrane-associated human proteins. A similar result was obtained by the membrane protein array assay showing that V_H-Fc ab8 did not bind to any of 5,300 human membrane-associated proteins, indicating its lack of non-specificity and thus low potential for off-target toxicity when used *in vivo*. Besides, unlike camel V_HHs, the V_H ab8 sequence is fully human and therefore likely less immunogenic than that of camelid V_HHs.

Multiple structures are now available for the SARS-CoV-2 S protein trimer in complex with various neutralizing antibodies, offering insight into antigenic epitopes and inhibitory mechanisms critical for S protein neutralization. Epitopes on the SARS-CoV-2 S protein RBD have emerged as effective targets, as evidenced by the action of several RBD binding antibodies including CR3022, B38, C105, CB6, H014, and S309 (Barnes et al., 2020; Lv et al., 2020; Pinto et al., 2020; Shi et al., 2020; Wu et al., 2020b). While B38, C105, and CB6 directly compete with ACE2 for binding sites on the RBD surface, H014 occupies a position distinct from these binding sites, precluding ACE2 binding *via* steric inhibition (Lv et al., 2020). S309 targets the RBD of the S protein both in closed and open S protein conformations, exhibiting a different mechanism of neutralization (Pinto et al., 2020). A recent study of the structure of the S protein trimer in complex with the nanobody H11-D4 (PDB ID: 6Z43) revealed full occupancy of the nanobody on all three RBDs in a "one up and two down" conformation (Huo et al., 2020), similar to what we report here. Our structural analysis demonstrates that the location of the V_H ab8 bound to the trimeric S ectodomain directly overlaps the region that would be occupied by ACE2 when bound to the S protein. The ACE2 blocking is likely the major mechanism of the V_H-Fc ab8 neutralizing activity, which is significantly augmented by avidity effects due to its bivalency. The narrow neutralization concentration range in the live virus neutralization (10-200 ng/ml for 0%-100% neutralization) (**Figure 5D**) indicates a plausible cooperative neutralization mechanism, probably due to the synergistic binding of V_H molecules in V_H-Fc ab8 to RBDs. Due to its small size, V_H may facilitate targeting occluded epitopes on RBD that are otherwise inaccessible to full-length IgGs, which is important because the SARS-CoV-2 S protein is conformationally heterogenous, exposing neutralizing epitopes to varying degrees (Yan et al., 2020). The structural analysis shows that V_H ab8 is able to simultaneously target all three RBD epitopes in both "up" and "down" conformations, which may provide a structural basis for a unique cooperative neutralization mechanism for V_H-Fc ab8. V_H-Fc ab8 with a long flexible linker between V_H and Fc may allow two

V_H molecules to bind simultaneously two protomers in the same S trimer or cross-link two different protomers from different S trimers.

The ab8 epitope is distal to the CR3022 epitope, explaining its lack of competition with CR3022. The ab8 contact residue F486 (L472 in SARS-CoV) is not conserved which likely explains its lack of cross-reactivity to SARS-CoV. From the GISAID and NCBI databases, we found nine mutations in RBD with relatively high frequencies in current circulating SARS-COV-2. Six of them are in the core domain (F342L, N354D, N354D/D364Y, V367F, R408I and W436R) and three in the RBM (K458R, G476S, V483A). The core domain mutations are far away from the ab8 epitope, thus these mutations do not affect V_H-Fc ab8 binding to RBD. Those three RBM mutations also did not affect ab8 binding although they are close to the ab8 epitope, suggesting that these mutations may not affect ab8 neutralizing activity although neutralization of whole virus carrying these mutations is needed to definitely demonstrate this possibility. Interestingly, V_H-Fc ab8 effectively inhibited the mouse ACE2 adapted SARS-CoV-2 with a Q498T/P499Y mutation in RBD, indicating that this double mutation also does not affect V_H-Fc ab8 binding to RBD. These results suggest that V_H-Fc ab8 may be a broadly cross-reactive SARS-CoV-2 neutralizing antibody.

In conclusion, we identified a fully human antibody V_H domain that shows strong competition with ACE2 for binding to RBD and potent neutralization of SARS-CoV-2 in vitro and in two animal models. This potent neutralizing activity combined with its specificity and good developability properties warrants its further evaluation for prophylaxis and therapy of SARS-CoV-2 infection. Our elucidation of its unique epitope and mechanism of neutralization could also help in the discovery of more potent inhibitors and vaccines.

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AUTHOR CONTRIBUTIONS. DSD, RSB, CTT, JWM, SS, DF and WL conceived and designed the research; WL identified and characterized antibodies; XL and ZS helped to make libraries, characterized antibodies and performed the cell fusion pseudovirus assays. CC made the RBD, ACE2; LZ made and characterized reagents; MU and EP characterized proteins and helped with the proteome assay; DM and AD performed the live virus

neutralization assays; AS, SSK, DF and SL performed the animal studies; AB, SC, KL, DM, SS, XZ and SS produced and purified the S trimer, carried out the EM experiments and analyzed the structure-related results; DSD and WL wrote the first draft of the article, and all authors discussed the results and contributed to the manuscript.

DECLARATION OF INTERESTS. Wei Li, Chuan Chen, Zehua Sun, John W. Mellors and Dimiter S. Dimitrov are co-inventors of a patent, filed on March 12 by the University of Pittsburgh, related to ab8 described in this paper.

FIGURE LEGENDS

Figure 1. Binding of V_H ab8 and V_H-Fc ab8 to recombinant SARS-CoV-2 RBD and S1 proteins and cell membrane associated S. (A and **D)** V_H and V_H-Fc ab8 binding to recombinant RBD and S1 proteins measured by ELISA. The MERS-CoV antibody IgG1 m336 was used as a negative control. Experiments were performed in duplicate and the error bars denote ± SD, n =2. **(B** and **E)** Kinetics of V_H ab8 (**B**) and V_H-Fc ab8 (**E**) binding to RBD. **(C)** Binding of V_H-Fc ab8, ACE2-Fc and IgG1 CR3022 to S transiently transfected 293T cells (293T-S). The 293T cells without transfection serve as a control. Antibodies or proteins were evaluated at a concentration of 1 μM. (**D**) Concentration-dependent binding of V_H-Fc ab8 and ACE2-Fc to 293T-S cells. See also **Figure S2, panel A**.

Figure 2. Competition of V_H-Fc ab8 and V_H ab8 with ACE2, CR3022 for binding to SARS-CoV-2 RBD and lack of binding of V_H-Fc ab8 to SARS-CoV S1. (A) Competition of V_H-Fc ab8 and V_H ab8 with ACE2 for binding to SARS-CoV-2 RBD. RBD was coated and incubated with 5-fold serially diluted V_H-Fc ab8 and V_H ab8 in the presence of 2 nM ACE2-mFc (mouse Fc). **(B)** Inhibition of ACE2 binding to RBD by V_H-Fc ab8 as measured by Blitz. **(C)** Lack of binding to SARS-CoV S1 as tested by ELISA. SARS-CoV S1 was coated and incubated with V_H-Fc ab8. (**D**) Competition between V_H-Fc ab8 and CR3022 measured by Blitz. ELISA Experiments were performed in duplicate and the error bars denote ± SD. **See also Figure S2, panel B and C**.

Figure 3. Epitope mapping for V_H-Fc ab8 by using naturally occurring RBD mutants from circulating SARS-CoV-2 isolates and by alanine scanning. (**A**) Mapping of natural RBD mutants to RBD/ACE2 3D structure (PDB ID: 6M0J). RBD and ACE2 are represented as cyan and green cartoons with RBM highlighted by red color. The RBD mutants are represented by cyan (core domain mutants) and red (RBM) spheres. (**B**) Binding of V_H-Fc ab8 to those RBD mutant as measured by ELISA. (**C**) Design of Ala scanning mutants to explore the ab8 epitope. RBD/ACE2 structure is based the same PDB as panel **A**. Non-conservative residues spanning ACE2 footprint on RBD compared to SARS-CoV are selected and depicted by stick and sphere representations. (**D**) V_H-Fc ab8 binding to SARS-CoV-2 RBD alanine mutants as tested by ELISA. ELISA procedure is similar to the above described. (**E**) Normalized signals of V_H-Fc ab8 binding to those RBD mutants compared to the WT RBD at the concentration of 1.6 nM derived from the panel **D**. (**F**) Representation of portions of ab8 binding region on RBD based on the epitope mapping ELISA results. F486 in the distal RBM loop is the plausible direct contact residue for ab8. **See also Figure S2, panel D and E.**

Figure 4. Electron microscopic analysis of the SARS-CoV-2 S protein ectodomain complexed with V_H ab8. (A) Side and top views of the density map of S protein ectodomain (shown in gray) in complex with V_H ab8. The density that we associate with the bound V_H domain is colored red. The open-state structure of the SARS-CoV-2 S protein ectodomain (PDB ID: 6VYB, blue color ribbon) fits well into the map with the exception of the tip of the RBD from the "up" protomer. There appears to be a slight outward shift in the V_H ab8 complex. **(B)** Side and top views of the density map of S protein ectodomain in complex with soluble human ACE2 domain, with density for bound ACE2 shown in blue. **(C)** Superposition of the density maps from (**A**) and (**B**). **(D)** A closer view of the binding site that incorporates the known atomic model for the structure of the ACE2 complex with the RBD in the "up" conformation, delineating the regions of contact with the V_H density. A ribbon representation of the RBM distal loop and the F486 side chain are highlighted in yellow. **See also Figure S3.**

Figure 5. Inhibition of cell-cell fusion and neutralization of pseudotyped and authentic SARS-CoV-2 by V_H-Fc ab8 and V_H ab8. (**A**) Inhibition of cell fusion between 293T-S and 293T-ACE2 cells by V_H ab8, V_H-Fc ab8 and ACE2-Fc. **(B)** Neutralization of SARS-CoV-2 pseudovirus by V_H ab8, V_H-Fc ab8 and ACE2-Fc. **(C)** Neutralization of live SARS-CoV-2 tested in the nLuc reporter assay. **(D)** Neutralization of live virus by a microneutralization assay. Experiments were performed in duplicate and the error bars denote ± SD, n =2.

Figure 6. Evaluation of the prophylactic efficacy of V_H-Fc ab8 in a mouse ACE2 adapted model; and both prophylactic and therapeutic efficacy in a hamster model of SARS-CoV-2 infection. (**A**) V_H-Fc ab8 inhibited mouse ACE2 adapted SARS-CoV-2 in wild type BALB/c mice (two-tailed, unpaired *t* test, ** $p < 0.01$). (**B**) The same experiments as panel **A** except that the mice lung was perfused before viral titration (Mann-Whitney *U* test, **$p < 0.01$). (**C**) The viral RNA level change in the lung in the same mice of panel **B** as quantified by RT-qPCR and presented as $TCID_{50}$ equivalents (Mann-Whitney *U* test, **$p < 0.01$). (**D-F**) Evaluation of the prophylactic and therapeutic efficacy of V_H-Fc ab8 in the hamster model. Hamsters were injected intraperitoneally with 10 mg/kg of V_H-Fc ab8 antibody either one day before (prophylaxis) or six hours after (therapy) intranasal challenge of 1×10^5 $TCID_{50}$ of SARS-CoV-2. (**D**) The decrease of viral RNA in the hamster lung after averaging all lung lobes. (**E** and **F**) The decrease of viral RNA in hamster lung lobes: prophylaxis and therapy, respectively. (Mann-Whitney *U* test, ns: $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$). **See also Figure S4 and S5.**

Figure 7. Histopathology of hamster lung stained by hematoxylin and eosin stain (H&E) and immunohistochemistry (IHC); comparison of antibody concentrations in the hamster lung and sera between V_H-Fc ab8 and IgG1 ab1. (**A** and **C**) **Reduced pathological changes in lung tissue lobe with V_H-Fc ab8 treatment.** H&E staining of treated and control lung lobes in hamsters challenged with SARS-CoV-2. Arrows showed inflammatory cells and arrow head for alveolar hemorrhages. (**B** and **D**) **Prophylaxis and post-infection treatment with V_H-Fc ab8 decreased SARS-CoV-2 antigen staining in lung lobes of hamsters.** Immunohistochemistry detection of the nucleocapsid antigen of V_H-Fc ab8 prophylactically treated (**B**) and post-exposure treatment (**D**) and control hamster lungs following SARS-CoV-2 challenge. Arrow indicates nucleocapsid positive cells (brown) in lungs lobes of hamsters at day 5 post-infection. (**E** and **F**) Comparison of V_H-Fc ab8 and IgG1 ab1 concentration in the lung and sera of hamsters receiving post-exposure treatment of a dose of 10 mg/kg

(Two-way ANOVA analysis followed by Tukey test, ns, $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p <$ 0.0001).

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Schematic representation of V_H library construction strategy, characterization of the RBD-his-biotin as an antigen for panning and evaluation the aggregation propensity of V_H ab8. Related to Star Methods "Generation of a human V_H library, Selection of Binders and Conversion of V_H to V_H-Fc Fusion Protein". **(A)** Schematic representation of HCDRs grafting into their cognate positions on a stable scaffold. **(B)** ELISA of biotinylated $RBD_{330-532}$ binding to streptavidin-HRP. **(C)** ELISA measurement of binding of biotinylated RBD-his to ACE2. ~100 ng ACE2-Fc was coated on plate with incubation of serially diluted RBD-his-biotin. Binding was detected by using HRP conjugated streptavidin. Experiments were performed in duplicate and the error bars denote ± SD, n =2. (**D**) Evaluation of aggregation of V_H ab8 by DLS. V_H ab8 (4 mg/ml) in PBS was incubated at 37°C. On day 0, day 1 and day 6, samples were taken out for DLS measurement. All measurements were repeated by three times. (**F**) Scheme of conversion of V_H ab8 into V_H-Fc ab8 by fusing IgG1 Fc. The linker between V_H and Fc is the natural human IgG1 upper and lower hinge (DKTHTCPPCPAPELL). V_H ab8 and V_H-Fc ab8 structure is modeled by the online SWISS-MODEL sever (https://swissmodel.expasy.org/).

Figure S2. Concentration dependent binding of V_H-Fc ab8 and ACE2-Fc to cell surface associated SARS-CoV-2 S; evaluation of competition of ACE2 and V_H ab8 by ELISA and FACS; test of the conformation integrity of RBD mutants by using a polyclonal antibody and monoclonal antibody CR3022. Related to Figure 1, 2 and 3. (A) Cells were incubated with serially diluted antibodies or ACE2-Fc and subsequently with PE conjugated anti-human Fc antibody for flow cytometry analysis. Percentage of PE-A+ cells were defined by the above gate strategy in FlowJ, representing the percentage of V_H-Fc ab8 and ACE2-Fc bound 293T-S cells. (**B**) ACE2 blocking V_H ab8 for binding to RBD by ELISA. RBD was coated to plate and 10 nM of V_H ab8 in the presence of gradient concentration of ACE2 was added. Binding was detected by HRP conjugated anti FLAG tag antibody. (**C**) ACE2 blocking V_H ab8 for binding to cell surface associated S. S transiently transfected 293T was incubated with 1 μM V_H ab8 in the presence of various concentration of ACE2 (his tag). Binding of V_H ab8 was detected by the PE conjugated anti FLAG tag antibody. (**D** and **E**) Binding of a mouse polyclonal anti-SARS-CoV-2 RBD antibody and IgG1 CR3022 to the RBD mutants. RBD mutants were coated to plate and two concentrations of polyclonal anti-RBD antibody and CR3022 were added. Binding was detected by HRP conjugated anti mouse (Fc) antibody and anti-human (Fc) antibody. Experiments were performed in duplicate and the error bars denote ± SD, n =2.

Figure S3. Collection and analysis of electron microscopic data. Related to Figure 4. (A) Representative raw micrograph of the SARS-CoV-2 S protein ectodomain complex with V_H ab8. Scale bar 50 nm. **(B)** Selected 2D class averages. Scale bar 10 nm. **(C)** Plot of Fourier Shell Correlation (FSC) between maps constructed from two randomly selected halves of the particle projection images.

Figure S4. Detection of infectious virus and viral RNA in hamster nasal washes and oral swabs. Related to Figure 6. Hamsters were injected intraperitoneally with 10 mg/kg of V_H-Fc ab8 antibody either one day before (prophylaxis) or six hours after (therapy) intranasal challenge of 1×10^5 $TCID_{50}$ of SARS-CoV-2. Untreated hamsters were kept as a control. Nasal washes and oral swabs were collected at day one, three and five post infection (dpi) for virus titer titration by viral $TCID_{50}$ assays and viral RNA quantification by RT-qPCR. **(A** and **E).** Nasal washes viral titer in un-treated (control), pre-infection (prophylaxis) treatment and post-infection (therapy) treatment hamsters. **(B** and **F).** Nasal washes viral RNA levels in un-treated, pre-treated and post- treated hamsters. (**C** and **G**) Oral swab viral titer in un-treated, pre-treated and post-treated hamsters. Note that the prophylactic treatment of V_H-Fc ab8 largely decreased the viral tier in the oral swabs at one dpi, while there is almost no effect for the post-infection treatment. **(D** and **H)** Oral swab viral RNA levels in un-treated, pre-treated and post-treated hamsters.

Figure S5. Post-exposure treatment efficacy of V_H-Fc ab8 at two different doses in the hamster model. Related to Figure 6. V_H-Fc ab8 at doses of 10 mg/kg or 3 mg/kg was administered i.p. 6 h after virus intranasal challenge. The hamster shedding including nasal washes and oral swabs were collected at 1, 3, 5 dpi. All hamsters were euthanized on 5 dpi. At the euthanasia, lungs (different lobes) were collected viral RNA quantification by RT-qPCR. (**A** and **D**) Nasal washes viral titer and viral RNA in un-treated (control), 3 mg/kg and 10 mg/kg post-infection treated hamsters. (**B** and **E**) Oral swab viral titer and viral RNA in un-treated (control), 3 mg/kg and 10 mg/kg post-infection treated hamsters. (**C**) Comparison of antibody concentrations in hamster sera for those two doses. Hamsters were bled at one and five dpi for measuring antibody concentrations in sera by SARS-CoV-2 S1 ELISA. Sera was diluted 1:100 and binding was detected by using the goat anti human IgG-HRP. (**F**). Viral RNA levels in different lung lobes. RNA quantity was presented as the $TCID_{50}$ equivalence.

Figure S6. Absent or very low aggregation and high specificity of binding of V_H-Fc ab8. Related to Star Methods "Dynamic Light Scattering, Size Exclusion Chromatography and Membrane Proteome Array Assay". (A) Evaluation of the aggregation of V_H-Fc ab8 by DLS. V_H-Fc ab8 (4 mg/ml) buffered in PBS was incubated at 37°C. On day 0, day 1 and day 6, samples were taken out for DLS measurement on Zetasizer Nano ZS ZEN3600 (Malvern Instruments Limited, Westborough, MA) to determine the size distribution. All measurements were repeated by three times. **(B)** Evaluation of V_H-Fc ab8 aggregation by SEC. Size exclusion was performed by loading 0.22 μm membrane-filtered proteins (150 ul, 1.5 mg/mL) onto the Superdex 200 increase 10/300 GL column. Protein was eluted by PBS buffer in a flow rate of 1.5 mL/min. The arrows indicate the peaks of the MW standards in PBS. **(C)** Lack of non-specific binding measured by a Membrane Proteome Array (MPA). Specificity testing of V_H-Fc ab8 (20 μg/ml) was performed using the MPA platform which comprises 5,300 different human membrane proteins, each overexpressed in live cells. To ensure data validity, each array plate contained positive (SARS-CoV-2 S) and negative (empty vector) controls.

Figure S7. Binding of V_H-Fc ab8 to human FcγRs measured by ELISA. Related to Star Methods "ELISA for detection of the binding of V_H-Fc ab8 and IgG1 ab1 to human FcγRs". Recombinant FcγRs ectodomains (100 ng) were coated, and biotinylated V_H-Fc ab8 or IgG1 ab1 was added. Binding was detected by Streptavidin HRP. Experiments were performed in duplicate and the error bars denote ± SD, n =2.

STAR*METHODS

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KEY RESOURCES TABLE

RESOURCE AVAILABLITY

Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Dimiter Dimitrov (mit666666@pitt.edu).

Materials Availability

All requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact author. This includes antibodies, viruses, plasmids and proteins. All reagents will be made available on request after completion of a Material Transfer Agreement.

Data and Code Availability

Antibody nucleotide sequence has been deposited to GenBank with an accession number of MT943599. The antibody is only allowed for non-commercial use. All data supporting the findings of this study are available within the paper and are available from the corresponding author upon request.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Cells and virus

Vero E6 (CRL-1586, American Type Culture Collection (ATCC) and 293T (ATCC) were cultured at 37°C in Dulbecco's Modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 10 mM HEPES pH 7.3, 1 mM sodium pyruvate, and 100 U/mL of penicillin–streptomycin. 293T stably expressing SARS-CoV-2 and human ACE2 was cultured in DMEM medium containing 200 μg/ml Zeocin. HEK293F and expi293F were cultured in FreeStyle 293 serum free medium (ThermoFisher, Cat#12338018) and Expi293™ Expression Medium

(ThermoFisher, Cat# A1435103), respectively. The SARS-CoV-2 spike pseudotyped HIV-1 backboned virus is packaged in 293T cells after transfecting pNL4-3.luc.RE and pcDNA3.1 S plasmids. The SARS-CoV-2 (US_WA-1/2020) and SARS-CoV2/Canada/ON/VIDO-01/2020 obtained from Centers for Disease Control and Prevention were propagated in Vero E6 cells. The recombinant SARS-CoV-2-SeattlenLuc virus and the mouse ACE2 adapted SAR-CoV-2 virus (carrying a Q498T/P499Y mutation in RBD) recovered by the reverse genetics was produced in VeroE6 cells. All work with infectious SARS-CoV-2 was performed in Institutional Biosafety Committee approved BSL3 facilities using appropriate positive pressure air respirators and protective equipment.

Recombinant proteins

The recombinant proteins SARS-CoV-2 RBD-his, RBD mutants, RBD-Fc, ACE2-hFc were subcloned into pcDNA3.1 expression plasmids, and expressed in expi293F cells. Proteins with his tag were purified by Ni-NTA affinity chromatography and protein with Fc tag purified by protein A chromatography. Protein purity was estimated as >95% by SDS-PAGE and protein concentration was measured spectrophotometrically (NanoVue, GE Healthcare).

Monoclonal antibodies

V_H ab8 antibody was identified by panning of the phage library. V_H-Fc ab8 were constructed by fusing V_H to human IgG1 Fc with the native IgG1 hinge. IgG1 ab1 was obtained by our lab through panning of a Fab phage library. MERS-CoV-specific IgG1 m336 and SARS-CoV antibody IgG1 CR3022 sequences from other groups were subcloned into the pDR12 plasmid for expression. V_H ab8 (in a phagemid pComb3x with a Flag tag) was expressed in HB2151 *E. coli* and purified by Ni-NTA affinity chromatography. All other IgG1 were expressed in expi293 cells and purified with protein A chromatography.

Mouse and hamster experiments

For the mouse model, BALB/c mice purchased from Envigo (BALB/cAnNHsd, stock# 047, immunocompetent, 11-12 months of age, female) were used for all experiments. They are drug/test naïve and negative for pathogens. Animals were not involved in any previous studies. Animals were housed in groups of 5 animals per cage and fed standard chow diet. The study was carried out in accordance with the recommendations for care and use of animals by the Office of Laboratory Animal Welfare (OLAW), National Institutes of Health and the Institutional Animal Care. All mouse studies were performed at the University of North Carolina (Animal Welfare Assurance #A3410-01) using protocols (19-168) approved by the UNC Institutional Animal Care and Use Committee (IACUC) and all virus studies were performed in ABSL3 facilities at UNC. Virus inoculations were performed under anesthesia and all efforts were made to minimize animal suffering. For evaluating prophylactic efficacy of V_H-Fc ab8, mice were intraperitoneally treated (12 hours before infection) with different doses of V_H-Fc ab8 followed by intranasal challenge with 10^5 PFU of mouse-adapted SARS-CoV-2. Two days post infection, mice were sacrificed and perfused with 10 ml PBS. Then lung was harvested for viral titer as determined by the plaque assay. For the hamster model, studies were approved by the University Animal Care Committee (UACC) of the University of

Saskatchewan according to the guidelines of the Canadian Council on Animal Care (CCAC). Hamsters were purchased from Charles River (male, immunocompetent, healthy, drug/test naïve, free of pathogens). Hamsters were not involved in previous procedures. Hamsters are housed in microisolater cages, typically 3-7/cage. The cages have BioFresh bedding with Crinkle bedding added. Hamsters have access to food and water ab libitum. Food is Lab Diet 5P00 ProLab RMH300. Cages are changed weekly or as needed and spot cleaned. For experiment, hamsters were intraperitoneally treated with V_H-Fc ab8 either 24 hrs before (prophylaxis) or 6 hrs (therapy) after intranasal challenge of 1×10^5 $TCID_{50}$ of SARS-CoV-2. Nasal washes and oral swabs were collected at day 1, 3 and 5 post infection (dpi). Hamsters were bled at 1 and 5 dpi. All hamsters were euthanized on 5 dpi. At euthanasia, lungs were collected for RNA isolation. For viral titer determination, VeroE6 cells $TCID_{50}$ assay was used. For testing viral RNA, viral RNA RT-qPCR was used. For testing antibody concentration at sera and lung, SARS-CoV-2 S1 ELISA was used. For histopathology, 10% formalin fixed and paraffin embedded tissues were processed with either hematoxylin and eosin stain (H&E) or immunohistochemistry (IHC). Lung lobes were scored based on pathology using microscopy.

METHOD DETAILS

Generation, Expression and Characterization of SARS-CoV-2 RBD, S1-Fc, ACE2-Fc, IgG1 m336, and Fab CR3022. The SARS-CoV-2 S and the anti-SARS-CoV antibody IgG1 CR3022 and genes were synthesized by IDT (Coralville, Iowa). MERS-CoV-specific IgG1 m336 antibody was expressed in human mammalian cell as described previously (Ying et al., 2014a). Briefly, IgG1 m336 light chain and heavy chain Fd were subcloned into the pDR12 vector containing dual promoters and a IgG1 Fc cassette. The recombinant plasmid was sequenced and transfected into expi293 cells for expression. The human angiotensin converting enzyme 2 (ACE2) gene was ordered from OriGene (Rockville, MD). The RBD domain (residues 330-532) and S1 domain (residues 14-675) and ACE2 (residues 18-740) genes were cloned in frame to human IgG1 Fc in the mammalian cell expression plasmid pcDNA3.1. The RBD protein with an AviTag followed by a 6×His tag at C-terminal was subcloned similarly. These proteins were expressed with Expi293 expression system (Thermo Fisher Scientific) and purified with protein A resin (GenScript) and by nickel- nitrilotriacetic acid (Ni-NTA) resin (Thermo Fisher Scientific). The Fab CR3022 antibody gene with a His tag was cloned into pCAT2 plasmid (developed in house) for expression in HB2151 bacteria and purified with Ni-NTA resin. Protein purity was estimated as >95% by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) and protein concentration was measured spectrophotometrically (NanoVue, GE Healthcare).

Generation of a human V_H library, Selection of Binders and Conversion of V_H to V_H-Fc Fusion Protein. Unlike camel V_HHs, which naturally evolved to be autonomously stable, human V_H is usually unstable and easy to aggregate in the absence of V_L (Li et al., 2016; Nguyen et al., 2000). However, human V_H can be selected or engineered with high stability and solubility. To facilitate identification of stable V_H binders, we chose engineered germline V_H3-23 as our library scaffold (Chen et al., 2008b). Our human V_H phage display library was made by grafting heavy chain CDR1, 2, 3 genes derived from 12 healthy donors' peripheral blood monocytes (PBMCs) and

splenocytes (Takara, Cat. No. 636525) into their cognate positions of a stable scaffold (based on the germline V_H3-23) in a manner similar to the method we previously described but without mutagenesis of CDR1 (Chen et al., 2008a). Briefly, CDRs were PCR-amplified by using primers with degenerated adaptors covering CDRs edge regions from diverse V_H families in one end, and with sequences annealing to the V_H3-23 framework (FR) regions in the other end. The PCR products were then assembled by overlapping extension PCR by using primers with homologous ending. The whole V_H was assembled by overlapping FR1-CDR1-FR2-CDR2 and FR3-CDR3-FR4 fragments. After assembly, the V_H fragment was Sfi I digested followed by ligated into Sfi I linearized pComb3x phagemid. The recombinant phagemid was then purified, desalted and concentrated for electroporation of bacteria TG1, from which the V_H phage particles were rescued and produced. The library size was determined by tittering transformants. The library quality (diversity) was checked by randomly Sanger sequencing hundreds of V_H clones and also evaluated by panning of diverse antigens. This library contains very large number of clones (10^{11}). For panning, the V_H library was alternatively panned against biotinylated RBD-his and RBD-Fc proteins. RBD biotinylation occurred through biotin ligase (BirA) mediated enzymatic conjugation of a single biotin on AviTag (GLNDIFEAQKIEWHE) (Fairhead and Howarth, 2015). The panning was for 3 rounds with input antigens of 10 μg RBD-his, 2 μg RBD-Fc and 0.5 μg RBD-his for the 1st, 2nd and 3rd round, respectively. The panning process begun with incubation of antigens with 10^{12} V_H phage particles followed by washing with phosphate-buffered saline (PBS) containing 0.1% Tween-20. Bound phage pulled down by streptavidin-M280-Dynabeads were rescued by log-phase TG1 cells with the M13KO7 helper phage. After the 3rd round panning, positive clones were selected by soluble expression monoclonal (SEM) ELISA followed by sequencing (Chen et al., 2008b). V_H binders were further screened for their binding affinity, stability and ACE2 competition. For conversion to Fc-fusion, the V_H gene was subcloned into pSecTag B vector containing human IgG1 Fc fragment. V_H-Fc ab8 was expressed as described above.

Enzyme-Linked Immunosorbent Assays (ELISAs). For detection of RBD biotinylation efficacy, horseradish peroxidase (HRP) conjugated streptavidin was used. For conformation of function of RBD-his after biotinylation, 100 ng ACE2-Fc was coated into the plates followed by addition of serially diluted biotinylated RBD-his. HRP conjugated streptavidin was used for detection. For other ELISAs, the SARS-CoV-2 RBD (residues 330-532) protein was coated on 96-well plates (Costar) at 100 ng/well in PBS overnight at 4°C. For screening SEM ELISA, clones randomly picked from the infected TG1 cells were incubated with immobilized antigen. Bound phages were detected with HRP-conjugated mouse anti-FLAG tag Ab (Sigma-Aldrich). For the V_H-Fc binding assay, HRP-conjugated goat anti-human IgG Fc (Sigma-Aldrich) was used for detection. For the competition ELISA with hACE2, 2 nM of human ACE2-mouse Fc was incubated with serially diluted V_H, or V_H-Fc, and the mixtures were added to RBD coated wells. After washing, bound ACE2-mouse Fc was detected by HRP-conjugated anti mouse IgG (Fc specific) (Sigma-Aldrich). For evaluation of ACE2 blocking of V_H ab8 binding to RBD, 10 nM V_H ab8 was incubated with coated RBD in the presence of various concentration of ACE2-His (Sino Biological), and the bound V_H ab8 was detected by HRP conjugated anti FLAG antibody. For evaluation of conformational changes of the epitope mapping RBD mutants, we used a mouse polyclonal anti SARS-CoV-2 RBD antibody (Sino biological, Cat. No. 40592-MP01) and the human IgG1 CR3022 antibody. For measuring the binding of V_H-Fc ab8 to RBD mutants, 100 ng RBD mutant was coated on 96-wells plates and incubated with V_H-Fc ab8 with binding detected by using

HRP conjugated anti human Fc antibody. To evaluate the binding of V_H-Fc ab8 and IgG1 ab1 to human FcγRs, recombinant human FcγRIA, IIA, IIIA were coated on 96-wells plates followed by addition of biotinylated V_H-Fc ab8 and IgG1 ab1. Binding was detected by the streptavidin-HRP. All colors were developed by 3,3′,5,5′-tetramethylbenzidine (TMB, Sigma) and stopped by 1 M H_2SO_4 followed by recording absorbance at 450 nm. Experiments were performed in duplicate and the error bars denote ± 1 SD.

BLItz. Antibody affinities and avidities were analyzed by the biolayer interferometry BLItz (ForteBio, Menlo Park, CA). For measuring V_H ab8 affinity, the RBD-Fc was mounted on the protein A sensor (ForteBio: 18-5010). 125 nM, 250 nM and 500 nM V_H ab8 were used for association. For measuring avidity of V_H-Fc ab8, biotinylated RBD-Fc was immobilized on streptavidin biosensors (ForteBio: 18–5019) for 2 min and equilibrated with Dulbecco's phosphate-buffered saline (DPBS) (pH = 7.4) to establish baselines. 50 nM, 100 nM and 200 nM V_H-Fc ab8 were chosen for association. The association was monitored for 2 min and then the antibody was allowed to dissociate in DPBS for 4 min. The k_a and k_d were derived from sensorgrams fittings and used for K_d calculation. For the competitive Blitz, 500 nM V_H-Fc ab8 was loaded onto the RBD-Fc coated sensor for 300 s to reach saturation followed by dipping the sensor into a 100 nM ACE2-Fc or Fab CR3022 solution in the presence of 500 nM V_H-Fc ab8. The association was monitored for 300 s. The signals from100 nM hACE2 or CR3022 binding to the RBD-Fc coated sensor in the absence of V_H-Fc ab8 was independently recorded in parallel. Competition was determined by the percentage of signal in the presence of V_H-Fc ab8 to signal in the absence of V_H-Fc ab8 (< 0.7 is considered to be competitive) (Wu et al., 2020a).

SARS-CoV-2 RBD Mutants and Epitope Mapping by Ala Scanning. RBD mutants, N354D, N354D/D364Y, V367F, R408I, W436R were purchased from Acro Biosystems. F342L and K458R were bought from Sino Biological. RBD mutants G476S and V483A, plus the alanine (Ala) scanning mutants N439A, G446L, L455A, F456A, A475I, F486A, Q493A, Q498A, N501A, Y505A were constructed by site-directed mutagenesis using QuikChange II XL Site-Directed Mutagenesis Kit (Agilent, cat. no. 200521). Mutants were expressed and purified according to the abovementioned RBD purification procedures. ELISA was used to evaluate the binding of these mutants compared to the wild type RBD.

Electron Microscopy for SARS-CoV-2 S Trimer Complexed with V_H ab8.

A. Expression and Purification. The codon optimized SARS-CoV-2 2P S protein ectodomain construct (GenBank: YP_009724390.1) was C-terminally tagged with 8xHis and a twin Strep tag and cloned into the mammalian expression vector pcDNA 3.1 (Synbio). HEK293F cells were grown in suspension culture using FreeStyle media (ThermoFisher) at 37 °C in a humidified CO_2 incubator (8% CO_2). Cells were transiently transfected at a density of 1 x 10^6 cells/ml using branched polyethylenimine (PEI) (Sigma) (Portolano et al., 2014). Media was exchanged after 24 h and supplemented with 2.2 mM valproic acid. Supernatant was harvested by centrifugation after 4 days, filtered and loaded onto a 5 ml HisTrap HP column (Cytiva). The column was washed with buffer (20 mM Tris pH 8.0, 500 mM NaCl, 20 mM imidazole) and the protein was eluted with buffer (20 mM Tris pH 8.0, 500 mM NaCl, 500 mM imidazole). Purified protein was concentrated (Amicon Ultra 100 kDa cut off, Millipore Sigma) and loaded onto a

Superose 6 column (Cytiva) equilibrated with GF buffer (20 mM Tris pH 8.0 and 150 mM NaCl). Peak fractions were pooled and concentrated to 1.3 mg/ml (Amicon Ultra 100 kDa cut off, Millipore Sigma).

B. Electron Microscopy Specimen Preparation and Data Collection. Purified S protein ectodomain (0.04 mg/ml) was mixed with V_H ab8 (0.02 mg/ml) or soluble ACE2 (0.02 mg/mL) and incubated on ice for 10 mins. For the competition experiment, the S protein (0.04 mg/ml) was first incubated on ice with V_H ab8 (0.02 mg/ml) for 10 mins then followed by addition of ACE2 (0.02 mg/mL) for another 10 mins. The mixtures (4.8 µl) were applied to 300-mesh copper grids coated with continuous ultrathin carbon. Grids were plasma cleaned using an H_2/O_2 gas mixture for 15 s in a Solarus plasma cleaner (Gatan Inc.) prior to adding the sample. Samples were allowed to adsorb for 30 s before blotting away excess liquid, followed by a brief wash with MilliQ H_2O. Grids were stained by three successive applications of 2% (w/v) uranyl formate (20 s, 20 s, 60 s). Grids containing S protein ectodomain with V_H ab8, and S protein ectodomain mixed with both V_H ab8 and soluble ACE2 were imaged using a 200 kV Glacios transmission electron microscope (ThermoFisher Scientific) equipped with a Falcon3 camera operated in linear mode. Using EPU automated acquisition software (ThermoFisher Scientific), 15-frame movies were collected at 92,000x magnification (corresponding to a physical pixel size of 1.6 □) over a defocus range of -0.5 to -3.0 µm with an accumulated total dose of 40 $e^-/Å^2$/movie. Grids containing purified S protein ectodomain (0.04 mg/mL) with soluble ACE2 (0.02 mg/mL) were imaged using a 200kV Glacios transmission electron microscope equipped with a Ceta 16M CMOS camera (ThermoFisher Scientific). Micrographs were collected at 92,000x magnification (physical pixel 1.6 □) over a defocus range of -0.5 to -3.0 µm with a total dose of 50 $e^-/Å^2$ using EPU automated acquisition software.

C. Image Processing. Motion correction and CTF estimation were performed in RELION (3.1) (Scheres, 2012). Particles were picked by crYOLO (1.7.4) (Wagner et al., 2019) with pre-trained model for negative stain data. After extraction, particles were imported to cryoSPARC live (v2.15.1) (Punjani et al., 2017) and subjected to 2D classification and 3D heterogeneous classification. Final density maps were obtained by 3D homogeneous refinement. Figures were prepared using UCSF Chimera (Pettersen et al., 2004).

Flow Cytometry Analysis (FACS). Full-length S protein of SARS-CoV-2 with native signal peptide replaced by the CD5 signal peptide were codon-optimized and synthesized by IDT. The S gene was subcloned into our in-house mammalian cell expression plasmid, which were used to transiently transfect 293T cells cultured in Dulbecco's Modified Eagle's Medium (DMEM) with 10% FBS, 1% penicillin-streptomycin (P/S). The comparisons of ACE2-Fc, IgG1 CR3022 and V_H-Fc ab8 binding to both blank 293T and 293T overexpressing S (293T-S) were performed. For the determination of binding avidity of V_H-Fc ab8 and ACE2-Fc to the cell surface S, serially diluted antibodies or ACE2-Fc with highest concentration of 1 µM were incubated with cells, and after washing, bound antibodies were detected by phycoerythrin (PE) conjugated anti-human Fc antibody (Sigma-Aldrich). PE-A+ cells were detected by flow cytometry using BD LSR II (San Jose, CA). The gating of PE-A+ population was performed by the FlowJo software, which was plotted against the concentrations of proteins to calculate FC_{50} by non-linear fitting in Graphpad Prism 7 (San Diego, CA). To evaluate ACE2 blocking of V_H ab8 binding to cell surface associated S,

gradient concentrations of ACE2-his in the presence of 1 μM V_H ab8 (Flag tag) were incubated with 293-S cells. After washing, V_H ab8 binding was detected by PE conjugated anti FLAG tag antibody.

Cell-Cell Fusion Inhibition Assay. To test antibody mediated inhibition of cell fusion, the β-galactosidase (β-gal) reporter gene based quantitative cell fusion assay was used (Xiao et al., 2003). In this assay, 293T-S cell expression of T7 RNA polymerase was achieved by infection with vaccinia virus VTF7.3, while 293T-ACE2 cell expression of T7 promoter controlled β-Gal was obtained by infection with vaccinia virus VCB21R. β-Gal will be expressed only after fusion of the two types of cells, which can be monitored by chromogenic reactions using β-Gal substrate. To assay cell-cell fusion, 293T cells stably expressing SARS-CoV-2 S (293T-S) cells were infected with T7 polymerase-expressing vaccinia virus (vTF7-3), and 293T cells stably expressing ACE2 (293T-ACE2) were infected with vaccinia virus (vCB21R Lac-Z) encoding T7 promotor controlled β-gal. Two hours after infection, cells were incubated with fresh medium and transferred to 37 °C for overnight incubation. The next day, 293T-S cells were pre-mixed with serially diluted antibodies or ACE2-Fc at 37 °C for 1 h followed by incubation with 293T-ACE2 cells at a 1:1 ratio for 3 h at 37°C. Then cells were then lysed, and the β-gal activity was measured using β□ galactosidase assay kit (substrate CPRG, G-Biosciences, St. Louis, MO) following the manufacturer's protocol. Fusion inhibition percentage (sample reading, F) was normalized by maximal fusion (reading, F_{max}) of 293T-S and 293T-ACE2 cells in the absence of antibodies using this formula: Fusion inhibition % = $[(F_{max}-F)/(F_{max} - F_{blank})] \times 100\%$, in which F_{blank} refers to the OD reading of 293T-S and 293T incubation wells. Fusion inhibition percentage was plotted against antibody concentrations. Experiments were performed in duplicate and the error bars denote ± 1 SD.

Pseudovirus Neutralization Assay. Pseudovirus neutralization assay was performed based on previous protocols (Zhao et al., 2013). Briefly, HIV-1 backbone based pseudovirus was produced in 293T cells by co-transfection with plasmid encoding SARS-CoV-2 S protein and plasmid encoding luciferase expressing HIV-1 genome (pNL4-3.luc.RE) using PEI. Pseudovirus-containing supernatants were collected 48 h later and concentrated using Lenti-X™ concentrator kit (Takara, CA). Pseudovirus neutralization assay was then performed by incubation of SARS-CoV-2 pseudovirus with serially diluted antibodies or ACE2-Fc for 1 h at 37 °C, followed by addition of the mixture into pre-seeded 293T-ACE2 cells. The mixture was then centrifuged at 1000 × g for 1 hour at room temperature. The medium was replaced 4 hrs later. After 24 h, luciferase expression was determined by Bright-Glo kits (Promega, Madison, WI) using BioTek synergy multi-mode reader (Winooski, VT). Cells only and virus only wells were included and used for normalization. The 50% pseudovirus neutralizing antibody titer (IC_{50}) was calculated using Graphpad Prism 7. Experiments were performed in duplicate and the error bars denote ± 1 SD.

SARS-CoV and SARS-CoV-2 Microneutralization Assay. The standard live virus-based microneutralization (MN) assay was used as previously described (Agrawal et al., 2016a; Agrawal et al., 2016b; Du et al., 2013; Du et al., 2014). Briefly, serially three-fold and duplicate dilutions of individual monoclonal antibodies (mAbs) were incubated with 120 pfu of SARS-CoV or SARS-CoV-2 at room temperature for 2 h before transferring into designated wells of confluent Vero E6 cells grown in 96-well microtiter plates. Vero E6 cells cultured with medium with or without virus were included as positive and negative controls, respectively. MERS-CoV RBD-specific

neutralizing m336 mAb (Ying et al., 2014a) were used as additional controls. After incubation at 37 °C for 4 days, individual wells were observed under the microcopy for the status of virus-induced formation of cytopathic effect. The efficacy of individual mAbs was expressed as the lowest concentration capable of completely preventing virus-induced cytopathic effect in 100% of the wells.

SARS-CoV and SARS-CoV-2 Reporter Gene Neutralization Assay. Full-length viruses expressing luciferase were designed and recovered via reverse genetics as described previously (Scobey et al., 2013; Yount et al., 2003). Briefly, the SARS-CoV-2 RNA from infected cell culture was reverse-transcribled and constructed into the seven contiguous genomic cDNA subclones with interconnecting junctions, which were then BsaI/BsmBI digested and ligated into a full-length SARS-CoV-2 genome cDNA through the cohesive ends. A silent mutation of T15102A was introduced into a conserved region in nsp12 to differentiate our recombinant viruses from the circulating SARS-CoV-2 strains through Sanger sequencing. The reporter viruse was synthesized by replacing a 276-bp region in ORF7 with a GFP-fused nanoluciferase (nLuc) gene. After assembly into full-length cDNA, full-length RNA was in vitro transcribed and was electroporated into Vero E6 cells. Virus stocks were propagated on Vero E6 cells in minimal essential medium containing 10% fetal bovine serum (HyClone) and supplemented with penicillin/kanamycin (Gibico). Viruses were tittered in Vero E6 USAMRID cells to obtain a relative light units (RLU) signal of at least 20× the cell only control background. Ab or ACE2-Fc were serially diluted 4-fold up to eight dilution spots with at a starting dilution 100 ∝g/ml, and were incubated with SARS-CoV-UrbaninLuc and SARS-CoV-2-SeattlenLuc viruses at 37℃ with 5% CO_2 for 1 hour. Then virus-antibody dilution complexes were added to the pre-seeding E6 USAMRID cells (20,000) in duplicate. Virus-only controls and cell-only controls were included in each neutralization assay plate. Following infection, plates were incubated at 37 ℃ with 5% CO_2 for 48 hours. Then cells were lysed and luciferase activity was measured via Nano-Glo Luciferase Assay System (Promega) according to the manufacturer specifications. SARS-CoV and SARS-CoV-2 neutralization IC_{50} were defined as the sample concentration at which a 50% reduction in RLU was observed relative to the average of the virus control wells. Experiments were performed in duplicate and IC_{50} was obtained by the non-linear fitting of neutralization curves in Graphpad Prism 7.

Evaluation of the V_H-Fc ab8 Protective Efficacy in a Mouse Adapted SARS-CoV-2 Model. A recombinant mouse ACE2 adapt SARS-CoV-2 variant was constructed by introduction of two amino acid changes (Q498T/P499Y) at the ACE2 binding pocket in RBD. Virus stocks were grown on Vero E6 cells and viral titer was determined by plaque assay (Dinnon et al., 2020). Groups of 5 each of 10 to 12-month old female BALB/c mice (Envigo, #047) were treated prophylactically (12 hours before infection) by intraperitoneal injection with 36, 8, or 2 mg/kg of V_H-Fc ab8, respectively. Mice were challenged intranasally with 10^5 PFU of mouse-adapted SARS-CoV-2. Two days post infection, mice were sacrificed and lung viral titer was determined by the plaque assay. To exclude the residual lung antibody impact on viral titration, mice were euthanized and perfused with 10 ml of PBS via cardiac puncture before lung harvest for viral titration. For virus titration, the caudal lobe of the right lung was homogenized in PBS. The resulting homogenate was serial-diluted and inoculated onto confluent monolayers of Vero E6 cells, followed by agarose overlay. Plaques were visualized via staining with Neutral Red on day 2 post

infection. To measure the viral RNA in the lung, tissue homogenate lysed in Trizol LS (Thermofischer) was then processed with Thermofischer Trizol RNA isolation protocol followed by RT-qPCR using the QuantiFast Probe RT-PCR kit (Qiagen) to amplify a portion of upE gene. The 50% tissue culture infectious doses ($TCID_{50}$) equivalence were estimated by running serial dilutions of known $TCID_{50}$ standards.

Evaluation of the V_H-Fc ab8 Prophylactic and Therapeutic Efficacy in a Hamster Model of SARS-CoV-2 Infection. SARS-CoV2/Canada/ON/VIDO-01/2020 was propagated on Vero'76 cells using DMEM with 2% FBS and 1μg/ml L-(tosylamido-2-phenyl) ethyl chloromethyl ketone (TCPK) trypsin. Infectious work with SARS-CoV-2 was approved by the Biosafety Protocol Approval Committee (BPAC) at the University of Saskatchewan and performed in the high containment laboratories at VIDO-InterVac. Male hamsters (9-week-old) were obtained from Charles River (Montreal, QC). For evaluations of prophylactic efficacy, all hamsters (n=7) were injected intraperitoneally with 10 mg/kg of V_H-Fc ab8 24 hours prior to intranasal challenge of 50 μl/nare containing a total of 1×10^5 $TCID_{50}$ of SARS-CoV-2. For the therapeutic group, hamsters were infected as above and treated intraperitoneally with 10 mg/kg (n=3) or 3 mg/kg (n=4) of V_H-Fc ab8 6 hours post-infection. Untreated hamsters were kept as a control. Nasal washes and oral swabs were collected at day 1, 3 and 5 post infection (dpi). Hamsters were bled at 1 and 5 dpi. All hamsters were euthanized on 5 dpi. At euthanasia, lung lobes were collected for virus titration and RNA isolation. For viral titer determination, nasal washes were diluted in a 10-fold dilution series and absorbed on Vero'76 cells in triplicates for 1 hour at 37°C. Inoculum was removed and replaced with fresh DMEM containing 2% FBS, penn/strep and 1μg/ml TPCK. Cytopathic effect was scored on day 3 and day 5 post infection. The limit of detection is 13.6 $TCID_{50}$. For testing viral RNA, viral RNA isolated from nasal and oral swabs using the QiaAmp Viral RNA mini kit (Qiagen) and the QuantiFast Probe RT-PCR kit (Qiagen) to amplify a portion of upE gene. For RNA levels in tissues, 30 mg of tissue homogenate in buffer RLT were processed with the RNeasy kit (Qiagen) followed by RT-qPCR as above. $TCID_{50}$ equivalence were estimated by running serial dilutions of known $TCID_{50}$ standards. For testing Ab8 concentrations post injection at hamster sera and lung tissue, SARS-CoV-2 spike-1 ELISA was used. S1 protein was coated at 1 μg/ml overnight at 4°C in PBS onto MaxiSorp plates (Nunc). The following day plates were blocked with 5% skim milk and 0.05%Tween20. Serum collected on day 1 and day 5 post-challenge was diluted 1:100 and absorbed for 1 hour at 37 °C. Plates were washed and goat anti human IgG-HRP was added. Plates were washed and subsequently developed with OPD (o-phenylenediamine dihydrochloride) substrate. Optical density was measured at 450 nm after 30 mins of incubation. For lung tissues, after blocking homogenates were diluted 1:10 and absorbed overnight at 4°C followed by detection with anti-human IgG-HRP and substrate as stated above. The control hamster lung homogenate was used for background correction. For histopathology on day 5 p.i., 10% formalin fixed and paraffin embedded tissues were processed with either hematoxylin and eosin stain (H&E) or immunohistochemistry (IHC) for detection of SARS-CoV2 antigen; in IHC after blocking tissue slides were treated with anti-nucleocapsid rabbit polyclonal antibodies followed with anti-rabbit HRP antibody.

Dynamic Light Scattering (DLS). For evaluation of aggregation propensity, V_H ab8 and V_H-Fc ab8 were buffer-changed to DPBS and filtered through a 0.22 μm filter. The concentration was adjusted to 4 mg/mL; 500 μL samples

were incubated at 37 °C. On day 0, day 1 and day 6, samples were taken out for DLS measurement on Zetasizer Nano ZS ZEN3600 (Malvern Instruments Limited, Westborough, MA) to determine the size distributions of protein particles.

Size Exclusion Chromatography (SEC). The Superdex 200 Increase 10/300 GL chromatography (GE Healthcare, Cat. No. 28990944) was used. The column was calibrated with protein molecular mass standards of Ferritin (Mr 440 000 kDa), Aldolase (Mr 158 000 kDa), Conalbumin (Mr 75 000 kDa), Ovalbumin (Mr 44 000 kDa), Carbonic anhydrase (Mr 29 000 kDa), Ribonuclease A (Mr 13 700 kDa). 150 µl filtered proteins (1.5 mg/ml) in PBS were used for analysis. Protein was eluted by DPBS buffer at a flow rate of 0.5 ml/min.

Membrane Proteome Array Assay. Integral Molecular, Inc. (Philadelphia, PA) performed specificity testing of V_H-Fc ab8 using the Membrane Proteome Array (MPA) platform. The MPA comprises 5,300 different human membrane protein clones, each overexpressed in live cells from expression plasmids that are individually transfected in separate wells of a 384-well plate (Tucker et al., 2018). The entire library of plasmids is arrayed in duplicate in a matrix format and transfected into HEK-293T cells, followed by incubation for 36 h to allow protein expression. Before specificity testing, optimal antibody concentrations for screening were determined by using cells expressing positive (membrane-tethered Protein A) and negative (mock-transfected) binding controls, followed by flow cytometric detection with an Alexa Fluor-conjugated secondary antibody (Jackson ImmunoResearch Laboratories). Based on the assay setup results, V_H-Fc ab8 (20 µg/ml) was added to the MPA. Binding across the protein library was measured on an iQue3 (Ann Arbor, MI) using the same fluorescently labeled secondary antibody. To ensure data validity, each array plate contained positive (Fc-binding; SARS-CoV-2 S protein) and negative (empty vector) controls. Identified targets were confirmed in a second flow cytometric experiment by using serial dilutions of the test antibody. The identity of each target was also confirmed by sequencing.

QUANTIFICATION AND STATISTICAL ANALYSIS

For the mouse model, the statistical significance of difference between V_H-Fc ab8 treated and control mice lung virus titers was determined by the two-tailed, unpaired, student *t* test calculated using GraphPad Prism 7.0. A p value < 0.05 was considered significant. ** $p < 0.01$. For the mice lung viral titer after perfusion, viral RNA and hamster lung viral RNA, statistical significance was determined by the Mann-Whitney *U* test. A p value < 0.05 was considered significant. ns: $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$. For comparing V_H-Fc ab8 and IgG1 ab1 concentration, significance analysis was determined by the two-way ANOVA followed by Tukey test in GraphPad Prism 7.0. A p value < 0.05 was considered significant. ns: $p > 0.05$, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$.

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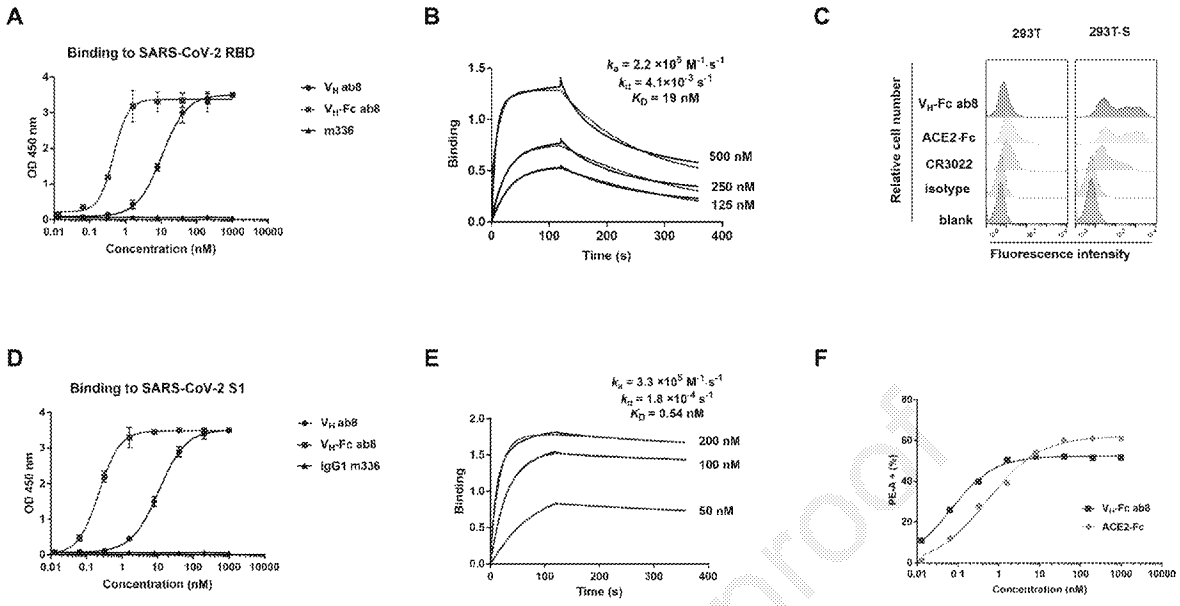
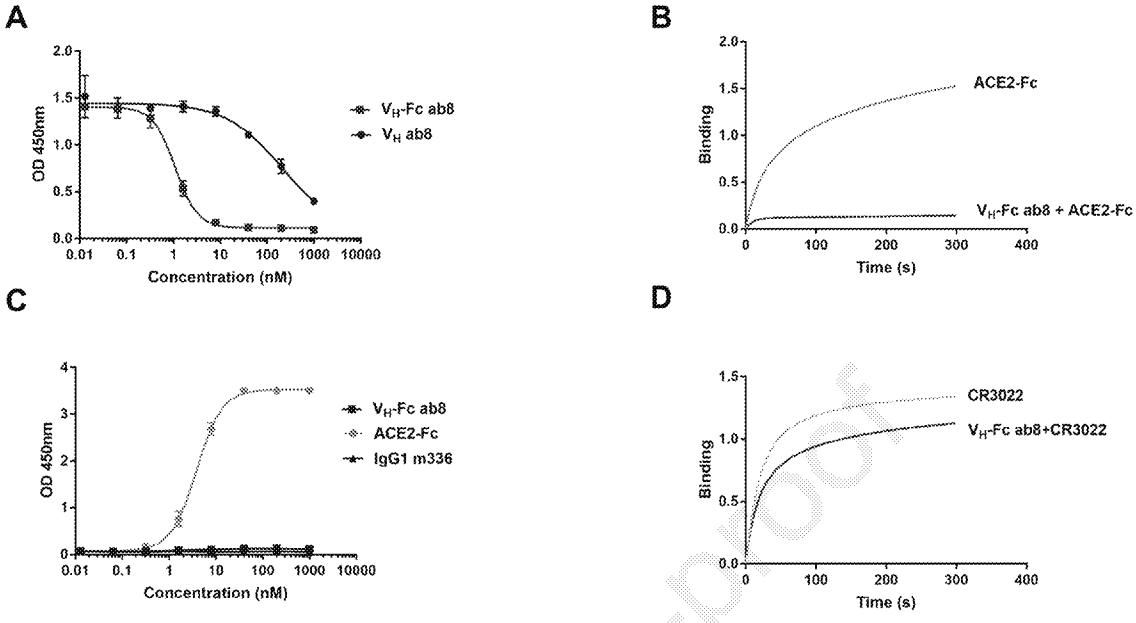
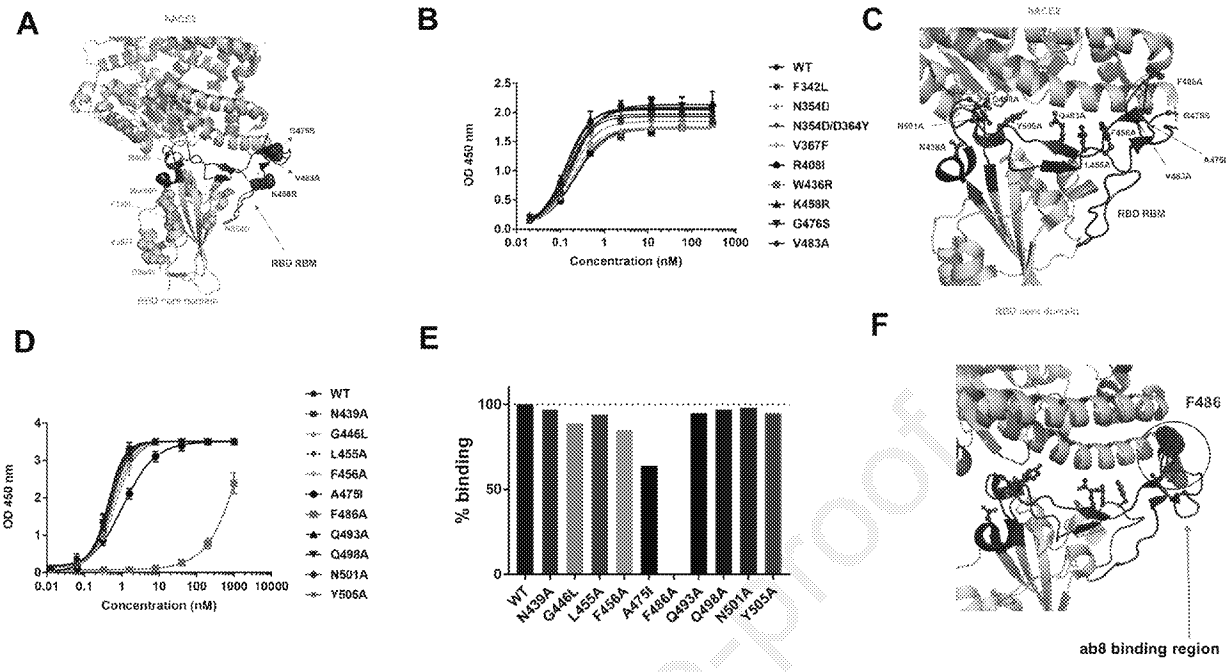
- A high-affinity human antibody domain, V_H ab8, specific for SARS-CoV-2 was selected
- V_H ab8 bound to all three S protomers competing with ACE2
- Bivalent V_H, V_H-Fc ab8, potently neutralized SARS-CoV-2 in vitro and in animals
- Small size and bivalency contribute to the high ab8 SARS-CoV-2 neutralizing potency

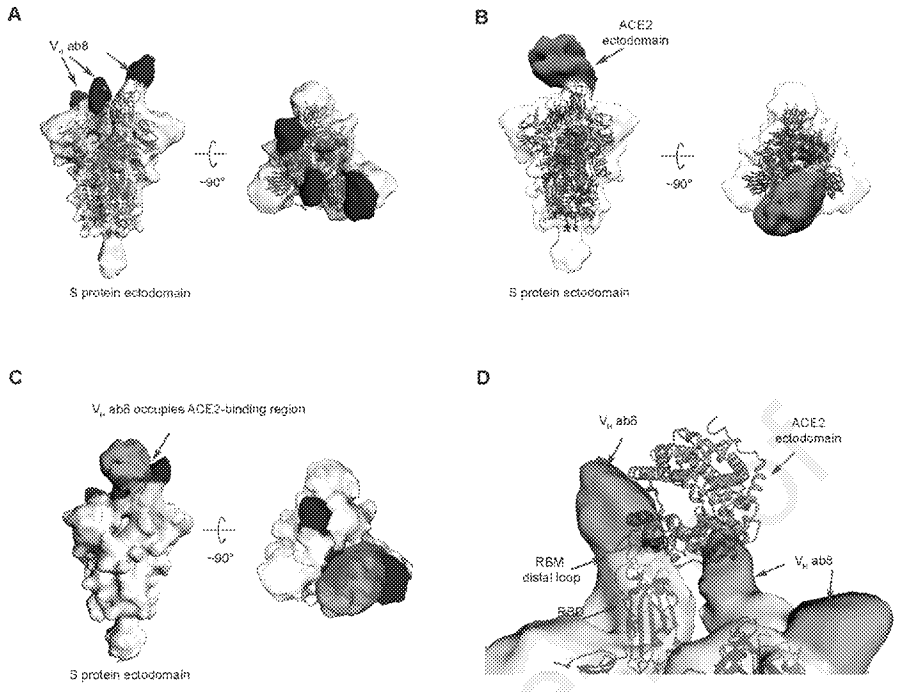
In brief summary:

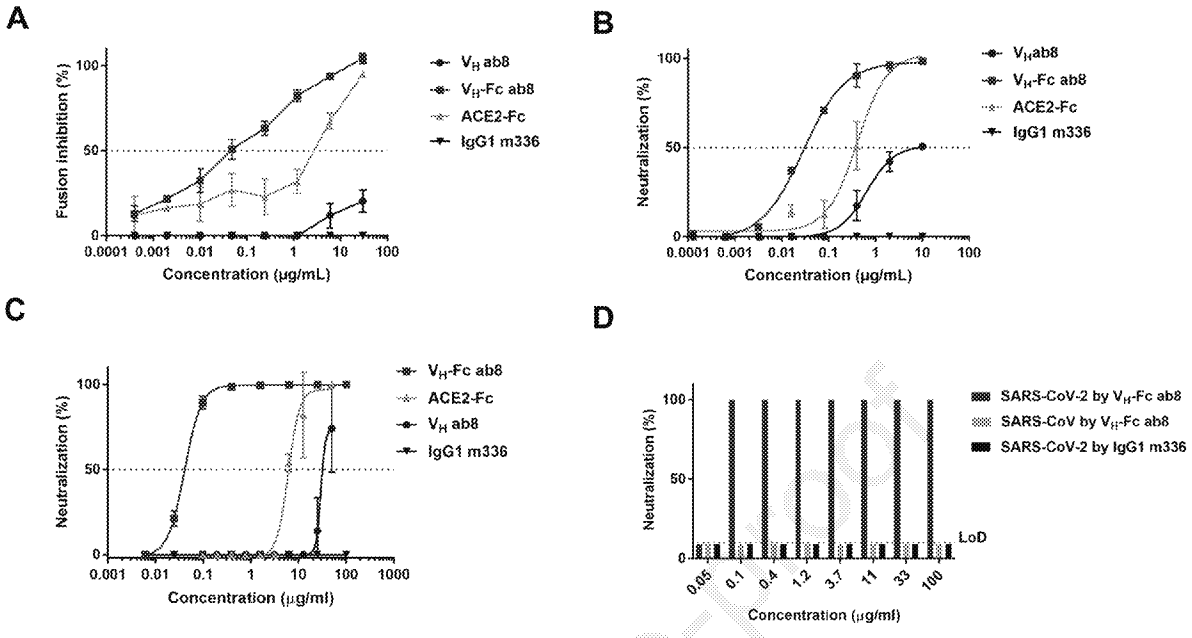
A high-affinity human antibody domain, V_H ab8, specific for SARS-CoV-2 bound to all three S protomers competing with ACE2. The relatively small size and bivalency of V_H-Fc ab8 contributed to its high potency in two animal models of infection.

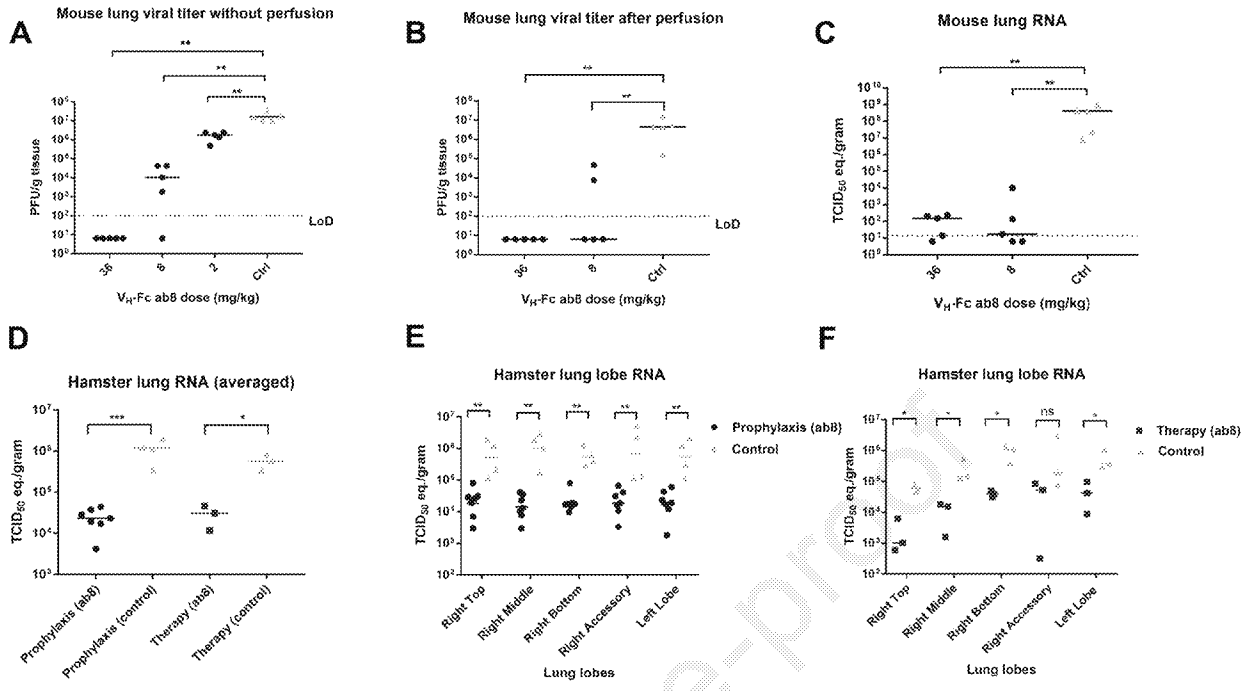


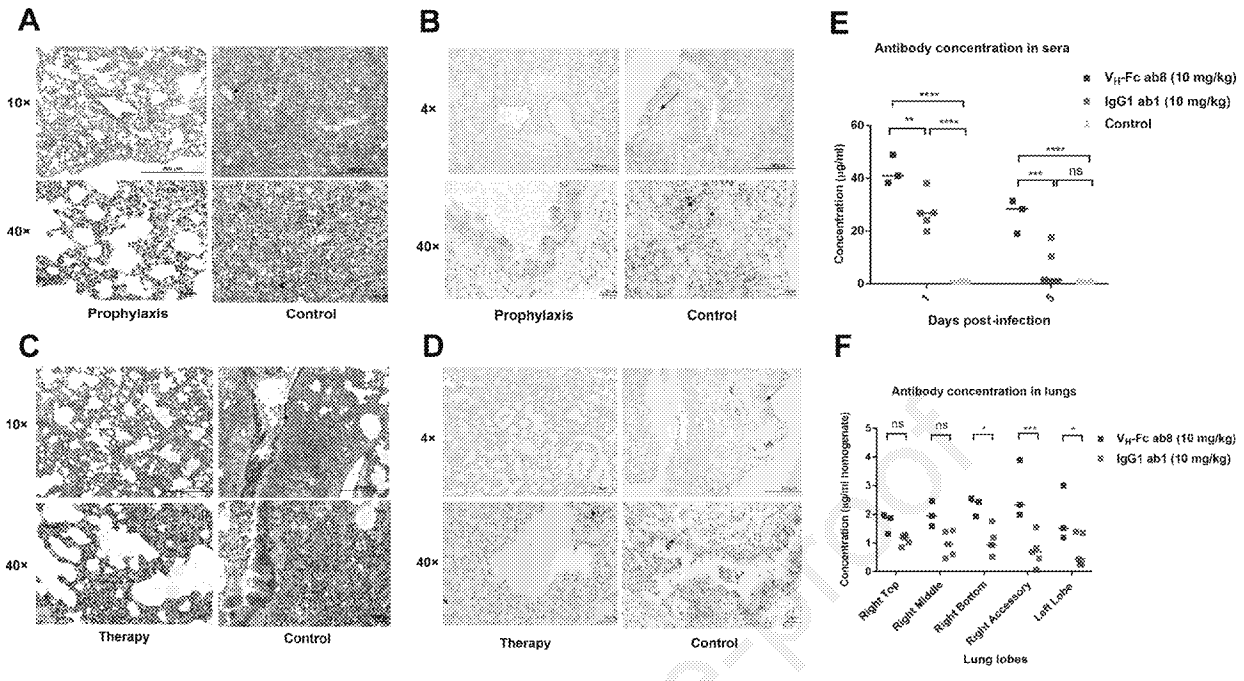












From: Liu, Shan-Lu [liu.6244@osu.edu]
Sent: 10/12/2020 8:46:29 PM
To: zhengzhiming4@gmail.com; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; Shan.lu@umassmed.edu; Hu, Haitao [haihu@UTMB.EDU]; wenzheho@temple.edu; Qfeng4@central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2@unl.edu; qiyi.tang@howard.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518@umd.edu; gaos8@upmc.edu; Wang,Penghua [pewang@uchc.edu]; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@163.com; xfyu1@zju.edu.cn; bzhao@partners.org; jianw@musc.edu; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jun.zhu@nih.gov; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; xiangguo.qiu@canada.ca; Feng Shao [shaofeng@nibs.ac.cn]; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan [Nan.Yan@UTSouthwestern.edu]; liliwang@upenn.edu; Linheng Li [LIL@stowers.org]; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; Liu, Shan-Lu [liu.6244@osu.edu]; wu@crystal.harvard.edu; Sun.Jie@mayo.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao [Haitao.Wen@osumc.edu]; Qu, Feng [qu.28@osu.edu]; Hezhao.Ji@umanitoba.ca; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; PZheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong [peshi@UTMB.EDU]; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong [wang.655@osu.edu]; shuping_tong_md@brown.edu; pinghuif@usc.edu; gaof@im.ac.cn; zihai@musc.edu; zqin@uams.edu; guoh4@upmc.edu; wma@missouri.edu; Feng.Li@uky.edu; xiaow@iu.edu; sli38@tulane.edu; guodeyin@mail.sysu.edu.cn
Subject: ACVA/SCBA-Virology 2020 meeting

Dear colleagues,

As you know, our ACVA/SCAB-Virology 2020 annual meeting originally scheduled in July was cancelled due to the pandemic. Now the Advisory Board has decided to have a virtual meeting on **December 30-31, 2020**. The date is chosen to specially mark the first public revelation of COVID-19 outbreak in Wuhan, which is December 30, 2019. The current board members will serve as organizing and also scientific program committees to facilitate the process.

The meeting will be held in the morning of December 30 and 31 (9-12 pm) and in the afternoon of December 30 (1:30-4:30 pm). Six scientific sessions focusing on the molecular virology, viral pathogenesis, and viral therapeutics and vaccines, etc. will be dedicated to this day-and-half event. Three focused panel discussions will also be arranged.

We are pleased that Drs. Susan Weiss and X.J. Meng have agreed to deliver keynote address during the meeting.

Xiang-Jin (X.J.) Meng, MD, PhD
Virginia Tech
"Expanding host range and extrahepatic manifestation of hepatitis E virus infection"

Susan R. Weiss, PhD
University of Pennsylvania
"Coronaviruses: Old and New"

Please submit your abstract to Dr. Tongqing Zhou (tzhou@mail.nih.gov) by Nov 30, 2020 for full consideration of selected talks. We especially encourage young investigators to submit abstracts and participate in this meeting. As we wish to cover as many topics as possible, the talk will be limited to 12 min of presentation plus 3 min of questions.

Please let me know if you have questions or suggestions.

P.S. This meeting will be open to all SCBA members (not restricted to the Virology Division). Will update.

Thank you.

Shan-Lu Liu, MD, PhD
ACVA/SCBA-Virology President
The Ohio State University

CENTER TO STOP COVID

From: 胡犇 [huben@wh.iov.cn]
Sent: 11/2/2020 2:41:30 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
CC: 石正丽 [zlshi@wh.iov.cn]
Subject: Invitation letter of the 9th International Symposium on Emerging Viral Diseases
Attachments: Invitation letter of 9th ISEVD_Prof Shi.pdf

Dear Prof. Shi,

The 9th International Symposium on Emerging Viral Diseases, organized by Wuhan Institute of Virology, Chinese Academy of Sciences, will be held in November 27th and 28th 2020 in Wuhan, China. This biennial symposium covers a variety of topics on emerging viruses, including virus discovery, pathogenesis, immunity, antivirals and vaccines, etc. It has become an event for Chinese and international virologists to discuss cutting-edge science on emerging viruses, as well as to foster international collaborations. This year, the meeting will focus on but not limited to SARS-CoV-2 and COVID-19. It will build an opportunity for global researchers to present their important research findings on SARS-CoV-2, and to exchange the latest understanding of this pandemic coronavirus and other emerging viruses.

You are one of the leading scientists on emerging viruses and have made distinguished research advance in SARS-CoV-2. It is our great pleasure to invite you to give a keynote speech about your outstanding research work at this symposium. For speakers outside China, the presentation will be given on-line via Zoom. Please find enclosed the formal invitation letter from the chairmen of the meeting, Prof.Zhengli Shi and Prof.Xi Zhou from Wuhan Institute of Virology.

If you accept this invitation, please reply to us by 8th November, and please let us know the available date and time of your talk.

We look forward to hearing from you.

Thank you!

Best regards

Ben Hu PhD
Wuhan Institute of Virology, CAS
Secretary of the 9th ISEVD

WUHAN INSTITUTE OF VIROLOGY
THE CHINESE ACADEMY OF SCIENCES

Address: Xiao Hong Shan 44, Wuchang, Wuhan 430071, Hubei, P. R. China
Tel: +86-27-87198593 Fax: +86-27-87198072 http://english.whiov.cas.cn/

November 2, 2020

Prof. Pei-Yong Shi
Department of Biochemistry and Molecular Biology, University of Texas Medical Branch, Galveston, TX, USA

Dear Prof. Shi,

The 9th International Symposium on Emerging Viral Diseases, organized by Wuhan Institute of Virology, Chinese Academy of Sciences, will be held in November 27th and 28th 2020 in Wuhan, China. This biennial symposium covers a variety of topics on emerging viruses, including virus discovery, pathogenesis, immunity, antivirals and vaccines, etc. It has become an event for Chinese and international virologists to discuss cutting-edge science on emerging viruses, as well as to foster international collaborations. This year, the meeting will focus on but not limited to SARS-CoV-2 and COVID-19. It will build an opportunity for global researchers to present their important research findings on SARS-CoV-2, and to exchange the latest understanding of this pandemic coronavirus and other emerging viruses.

It is our great pleasure to invite you to give a keynote speech about your outstanding research work at this symposium. The presentation will be given on-line via Zoom.

If you accept this invitation, please reply to the meeting secretary Dr. Ben Hu (huben@wh.iov.cn) by 8th November, and please let us know the available date and time of your talk. We look forward to hearing from you.

Sincerely Yours,

Zheng-Li SHI, PhD

Senior Scientist & Professor
Wuhan Institute of Virology, CAS
zlshi@wh.iov.cn
Tel: 86-27-87197240

Xi ZHOU, PhD

Senior Scientist & Professor
Wuhan Institute of Virology, CAS
zhouxi@wh.iov.cn
Tel: 86-27-87197727

From: 胡犇 [huben@wh.iov.cn]
Sent: 11/3/2020 1:31:28 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: Re: RE: Invitation letter of the 9th International Symposium on Emerging Viral Diseases

Dear Prof Shi,

Thanks a lot for your quick response.

We are very glad to know that you accept to participate in the meeting. We will contact you later when we make the meeting agenda.

Sincerely

Ben

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-11-02 21:47:41 (星期一)
收件人: "胡犇" <huben@wh.iov.cn>
抄送: "石正丽" <zlshi@wh.iov.cn>
主题: RE: Invitation letter of the 9th International Symposium on Emerging Viral Diseases

Dear Ben and Zhengli,

Thank you for the invitation. I will be happy to participate. Look forward to seeing you and other colleagues.

Best, Pei-Yong

Pei-Yong Shi, Ph.D.
John Sealy Distinguished Chair in Innovations in Molecular Biology
Vice Chair for Innovation and Commercialization
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch at Galveston
Phone: 409-772-6370

From: 胡犇 <huben@wh.iov.cn>
Sent: Monday, November 2, 2020 2:42 AM
To: Shi, Pei yong <peshi@UTMB.EDU>

Cc: 石正丽 <zlshi@wh.iov.cn>
Subject: Invitation letter of the 9th International Symposium on Emerging Viral Diseases

Dear Prof. Shi,

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You are one of the leading scientists on emerging viruses and have made distinguished research advance in SARS-CoV-2. It is our great pleasure to invite you to give a keynote speech about your outstanding research work at this symposium. For speakers outside China, the presentation will be given on-line via Zoom. Please find enclosed the formal invitation letter from the chairmen of the meeting, Prof.Zhengli Shi and Prof.Xi Zhou from Wuhan Institute of Virology.

If you accept this invitation, please reply to us by 8th November, and please let us know the available date and time of your talk.

We look forward to hearing from you.

Thank you!

Best regards

Ben Hu PhD
Wuhan Institute of Virology, CAS
Secretary of the 9th ISEVD

From: 胡犇 [huben@wh.iov.cn]
Sent: 11/25/2020 4:14:43 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: 9th ISEVD on-line speaker instruction
Attachments: 9th ISEVD meeting brochure.pdf

Dear speaker:

The 9th International Symposium on Emerging Viral Diseases will start in the morning of 27th November (Beijing time).

Please find enclosed the brochure of the two-day symposium, which include the final program, the information needed for zoom meeting log-in, and the biosketch collection of all speakers.

Please note that the time indicated in the program are generally in Beijing time (GMT +8). But for our speakers in other time zones, the scheduled time of your presentation in your local time zone are shown in bold.

Please use following information to join in our meeting by Zoom:

Zoom Meeting link:
https://us02web.zoom.us/j/3120552792?pwd= **552.136**

Meeting Topic: 9th ISEVD Day 1 / Day 2

Meeting ID: 3120552792

Password: **552.136**

All presentations are given in English. On-line speakers are welcome to join in the meeting throughout the symposium.

Please make sure that you have entered the zoom meeting at least 10 min before your presentation starts.

If you are afraid that some networking problem may happen when you give the talk and affect the quality of the live presentation, you can also make a video recording of your speech in advance, and send it to us at least 24 hours before the scheduled time of your talk.

Thank you for your support to the symposium!

We are looking forward to hearing your talks.

Best regards

Ben HU PhD

Wuhan Institute of Virology, CAS
Secretary of the 9th ISEVD

The 9th International Symposium on Emerging Viral Diseases

第九届新生病毒性疾病控制学术研讨会

Main Organizer /主办单位

Wuhan Institute of Virology, CAS
中国科学院武汉病毒研究所

Participating Organizers /承办单位

State Key Laboratory of Virology
病毒学国家重点实验室

Society of Microbiology, Hubei &Wuhan
湖北省暨武汉微生物学会

Center for Emerging Infectious Diseases, WIV, CAS
中国科学院武汉病毒研究所新发传染病研究中心

Key Laboratory of Special Pathogens and Biosafety, CAS
中国科学院高致病性病原生物学与生物安全重点实验室

Virologica Sinica
《中国病毒学（英）》期刊

November 26-28, 2020
Wuhan, China

Chairmen/主席

Zheng-Li SHI, Wuhan Institute of Virology, CAS

石正丽 研究员，中国科学院武汉病毒研究所

Xi ZHOU, Wuhan Institute of Virology, CAS

周溪 研究员，中国科学院武汉病毒研究所

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Contact Details:

Ms. Han ZHANG　张晗

Tel: 86-27-87197115　E-mail: zhanghan@wh.iov.cn

Dr. Ben HU　胡犇

Tel: 86-27-87197311　E-mail: huben@wh.iov.cn

Ms. Lei ZHANG　张磊

Tel: 86-27-87198536　E-mail: zhanglei@wh.iov.cn

Wuhan Institute of Virology, CAS

Xiao Hong Shan No.44, Wuhan, 430071, P.R. China

Program of
The 9th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间 (GMT +8)	Content 议程
Thursday 星期四 Nov. 26, 2020 11 月 26 日	**Venue 地点** 09:00-21:00	**Registration**/报到注册 Ground Floor, Optics Valley Kingdom Plaza Hotel/光谷金盾大酒店一楼大厅
		Day 1, Morning Session /第一天上午
	Venue 地点	Banquet Hall of Optics Valley Kingdom Plaza 3nd floor of the hotel 光谷金盾大酒店三楼宴会厅
	08:45-08:50	**Opening Address/开幕式致词** **By Zhengli Shi** Wuhan Institute of Virology, Chinese Academy of Sciences Chair of the 9th International Symposium on Emerging Viral Diseases
	08:50-09:05	**Title:** Fighting against SARS-CoV-2: Achievements by WIV **Speaker: Yanyi Wang** Director of Wuhan Institute of Virology, Chinese Academy of Sciences
	09:05-12:00	**Session 1: Antiviral treatment, vaccines and diagnosis** **Session Chair: Prof. Xi ZHOU**
Friday 星期五 Nov. 27, 2020 11 月 27 日	09:05-09:35 Keynote Speech S-01	**Title:** Drug Discovery Against COVID-19 **Speaker: Hualiang Jiang** **Academician of CAS** Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai
	09:35-10:05 Keynote Speech S-02	**Title:** Development of a highly effective pan-β-CoV_B vaccine **Speaker: Shibo Jiang (on-line presentation)** School of Basic Medical Sciences, Fudan University, Shanghai
	10:05-10:20	Group Photo of Symposium Participants/与会代表合影 Tea Break/茶歇
	10:20-10:45 S-03	**Title:** SARS-CoV-2 polymerase catalysis and remdesivir intervention **Speaker: Peng Gong** Wuhan Institute of Virology, Chinese Academy of Sciences
	10:45-11:10 S-04	**Title:** Method Development for rapid detection of emerging pathogens **Speaker: Hongping Wei** Wuhan Institute of Virology, Chinese Academy of Sciences
	11:10-11:35 S-05	**Title:** Development of neutralizing antibodies against SARS-CoV-2 **Speaker: Rui Gong** Wuhan Institute of Virology, Chinese Academy of Sciences

11:35-12:00 S-06	**Title:** Mechanisms of pathogenic RNA viruses triggered inflammatory responses and countermeasures **Speaker: Ke Peng** Wuhan Institute of Virology, Chinese Academy of Sciences
12:00-12:15 Sponsor Presentation	**Title:** Cryo EM application update and new product innovations **By Tianqing Zhang** Business Development Manager, Thermo Fisher Scientific
12:15-14:00	Lunch/午餐
Day 1, Afternoon Session /第一天下午	
14:00-17:50	**Session 2: Virus-host interaction** **Session Chair: Prof. Zhihong HU**
14:00-14:30 Keynote Speech S-07	**Title:** Adaptive immunity to COVID-19 **Speaker: Chen Dong (on-line presentation)** **Academician of CAS** Institute for Immunology and School of Medicine, Tsinghua University
14:30-14:55 S-08	**Title:** Take advantage of biosafety platforms and make contributions to the scientific combat against COVID-19 **Speaker: Zhiming Yuan** Wuhan Institute of Virology, Chinese Academy of Sciences
14:55-15:20 S-09	**Title:** Pathogenesis and Biomarkers of COVID-19 **Speaker: Xi Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
15:20-15:45 S-10	**Title:** Natural origin, global spread and genetic variation of SARS-CoV-2 **Speaker: Weifeng Shi (on-line presentation)** Shandong First Medical University and Shandong Academy of Medical Sciences
15:45-16:05	Tea Break/茶歇
16:05-16:35 **(GMT+1 9:05-9:35)** Keynote Speech S-11	**Title:** Comparative pathogenesis of SARS, MERS and COVID-19 **Speaker: Bart Haagmans (on-line presentation)** Viroscience Department, Erasmus MC, Rotterdam, the Netherlands
16:35-17:00 S-12	**Title:** Understanding virus-host interactions in the era of organoid **Speaker: Jie Zhou (on-line presentation)** Department of Microbiology, The University of Hong Kong

17:00-17:25 S-13	**Title:** Mechanism of genomic/subgenomic RNA replication and transcription of Coronaviruses **Speaker: Yu Chen** College of Life Sciences, Wuhan University
17:25-17:50 S-14	**Title:** SARS-CoV-2 cell tropism and multi-organ infection **Speaker: Manli Wang** Wuhan Institute of Virology, Chinese Academy of Sciences
18:00-20:00	Dinner/晚餐

Program of
The 9th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间 (GMT+8)	Content 议程
		Day 2. Morning Session /第二天上午
Saturday 星期六 Nov. 28, 2020 11 月 28 日	08:50-12:00	**Session 3: Pathogen biology and pathogenesis** **Session Chair: Prof. Peng ZHOU**
	08:50-09:20 **(GMT -5 19:50-20:20 27th Nov)** Keynote Speech S-15	**Title**: Interspecies transmission and global spread of emerging coronaviruses of humans and animals **Speaker**: **Linda J. Saif (on-line presentation)** Department of Veterinary Preventive Medicine, The Ohio State University, Wooster, OH, USA
	09:20-09:50 **(GMT -5 20:20-20:50 27th Nov)** Keynote Speech S-16	**Title:** Analyzing trends in global disease emergence to predict and prevent future pandemics **Speaker: Peter Daszak (on-line presentation)** Ecohealth Alliance, New York City, NY, USA
	09:50-10:20 **(GMT -6 19:50-20:20 27th Nov)** Keynote Speech S-17	**Title:** Mouse models for COVID-19 **Speaker: Stanley Perlman (on-line presentation)** Departments of Microbiology and Immunology, and Pediatrics, University of Iowa, Iowa City, IA
	10:20-10:40	Tea Break/茶歇
	10:40-11:10 **(GMT -6 20:40-21:10 27th Nov)** Keynote Speech S-18	**Title:** SARS-CoV-2 Biology and Countermeasure Development **Speaker: Pei-Yong Shi (on-line presentation)** Department of Biochemistry & Molecular Biology, University of Texas Medical Branch at Galveston, TX
	11:10-11:35 **(GMT -6 21:10-21:35 27th Nov)** S-19	**Title:** Development of Influenza A Virus Entry Inhibitors **Speaker: Lijun Rong (on-line presentation)** Department of Microbiology and Immunology, College of Medicine, University of Illinois at Chicago, IL

11:35-12:00 **(GMT -7** **20:35-21:00** **27th Nov)** S-20	**Title:** Medical countermeasure development against COVID19 in the rhesus macaques model **Speaker: Vincent J. Munster (on-line presentation)** Laboratory of Virology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, USA
12:00-14:00	Lunch/午餐
Day 2, Afternoon Session /第二天下午	
14:00-17:50	**Session 4: Pathogen biology** **Session Chair: Prof. Zhengli SHI**
14:00-14:30 Keynote Speech S-21	**Title:** Bats and viruses – in the context of COVID-19 **Speaker: Lin-Fa Wang (on-line presentation)** Programme in Emerging Infectious Diseases at Duke-NUS Medical School, Singapore
14:30-14:55 S-22	**Title:** When could we predict the emergence of the infectious diseases like weather forecast? **Speaker: Yongzhen Zhang** Shanghai Public Health Clinical Center, Fudan University, Shanghai
14:55-15:20 S-23	**Title:** Co-infection of SARS-CoV-2 and influenza virus **Speaker: Ke Xu** College of Life Sciences, Wuhan University
15:20-15:45 S-24	**Title:** Persistence of SARS-CoV-2 *in vivo* and *in vitro* **Speaker: Peng Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
15:45-16:00	Tea Break/茶歇
16:00-16:30 Keynote Speech S-25	**Title:** From SARS, 2003, to COVID-19, 2020 – Insight into SARS-CoV-2 replication and transcription machinery **Speaker: Zihe Rao** **Academician of CAS** School of Life Sciences and School of Medicine, Tsinghua University, Beijing
16:30-16:55 S-26	**Title:** SARS-CoV-2 and its transmission **Speaker: Leo Poon (on-line presentation)** School of Public Health, The University of Hong Kong
16:55-17:20 **(GMT +1** **9:55-10:20)** S-27	**Title:** Development of an RNA replicon vaccine for highly pathogenic human Coronaviruses **Speaker: Luis Enjuanes (on-line presentation)** Department of Molecular and Cell Biology. National Center of Biotechnology (CNB-CSIC), Madrid, Spain

17:20-17:45 **(GMT +1 10:20-10:45)** S-28	**Title:** SARS-CoV-2 entry into cells and its inhibition **Speaker: Stefan Pöhlmann (on-line presentation)** Infection Biology Unit, German Primate Center - Leibniz Institute for Primate Research, Göttingen, Germany
17:45-17:50	**Closing Remarks/闭幕致词** **By Xi Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences Chair of the 9th International Symposium on Emerging Viral Diseases
18:00-19:00	Dinner/晚餐

For our on-line speakers

- Please use following information to join in our meeting by Zoom:

Zoom Meeting link:

https://us02web.zoom.us/j/3120552792?pwd=552.136

552.136

Meeting Topic: 9th ISEVD Day 1 / Day 2

Meeting ID: 3120552792

Password: 552.136

- All presentations are given in English. On-line speakers are welcome to join in the meeting throughout the 2-day symposium.
- Please make sure that you have entered the zoom meeting at least 10 min before your presentation starts.

Biosketches of Speakers (In order of presentations)

报告专家简介（按照报告顺序）

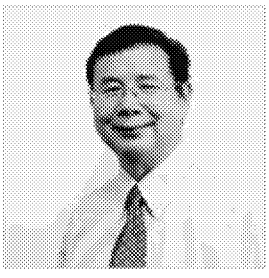
Dr. Hualiang Jiang, CAS Academician

Dr. Hualiang Jiang is a pharmaceutical scientist. He was conferred a bachelor's degree in Chemistry from the Nanjing University in 1987. He received his master's degree in Physical Chemistry (Quantum Chemistry) from East China Normal University in 1992. In 1995, he obtained his Ph.D. degree in Medicinal Chemistry from Shanghai Institute of Materia Medica (SIMM), Chinese Academy of Sciences (CAS). In 2004, he was appointed as Deputy Director of SIMM followed by his directorship from 2012 up to now. He was a chief scientist of two 973 National Basic Research Projects in drug discovery. He was a member of scientific committees of several major research programs in China, such as 863 National High Technology Program, National Basic Research Program, and Major Research Project of National Natural Science Foundation of China. He also served as Associate Editor of *Journal of Medicinal Chemistry* and editorial board members of several journals such as *The Journal of Biological Chemistry*. Over the years, Dr. Jiang has received numerous awards including the Natural Science Award of China, the 5th Prize of Yong Scientist Award of China, the Science and Technology Progress Prize from Ho Leung Ho Lee Foundation, etc. He was elected as Member of the Chinese Academy of Sciences in 2017.

Dr. Jiang's research is mainly focused on developing new computational methods for target identification and drug design and their applications in drug discovery. He has devised and developed a series of new computational methods for target identification and function predication. These methods have been widely used by big pharmaceutical companies and academic community at large. Employing the strategy of computational prediction combined with experimental validation, Dr. Jiang and his team have discovered and studied the druggable properties of a series of proteins. Targeting several diseases such as pulmonary hypertension, schizophrenia, type 2 diabetes, erectile disorder and Alzheimer's disease, Dr. Jiang and his co-workers obtained a number of drug candidates by using computational drug design, organic synthesis and drug development technologies. One compound has entered into phase II clinical trial, three are undergoing phase I clinical trial. Dr. Jiang has published more than 200 corresponding/co-corresponding author papers, 260 non-corresponding author papers, and 13 review articles in international journals and these papers have been cited more than 20,000 times. He was invited to write chapters for 4 books.

Shibo Jiang, M.D.

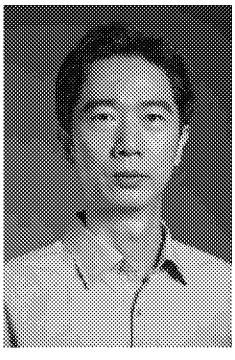
Professor, College of Basic Medical Science,
Fudan University, Shanghai, China
Email: shibojiang@fudan.edu.cn



Shibo Jiang was educated in China for getting M.S. and M.D. degrees. He received his postdoctoral training in the Rockefeller University in New York from 1987 to 1990, worked in the LFK Research Institute of the New York Blood Center as Member and Laboratory Head from 1990 to 2010, and joined Fudan University as a professor in late 2010. His major research interest is to research and develop antiviral therapeutics and vaccines against HIV, HPV, coronaviruses, and influenza viruses. So far, he has published 490 peer-reviewed papers, which have been cited 24,322 times, with an h-index of 82 (Google Scholar). He has obtained 25 US patents and 16 Chinese and PCT patents, 11 of which have been licensed out. Since the beginning of 2020, he has published 50 peer-reviewed papers in *The Lancet*, *Science* (x2), *Nature, Nat Rev Microbiol, Sci Transl Med.,* etc., making contribution in studying coronavirus fusion and entry mechanism and developing broad-spectrum anti-coronavirus therapeutic and vaccine candidates.

Prof. Peng GONG

Wuhan Institute of Virology, Center for Biosafety Mega-Science, Chinese Academy of Sciences, faculty member



B.S. 1998/M.S. 2001, Tsinghua University
PhD 2006, University of Massachusetts Amherst
Postdoctoral research associate, 2006-2007, University of Massachusetts Amherst
Postdoctoral research fellow/research scientist, 2007-2011, Colorado State University

Principal research interests:

Catalysis and regulation of viral RNA-dependent RNA polymerases (RdRPs); Intervention mechanisms of nucleotide analog targeting viral RdRPs.

Representative publications:

1. Structural basis for RNA replication by the SARS-CoV-2 polymerase. Wang et al., ***Cell*** 2020, 182(2):417-28.

2. Stringent control of the RNA-dependent RNA polymerase translocation revealed by multiple intermediate structures. Wang et al., ***Nat Commun*** 2020, 11:2605.

3. A conformation-based intra-molecular initiation factor identified in the flavivirus RNA-dependent RNA polymerase. Wu et al., ***PLoS Pathog*** 2020, 16(5):e1008484.

4. A unique intra-molecular fidelity-modulating mechanism identified in a viral RNA-dependent RNA polymerase. Liu et al., ***Nucleic Acids Res*** 2018, 46(20):10840-54.

5. Structural basis of viral RNA-dependent RNA polymerase catalysis and translocation. Shu and Gong, ***Proc Natl Acad Sci USA*** 2016, 113(28):E4005-4014.

6. Crystal structure of the full-length Japanese encephalitis virus NS5 reveals a conserved methyltransferase-polymerase interface. Lu and Gong, ***PLoS Pathog*** 2013, 9(8):e1003549.

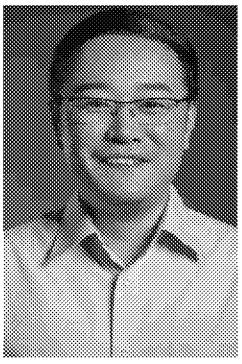
Hongping Wei, Dr., Professor

Principle Investigator of Diagnostic Microbiology
Director of African Swine Fever Regional Laboratory of China (Wuhan)
Vice-Director of Center for Emerging Infectious Diseases,
Wuhan Institute of Virology, Chinese Academy of Sciences
Email: hpwei@wh.iov.cn

Prof Wei's main research interests are developing rapid methods for infectious pathogens and bacteriophage therapy. His group has developed RT-PCR kits for viruses, such as SARS-CoV-2 and African Swine fever virus and rapid drug susceptibility tests for bacteria such as *Mycobacterium Tuberculosis*. In order to find new treatments for drug-resistant bacteria, his group has found a few highly active lysins from bacteriophages. Prof Wei has published about 40 research papers and commercialized a few products such as RT-PCR kit for detection of SARS-CoV-2 by cooperation with companies.

Rui Gong

Professor, Head of Antibody Engineering Group
Wuhan Institute of Virology, Chinese Academy of Sciences
No.44 Xiao Hong Shan, Wuhan, Hubei 430071, P. R. China
Tel: +86-27-87199331, +86-27-87806108
Fax: +86-27-87806108
E-mail: gongr@wh.iov.cn



Education:

9/2002 – 6/2007 Ph.D. (Microbiology), College of Life Sciences, Wuhan University, China
9/1998 – 6/2002 B.S. (Biomedicine), College of Life Sciences, Wuhan University, China

Brief Chronology of Employment:

9/2012 – Date Professor, Head of Antibody Engineering Group
9/2007 – 8/2012 Postdoctoral Fellow, National Cancer Institute (NCI), National Institute of Health (NIH), Frederick, MD, USA

Honors & Other Special Scientific Recognition:

1. Rui Gong, Federal Technology Transfer Award, NCI, NIH, USA, 2011.
2. Rui Gong, Federal Technology Transfer Award, NCI, NIH, USA, 2012.

Biography

Rui Gong, Ph.D., Head of Antibody Engineering Group, Professor, Ph.D. Supervisor. Dr. Gong graduated from Wuhan University in 2002 and received his Ph.D. also in Wuhan University in 2007. He went to National Cancer Institute, National Institute of Health, USA in 2007 for his training as a postdoctoral fellow, and joined Wuhan Institute of Virology, Chinese Academy of Sciences and established Antibody Engineering Group for antibody engineering-related research in 2012. Dr. Gong won Federal Technology Transfer Award (NIH, USA) in 2011 and 2012. He has more than thirty publications and several patents. He is hosting or hosted the grants of the Strategic Priority, Research Program of the Chinese Academy of Sciences, Young Scientist Subject of the National High Technology Research and Development Program of China (863 Project), and National Natural Science Foundation of China, etc.

Research Interests:

The long-term goal is to develop therapeutic antibodies and vaccines against virus. Our work includes selection of full-length antibodies and antibody fragments against important and emerging viruses by phage display, yeast display, and other high throughput screening technologies; identification of the epitopes for vaccine design; development of novel C-based single domain antibodies (C-sdAbs) based on scaffolds derived from antibody constant CH2 domains in antibody Fc fragments; and improvement of biological activities of Fc fragments. We try to elucidate the basic questions in virology, and solve several difficulties for improvement of efficacy of therapeutic antibodies and vaccines.

Publications

*corresponding author

1. Cao G, Gao X, Zhan Y, Wang Q, Zhang Z, Dimitrov DS, **Gong R***. An engineered human IgG1 CH2 domain with decreased aggregation and nonspecific binding. **MAbs.** 2020, 12(1):1689027.

2. Li M, Chen L, Wang Q, Hao M, Zhang X, Liu L, Yu X, Yang C, Xu J*, Chen J*, **Gong R***. A cross-reactive human monoclonal antibody targets the conserved H7 antigenic site A from fifth wave H7N9-infected humans. **Antiviral Res.** 2019, 170:104556.

3. Gao X, Conard A, Yang C, Zhan Y, Zeng F, Shi J, Li W, Dimitrov DS, **Gong R***. Optimization of the C-Terminus of an Autonomous Human IgG1 CH2 Domain for Stability and Aggregation Resistance. **Mol Pharm.** 2019, 16(8):3647-3656.

4. Yang C, Zeng F, Gao X, Zhao S, Li X, Liu S, Li N, Deng C, Zhang B, **Gong R***. Characterization of two engineered dimeric Zika virus envelope proteins as immunogens for neutralizing antibody selection and vaccine design. **J Biol Chem.** 2019, 294(27):10638-10648.

5. Yang C, **Gong R***, de Val N*. Development of Neutralizing Antibodies against Zika Virus Based on Its Envelope Protein Structure. **Virol Sin.** 2019, 34(2): 168-174.

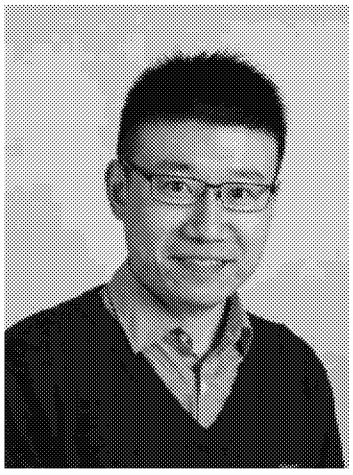
6. Zeng F, Yang C, Gao X, Li X, Zhang Z, **Gong R***. Comprehensive elucidation of the structural and functional roles of engineered disulfide bonds in antibody Fc fragment. **J Biol Chem.** 2018, 293(49):19127-19135.

7. Yang C, Gao X, **Gong R***. Engineering of Fc Fragments with Optimized Physicochemical Properties Implying Improvement of Clinical Potentials for Fc-Based Therapeutics. **Front Immunol.** 2018, 8:1860.

8. Sun Y, Zhang H, Shi J, Zhang Z, **Gong R***. Identification of a Novel Inhibitor against Middle East Respiratory Syndrome Coronavirus. **Viruses.** 2017, 9(9).

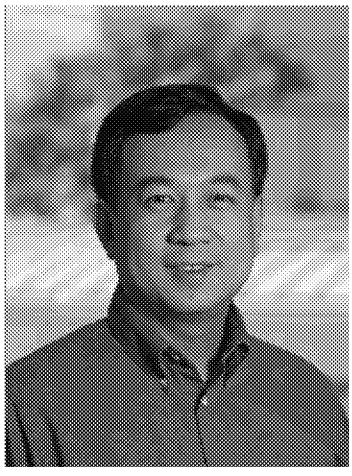
9. Chen X, Zeng F, Huang T, Cheng L, **Liu H***, **Gong R***. Optimization on Fc for Improvement of Stability and Aggregation Resistance. **Curr Pharm Biotechnol.** 2016, 17(15):1353-1359.

10. **Gong R***. Editorial (Thematic Issue: Fc-related Antibody Engineering). **Curr Pharm Biotechnol.** 2016, 17(15):1296-1297.



Prof. Dr. Ke Peng, principle investigator of the State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences. Ke Peng received his PhD training through the Chinese Academy of Sciences and the Dutch Royal Academy of Sciences joint-PhD program in the Wuhan Institute of Virology and Wageningen University in the Netherlands, after which he did post-doctoral research in the field of HIV-1 replication and pathogenesis in the Medical School of Heidelberg University in Germany. Since 2016.10 he set up the research group of Virus-Host Interactions to study the pathogenesis mechanisms of pathogenic RNA viruses including bunyavirus, SARS-CoV-2 and HIV-1. The recent research progresses in his group focused on: 1) pathogenesis and inflammatory mechanisms of bunyavirus infection and antiviral drug development (*Cell Research* **2019**, *Cell Reports* **2020**, *Cell Discovery* **2020**, *ACS Infectious Diseases* **2020**); 2) mechanisms of SARS-CoV-2 triggered inflammatory responses (*Signal Transduction Targeted Therapy* **2020**); and 3) mechanisms of HIV-1 nuclear entry and integration (*eLife* **2019**). The mechanisms of RNA virus triggered inflammatory responses and anti-viral drug development would be the two long-term pursued research topics in his group.

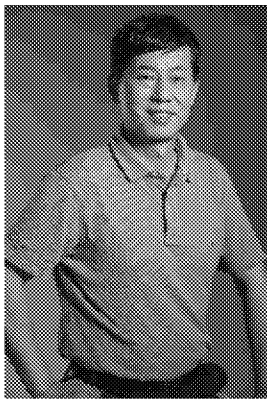
Chen Dong, Ph.D, CAS Academician



Dr. Dong is Professor and Director of the Institute for Immunology at Tsinghua University, Beijing, China. He is a member of the Chinese Academy of Sciences. Dr. Dong was Dean of the School of Medicine at Tsinghua University, he also served as a Professor of Immunology and the Director of the Center for inflammation and Cancer at the University of Texas MD Anderson Cancer Center before his move to Tsinghua University. Dr. Dong's research is to understand the molecular mechanisms whereby immune and inflammatory responses are normally regulated, and to apply this knowledge to the understanding and treatment of autoimmunity and allergy disorders as well as cancer. The work from Dr. Dong's group has led to the discoveries of Th17 and T follicular helper (Tfh) cell subsets in the immune system and elucidation of their biological and pathological functions. Dr. Dong has over 200 publications and was rated highly cited researcher for six years from 2014 to 2019. The honors he has received include the 2009 American Association of Immunologists-BD Bioscience Investigator Award and 2019 International Cytokine and Interferon Society Biolegend-William E. Paul Award. He is a fellow of the American Association for the advancement of Science and a member of the Chinese Academy of Sciences. He is currently an Editor for Immunity, Editor-in-chief for Frontiers in Immunology- T Cell Biology and Associate Editor for China Sciences- Life Sciences.

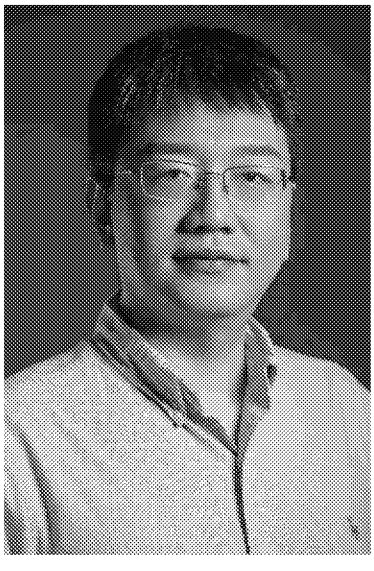
Zhiming Yuan

Ph.D., Principle Investigator
Wuhan Institute of Virology, CAS



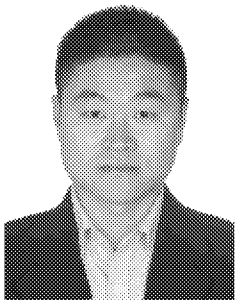
Yuan Zhiming got his PhD on microbiology and biotechnology at Sun Yat-sen University, and then trained and worked in France, Denmark, and United States for several years. He has been working as a Professor in Wuhan Institute of Virology, the President of Wuhan Branch, Chinese Academy of Sciences since year 2000. As a principal investigator, his research group works on the diagnosis and drug discovery of aborviruses, genomics, insecticidal proteins and their mode of action, genetically modification of entomopathogenic bacteria (Bacillus spp), as well as the production, standardization and application of bio-pesticide and other microbial agents. Since 2003, he was appointed the Chairman of Institutional Biosafety Committee, member of National Laboratory Biosafety Committee, advisor of different national technical committees on biosafety management, general manager of National High-Level Biosafety Laboratory in Wuhan. He also works as a group leader on Sino-French biosafety legislation cooperation. In addition, he was elected as President of Hubei Society for Microbiology in 2008. Along providing expertise and consultative services to both private companies and government institutions on matters of biotechnology and biosafety, he has given many lectures to national and international audiences. He published more than 150 scientific papers on Bacillus spp and aborviruses during his career.

Dr. Xi Zhou



Dr. Xi Zhou got his Ph.D. degree and postdoctoral training in the University of Texas GSBS at Houston, and the University of Texas, M.D. Anderson Cancer Center. He is currently a professor and the deputy director of State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences (CAS). Before this current position, Dr. Zhou was the Luojia Distinguished Professor and Deputy Chair, Dept. of Virology, Wuhan University, China. Dr. Zhou's research interest is focused on RNA viruses, antiviral immunity and antiviral therapy. His group uses important human and vector-borne pathogenic RNA viruses (such as coronavirus, enterovirus, flavivirus, etc.) to study many aspects of RNA virology and immunology. Since the outbreak of COVID-19, his group is also working on the virus-host interactions and pathogenesis of SARS-CoV-2 and COVID-19. After establishing his own group in 2011, he has authored more than 50 papers in peer reviewed journals, including Immunity, Cell Host Microbe, Cell Research, National Science Review, Science Advances, eLife, PLOS Pathogens, Nucleic Acids Res., Cell Mol Immunol., J. Virol. etc., as corresponding author. Dr. Zhou is the recipient of the National Excellent Young Scientist Fund of China, the Young Scientist Fund of National High-Tech R&D (863) Project of China, and the Newton Advanced Fellowship of the Royal Society/Academy of Medical Sciences (UK), and the Christopher Mérieux Award for Young Virologist of Chinese Society for Virology and Mérieux Institut. He is currently serving as the Vice President of Hubei Society for Microbiology, and the Vice President of Wuhan Society for Microbiology, and editorial member of Viruses and Virological Sinica.

Weifeng Shi



PhD in Bioinformatics and Professor in Basic Medicine

Research interests: i. Origin, transmission and evolution of emerging virus diseases; ii. Molecular epidemiology and pathogenic mechanisms of human enteroviruses; iii. Virome and novel virus discovery

Honors:

1. 2020 "Chang Jiang Scholars program" – Special Position for SARS-CoV-2
2. 2019 "Chang Jiang Scholars program" – Young Scholars
3. 2019 Natural Science Prize of Shandong Province (Second class)
4. 2018 Young Scientist Prize of Shandong Province
5. 2015 Taishan Scholars program of Shandong Province

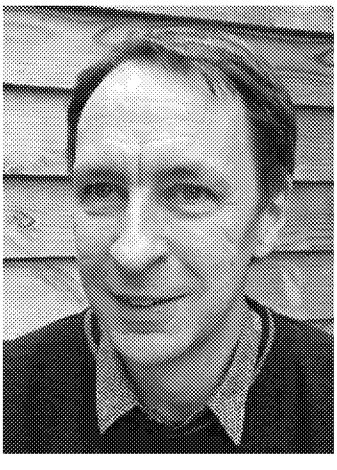
Academic achievements:

As of November 2020, I have published >120 publications in peer-reviewed journals, including Lancet, Nature, Nature Reviews Microbiology, Nature Communications, Cell Host & Microbe, and Current Biology, with a total of > 15000 citations.

Selected publications on SARS-CoV-2:

1. Roujian Lu#, Xiang Zhao#, Juan Li#, Peihua Niu#, Bo Yang#, Honglong Wu#, Wenling Wang, Hao Song, Baoying Huang, Na Zhu, Yuhai Bi, Xuejun Ma, Faxian Zhan, Liang Wang, Tao Hu, Hong Zhou, Zhenhong Hu, Weimin Zhou, Li Zhao, Jing Chen, Yao Meng, Ji Wang, Yang Lin, Jianying Yuan, Zhihao Xie, Jinmin Ma, William J. Liu, Dayan Wang, Wenbo Xu, Edward C. Holmes, George F. Gao, Guizhen Wu*, Weijun Chen*, **Weifeng Shi***, Wenjie Tan*. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. ***Lancet***, 2020, 395(10224): 565-574.
2. Hong Zhou#, Xing Chen#, Tao Hu#, Juan Li#, Hao Song, Yanran Liu, Peihan Wang, Di Liu, Jing Yang, Edward C. Holmes, Alice C. Hughes*, Yuhai Bi*, **Weifeng Shi***. A novel bat coronavirus closely related to SARS-CoV-2 contains natural insertions at the S1/S2 cleavage site of the spike protein. ***Curr Biol***, 2020, 30: 2196-2203.
3. Jing Yang#, Juan Li#, Shengjie Lai#*, Corrine W. Ruktanonchai, Weijia Xing, Alessandra Carioli, Peihan Wang, Nick W. Ruktanonchai, Ruiyun Li, Jessica R. Floyd, Liang Wang, Yuhai Bi*, **Weifeng Shi***, Andrew J. Tatem. Uncovering intercontinental COVID-19 transmission dynamics using global travel network and phylogenetic analyses. ***Journal of Travel Medicine***, in press.
4. Na Zhu#, Dingyu Zhang#, Wenling Wang#, Xinwang Li#, Bo Yang#, Jingdong Song, Xiang Zhao, Baoying Huang, **Weifeng Shi**, Roujian Lu, PeihuaNiu, Faxian Zhan, Xuejun Ma, Dayan Wang, Wenbo Xu, Guizhen Wu*, George F. Gao*, Wenjie Tan*. A Novel Coronavirus from Patients with Pneumonia in China, 2019. ***N Engl J Med***, 2020, 382(8): 727-733.

Prof. Bart Haagmans



Bart Haagmans is a workgroup leader at the department of Viroscience of the Erasmus Medical Center in Rotterdam. He did his training at the Utrecht University and holds a PhD from the same university. His main interest is the pathogenesis of emerging viral infections including SARS and MERS coronavirus. Receptor usage and zoonotic transmission are studied with the aim to further understand the biology of coronaviruses and to develop candidate vaccines.

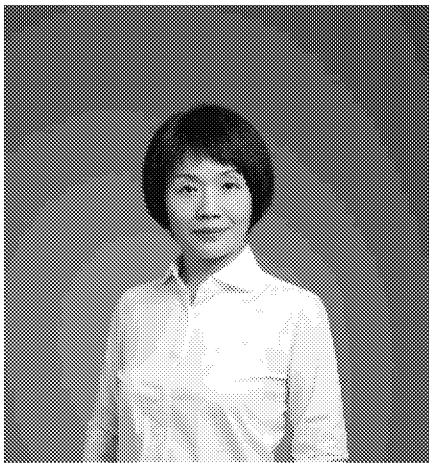
Understanding virus-host interactions in the era of organoid

Department of Microbiology, The University of Hong Kong, Hong Kong, China

Recent advances in stem cell biology allow the *in vitro* growth of 3-dimensional organoids that recapitulate essential attributes of their counterpart-organs *in vivo*. Organoids can be grown from pluripotent stem cells or tissue-resident adult stem cells (ASC). ASC-derived organoids consist exclusively of epithelial cells and can be generated from a variety of human organs. Our study published in 2018 has ushered in a brand-new long-term expandable culture model of human respiratory epithelium to the world, the human airway organoids. These human airway organoids can faithfully simulate the multicellular complexity and functionality of human airway epithelium to a near-physiological level. We demonstrated that these human airway organoids can predict the infectivity of emerging influenza viruses, which has been a long-standing challenge for influenza research and public health worldwide. Leveraging human intestinal organoids, we reported that human intestinal tract is an alternative route to acquire MERS-CoV infection (Science Advances, 2017).

In the early outbreak of COVID-19, we tested the infectivity of SARS-CoV-2 in human intestinal organoids since some COVID-19 patients developed gastrointestinal symptoms. We demonstrate robust replication of SARS-CoV-2 in both large and small intestinal organoids, suggesting enteric infection in COVID-19 patients (Nature Medicine 2020). The human lung organoids and intestinal organoids in our lab have become powerful and versatile technical platforms, which can be applied to various applications including assessing pathogenicity of human pathogens, understanding pathogenesis, and evaluating therapeutic efficacy.

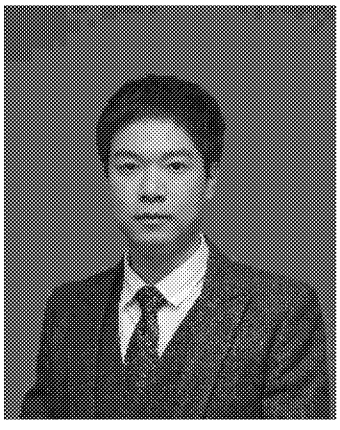
In addition, we established bat intestinal organoids which can simulate the native intestinal epithelium of bats. The intestinal organoids derived from Chinese horseshoe bat are highly susceptible to SARS-CoV-2 and sustain active viral replication, implicating that bat intestinal cells may support the natural infection by SARS-CoV-2 and its progenitor(s). Importantly, these bat intestinal organoids open up a new avenue for isolating and cultivating other bat viruses, which has been a long-standing challenge for studying numerous bat viruses of high zoonotic potential.



Jie Zhou, PhD

Biography

Dr. Jie Zhou graduated from Xi'An Medical University and served as a clinical pathologist in the affiliated hospitals in Peking University. She started her PhD training of Virology in The University of Hong Kong in 2003. After her postdoctoral training in UC San Francisco, she moved back to HKU. Now she is an assistant professor in HKU Microbiology. Her research interests are virus-host interaction and pathogenesis of human viral infections. In the past few years, her team have been working on establishing human organoids for virus research.



陈 宇

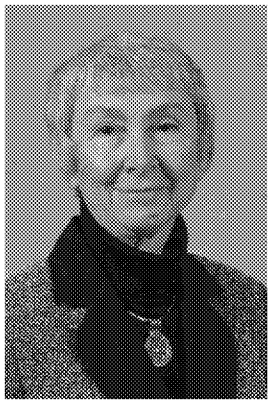
武汉大学病毒学国家重点实验室

chenyu@whu.edu.cn

陈宇，博士，教授，武汉大学病毒学国家重点实验室 PI，生命科学学院病毒系副主任，长江学者奖励计划特岗教授，中央高校拔尖创新人才，湖北省自然科学基金杰出青年基金获得者；2009 年毕业于武汉大学生命科学学院病毒学专业，获博士学位；赫尔辛基大学访问学者。从事冠状病毒复制与致病机制及病毒防治研究，承担、参与国家自然科学基金重大项目、科技部“973”、“十二五”、“十三五”传染病重大专项、科技部病毒与免疫创新团队等项目。解析了 SARS 冠状病毒 RNA 甲基转移酶、主蛋白酶、N 蛋白等的功能、结构及其作用机制，开发了 4 种靶向抗冠状病毒抑制剂；系统研究了 SARS 及新冠病毒亚基因组复制转录机制，解析新冠病毒亚基因组新特性，发现其不连续转录复制新机制；合作完成了新冠病毒病原鉴定；鉴定了气溶胶新冠病毒载量及传播特性；发展了高灵敏度的新冠病毒核酸检测方法；发表了新冠患者 BALF 和 PBMC 转录组数据。在 *Nature, Nature Immunology, PNAS, PLoS Pathog, Emerg Microbe Infect, J Virol* 等期刊发表论文 30 余篇，引用 1700 余次，申请发明专利 10 项，实现成果转化 1 项。

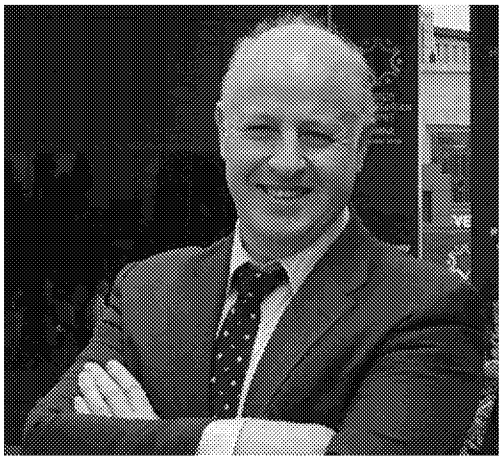
Prof. Manli Wang got her doctoral degree from Wuhan Institute of Virology, CAS in 2009 and has been working there since then. She has been focusing on the mechanism of virus entry and antiviral research by taking several important viruses as models. A serials of important scientific findings have been achieved, including **(1)** Thoroughly disclosed the evelope fusion protein-mediated baculovirus entry mechanism, revealed the roadblocks to mammalian cell entry of baculovirus, thus providing new strategies for improving baculovirus-based gene delivery and therapy. **(2)** Disclosed the multistep entry process and the dynamic virus-host interactions of the severe fever with thrombocytopenia syndrome virus (SFTSV) by using single-particle trafficking and quantitative proteomic technologies, providing potential targets for SFTS prevention and control. **(3)** Recently, she focuses on drug screening and virus pathogenesis of SARS-CoV-2. Her team reported several drugs, including remdesivir (GS-5734), chloroquine (CQ), hydroxychloroquine (HCQ) and arbidol, could efficiently inhibit SARS-CoV-2 infection *in vitro*. In addition, her team systematically analyzed the organotropism and cell tropism of SARS-CoV-2 by using human and animal samples. Dr. Wang has published 40 (co-)first/(co-)corresponding authored papers in SCI journals, including Cell Res (1), Small (1), Small Methods (1), Cell Discovery (3), Journal of Virology (10), et al. Her PhD thesis has won "Top 50 Excellent PhD Thesis Award of Chinese Academy of Sciences" (year 2010).

Linda J. Saif



Dr. Linda Saif is a Distinguished University Professor at The Ohio State University (OSU) in the Food Animal Health Research Program (College of Food, Agriculture and Environmental Sciences) and the Veterinary Preventive Medicine Department (College of Veterinary Medicine). She is Co-Director of the Viruses and Emerging Pathogens Program of the OSU Infectious Diseases Institute. She is a virologist and mucosal immunologist, whose coronavirus research spans 4 decades, focusing on pathogenesis, immunity and vaccines for animal coronaviruses. Her team's discovery of the gut-mammary secretory IgA axis (initial description of a common mucosal immune system) in swine was a breakthrough for development of maternal coronavirus vaccines to passively protect neonatal animals. Her lab also investigates the interrelationships among animal coronaviruses, and their human counterparts to assess their zoonotic potential and mechanisms of interspecies transmission. Besides research on enteric viruses (rotaviruses noroviruses), her lab investigates the impacts of probiotics and the gut microbiota on the neonatal immune system and vaccines. Dr. Saif worked with WHO and CDC during the Severe Acute Respiratory Syndrome (SARS) outbreak and with the Ministry of Agriculture in Saudi Arabia on the Middle East Respiratory Syndrome (MERS) coronavirus in camels. Her laboratory is a WHO International Reference Lab for Animal coronaviruses in the SARS/BEI network and was an International Reference Lab for TGEV porcine coronavirus for the Office International des Epizooties (OIE), Paris, France. She is a member of the U.S. National Academy of Sciences and the National Academy of Inventors. She is an elected Fellow of the American College of Veterinary Microbiologists, the AAAS, and the American Academy of Microbiology. In 2015, she was the first woman to receive the Wolf Prize in Agriculture. She has authored or coauthored over 390 journal publications and 77 book chapters.

Dr. Peter Daszak, Ph.D



Dr. Peter Daszak is President of EcoHealth Alliance, a US-based organization that conducts research and outreach on global health and conservation. Dr. Daszak's research is focused on the origins and impact of emerging diseases, and includes identifying the bat origin of SARS-CoV, the drivers of Nipah virus emergence, publishing the first global emerging disease 'hotspots' map, discovering SADS coronavirus, launching the Global Virome Project, identifying the first case of a disease causing species extinction, and discovering chytridiomycosis as the cause global amphibian declines. Dr. Daszak is a member of the National Academy of Medicine, Chair of the NASEM's Forum on Microbial Threats, a member of the NRC Advisory Committee to the US Global Change Research Program, and a member of the NASEM Standing Committee on Emerging Infectious Diseases and 21st Century Health Threats that advises HHS ASPR and the US White House COVID Taskforce. He serves on the Supervisory Board of the One Health Platform, the One Health Commission Council of Advisors, *The Lancet* One Health Commission, *The Lancet* COVID-19 Commission, the Future Earth Health KAN Steering Committee, the CEEZAD External Advisory Board, and is a member of the Cosmos Club. He has served on the IOM Committee on global surveillance for emerging zoonoses, the NRC committee on the future of veterinary research, the International Standing Advisory Board of the Australian Biosecurity CRC; and has advised the Director for Medical Preparedness Policy in the White House National Security Staff, and is a member of the WHO R&D Blueprint program for pathogen prioritization. Dr. Daszak won the 2000 CSIRO medal for collaborative research on the discovery of amphibian chytridiomycosis, and is Editor-in-Chief of the journal *Ecohealth*. He has authored over 300 scientific papers, is a Web of Science *Highly Cited Researcher* for 2018 & 2019, and his work has been the focus of extensive media coverage.

Dr. Stanley Perlman

The University of Iowa
Professor of Microbiology and Immunology, and of Pediatrics
USA

Dr. Perlman received his Ph.D. in Biophysics from M.I.T., Cambridge, Massachusetts and his M.D. from the University of Miami, Miami, Florida. He was trained in Pediatrics and Pediatric Infectious Diseases at Boston Children's Hospital, Boston, Massachusetts. His current research efforts are focused on coronavirus pathogenesis, including virus-induced demyelination and the Severe Acute Respiratory Syndrome (SARS), the Middle East Respiratory Syndrome (MERS) and COVID-19.

His laboratory has developed several novel animal models useful for studying pathogenesis and evaluating vaccines and anti-viral therapies. His studies are directed at understanding why aged patients and mice developed more severe disease than younger individuals after infection with SARS-CoV or SARS-CoV-2 and also on why there is a male predominance in patients with more severe disease after infection with SARS-CoV, MERS-CoV or SARS-CoV-2. He and his colleagues demonstrated that transduction of mice with an adenovirus expressing the human receptor for MERS-CoV, DPP4, rendered them sensitive to infection, providing the first rodent model useful for studying MERS. Similar approaches have been used to develop a mouse model for COVID-19. He has also developed models for the loss of sense of smell (anosmia) observed in patients with COVID-19.

Pei-Yong Shi, Ph.D.

John Sealy Distinguished Chair in Innovations in Molecular Biology
University of Texas Medical Branch at Galveston, Texas, USA

Pei-Yong Shi is John Sealy Distinguished Chair in Innovations in Molecular Biology at University of Texas Medical Branch and Fellow of American Academy of Microbiology. He works on RNA virus replication, antiviral drug discovery, and vaccine research. His unique expertise in public health laboratory (Wadsworth Center, New York State Department of Health; 8 years), pharmaceutical companies (Novartis and Bristol-Myers Squibb; total 10 years), and academia (University of Texas Medical Branch, Yale, and other universities; total 11 years) allows him to work on both basic and translational research. He has published over 300 peer-reviewed papers in leading journals, including *Nature*, *Science*, *Cell*, and *Nature Medicine*. His work has generated bodies of knowledge that has significantly advanced the fields of RNA viral replication, diagnostics, drug discovery, and vaccine development. His group developed the first reverse genetic systems for the epidemic West Nile virus and Zika virus, and discovered flavivirus N7 and 2'O methyltransferase activities. In response to the recent COVID pandemic, his team published the first peer-reviewed infectious clone and reporter virus for SARS-CoV-2; these reagents have been shared around world to fight the COVID pandemic. Besides academic excellence, he also has a stellar track record of senior leadership role at major pharmaceutical companies (*e.g.*, Executive Director at Novartis Institute for Tropical Diseases) where he set up antiviral strategies and executed drug discovery and development. He contributed to the development of Fostemsavir, an FDA-approved HIV drug. Many of his technologies have been licensed to leading pharmaceutical companies for diagnostic and countermeasure development. A recent example is his reporter neutralization assay that has enabled the rapid development of Pfizer's COVID-19 vaccine, the first vaccine with >90% efficacy in humans.

Dr. Lijun Rong

Professor of Microbiology and Immunology
Director of High-Throughput Screening Facility
University of Illinois, Chicago

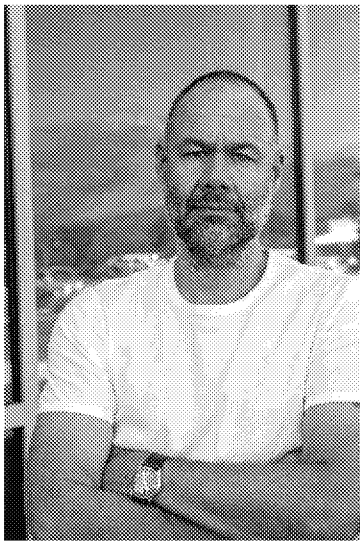
Positions and Employment

1998-2004	Assistant Professor, Dept. of Microbiology & Immunology, School of Medicine, University of Illinois, Chicago, Illinois.
2004-2015	Associate Professor, Dept. of Microbiology & Immunology, School of Medicine, University of Illinois, Chicago, Illinois.
2015-	Professor, Dept. of Microbiology & Immunology, School of Medicine, University of Illinois, Chicago, Illinois.
2010-	Director of High-throughput Screening Facility. University of Illinois, Chicago, Illinois
2019-	Visiting Professor of Shandong University of Chinese Traditional Medicine, Jinan, Shandong, China
2019-	Visiting Professor of Institute of Pathogen Biology, Chinese Academy of Medical Sciences and &Peking Union Medical College, Beijing, China

Selected publications on antiviral drug discovery in 2020

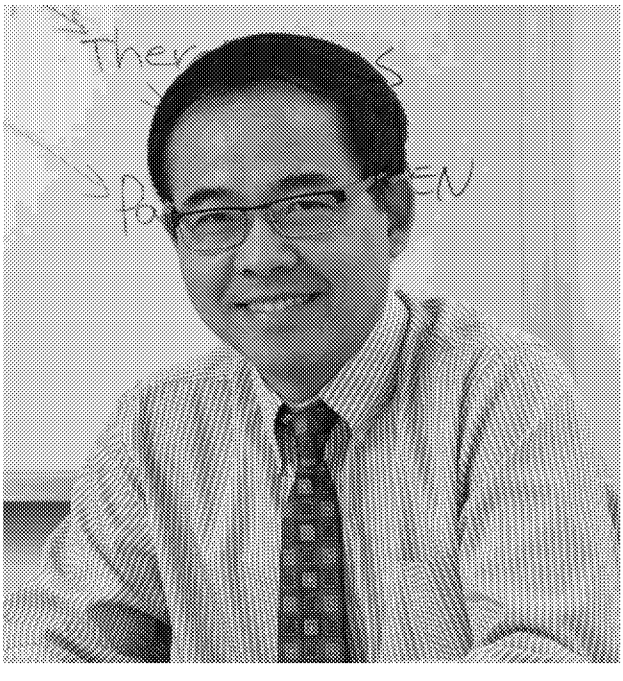
1. Cooper L, Schafer A, Li Y, Cheng H, Medegan Fagla B, Shen Z, Nowar R, Dye K, Anantpadma M, Davey RA, Thatcher GRJ, **Rong L**, Xiong R. Screening and Reverse-Engineering of Estrogen Receptor Ligands as Potent Pan-Filovirus Inhibitors. J Med Chem. 2020 Sep 22;. doi: 10.1021/acs.jmedchem.0c01001. [Epub ahead of print] PubMed PMID: 32886512. (**Cover**)
2. Gaisina IN, Peet NP, Wong L, Schafer AM, Cheng H, Anantpadma M, Davey RA, Thatcher GRJ, **Rong L**. Discovery and Structural Optimization of 4-(Aminomethyl)benzamides as Potent Entry Inhibitors of Ebola and Marburg Virus Infections. J Med Chem. 2020 Jul 9;63(13):7211-7225. doi: 10.1021/acs.jmedchem.0c00463. Epub 2020 Jun 17. PubMed PMID: 32490678.
3. Gao Y, Cheng H, Khan S, Xiao G, **Rong L**, Bai C. Development of coumarine derivatives as potent anti-filovirus entry inhibitors targeting viral glycoprotein. Eur J Med Chem. 2020 Oct 15;204:112595. doi: 10.1016/j.ejmech.2020.112595. Epub 2020 Jul 12. PubMed PMID: 32707357; PubMed Central PMCID: PMC7529935
4. Gaisina IN, Peet NP, Cheng H, Li P, Du R, Cui Q, Furlong K, Manicassamy B, Caffrey M, Thatcher GRJ, **Rong L**. Optimization of 4-Aminopiperidines as Inhibitors of Influenza A Viral Entry That Are Synergistic with Oseltamivir. J Med Chem. 2020 Mar 26;63(6):3120-3130. doi: 10.1021/acs.jmedchem.9b01900. Epub 2020 Mar 2. PubMed PMID: 32069052.

Dr. Vincent Munster



Dr. Vincent Munster is the chief of the Virus Ecology Section at NIAIDs Rocky Mountain Laboratories. He received his Ph.D. in virology from Erasmus University, Rotterdam, the Netherlands, in 2006. During his Ph.D. studies, Dr. Munster studied the ecology, evolution, and pathogenesis of avian influenza viruses. He continued his training at the Erasmus Medical Center from 2006 to 2009, where he worked within the Center for Research on Influenza Pathogenesis and Surveillance (CRIPS) focusing on pathogenicity and human-to-human transmission of influenza A viruses. Dr. Munster joined the NIAIDs Laboratory of Virology as a visiting fellow in 2009 to study the ecology of emerging viruses such as Ebola virus. In 2013, Dr. Munster established the Virus Ecology Unit as an independent tenure-track investigator. His lab is working to elucidate the ecology of emerging viruses and drivers of zoonotic and cross-species transmission. The lab uses a combined field and experimental research approach and conducts research at the state-of-the-art high- and maximum-containment facilities of the Rocky Mountain Laboratories, as well as at field study sites in Africa (the Republic of the Congo, Mali, Ghana, Liberia) and the Middle East (Jordan). Dr. Munster has been actively involved in the response to MERS-CoV, Ebola virus and COVID19 outbreaks. With the current COVID19 pandemic he is actively involved in the development of medical countermeasures and providing critical experimental data supporting direct public health decisions and interventions.

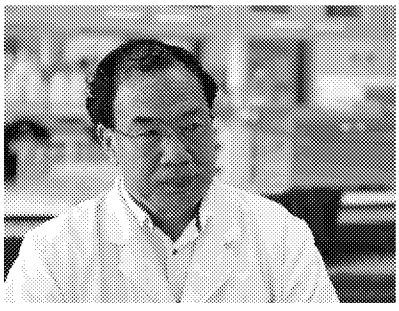
Prof Linfa Wang



Prof Linfa Wang is a professor in the Programme in Emerging Infectious Diseases at Duke-NUS Medical School, Singapore. He is an international leader in the field of emerging zoonotic viruses and virus-host interaction. His current research focuses on why bats are such an important reservoir for emerging viruses and on how we can learn from bats to make us more resilience to infection and diseases in general. He is a member of the WHO SARS Scientific Research Advisory Committee and played a key role in identification of bats as the natural host of SARS-like viruses. Currently, he is serving on multiple WHO committees for COVID-19, including the WHO IHR Emergency Committee. Prof Wang has more than 400 scientific publications, including papers in *Science*, *Nature and Lancet*. He is currently the Editor-in-Chief for the open access Virology Journal. In 2010, Prof Wang was elected to the Australian Academy of Technological Sciences and Engineering.

Yong-Zhen Zhang

Shanghai Public Health Clinic Center & School of Life Sciences, Fudan University, Shanghai



Since the end of 1998 when Zhang finished his PhD course at Kunming Institute of Zoology of the Chinese Academy of Sciences, he had been worked at National Institute for Communicable Disease Control and Prevention of China CDC in Beijing, and have moved to Shanghai in this year. He performed the epidemiologic research and the control and prevention of rabies and hemorrhagic fever with renal syndrome before 2012. Subsequently, he focused on the virus diversity, evolution, ecology, and transmission, as well as the etiologic agents and clinic features of the infectious disease that could not be diagnosed clinically based on a surveillance network including local CDC and hospitals in China.

Ke XU, Ph.D.

Professor
State Key Laboratory of Virology
College of Life Sciences
Wuhan University

Dr. Xu graduated from Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences as Ph.D. in the year 2009, major in Biochemistry and Biomedicine. She was the investigator in Institut Pasteur of Shanghai, Chinese Academy of Sciences 2009-2018. Since 2019, she is a professor in the State Key Laboratory of Virology of Wuhan University. Dr. Xu mainly works on the molecular mechanisms underlying viral-host interplay and identifying drug targets for emerging and re-emerging viruses, such as SARS-CoV and influenza A virus. She reported that NS1 and NP proteins of influenza A viruses are sumoylated which is essential for virus survival to antagonize IFN response (***Journal of Virology 2011***; ***Journal of Virology 2014***). She discovered that epigenetic modifications on influenza A virus NP protein play an important role in RNA virus replication (***Nature Communications 2017; PLoS Pathogens 2017***). She also developed site-targeted antivirals against emerging viruses and identified host DHODH enzyme as an efficient drug target for SARS-CoV-2 and other acute-viral infections ***(Protein & Cell 2020).*** She was also awarded to ESWI young scientist award (2014), Shanghai Rising-Star Talent (2015), and the NSFC excellent young scientist (2019). She served as an advisory board member of Archives of Virology and scientific reviewers for several SCI journals.

Dr. Peng ZHOU

Professor, Center for Emerging Infectious Diseases, Wuhan Institute of Virology, Chinese Academy of Sciences, China

Academic qualifications:
PhD of molecular biology, Wuhan Institute of Virology (WIV), Chinese Academy of Sciences (CAS), Wuhan, China, 2010;
Joint PhD study, Australian Animal Health Laboratory (AAHL), CSIRO, Australia, 2009-2010
Bachelor of bioengineering, Henan University, Kaifeng, China, 2004.

Research interests: Bat innate immunity; virus host interface; pathogens discovery

Publication track record: more than 50-refereed publications in journals including *Nature*, *Science, Cell Host and Microbe, PNAS, Journal of Virology and Journal of Immunology* covering virology and immunology. Publications also include one book chapter on bat immunology

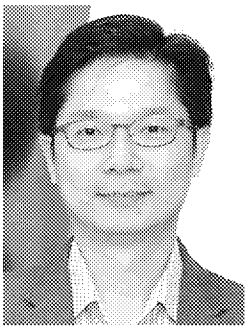
Selected Publications:

1. **Zhou P**, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li B, Huang CL, Chen HD, Chen J, Luo Y, Guo H, Jiang RD, Liu MQ, Chen Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan B, Zhan FX, Wang YY, Xiao GF, Shi ZL*. **Nature**. 2020 Feb 3. doi: 10.1038/s41586-020-2012-7.
2. Zhang W, Du RH, Li B, Zheng XS, Yang XL, Hu B, Wang YY, Xiao GF, Yan B, Shi ZL* & **Zhou P***. Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes. ***Emerg Micro Infect***, 9:1, 386-389, DOI: 10.1080/22221751.2020.1729071.
3. Li B, Si HR, Zhu Y, Yang XL, Anderson DE, Shi ZL, Wang LF*, **Zhou P***. Discovery of bat coronaviruses through surveillance and probe capture-based next generation sequencing. ***mSphere*** 10.1128/mSphere.00807-19.
4. **Zhou Peng**, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y, Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson D, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ, Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XLL, Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, Wang LF, Shi ZL, Tong YG, Ma JY. (2018) Fatal swine acute diarrhea syndrome caused by an HKU-2 related coronavirus of bat origin. ***Nature*** 255-258, vol 556, April 4 2018
5. Xie J, Li Y, She X, Goh G, Zhu Y, Cui J, Wang L-F, Shi ZL*, **Zhou P*** (2018) Dampened STING-dependent interferon activation in bats. ***Cell Host Micro*** 23, 1–5, March 14 2018.

Prof. Zihe Rao, CAS Academician

Prof. Zihe Rao, Head of Laboratory for Structural Biology, Tsinghua University, the member of the Presidium of the CAS Academic Divisions, the member of Standing Committee of the National Committee of the Political Consultative Conference, Founder and Editor-in-Chief of Protein & Cell (IF 10.164 Year 2019), the former President of Nankai University, the former Director-General of Institute of Biophysics (CAS), the former President of the International Union for Pure and Applied Biophysics (IUPAB). Prof. Zihe Rao dedicates in studying the mechanisms underlying pathogenic infectious agents with significant concerns on global public health throughout his academic career. He provides the insight into virus lifecycle and antiviral research on coronaviruses (SARS-CoV and SARS-CoV-2), picornaviruses, flaviviruses, avian influenza virus and retrovirus. He also works to develop the innovative technics to dissect the assembly giant viruses, including Africa swine fever virus and herpesvirus. Amongst his studies on viruses, his recent works provide groundbreaking insights into energy and metabolite transport, drug resistance and cell wall synthesis in M. tuberculosis with invaluable information for anti-TB drug discovery. In the recent global pandemic of COVID-19, he determined the structures of two key targets for antiviral development, main protease and RNA-dependent RNA polymerase, accelerating the global efforts against COVID-19 (Nature 2020, Science 2020). To date, he has published more than 380 peer reviewed research papers, including 22 pieces of research papers in Cell, Nature and Science, with more than 17,500 citations (google scholar 2020 Nov 13) in total.

香 港 大 學
THE UNIVERSITY OF HONG KONG



Professor Leo L. M. POON
School of Public Health, LKS Faculty of Medicine
The University of Hong Kong
E-mail: llmpoon@hku.hk
Website: https://sph.hku.hk/en/about-us/faculty-and-staff/academic-staff/poon,-lit-man-leo
Research interest: Public Health, Infectious Diseases and Virology

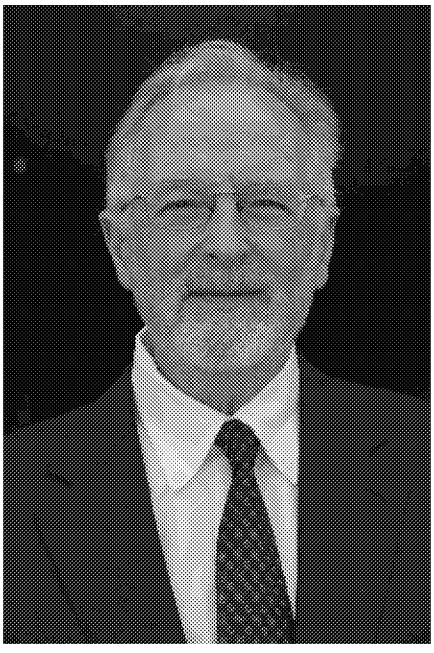
Short Biography

Professor Leo Poon was born and raised in Hong Kong. He received his doctoral training in Sir William Dunn School of Pathology in University of Oxford (1999). He joined HKU in 2001. He is a now a professor in School of Public Health and he is the division head of Public Health Laboratory Sciences in this school.

Leo Poon has strong research interests related to emerging viruses, ranging from basic science to clinical virology. His work primarily focuses on influenza virus and coronavirus (e.g. SARS and MERS, SARS-CoV-2). He has published over 220 publications. He has been ranked as a top 1% most-cited scientist since 2005. He is a founding member of the Hong Kong Young Academy of Sciences.

Apart from serving in his capacity within HKU, he serves as an expert in various international health care organizations (e.g. WHO and OIE). He serves in a number of task force groups in these organizations to develop infectious disease control policy. His division serves as a WHO reference laboratory for H5 influenza virus and COVID-19. He organized workshops to train frontline medical scientists in various regional and international disease control programs. He conducted overseas missions and outbreak investigations for controlling infectious diseases.

Prof Luis Enjuanes



Luis Enjuanes has been working in the virology field for more than 40 years, including 35 years in coronaviruses. His present interest is the study of the mechanism of replication, transcription, virulence and virus-host interaction in coronavirus. He has published more than 220 peer reviewed articles and 65 book chapters. At present, he is Research Professor and Head of the Coronavirus Laboratory at the National Center of Biotechnology of the Spanish National Research Council (CNB-CSIC). He has been an NIH Fogarty Visiting Fellow at Bethesda, MD, and a Visiting Scientist at FCRC, NIH, MD. He is Professor of Virology at the University of Madrid and the Institute Pasteur of Paris. He has been named "Distinguish Senior Virologist" by the Spanish Society of Virology, and a Member of the Royal Academy of Exact, Physical and Natural Sciences. He is also a member of the American Academy of Microbiology. He has been Editor-in-Chief of Virus Research. Enjuanes has received from the Government of Spain the Medal to the Merit for Scientific Research and University Teaching.

Stefan Pöhlmann, Prof. Dr.

Professor, Head of the Infection Biology Unit,
German Primate Center

2000: Ph.D., Friedrich-Alexander-Universität Erlangen-Nürnberg
2000-2003: Postdoctoral Fellow, University of Pennsylvania
2003-2007: Head of a SFB Junior Research Group, Institute of Clinical and Molecular Virology, Friedrich-Alexander-University Erlangen-Nürnberg
2007-2010: Professor for Experimental Virology, Hannover Medical School
2010: Professor for Infection Biology at Georg-August-University Göttingen (Brückenprofessur) and Head of the Infection Biology Unit of the German Primate Center

Major Research Interests

Influenza viruses pose a global health threat. These viruses constantly change and therapeutics may thus cease to be effective. Therefore, we seek to develop novel influenza therapies. One focus of our work is on the host cell protease TMPRSS2 since we obtained evidence that influenza viruses depend on this enzyme for acquisition of infectivity. Moreover, we are investigating how defective interfering particles (DIPs) can be developed as novel therapeutics.

Emerging viruses may cause severe disease. Outbreaks frequently occur abroad but the agents can be imported into Germany via infected travelers. We are investigating how emerging viruses interact with host cells and cause disease. Our focus in on lymphocytic choriomeningitis virus, Ebola virus and SARS coronavirus. One aim of our research is to develop cell culture systems that allow predicting transmissibility and thus pandemic potential of emerging viruses.

Another focus of our research is on primate herpesviruses. The transmission of herpes B virus from macaques to humans can cause serve disease while closely related viruses seem to be apathogenic in humans. We are investigating which viral and host factors determine whether infection will result in severe disease. Moreover, we are developing diagnostics for herpesvirus infections of non-human primates.

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 11/26/2020 9:00:39 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: Fw: Re: RE: paper-2020526
Attachments: GLP2R-20201126.docx; GLP2R 20201124.pptx

-----原始邮件-----
发件人:"陈新文" <chenxw@wh.iov.cn>
发送时间:2020-11-26 22:27:51 (星期四)
收件人: "Shi, Pei yong" <peshi@UTMB.EDU>
抄送:
主题: Re: RE: paper-2020526

Pei-yong,

Here is the update draft of the paper. I would like invite you go through the MS.Thank you very much !

I am looking forward to hearing from you.

All mm regards,

Xinwen

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-05-27 20:29:20 (星期三)
收件人: "陈新文" <chenxw@wh.iov.cn>
抄送:
主题: RE: paper-2020526

Hi Xinwen,

I quickly went through the manuscript. Let's have a call to (i) go through the data and (ii) discuss the way forward. Please let me know when you have time to call.

Best,

- Pei-Yong

From: 陈新文 <chenxw@wh.iov.cn>
Sent: Tuesday, May 26, 2020 10:30 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: paper-2020526

佩勇，

附件是文章的结果。文章很初步，整体结构也需要大的调整。我想这是第一次请教，请你审核数据（文章的主体部分和图表），期待意见和建议，特别是：

1）需要补充的其他实验；

2）文章写作思路和整体布局

另外， 我们正在补充的数据包括：

1）GLP2R蛋白的ECL1结构域和E蛋白DIII直接相互作用证据（合成多肽，SPR分析），

2）缺陷小鼠感染实验（已经构建成功，正在繁殖）。

将在你意见和建议的基础上重新架构文章。

非常感谢！

祝好！

新文

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 12/5/2020 10:50:25 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: GLP2R-20201206
Attachments: Extended Data Figs-20201206.docx; GLP2R-20201206.docx

Pei-Yong,

Please find the update version. Looking forward to hearing from you.

All my regards,

Xinwen

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 12/7/2020 2:49:44 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: GLP2R-20201207
Attachments: Extended Data Figs20201207.docx; GLP2R-20201207.docx

Pei-Yong,

I have not received your comments. Here I would like send your the new version of the MS. We have checked the MS in more detail,and redrawn all figures. If possible, You could work on this files.

All my regards,

Xinwen

From: 陈新文 [chenxw@wh.iov.cn]
Sent: 12/9/2020 5:32:08 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
Subject: Extended Data Dec 10 2020
Attachments: Extended Data Dec 10 2020.docx; GLP2R Dec 10 2020.docx; Supplementary Tables 1-7 Dec 10 2020.docx

Pei-Yong,

Here is the new version.

All my regards,

Xinwen

From: Liu, Shan-Lu [liu.6244@osu.edu]
Sent: 1/2/2021 4:09:25 PM
To: zhengzhiming4@gmail.com; tzhou@mail.nih.gov; GCheng@mednet.ucla.edu; liangy@umn.edu; rli@vcu.edu; xjmeng@vt.edu; Zhijian.Chen@UTSouthwestern.edu; mluo@gsu.edu; zhangyj@umd.edu; xzhu1@umd.edu; jqiu@kumc.edu; lijun@uic.edu; fengwei.bai@usm.edu; andyu@iupui.edu; reachxw@vt.edu; gluo@uab.edu; ldu@nybc.org; hxu@tulane.edu; liu_fy@berkeley.edu; Shan.lu@umassmed.edu; Hu, Haitao [haihu@UTMB.EDU]; wenzheho@temple.edu; Qfeng4@central.uh.edu; tang@bio.fsu.edu; feng.li@sdstate.edu; ruilu@lsu.edu; sxiang2@unl.edu; qiyi.tang@howard.edu; dingsw@ucr.edu; guohua@missouri.edu; bling@tulane.edu; junwang@pharmacy.arizona.edu; lifang@umn.edu; wang518@umd.edu; gaos8@upmc.edu; Wang,Penghua [pewang@uchc.edu]; xiangy@uthscsa.edu; fzhu@bio.fsu.edu; chen.liang@mcgill.ca; lyuan@vt.edu; fgao@duke.edu; wangjw28@163.com; xfyu1@zju.edu.cn; bzhao@partners.org; jianw@musc.edu; zyang@ksu.edu; yu.cong@nih.gov; weiming.yuan@usc.edu; Zongdi.feng@nationwidechildrens.org; juh13@psu.edu; hengx@missouri.edu; lsu@med.unc.edu; ywu8@gmu.edu; jwu@whu.edu.cn; tshuo@uic.edu; Shibojiang@fudan.edu.cn; sjiang@nybc.org; pinwang@usc.edu; rzhao@som.umaryland.edu; shuylong@mail.sysu.edu.cn; xuefeng.liu@georgetown.edu; yuxingli@som.umaryland.edu; shixia.wang@umassmed.edu; yhe@ipbcams.ac.cn; Pinghui.feng@usc.edu; ju-tao.guo@bblumberg.org; lin.liu@okstate.edu; hua.zhu@rutgers.edu; Jinhong.chang@bblumberg.org; jianzhu1012@gmail.com; ronghai@ucr.edu; jliu4@uams.edu; xiangpeng.kong@med.nyu.edu; haoquanwu@outlook.com; Wenjun.liu@defence.gov.au; Liang.shan@wustl.edu; hliao@duke.edu; yuan2@upenn.edu; zxing@umn.edu; hongmin.li@health.ny.gov; pzheng@ihv.umaryland.edu; yaliu@ihv.umaryland.edu; jxw103@case.edu; Feng Shao [shaofeng@nibs.ac.cn]; zlshi@wh.iov.cn; klan@whu.edu.cn; zengmsh@mail.sysu.edu.cn; Nan Yan [Nan.Yan@UTSouthwestern.edu]; liliwang@upenn.edu; Linheng Li [LIL@stowers.org]; kli1@uthsc.edu; tsx@case.edu; ssun@mdanderson.org; ysang@tnstate.edu; wu@crystal.harvard.edu; Sun.Jie@mayo.edu; peijun@strubi.ox.ac.uk; jiayu@coh.org; bchen@crystal.harvard.edu; Wen, Haitao [Haitao.Wen@osumc.edu]; Qu, Feng [qu.28@osu.edu]; Hezhao.Ji@umanitoba.ca; zhengyo@msu.edu; zhanglinqi@tsinghua.edu.cn; Whu@temple.edu; RSun@mednet.ucla.edu; Guangping.Gao@umassmed.edu; pzheng@ihv.umaryland.edu; GMSWANG@nus.edu.sg; Shi, Pei yong [peshi@UTMB.EDU]; yaliu@ihv.umaryland.edu; ziying-yan@uiowa.edu; lqiao@luc.edu; yong.xiong@yale.edu; Wang, Qiuhong [wang.655@osu.edu]; shuping_tong_md@brown.edu; Pinghui Feng [pinghuif@usc.edu]; gaof@im.ac.cn; zihai@musc.edu; zqin@uams.edu; guoh4@upmc.edu; wma@missouri.edu; Feng.Li@uky.edu; xiaow@iu.edu; sli38@tulane.edu; guodeyin@mail.sysu.edu.cn; hli1@pharmacy.arizona.edu; xiaow@iu.edu; ashuang@caltech.edu; jamesou@usc.edu; cwood1@unl.edu
Subject: SCBA-Virology Division 2020 Year in Review
Attachments: SCBA-Virology Division 2020 Year in Review_SLL.pdf

Dear Colleagues and Friends:

As in the past, I have summarized the activity of our WeChat group for last year, kindly find attached.

If you wish to join the WeChat group, please also let me or Haitao Guo know.

Best wishes.

Shan-Lu

From: "Liu, Shan-Lu" <liu.6244@osu.edu>
Date: Friday, January 1, 2021 at 10:03 AM
To: "zhengzhiming4@gmail.com" <zhengzhiming4@gmail.com>, "tzhou@mail.nih.gov" <tzhou@mail.nih.gov>, "GCheng@mednet.ucla.edu" <GCheng@mednet.ucla.edu>, "liangy@umn.edu" <liangy@umn.edu>, "rli@vcu.edu" <rli@vcu.edu>, "xjmeng@vt.edu" <xjmeng@vt.edu>, "Zhijian.Chen@UTSouthwestern.edu" <Zhijian.Chen@UTSouthwestern.edu>, "mluo@gsu.edu"

<mluo@gsu.edu>, "zhangyj@umd.edu" <zhangyj@umd.edu>, "xzhu1@umd.edu" <xzhu1@umd.edu>, "jqiu@kumc.edu" <jqiu@kumc.edu>, "lijun@uic.edu" <lijun@uic.edu>, "fengwei.bai@usm.edu" <fengwei.bai@usm.edu>, "andyu@iupui.edu" <andyu@iupui.edu>, "reachxw@vt.edu" <reachxw@vt.edu>, "gluo@uab.edu" <gluo@uab.edu>, "ldu@nybc.org" <ldu@nybc.org>, "hxu@tulane.edu" <hxu@tulane.edu>, "liu_fy@berkeley.edu" <liu_fy@berkeley.edu>, "Shan.lu@umassmed.edu" <Shan.lu@umassmed.edu>, "haihu@UTMB.edu" <haihu@UTMB.edu>, "wenzheho@temple.edu" <wenzheho@temple.edu>, "Qfeng4@central.uh.edu" <Qfeng4@central.uh.edu>, "tang@bio.fsu.edu" <tang@bio.fsu.edu>, "feng.li@sdstate.edu" <feng.li@sdstate.edu>, "ruilu@lsu.edu" <ruilu@lsu.edu>, "sxiang2@unl.edu" <sxiang2@unl.edu>, "qiyi.tang@howard.edu" <qiyi.tang@howard.edu>, "dingsw@ucr.edu" <dingsw@ucr.edu>, "guohua@missouri.edu" <guohua@missouri.edu>, "bling@tulane.edu" <bling@tulane.edu>, "junwang@pharmacy.arizona.edu" <junwang@pharmacy.arizona.edu>, "lifang@umn.edu" <lifang@umn.edu>, "wang518@umd.edu" <wang518@umd.edu>, "gaos8@upmc.edu" <gaos8@upmc.edu>, "pewang@uchc.edu" <pewang@uchc.edu>, "xiangy@uthscsa.edu" <xiangy@uthscsa.edu>, "fzhu@bio.fsu.edu" <fzhu@bio.fsu.edu>, "chen.liang@mcgill.ca" <chen.liang@mcgill.ca>, "lyuan@vt.edu" <lyuan@vt.edu>, Feng Gao <fgao@duke.edu>, "wangjw28@163.com" <wangjw28@163.com>, "xfyu1@zju.edu.cn" <xfyu1@zju.edu.cn>, "bzhao@partners.org" <bzhao@partners.org>, "jianw@musc.edu" <jianw@musc.edu>, "zyang@ksu.edu" <zyang@ksu.edu>, "yu.cong@nih.gov" <yu.cong@nih.gov>, "weiming.yuan@usc.edu" <weiming.yuan@usc.edu>, "Zongdi.feng@nationwidechildrens.org" <Zongdi.feng@nationwidechildrens.org>, "juh13@psu.edu" <juh13@psu.edu>, "hengx@missouri.edu" <hengx@missouri.edu>, "lsu@med.unc.edu" <lsu@med.unc.edu>, "ywu8@gmu.edu" <ywu8@gmu.edu>, "jwu@whu.edu.cn" <jwu@whu.edu.cn>, "tshuo@uic.edu" <tshuo@uic.edu>, "Shibojiang@fudan.edu.cn" <Shibojiang@fudan.edu.cn>, "sjiang@nybc.org" <sjiang@nybc.org>, "pinwang@usc.edu" <pinwang@usc.edu>, "rzhao@som.umaryland.edu" <rzhao@som.umaryland.edu>, "shuylong@mail.sysu.edu.cn" <shuylong@mail.sysu.edu.cn>, "xuefeng.liu@georgetown.edu" <xuefeng.liu@georgetown.edu>, "yuxingli@som.umaryland.edu" <yuxingli@som.umaryland.edu>, "shixia.wang@umassmed.edu" <shixia.wang@umassmed.edu>, "yhe@ipbcams.ac.cn" <yhe@ipbcams.ac.cn>, "Pinghui.feng@usc.edu" <Pinghui.feng@usc.edu>, "ju-tao.guo@bblumberg.org" <ju-tao.guo@bblumberg.org>, "lin.liu@okstate.edu" <lin.liu@okstate.edu>, "hua.zhu@rutgers.edu" <hua.zhu@rutgers.edu>, "Jinhong.chang@bblumberg.org" <Jinhong.chang@bblumberg.org>, "jianzhu1012@gmail.com" <jianzhu1012@gmail.com>, "ronghai@ucr.edu" <ronghai@ucr.edu>, "jliu4@uams.edu" <jliu4@uams.edu>, "xiangpeng.kong@med.nyu.edu" <xiangpeng.kong@med.nyu.edu>, "haoquanwu@outlook.com" <haoquanwu@outlook.com>, "Wenjun.liu@defence.gov.au" <Wenjun.liu@defence.gov.au>, "Liang.shan@wustl.edu" <Liang.shan@wustl.edu>, "hliao@duke.edu" <hliao@duke.edu>, "yuan2@upenn.edu" <yuan2@upenn.edu>, "zxing@umn.edu" <zxing@umn.edu>, "hongmin.li@health.ny.gov" <hongmin.li@health.ny.gov>, "pzheng@ihv.umaryland.edu" <pzheng@ihv.umaryland.edu>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "jxw103@case.edu" <jxw103@case.edu>, Feng Shao <shaofeng@nibs.ac.cn>, "zlshi@wh.iov.cn" <zlshi@wh.iov.cn>, "klan@whu.edu.cn" <klan@whu.edu.cn>, "zengmsh@mail.sysu.edu.cn" <zengmsh@mail.sysu.edu.cn>, Nan Yan <Nan.Yan@UTSouthwestern.edu>, "liliwang@upenn.edu" <liliwang@upenn.edu>, Linheng Li <LIL@stowers.org>, "kli1@uthsc.edu" <kli1@uthsc.edu>, "tsx@case.edu" <tsx@case.edu>, "ssun@mdanderson.org" <ssun@mdanderson.org>, "ysang@tnstate.edu" <ysang@tnstate.edu>, "Liu, Shan-Lu" <liu.6244@osu.edu>, "wu@crystal.harvard.edu" <wu@crystal.harvard.edu>, "Sun.Jie@mayo.edu" <Sun.Jie@mayo.edu>, "peijun@strubi.ox.ac.uk" <peijun@strubi.ox.ac.uk>, "jiayu@coh.org" <jiayu@coh.org>, "bchen@crystal.harvard.edu" <bchen@crystal.harvard.edu>, "Wen, Haitao" <Haitao.Wen@osumc.edu>, "Qu, Feng" <qu.28@osu.edu>, "Hezhao.Ji@umanitoba.ca" <Hezhao.Ji@umanitoba.ca>, "zhengyo@msu.edu" <zhengyo@msu.edu>, "zhanglinqi@tsinghua.edu.cn" <zhanglinqi@tsinghua.edu.cn>, "Whu@temple.edu" <Whu@temple.edu>, Ren Sun <RSun@mednet.ucla.edu>, "Guangping.Gao@umassmed.edu" <Guangping.Gao@umassmed.edu>, "pzheng@ihv.umaryland.edu" <pzheng@ihv.umaryland.edu>, "GMSWANG@nus.edu.sg"

<GMSWANG@nus.edu.sg>, "peshi@UTMB.EDU" <peshi@UTMB.EDU>, "yaliu@ihv.umaryland.edu" <yaliu@ihv.umaryland.edu>, "ziying-yan@uiowa.edu" <ziying-yan@uiowa.edu>, "lqiao@luc.edu" <lqiao@luc.edu>, "yong.xiong@yale.edu" <yong.xiong@yale.edu>, "Wang, Qiuhong" <wang.655@osu.edu>, "shuping_tong_md@brown.edu" <shuping_tong_md@brown.edu>, Pinghui Feng <pinghuif@usc.edu>, "gaof@im.ac.cn" <gaof@im.ac.cn>, "zihai@musc.edu" <zihai@musc.edu>, "zqin@uams.edu" <zqin@uams.edu>, "guoh4@upmc.edu" <guoh4@upmc.edu>, "wma@missouri.edu" <wma@missouri.edu>, "Feng.Li@uky.edu" <Feng.Li@uky.edu>, "xiaow@iu.edu" <xiaow@iu.edu>, "sli38@tulane.edu" <sli38@tulane.edu>, "guodeyin@mail.sysu.edu.cn" <guodeyin@mail.sysu.edu.cn>, "hli1@pharmacy.arizona.edu" <hli1@pharmacy.arizona.edu>, "xiaow@iu.edu" <xiaow@iu.edu>, "ashuang@caltech.edu" <ashuang@caltech.edu>, "Weiss, Susan" <weisssr@pennmedicine.upenn.edu>, "jamesou@usc.edu" <jamesou@usc.edu>, "cwood1@unl.edu" <cwood1@unl.edu>
Subject: Thank you and happy new year!

Dear colleagues:

Greetings and happy new year!

I hope that you all have enjoyed our annual meeting last two days, which I consider as a success. There were more than 300 registrations, and in each session, there were at least 100 attendees at various times. Once again, I wish to thank all the speakers, cochairs, panelists and all of you for your participation and discussion. I especially want to thank the organizing committee members, Genhong Cheng, Haitao Guo, Renfeng Li, Yuying Liang, Wenjun Ma, Tongqing Zhou, and hi-Ming Zheng for their help that made this symposium possible. I would hope that our annual meeting next year will happen in person.

As I finish my term as the Founding President of this association, which is effective today, I would like to offer my most sincere appreciation and thanks for your care, trust, understanding, patience, and support. It is all because of you last few years that this association and the WeChat group is so strong, entertaining, and full of fun!

In the meantime, I would like to introduce the new leadership team of SCBA-Virology Division as follows:

President: Haitao Guo, Ph.D, University of Pittsburgh School of Medicine
Secretary: Tongqing Zhou, Ph.D, Vaccine Research Center, NIAID, NIH
Treasurers: Yuying Liang , Ph.D, University of Minnesota, and Wenjun Ma, Ph.D, University of Missouri

I wish you all a happy, healthy, and prosperous 2021!

Shan-Lu

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
The Ohio State University
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

SCBA-Virology Division 2020 Year in Review: Focused Responses to COVID-19

By Shan-Lu Liu

This past year has been unprecedented as we grapple with the COVID-19 pandemic around the globe. The SCBA-Virology Division has had many exciting and intriguing discussions over this year; I have summarized some key highlights below.

Dec 30, 2019: Immediate response and discussion about the first public revelation of mysterious pneumonia in Wuhan, China.

Jan 2-5, 2020: Response and lively discussion about the suspected pathogen for the Wuhan pneumonia and the possibility of human-to-human transmission.

Jan 4, 2020: Focused discussion on endogenous retroviruses and their roles in animal and human physiology, pathology and evolution.

Jan 5, 2020: Focused discussion on Koch's postulates and how to apply them in identifying the suspicious pathogens, including Zhi-Ming Zheng's suggestion to detect IgM within 2 weeks of infection and 4-fold titer increase for specific IgG in paired sera. Overwhelming calls from colleagues, including many in mainland China like Dr. Yuelong Shu, to release the name of the pathogen.

Jan 9, 2020: Overwhelming responses to the Walls Street Journal news on COVID-19.

Jan 10-11, 2020: Debate on naming the new coronavirus, in particular regarding whether "Wuhan" should be included.

Jan 10, 2020: Immediate dissemination and focused discussion on the full genome sequence of SARS-CoV-2 released by Yongzhen Zhang and Edward Holmes.

Jan 19-22, 2020: Response and discussion about the correspondence by Shan-Lu Liu in Nature entitled "New virus in China requires international control effort" that calls for investigation of human-to-human transmission, and commentary in Viruses entitled "Emerging Viruses without Borders: The Wuhan Coronavirus" that appeals for continued US-China scientific collaboration.

Jan 23, 2020: Response and discussion regarding the lockdown of Wuhan.

Jan 23, 2020: Proposal by Shan Lu and members of the society to China CDC and other agencies for effective control of the spreading virus, entitled
"分层管理，集中分筛可疑人群是当前控制新型冠状病毒的关键".

Since Jan 27, 2020, members of this society have actively participated in media interviews, including Shou-Jiang Gao, Haitao Guo, Qi Huang, Shibo Jiang, Dong-Yan Jin, Ke Lan, Shan-Lu Liu, Shan Lu, Lijun Rong, Zhengli Shi, Lishan Su, Jun Wang, Qiuhong Wang, Yan Xiang, Zhi-Ming Zheng, Richard Zhao, and many more.

Jan 27, 2020: Active discussion on a Lancet paper by Kwok-Yung Yuen and colleagues that reported the first family-clustered cases of person-to-person transmission of SARS-CoV-2.

Feb 2, 2020: Lively discussion on a preprint by Indian scientists claiming an association between SARS-CoV-2 and HIV; this led to an article by corresponding author Feng Gao and coauthors Chuan Xiao, Shou-Jiang Gao, Yongming Sang published in Emerging Microbes and Infections (EMI).

Feb 19, 2020: Themed discussion on the role of selective pressure in generating recombinants that may have contributed to the origin of SARS-CoV-2.

Feb 19, 2020: Congratulations to Dong-Yan Jin for election into the American Academy of Microbiology.

Feb 20, 2020: Strong debate on the naming of SARS-CoV-2, resulting in an article entitled "SARS-CoV-2 is an appropriate name for the new coronavirus" by members Yuntao Wu, Wenzhe Ho, Dong-Yan Jin, Shan-Lu Liu, Xuefeng Liu, Jianming Qiu, Yongming Sang, Qiuhong Wang, and Zhi-Ming Zheng, etc.

Feb 23, 2020: Themed discussion on the possible origin of SARS-CoV-2 and RaTG13, specifically on whether or not SARS-CoV-2 is artificially engineered; this led to an article entitled "No credible evidence supporting claims of the laboratory engineering of SARS-CoV-2" by Lishan Su and Shan-Lu Liu and others published in EMI. This paper received 75000 downloads, ranking as the third most downloaded paper among 2500 journals in the Taylor & Francis family.

March 19, 2020: Response, discussion, and support of Dr. Kwok-Yung Yuen's commentary published in a Hong Kong Newspaper regarding the frequent spillover of animal viruses to humans and lessons learned from 2003/SARS and COVID-19.

May 17, 2020: Themed discussion on selective pressure that drives both the SARS-CoV-2 Spike and ACE2 receptor co-evolution.

May - August, 2020: Xuefeng Liu co-organized a series of COVID-19 seminars sponsored by the Wuhan University Alumni Association; speakers include Genhong Cheng, Haitao Guo, Deyin Guo, Jianming Hu, Shibo Jiang, Ke Lan, Xuefeng Liu, Dongfang Liu, Yang Liu, Zheng-Li Shi, Jun Wang, Yuntao Wu, Zhi-Ming Zheng, Tongqing Zhou, Fanxiu Zhu, etc.

August 30, 2020: Themed discussion on antibody-dependent enhancement (ADE) and possible impact on COVID-19 pathogenesis and vaccines.

Sept 1, 2020: Focused discussion on scientific contributions of Dr. Louise Chow and the lack of recognition by Nobel committee and other organizations for her tremendous contribution to RNA splicing.

Sept 8, 2020: Response and discussion about a Xinhua News Agency's report on the timeline of discovery of SARS-CoV-2, particularly on the important contribution of Yongzhen Zhang, who was the first to publicly release the genome sequence of SARS-CoV-2.

Sept 23, 2020: Response and congratulations to Zheng-Li Shi and Yongzhen Zhang as "The 100 Most Influential People of 2020" selected by TIME magazine.

Sept 24, 2020: Response and congratulations to Yang Liu and Pan Zheng's breakthrough on CD24Fc treatment for COVID-19.

Oct 5, 2020: Active discussion regarding the announcement of 2020 Nobel Prize winners, with special congratulations to virology colleagues Drs. Charles Rice, Harvey Alter and Michael Houghton to science and recognition of their connections to the Chinese virology community.

Nov 25, 2025: Response and congratulations to Fanxiu Zhu and Shan-Lu Liu for being elected as fellows of the American Association for the Advancement of Science.

Oct - Dec, 2020: Continuous discussion and debate on COVID-19 vaccines: safety, efficacy and distribution.

Dec 30-31: The 3rd Symposium of SCBA-Virology was held virtually and successfully. Invited speakers were Drs. Susan Weiss and Xiang-Jin (XJ) Meng, who had given outstanding speeches. There were ~320 registrations from at least 7 counties and regions. Three sessions include: (1) COVID-19/SARS-CoV-2, (2) Host response, pathogenesis, and antivirals, and (3) Viral replication and spread. All sessions were followed by a panel discussion, which was informative, interactive, and entertaining

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; 'Nancy Connell'[NancyConnell@jhu.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 6/8/2020 11:02:00 PM (UTC-05:00)
Subject: RE: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET
Immunity topics plus Gao for 3rd China U.S. Dialogue v2.docx
Chinese Participants-0610.docx

Greetings,

I have attached the list of Chinese participants for the meeting tomorrow (that I just received). There will be fewer people on their side this time (at our request). **Please let me know if you are not planning to participate.**

I have also attached the **American version** of the agenda / list of questions. Recall that their version lists Harvey Fineberg and Ralph Baric as discussants to answer Dr. Gao's questions but not the other names.

FYI the Zoom link for the meeting is:
https://nasem.zoom.us/j/95921551654?pwd= **552.136**

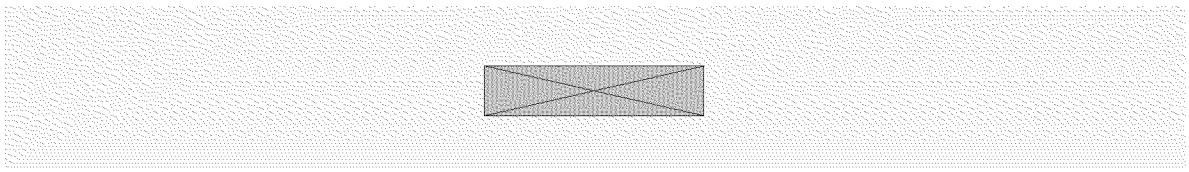
Please let me know if you have any questions or concerns. Thanks again for taking the time to participate in these meetings.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 11:28 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET



Meeting link:
https://nasem.zoom.us/j/95921551654?pwd=

552.136

552.136

Meeting Topic: **Third Virtual U.S. China Bio Dialogue Meeting**

Meeting Time: **Jun 9, 2020 9:00 - 11:00 PM Eastern Time**

Add to Calendar Add to Google Calendar Add to Yahoo Calendar

Start Meeting

If the above button is not clickable, try copying and pasting the following link into the address bar of your web browser

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Or join meeting with the following methods

Phone one-tap

Phone one-tap: US: +14702509358,,95921551654# or +16465189805,,95921551654#

Join by Telephone

For higher quality, dial a number based on your current location.

Dial: US : +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or +1 213 338 8477 or +1 253 215 8782 or 877 853 5257 (Toll Free) or 888 475 4499 (Toll Free)

Meeting ID: 959 2155 1654

Password: **552.136**

International numbers

Join from an H.323/SIP room system

H.323: 162.255.37.11 (US West)
162.255.36.11 (US East)
221.122.88.195 (China)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (EMEA)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)

Meeting ID: 959 2155 1654

Password: **552.136**

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Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

Questions:

Immune Response and Immunotherapy

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection (Le Duc)
  - How is immune response being measured?
  - Was there standardization of testing tools?
- **What is the overall situation of serologic investigation in the US? (Fineberg)**
- What can be said about the characterization of the (Perlman)
  - Innate immune responses?
  - humoral immune response?
  - cellular immune response?
- What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection? (Hamburg)
  - Is the use of immune plasma effective?
  - Have there been any complications?
- What has been China's experience with human monoclonal antibodies for treatment and prevention? (Hamburg)
  - Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?
- What immunopathologies are evident in the patients with COVID-19? (Relman)
  - Are there any biomarkers in patients who develop systemic inflammation?
  - What is the most effective treatment for patients who develop a cytokine storm?

Immunity

- After recovery, what types of antiviral immune responses are present? (Saif)
  - Do these immune responses protect from re-infection?
  - What is known about the durability of neutralizing antibody and longevity of protective immunity?

  Did recovery from SARS provide any protection from infection with SARS-CoV-2?
- **Progress in the development of vaccine in the U.S. especially mRNA vaccine? (Baric)**

Reactivation or Reinfection of Recovered Patients/Fall resurgence

- Has reactivation of latent virus or re-infection been seen among survivors? (Shi)
- Is reactivation/reinfection a concern with respect to a fall resurgence?
- What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)

- **What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the U.S.? (Fineberg)**

Chinese Participants

Ling Chen: Dr. Ling Chen is a professor and founding director of CAS Guangzhou Institute of Biomedicine and Health, former deputy director of State Key Lab of Respiratory Disease.

Chen Dong: Dr. Chen Dong is Director and a professor of the Institute for Immunology, Dean of the School of Medicine at Tsinghua University, CAS member.

George F. Gao: Dr. George F. Gao is Director-General of CCDC, a professor at the CAS Institute of Microbiology, CAS member.

Qihan Li: Dr. Qihan Li is a professor of the Institute of Medical Biology, Chinese Academy of Medical Science, Peking Union Medical College. His research focuses on viral vaccine and viral immunology.

Wenjie Tan: Dr. Wenjie Tan is Chief and a professor of the Biotech Center for Viral Disease Emergency, National Institute for Viral Disease Control and Prevention, CCDC.

Jianqing Xu: Dr. Jianqing Xu is a professor of the Institutes of Biomedical Sciences, Fudan University.

Zhiming Yuan: Dr. Zhiming Yuan is a professor of CAS Wuhan Institute of Virology, Director of Wuhan P4 lab.

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Mon 5/25/2020 7:07:49 AM (UTC-05:00)
Subject: Questions - reply requested

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April?

Look forward to hearing from you.

best wishes
Marcus Williamson

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=02%7C01%7Cvimenach%40utmb.edu%7C3e9682604d1b4dd4576c08d800a46f62%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637260053589056828&sdata=MT2x0NrVZ0s36xv1ZYOiCc6nFzke74WdSvIQ9tOW9bE%3D&reserved=0

which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Wed 5/27/2020 8:32:20 AM (UTC-05:00)
Subject: Questions - reply requested

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=02%7C01%7Cvimenach%40utmb.edu%7C64578e64cd5e4a871db008d8024292a7%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637261832237357144&sdata=IKTGXQqL9v0f2xfWhmL61MXLnS%2FwQ%2Fz3W5PGYLfoymw%3D&reserved=0

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Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov];
Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov];
Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov];
John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov];
Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov];
Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov];
Terry.Nealey@leg.wa.gov[Terry.Nealey@leg.wa.gov]; Sharon.Nelson@leg.wa.gov[Sharon.Nelson@leg.wa.gov];
Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov];
Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov];
Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov];
Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov];
Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov];
Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov];
Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov];
Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov];
Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov];
Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov];
Cindy.Ryu@leg.wa.gov[Cindy.Ryu@leg.wa.gov]; Rebecca.Saldana@leg.wa.gov[Rebecca.Saldana@leg.wa.gov];
SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov];
Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov];
Mike.Sells@leg.wa.gov[Mike.Sells@leg.wa.gov]; Tana.Senn@leg.wa.gov[Tana.Senn@leg.wa.gov];
Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov];
Shelly.Short@leg.wa.gov[Shelly.Short@leg.wa.gov]; Vandana.Slatter@leg.wa.gov[Vandana.Slatter@leg.wa.gov];
Norma.Smith@leg.wa.gov[Norma.Smith@leg.wa.gov]; Larry.Springer@leg.wa.gov[Larry.Springer@leg.wa.gov];
Melanie.Stambaugh@leg.wa.gov[Melanie.Stambaugh@leg.wa.gov]; Derek.Stanford@leg.wa.gov[Derek.Stanford@leg.wa.gov];
mike.steele@leg.wa.gov[mike.steele@leg.wa.gov]; Drew.Stokesbary@leg.wa.gov[Drew.Stokesbary@leg.wa.gov];
Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov];
Dean.Takko@leg.wa.gov[Dean.Takko@leg.wa.gov]; Gael.Tarleton@leg.wa.gov[Gael.Tarleton@leg.wa.gov];
David.Taylor@leg.wa.gov[David.Taylor@leg.wa.gov]; Steve.Tharinger@leg.wa.gov[Steve.Tharinger@leg.wa.gov];
Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov];
Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov];
Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov];
Jim.Walsh@leg.wa.gov[Jim.Walsh@leg.wa.gov]; Maureen.Walsh@leg.wa.gov[Maureen.Walsh@leg.wa.gov];
Judy.Warnick@leg.wa.gov[Judy.Warnick@leg.wa.gov]; Lisa.Wellman@leg.wa.gov[Lisa.Wellman@leg.wa.gov];
JT.Wilcox@leg.wa.gov[JT.Wilcox@leg.wa.gov]; Lynda.Wilson@leg.wa.gov[Lynda.Wilson@leg.wa.gov];
Sharon.Wylie@leg.wa.gov[Sharon.Wylie@leg.wa.gov]; Jesse.Young@leg.wa.gov[Jesse.Young@leg.wa.gov];
Hans.Zeiger@leg.wa.gov[Hans.Zeiger@leg.wa.gov]; kanchanmvk@yahoo.com[kanchanmvk@yahoo.com];
ushamvk@yahoo.co.in[ushamvk@yahoo.co.in]; mike.agogliati@wfsb.com[mike.agogliati@wfsb.com];
fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com]; wjbkwebteam@foxtv.com;[wjbkwebteam@foxtv.com];
sanjay.mishra@Vanderbilt.Edu[sanjay.mishra@Vanderbilt.Edu]; kienym@who.int[kienym@who.int];
Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu]; sbaldwin@idri.org[sbaldwin@idri.org];
friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov]; Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org];
cww@austin.utexas.edu[cww@austin.utexas.edu]; mail@wired.com[mail@wired.com]; submit@wired.com[submit@wired.com];
megan_molteni@wired.com[megan_molteni@wired.com]; tyagi@ebi.ac.uk[tyagi@ebi.ac.uk];
Nick.Furnham@lshtm.ac.uk[Nick.Furnham@lshtm.ac.uk]; betsy.mckay@wsj.com[betsy.mckay@wsj.com];
spencer.macnaughton@wsj.com[spencer.macnaughton@wsj.com]; conall.jones@wsj.com[conall.jones@wsj.com];
brianna.abbott@wsj.com[brianna.abbott@wsj.com]; Christopher.Weaver@wsj.com[Christopher.Weaver@wsj.com];
jared.hopkins@wsj.com[jared.hopkins@wsj.com]; Peter.Loftus@dowjones.com[Peter.Loftus@dowjones.com];
dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int];
wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com];
lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk];
mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk];
Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com];
Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de];
zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com];
badrishanthi@hotmail.com[badrishanthi@hotmail.com]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au];
ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com]; suoban@simm.ac.cn[suoban@simm.ac.cn];
wiv@wh.iov.cn[wiv@wh.iov.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg];
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david.szymkowski@xencor.com[david.szymkowski@xencor.com]; media.relations@roche.com[media.relations@roche.com];
murthy.aditya@gene.com[murthy.aditya@gene.com]; joshua.wallach@yale.edu[joshua.wallach@yale.edu];
alexander.egilman@yale.edu[alexander.egilman@yale.edu]; margaret.e.mccarthy@yale.edu[margaret.e.mccarthy@yale.edu];
jennifer.miller@nyumc.org[jennifer.miller@nyumc.org]; steven.woloshin@dartmouth.edu[steven.woloshin@dartmouth.edu];
lisa.schwartz@dartmouth.edu[lisa.schwartz@dartmouth.edu]; joseph.ross@yale.edu[joseph.ross@yale.edu];
johan.neyts@kuleuven.be[johan.neyts@kuleuven.be]; kai.dallmeier@kuleuven.be[kai.dallmeier@kuleuven.be];
hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; manjunath.k@zyduscadila.com[manjunath.k@zyduscadila.com];
rajeshbahekar@zyduscadila.com[rajeshbahekar@zyduscadila.com];

ashokd.jaiswal@zyduscadila.com[ashokd.jaiswal@zyduscadila.com];
kevinkumarkansagra@zyduscadila.com[kevinkumarkansagra@zyduscadila.com];
poonamgiri@zyduscadila.com[poonamgiri@zyduscadila.com]; mukul.jain@zyduscadila.com[mukul.jain@zyduscadila.com];
abhijitchatterjee@zyduscadila.com[abhijitchatterjee@zyduscadila.com];
amitjoharapurkar@zyduscadila.com[amitjoharapurkar@zyduscadila.com];
nuggehally.srinivas@zyduscadila.com[nuggehally.srinivas@zyduscadila.com];
sameeragarwal@zyduscadila.com[sameeragarwal@zyduscadila.com];
Deven.Parmar@zyduscadila.com[Deven.Parmar@zyduscadila.com];
maulikr.patel@zyduscadila.com[maulikr.patel@zyduscadila.com]; gattinoniluciano@gmail.com[gattinoniluciano@gmail.com];
sapna@jhmi.edu[sapna@jhmi.edu]; aluks@uw.edu[aluks@uw.edu]; hooman.poor@mssm.edu[hooman.poor@mssm.edu];
christoph.steininger@meduniwien.ac.at[christoph.steininger@meduniwien.ac.at];
jkorzenik@bwh.harvard.edu[jkorzenik@bwh.harvard.edu]; mdlarsen@health.sdu.dk[mdlarsen@health.sdu.dk];
jan.nielsen2@rsyd.dk[jan.nielsen2@rsyd.dk]; jens.kjeldsen@rsyd.dk[jens.kjeldsen@rsyd.dk];
bente.noergaard@rsyd.dk[bente.noergaard@rsyd.dk]; akavanaugh@ucsd.edu[akavanaugh@ucsd.edu];
philipose.jobin@gmail.com[philipose.jobin@gmail.com]; Kenneth-gordon@northwestern.edu[Kenneth-gordon@northwestern.edu];
Richard.Colletti@uvm.edu[Richard.Colletti@uvm.edu]; melinda.engevik@bcm.edu[melinda.engevik@bcm.edu];
bruce.sands@mssm.edu[bruce.sands@mssm.edu]; bryce.a.mendelsohn@kp.org[bryce.a.mendelsohn@kp.org];
ferrislk@upmc.edu[ferrislk@upmc.edu]; graghu@u.washington.edu[graghu@u.washington.edu];
jack.mzhou@gmail.com[jack.mzhou@gmail.com]; joaquimjferreira@gmail.com[joaquimjferreira@gmail.com];
luca.richeldi@policlinicogemelli.it[luca.richeldi@policlinicogemelli.it]; mark@tetratherapeutics.com[mark@tetratherapeutics.com];
neb225@gmail.com[neb225@gmail.com]; rbhild@rbht.nhs.uk[rbhild@rbht.nhs.uk];
rfarrell@caregroup.harvard.edu[rfarrell@caregroup.harvard.edu]; rxx@case.edu[rxx@case.edu];
vivek.rudrapatna@ucsf.edu[vivek.rudrapatna@ucsf.edu]
From: vinu arumugham[igesynth@yahoo.com]
Sent: Fri 8/14/2020 3:10:51 PM (UTC-05:00)
Subject: Prof. Kounis and I link Kounis syndrome to COVID-19, dengue; Famotidine/Cetirizine improve COVID-19 outcomes; Make them standard of care, NOW.

Prof. Kounis' team and I, describe the common immunological mechanisms involved in cardiac injury in COVID-19, severe dengue infection and allergic reactions/anaphylaxis (Kounis syndrome). The medications for prevention/treatment include famotidine/cetirizine.

The passepartout wayfares of Covid-19, Cytokine storm and Kounis syndrome

https://doi.org/10.5281/zenodo.3977923
Dual-Histamine Blockade with Cetirizine - Famotidine Reduces Pulmonary Symptoms in COVID-19 Patients
https://www.medrxiv.org/content/10.1101/2020.06.30.20137752v1

I predicted in **JANUARY 2020** (email below) that mast cell stabilizers and antihistamines can help in COVID-19. I notified health authorities and thousands of doctors/researchers, worldwide. Hundreds of thousands of lives could have been saved.

The **key is to understand that COVID-19 severity is a result of an allergic reaction to the virus**, a "slow rolling anaphylaxis". **WE HAVE PROVEN TREATMENTS FOR ANAPHYLAXIS. NO CLINICAL TRIALS NEEDED.**

The diagnosis and management of anaphylaxis: An updated practice parameter

https://www.jacionline.org/article/S0091-6749(05)00115-6/fulltext

"These protocols have recommended the administration of **H1 and H2 antagonists, β-agonists, antileukotrienes, and corticosteroids**."

Cetirizine is an histamine H1 blocker or antagonist. Famotidine is an histamine H2 blocker or antagonist.

These safe, OTC drugs above can be used immediately upon COVID-19 symptoms (or even a low dose if

exposure is suspected). Mast cell stabilizers, β-agonists, antileukotrienes, and corticosteroids can be prescribed as standard of care. Hundreds of thousands of lives can be saved.

As I wrote in my comment posted in the Annals of Internal Medicine:

Please see comments section:

https://annals.org/aim/fullarticle/2764199/use-hydroxychloroquine-chloroquine-during-covid-19-pandemic-what-every-clinician

Understanding mechanisms is better than demanding clinical trials in the middle of a pandemic

More details:

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
https://www.researchsquare.com/article/rs-30934/v2

Repositioning Chromones for Early Anti-inflammatory Treatment of COVID-19

https://www.frontiersin.org/articles/10.3389/fphar.2020.00854/full

Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy

https://pubmed.ncbi.nlm.nih.gov/32013309/

Thanks,
Vinu

-------- Forwarded Message --------

Subject: Wuhan 2019-nCoV treatment; Vaccines induce autoimmunity: Epitope database evidence; Ebola vaccine will cause rice allergy epidemic
Date: Fri, 24 Jan 2020 17:42:02 -0800
From: vinu arumugham <igesynth@yahoo.com>
To: jay.slater@fda.hhs.gov <jay.slater@fda.hhs.gov>, jane.woo@fda.hhs.gov <jane.woo@fda.hhs.gov>, maureen.hess@fda.hhs.gov <maureen.hess@fda.hhs.gov>, Richard.Forshee@fda.hhs.gov <Richard.Forshee@fda.hhs.gov>, Mark.Walderhaug@fda.hhs.gov <Mark.Walderhaug@fda.hhs.gov>, CBER OCOD Consumer Account <cberocod@fda.hhs.gov>, Destefano, Frank (CDC/OID/NCEZID) <fxd1@cdc.gov>, isq8@cdc.gov <isq8@cdc.gov>, nar5@cdc.gov <nar5@cdc.gov>, hjn0@cdc.gov <hjn0@cdc.gov>, Secretary@HHS.gov <Secretary@HHS.gov>, CommissionerFDA@fda.hhs.gov <CommissionerFDA@fda.hhs.gov>, olx1@cdc.gov <olx1@cdc.gov>, directorsincoming@cdc.gov <directorsincoming@cdc.gov>, francis.collins@nih.gov <francis.collins@nih.gov>, mrolfes1@cdc.gov <mrolfes1@cdc.gov>, xzd2@cdc.gov <xzd2@cdc.gov>, acy9@cdc.gov <acy9@cdc.gov>, dbj0@cdc.gov <dbj0@cdc.gov>, jmk9@cdc.gov <jmk9@cdc.gov>, tft9@cdc.gov <tft9@cdc.gov>, gll9@cdc.gov <gll9@cdc.gov>, sharplessne@nih.hhs.gov <sharplessne@nih.hhs.gov>, tnc4@cdc.gov <tnc4@cdc.gov>, kok4@cdc.gov <kok4@cdc.gov>, rxl3@cdc.gov <rxl3@cdc.gov>, gbq7@cdc.gov <gbq7@cdc.gov>, fwf7@cdc.gov <fwf7@cdc.gov>, megan.mcseveney@fda.hhs.gov <megan.mcseveney@fda.hhs.gov>, afauci@niaid.nih.gov <afauci@niaid.nih.gov>, Emelia.Benjamin@bmc.org <Emelia.Benjamin@bmc.org>, mjessup@leducq.com <mjessup@leducq.com>, tavori@ohsu.edu <tavori@ohsu.edu>,

jessica.lilley@vanderbilt.edu <jessica.lilley@vanderbilt.edu>, web@beasleyallen.com <web@beasleyallen.com>, dr.flegg@bfwhospitals.nhs.uk <dr.flegg@bfwhospitals.nhs.uk>

IgE mediated sensitization to peptides that have homology to 2019-nCoV peptides may contribute to disease severity. In that case, antihistamines and other allergy treatments such as mast cell stabilizers may help reduce infection severity.

A BLASTP analysis of 2019-nCoV proteome against common vaccine antigens was performed. Preliminary results suggest that IgE mediated sensitization to common vaccine antigens can result in cross reactive immune responses to 2019-nCoV.

Please see details of the mechanisms here:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

https://www.quora.com/Why-was-the-flu-so-deadly-in-outbreaks-in-the-past-And-what-made-the-flu-become-less-deadly/answers/86456279

"Scientists" at the global vaccine safety summit spill the beans: There is no science behind vaccine safety claims, it's a fairy tale.

The party is over folks.

https://youtu.be/s2IujhTdCLE

ERVEBO Ebola vaccine will create a rice allergy epidemic, add to numerous autoimmune diseases, cancer and make Ebola disease even more severe. Design for safety and vaccine safety regulation remain abject failures. Incompetence or indifference?
https://doi.org/10.5281/zenodo.3595020

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

https://doi.org/10.5281/zenodo.3603480

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

Vinu Arumugham
Jan 2020
vinucubeacc@gmail.com

Lay summary

Proteins are a chain of amino acids. Proteins can have up to several hundred amino acids. Snippets of proteins (peptides), 7-15 amino acids in length are important in immunology. There are 20 types of amino acids. Each is assigned a letter (1 letter code).

Antibodies are proteins that can bind to peptides that have a specific amino acid sequence. Such a target peptide is known as an epitope. When an antibody binds to a peptide (which is part of a protein, which in turn may be part of a cell surface), it can trigger an immune attack on the cell. If the cell were a bacterium, the bacterium would be killed.

Humans (like all organisms) are made of numerous proteins (self proteins). So we have self-proteins, self-peptides and self-epitopes. In a healthy person, the body will not make antibodies that bind strongly to self-peptides (self-tolerance).

DNA is a chain of base-pairs. The DNA base-pair sequence determines the amino acid sequence in the protein produced. If there is a mutation that alters a single base-pair, the resulting protein will have a single amino acid that is altered. To prevent cancer, the immune system is capable of making antibodies against such altered peptides. Such antibodies can also weakly bind (cross react) to the unaltered normal peptide thus resulting in destruction of some healthy cells.

Say a normal protein has the following peptide (10 amino acids, each represented by its 1 letter code):

ALSTLVVNKI

Say DNA in a cell mutates due to a carcinogen exposure and it alters the protein thus resulting in this peptide with a single amino acid change:

ALSTLVV**S**KI

When the immune system makes antibodies targeted at ALSTLVV**S**KI (to attack the cell with the DNA mutation), the same antibodies can weakly bind to the normal ALSTLVVNKI peptide.

ALSTLVVNKI is an epitope associated with rheumatoid arthritis (RA).

So as a result of the immune system defending against cancer, the person can develop RA.

Now consider vaccines containing animal proteins. Animal proteins are very similar to human proteins, containing only occasional amino acid differences. An animal peptide could therefore have the ALSTLVV**S**KI sequence. Such a vaccine would fool the immune system into creating an anti-cancer immune response, creating antibodies targeted at ALSTLVV**S**KI. The result is vaccine induced RA.

Therefore one can predict that analyzing epitopes associated with autoimmune diseases, such single amino acid difference compared to animal peptides present in vaccines, would occur more frequently than can be expected merely by chance. The analysis confirms that this prediction is valid.

Abstract

The National Institute of Allergy and Infectious Diseases (NIAID) sponsors the Immune Epitope Data Base (IEDB). IEDB contains epitopes identified from the medical literature and organized by diseases and categories of diseases. All epitopes (23000+) associated with 82 autoimmune diseases in humans were analyzed.

The role of animal, plant, fungal proteins contained in vaccines in the etiology of autoimmune diseases have been described in humans and animals. BLASTP was used to analyze IEDB derived epitopes for sequence alignment to animal, plant, fungal (APF) proteins present in vaccines and biologics. Specifically, the search was performed against bovine, chicken, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes.

The results show that 57% of epitopes differed by exactly one amino acid residue from an APF peptide. 78% of the epitopes differed by up to two amino acid residues from an APF peptide. The rest of the epitopes were either identical or differed by more than two amino acid residues.

A majority of IEDB epitopes analyzed were 9-mer peptides. Comparing randomly selected 9-mer human peptides with APF proteomes, the probability of single amino acid residue difference (SAARD) outcomes was derived. This was used to

estimate the probability that actual IEDB SAARD alignments to APF peptides were merely a chance outcome. The estimates show that the probability that the observed IEDB alignments to APF being merely a chance outcome are vanishingly small. So the results make it absolutely clear that APF proteins in vaccines cause all these autoimmune diseases.

Introduction

Vaccines contain thousands of residual animal, plant and fungal (APF) proteins from the manufacturing process (1–6). 293 chicken proteins were identified in the influenza vaccine (7), for example. Actin and vimentin proteins were detected in the Priorix Tetra vaccine (8). Immunization with homologous xenogeneic antigens resulting in autoimmune diseases has been known for at least 40 years (9). Vaccines that contain bovine proteins caused autoimmunity in dogs (10). We previously described the immunological mechanism involved in autoimmunity induction by immunization with homologous xenogeneic antigens (11).

Cancer cells have minor differences when compared to healthy cells. Due to mutation of the DNA encoding the proteins, cancer cells can display altered proteins on their surface. Healthy cancer defense mechanisms include immune responses directed at such altered proteins. Therefore an immune response directed against cancer cells always carries a risk of cross reactive immune responses against healthy cells displaying the unaltered protein. Therefore, cancer induced autoimmune responses are a consequence of normal, healthy immune system behavior.

Animal proteins have minor differences compared to human proteins. Peptides that are identical between humans and animals are unlikely to cause any problem due to strong self tolerance. However, peptides with one amino acid residue difference produce the strongest cross reactive immune responses (11). They are ideally suited to induce autoimmune diseases. Injecting animal proteins results in anti-cancer immune responses because the immune system perceives animal proteins as altered human proteins. Adjuvants in the vaccine boost this anti-cancer immune response. This artificial anti-cancer response directed at thousands of APF proteins in vaccines or biologics, therefore cross react and cause numerous autoimmune disorders.

For this reason, one can predict that single amino acid residue difference (SAARD) between autoimmune disease related epitopes in the IEDB and homologous APF peptides in vaccines, would occur at a higher probability than by mere chance. We perform a BLASTP analysis to verify.

Methods

Basic local alignment search tool for proteins (BLASTP) (12), Universal Protein Resource (UniProt)(13) and the Immune Epitope Database (IEDB) (14) were used for bioinformatics analysis.

Specifically, the BLASTP sequence alignment of IEDB peptides was performed against bovine, chick, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes. Vaccines and biologics contain residual proteins from all these organism due to media used to grow viruses or bacteria, recombinant cells/organisms used for protein expression or as excipients.

Results

57% of IEDB peptides have a SAARD and 78% have up to two amino acid differences compared to animal, fungal or plant peptides present in vaccines.

Discussion

Could this result be a chance occurrence?

A majority of IEDB epitopes analyzed were 9-mer peptides. Five thousand 9-mer peptides were chosen at random from the human proteome. BLASTP was run using these peptides to compare against each organism's proteome or a subset. This provides us the probability that randomly selected human peptides have an alignment providing a SAARD compared to peptides from these organisms. These are listed in table 1 under " Random SAARD alignment". Given this, we can compute the probability of the actual SAARD alignment to IEDB epitopes, occurring by chance. This is listed in table 1 under "Estimated probability of actual SAARD outcome occurring just by chance".

For a simple coin toss example, we would perform the calculation as follows:

Computing probability of say a 7 heads, 3 tails outcome of 10 trials of a fair coin:

Probability = (0.5^7) x (0.5^3) x 10! / (7! x 3!)

Where:

0.5 is the probability of a head or tail outcome of a fair coin.

For an unfair coin, say probability of head outcome = 0.4 and tail outcome 0.6, we would have:

Probability = (0.4^7) x (0.6^3) x 10! / (7! x 3!)

For the IEDB peptide probability analysis, the outcome is for 23192 trials (peptides).

The "head outcome" is the "Random SAARD alignment " entries in table 1. The "tail outcome" probability is 1-"head

outcome".

Sample calculation for Chinese Hamster:

Probability = ((889/5000)^4574) x ((4111/5000)^18618) x 23192! / (4574! x 18618!)

Probability = 1.488e-15

Where: 889*100/5000 = 17.8% is the entry in Table 1 for Chinese Hamster. BLASTP analysis shows 889 SAARD out of 5000 peptides analyzed.

And, 4574*100/23192=19.7% is the IEDB entry in Table 1 for Chinese Hamster. BLASTP analysis shows 4574 SAARD out of 23192 peptides analyzed.

So the 1.488e-15 value is the probability that we will have exactly 4574 SAARD alignments out of 23192 peptides. The probability goes down for all values > 4574. Conservatively, applying the same probability as for 4574, to all values >4574, we can calculate the probability of the chance occurrence of 4574 or greater number of SAARD alignments as 1.488e15 * 18618 = 27e-12, entry in table.

The Gnome calculator was used to perform these calculations and the results were verified using the Qalculate! calculator and WolframAlpha (15) since spreadsheets are unable to perform these calculations.

Table 1

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
African green monkey (*Chlorocebus aethiops*)	26 (0.5)	420 (1.8)	~1.7e-96	Probabilit is vanishi vaccines,
Cow (*Bos taurus*)	936 (18.7)	4385 (18.9)	~1	There are occurred j cow protei amount is bovine gel vaccines. tissues in other cow more likel entry belo
Cow's Milk (*Bos taurus*)	0 (0)	12 (0.05)	0	Probabilit is 0. So th these disea
Chinese Hamster (*Cricetulus griseus*)	889 (17.8)	4574 (19.7)	~27e-12	Probabilit is vanishi vaccines,
Chicken (*Gallus gallus*)	536 (10.7)	3901 (16.8)	<1e-100	Probabilit is vanishi vaccines, porcine an embryo is proteins ca
Guinea Pig (*Cavia porcellus*)	837 (16.7)	4439 (19.1)	~1e-18	Probabilit is vanishi vaccines,
Mice (*Mus musculus*)	940 (18.8)	4467 (19.3)	~1	There are occurred j

				mice prote amount is cells are u proteins pr present in be present
Maize (*Zea mays*)	303 (6.1)	1667 (7.2)	~5e-9	Probability is vanishin vaccines,
Peanut (*Arachis hypogaea)*	223 (4.5)	1697 (7.3)	~79e-81	Probability is vanishin vaccines,
Yeast *(Saccharomyces cerevisiae)*	64 (1.3)	828 (3.6)	<1e-100	Probability is vanishin vaccines,
Sesame (*Sesamum indicum*)	155 (3.1)	1398 (6.0)	<1e-100	Probability is vanishin vaccines,
Soy (*Glycine max)*	215 (4.3)	1548 (6.7)	~86e-59	Probability is vanishin vaccines,
Pig (*Sus scrofa*)	963 (19.3)	4407 (19.0)	~1	There are occurred ju porcine pr amount is used in va present in vaccines b present. T
Wheat (*Triticum aestivum*)	138 (2.8)	977 (4.2)	~18e-33	Probability is vanishin vaccines,

The calculations make it clear that the findings cannot be merely a chance outcome and that immunization against animal/plant/fungal antigens in the vaccines do cause these autoimmune diseases in the IEDB.

Conclusion

Vaccines containing animal, plant or fungal proteins are extremely dangerous and cause numerous autoimmune diseases and cancer (16–19). All non-target proteins in vaccines must be immediately removed using processes such affinity chromatography (20).

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To: sanjay.mishra@Vanderbilt.Edu[sanjay.mishra@Vanderbilt.Edu]; kienym@who.int[kienym@who.int]; Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu]; sbaldwin@idri.org[sbaldwin@idri.org]; friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov]; Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org]; cww@austin.utexas.edu[cww@austin.utexas.edu]; henaorestrepoa@who.int[henaorestrepoa@who.int]; www.felix@konpotey-ahulu.com[www.felix@konpotey-ahulu.com]; Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov]; Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov]; Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov]; John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov]; Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov]; Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov]; Terry.Nealey@leg.wa.gov[Terry.Nealey@leg.wa.gov]; Sharon.Nelson@leg.wa.gov[Sharon.Nelson@leg.wa.gov]; Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov]; Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov]; Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov]; Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov]; Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov]; Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov]; Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov]; Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov]; Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov]; Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov]; Cindy.Ryu@leg.wa.gov[Cindy.Ryu@leg.wa.gov]; Rebecca.Saldana@leg.wa.gov[Rebecca.Saldana@leg.wa.gov]; SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov]; Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov]; Mike.Sells@leg.wa.gov[Mike.Sells@leg.wa.gov]; Tana.Senn@leg.wa.gov[Tana.Senn@leg.wa.gov]; Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov]; Shelly.Short@leg.wa.gov[Shelly.Short@leg.wa.gov]; Vandana.Slatter@leg.wa.gov[Vandana.Slatter@leg.wa.gov]; Norma.Smith@leg.wa.gov[Norma.Smith@leg.wa.gov]; Larry.Springer@leg.wa.gov[Larry.Springer@leg.wa.gov]; Melanie.Stambaugh@leg.wa.gov[Melanie.Stambaugh@leg.wa.gov]; Derek.Stanford@leg.wa.gov[Derek.Stanford@leg.wa.gov]; mike.steele@leg.wa.gov[mike.steele@leg.wa.gov]; Drew.Stokesbary@leg.wa.gov[Drew.Stokesbary@leg.wa.gov]; Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov]; Dean.Takko@leg.wa.gov[Dean.Takko@leg.wa.gov]; Gael.Tarleton@leg.wa.gov[Gael.Tarleton@leg.wa.gov]; David.Taylor@leg.wa.gov[David.Taylor@leg.wa.gov]; Steve.Tharinger@leg.wa.gov[Steve.Tharinger@leg.wa.gov]; Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov]; Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov]; Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov]; Jim.Walsh@leg.wa.gov[Jim.Walsh@leg.wa.gov]; Maureen.Walsh@leg.wa.gov[Maureen.Walsh@leg.wa.gov]; Judy.Warnick@leg.wa.gov[Judy.Warnick@leg.wa.gov]; Lisa.Wellman@leg.wa.gov[Lisa.Wellman@leg.wa.gov]; JT.Wilcox@leg.wa.gov[JT.Wilcox@leg.wa.gov]; Lynda.Wilson@leg.wa.gov[Lynda.Wilson@leg.wa.gov]; Sharon.Wylie@leg.wa.gov[Sharon.Wylie@leg.wa.gov]; Jesse.Young@leg.wa.gov[Jesse.Young@leg.wa.gov]; Hans.Zeiger@leg.wa.gov[Hans.Zeiger@leg.wa.gov]; dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int]; wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com]; lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk]; mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de]; zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com]; badrishanthi@hotmail.com[badrishanthi@hotmail.com]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au]; ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com]; suoban@simm.ac.cn[suoban@simm.ac.cn]; wiv@wh.iov.cn[wiv@wh.iov.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg]; oon_tek_ng@ncid.sg[oon_tek_ng@ncid.sg]; Linfa.wang@csiro.au[Linfa.wang@csiro.au]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; david.szymkowski@xencor.com[david.szymkowski@xencor.com]; media.relations@roche.com[media.relations@roche.com]; murthy.aditya@gene.com[murthy.aditya@gene.com]; joshua.wallach@yale.edu[joshua.wallach@yale.edu]; alexander.egilman@yale.edu[alexander.egilman@yale.edu]; margaret.e.mccarthy@yale.edu[margaret.e.mccarthy@yale.edu]; jennifer.miller@nyumc.org[jennifer.miller@nyumc.org]; steven.woloshin@dartmouth.edu[steven.woloshin@dartmouth.edu]; lisa.schwartz@dartmouth.edu[lisa.schwartz@dartmouth.edu]; joseph.ross@yale.edu[joseph.ross@yale.edu]; johan.neyts@kuleuven.be[johan.neyts@kuleuven.be]; kai.dallmeier@kuleuven.be[kai.dallmeier@kuleuven.be]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; manjunath.k@zyduscadila.com[manjunath.k@zyduscadila.com]; rajeshbahekar@zyduscadila.com[rajeshbahekar@zyduscadila.com]; 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Deven.Parmar@zyduscadila.com[Deven.Parmar@zyduscadila.com];
maulikr.patel@zyduscadila.com[maulikr.patel@zyduscadila.com]; gattinoniluciano@gmail.com[gattinoniluciano@gmail.com];
sapna@jhmi.edu[sapna@jhmi.edu]; aluks@uw.edu[aluks@uw.edu]; hooman.poor@mssm.edu[hooman.poor@mssm.edu];
christoph.steininger@meduniwien.ac.at[christoph.steininger@meduniwien.ac.at]; abhauber@rti.org[abhauber@rti.org];
husnie@ccf.org[husnie@ccf.org]; mjbergman@prodigy.net[mjbergman@prodigy.net];
masellicacer@uthscsa.edu[masellicacer@uthscsa.edu]
From: vinu arumugham[vaccine.safety@aol.com]
Sent: Sun 9/27/2020 4:03:23 PM (UTC-05:00)
Subject: Flu shot makes COVID-19 worse, confirmed by Cleveland Clinic; Make Famotidine/Cetirizine SOC for COVID-19; COVID-19 vaccines are unsafe

Mechanistic evidence (prediction)

Proteins that contaminate influenza vaccines have high homology to SARS-CoV-2 proteins thus increasing risk of severe COVID-19 disease and mortality
https://doi.org/10.5281/zenodo.3996984

Epidemiological evidence (confirmation)

Flu shot increases risk of COVID-19 Hospitalization **240%**, ICU admission **204%**, Hospital mortality **232%**.

Safety of Influenza Vaccine during COVID-19

https://doi.org/10.1017/cts.2020.543

"Among individuals with a positive SARS-CoV-2 test, patients previously vaccinated for influenza in 2019 were more likely to be hospitalized. Once hospitalized, they were more likely to be admitted to the ICU and die during hospitalization."

From Table 1:

	Never Vaccinated (N=1,125)	Vaccinated in 2019 (N=309)
Hospitalization - no.(%)	192 (17.1)	127 (41.1)
ICU Admission - no.(%)	77 (6.8)	43 (13.9)
Hospital Mortality - no.(%)	32 (2.8)	20 (6.5)

My comment posted in the Annals of Internal Medicine

The iatrogenic cascade of illnesses

https://www.acpjournals.org/doi/full/10.7326/M20-2470#_comments

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COVID-19 vaccines are **fundamentally flawed and unsafe**. Details below:

The CanSino Biologics vaccine:

https://publons.com/r/9024531/

The Oxford vaccine:

https://publons.com/r/9015091/

The Moderna mRNA vaccine:

https://publons.com/r/9025990/

The Pfizer/BioNTech vaccine:

https://publons.com/r/9026177/

The Novavax vaccine

https://publons.com/review/9108287/

Prof. Kounis' team and I, describe the common immunological mechanisms involved in cardiac injury in COVID-19, severe dengue infection and allergic reactions/anaphylaxis (Kounis syndrome). The medications for prevention/treatment include famotidine/cetirizine.

The passepartout wayfares of Covid-19, Cytokine storm and Kounis syndrome

https://doi.org/10.5281/zenodo.3977923
Dual-Histamine Blockade with Cetirizine - Famotidine Reduces Pulmonary Symptoms in COVID-19 Patients
https://www.medrxiv.org/content/10.1101/2020.06.30.20137752v1

I predicted in **JANUARY 2020** (email below) that mast cell stabilizers and antihistamines can help in COVID-19. I notified health authorities and thousands of doctors/researchers, worldwide. Hundreds of thousands of lives could have been saved.

The **key is to understand that COVID-19 severity is a result of an allergic reaction to the virus**, a "slow rolling anaphylaxis". **WE HAVE PROVEN TREATMENTS FOR ANAPHYLAXIS. NO CLINICAL TRIALS NEEDED.**

The diagnosis and management of anaphylaxis: An updated practice parameter

https://www.jacionline.org/article/S0091-6749(05)00115-6/fulltext

"These protocols have recommended the administration of **H1 and H2 antagonists, ??-agonists, antileukotrienes, and corticosteroids**."

Cetirizine is an histamine H1 blocker or antagonist. Famotidine is an histamine H2 blocker or antagonist.

These safe, OTC drugs above can be used immediately upon COVID-19 symptoms (or even a low dose if exposure is suspected). Mast cell stabilizers, ??-agonists, antileukotrienes, and corticosteroids can be prescribed as standard of care. Hundreds of thousands of lives can be saved.

As I wrote in my comment posted in the Annals of Internal Medicine:

Please see comments section:

https://annals.org/aim/fullarticle/2764199/use-hydroxychloroquine-chloroquine-during-covid-19-pandemic-what-every-clinician

Understanding mechanisms is better than demanding clinical trials in the middle of a pandemic

More details:

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
https://www.researchsquare.com/article/rs-30934/v2

Repositioning Chromones for Early Anti-inflammatory Treatment of COVID-19

https://www.frontiersin.org/articles/10.3389/fphar.2020.00854/full

Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy??

https://pubmed.ncbi.nlm.nih.gov/32013309/

Thanks,
Vinu

-------- Forwarded Message --------

Subject: Wuhan 2019-nCoV treatment; Vaccines induce autoimmunity: Epitope database evidence; Ebola vaccine will cause rice allergy epidemic
Date: Fri, 24 Jan 2020 17:42:02 -0800
From: vinu arumugham <igesynth@yahoo.com>
To: jay.slater@fda.hhs.gov <jay.slater@fda.hhs.gov>, jane.woo@fda.hhs.gov <jane.woo@fda.hhs.gov>, maureen.hess@fda.hhs.gov <maureen.hess@fda.hhs.gov>, Richard.Forshee@fda.hhs.gov <Richard.Forshee@fda.hhs.gov>, Mark.Walderhaug@fda.hhs.gov <Mark.Walderhaug@fda.hhs.gov>, CBER OCOD Consumer Account <cberocod@fda.hhs.gov>, Destefano, Frank (CDC/OID/NCEZID) <fxd1@cdc.gov>, isq8@cdc.gov <isq8@cdc.gov>, nar5@cdc.gov <nar5@cdc.gov>, hjn0@cdc.gov <hjn0@cdc.gov>, Secretary@HHS.gov <Secretary@HHS.gov>, CommissionerFDA@fda.hhs.gov <CommissionerFDA@fda.hhs.gov>, olx1@cdc.gov <olx1@cdc.gov>, directorsincoming@cdc.gov <directorsincoming@cdc.gov>, francis.collins@nih.gov <francis.collins@nih.gov>, mrolfes1@cdc.gov <mrolfes1@cdc.gov>, xzd2@cdc.gov <xzd2@cdc.gov>, acy9@cdc.gov <acy9@cdc.gov>, dbj0@cdc.gov <dbj0@cdc.gov>, jmk9@cdc.gov <jmk9@cdc.gov>, tft9@cdc.gov <tft9@cdc.gov>, gll9@cdc.gov <gll9@cdc.gov>, sharplessne@nih.hhs.gov <sharplessne@nih.hhs.gov>, tnc4@cdc.gov <tnc4@cdc.gov>, kok4@cdc.gov <kok4@cdc.gov>, rxl3@cdc.gov <rxl3@cdc.gov>, gbq7@cdc.gov <gbq7@cdc.gov>, fwf7@cdc.gov <fwf7@cdc.gov>, megan.mcseveney@fda.hhs.gov <megan.mcseveney@fda.hhs.gov>, afauci@niaid.nih.gov <afauci@niaid.nih.gov>, Emelia.Benjamin@bmc.org <Emelia.Benjamin@bmc.org>, mjessup@leducq.com <mjessup@leducq.com>, tavori@ohsu.edu <tavori@ohsu.edu>, jessica.lilley@vanderbilt.edu <jessica.lilley@vanderbilt.edu>, web@beasleyallen.com <web@beasleyallen.com>, dr.flegg@bfwhospitals.nhs.uk <dr.flegg@bfwhospitals.nhs.uk>

IgE mediated sensitization to peptides that have homology to 2019-nCoV peptides may contribute to disease severity. In that case, antihistamines and other allergy treatments such as mast cell stabilizers may help reduce infection severity.

A BLASTP analysis of 2019-nCoV proteome against common vaccine antigens was performed. Preliminary results suggest that IgE mediated sensitization to common vaccine antigens can result in cross reactive immune responses to 2019-nCoV.

Please see details of the mechanisms here:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

https://www.quora.com/Why-was-the-flu-so-deadly-in-outbreaks-in-the-past-And-what-made-the-flu-become-less-deadly/answers/86456279

"Scientists" at the global vaccine safety summit spill the beans: There is no science behind vaccine safety claims, it's a fairy tale.

The party is over folks.

https://youtu.be/s2IujhTdCLE

ERVEBO Ebola vaccine will create a rice allergy epidemic, add to numerous autoimmune diseases, cancer and make Ebola disease even more severe. Design for safety and vaccine safety regulation remain abject failures. Incompetence or indifference?
https://doi.org/10.5281/zenodo.3595020

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

https://doi.org/10.5281/zenodo.3603480

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

Vinu Arumugham
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vinucubeacc@gmail.com

Lay summary

Proteins are a chain of amino acids. Proteins can have up to several hundred amino acids. Snippets of proteins (peptides), 7-15 amino acids in length are important in immunology. There are 20 types of amino acids. Each is assigned a letter (1 letter

code).

Antibodies are proteins that can bind to peptides that have a specific amino acid sequence. Such a target peptide is known as an epitope.?? When an antibody binds to a peptide (which is part of a protein, which in turn may be part of a cell surface), it can trigger an immune attack on the cell. If the cell were a bacterium, the bacterium would be killed.

Humans (like all organisms) are made of numerous proteins (self proteins). So we have self-proteins, self-peptides and self-epitopes. In a healthy person, the body will not make antibodies that bind strongly to self-peptides (self-tolerance).

DNA is a chain of base-pairs. The DNA base-pair sequence determines the amino acid sequence in the protein produced. If there is a mutation that alters a single base-pair, the resulting protein will have a single amino acid that is altered. To prevent cancer, the immune system is capable of making antibodies against such altered peptides. Such antibodies can also weakly bind (cross react) to the unaltered normal peptide thus resulting in destruction of some healthy cells.

Say a normal protein has the following peptide (10 amino acids, each represented by its 1 letter code):

ALSTLVVNKI

Say DNA in a cell mutates due to a carcinogen exposure and it alters the protein thus resulting in this peptide with a single amino acid change:

ALSTLVV**S**KI

When the immune system makes antibodies targeted at ALSTLVV**S**KI (to attack the cell with the DNA mutation), the same antibodies can weakly bind to the normal ALSTLVVNKI peptide.

ALSTLVVNKI is an epitope associated with rheumatoid arthritis (RA).

So as a result of the immune system defending against cancer, the person can develop RA.

Now consider vaccines containing animal proteins. Animal proteins are very similar to human proteins, containing only occasional amino acid differences. An animal peptide could therefore have the ALSTLVV**S**KI sequence. Such a vaccine would fool the immune system into creating an anti-cancer immune response, creating antibodies targeted at ALSTLVV**S**KI. The result is vaccine induced RA.

Therefore one can predict that analyzing epitopes associated with autoimmune diseases, such single amino acid difference compared to animal peptides present in vaccines, would occur more frequently than can be expected merely by chance. The analysis confirms that this prediction is valid.

Abstract

The National Institute of Allergy and Infectious Diseases (NIAID) sponsors the Immune Epitope Data Base (IEDB). IEDB contains epitopes identified from the medical literature and organized by diseases and categories of diseases. All epitopes (23000+) associated with 82 autoimmune diseases in humans were analyzed.

The role of animal, plant, fungal proteins contained in vaccines in the etiology of autoimmune diseases have been described in humans and animals. BLASTP was used to analyze IEDB derived epitopes for sequence alignment to animal, plant, fungal (APF) proteins present in vaccines and biologics. Specifically, the search was performed against bovine, chicken, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes.

The results show that 57% of epitopes differed by exactly one amino acid residue from an APF peptide. 78% of the epitopes differed by up to two amino acid residues from an APF peptide. The rest of the epitopes were either identical or differed by more than two amino acid residues.

A majority of IEDB epitopes analyzed were 9-mer peptides. Comparing randomly selected 9-mer human peptides with APF proteomes, the probability of single amino acid residue difference (SAARD) outcomes was derived. This was used to estimate the probability that actual IEDB SAARD alignments to APF peptides were merely a chance outcome. The estimates show that the probability that the observed IEDB alignments to APF being merely a chance outcome are

vanishingly small. So the results make it absolutely clear that APF proteins in vaccines cause all these autoimmune diseases.

Introduction

Vaccines contain thousands of residual animal, plant and fungal (APF) proteins from the manufacturing process (1???6)???. 293 chicken proteins were identified in the influenza vaccine (7)???, for example. Actin and vimentin proteins were detected in the Priorix Tetra vaccine (8)???. Immunization with homologous xenogeneic antigens resulting in autoimmune diseases has been known for at least 40 years (9)???. Vaccines that contain bovine proteins caused autoimmunity in dogs (10)???. We previously described the immunological mechanism involved in autoimmunity induction by immunization with homologous xenogeneic antigens (11)???.

Cancer cells have minor differences when compared to healthy cells. Due to mutation of the DNA encoding the proteins, cancer cells can display altered proteins on their surface. Healthy cancer defense mechanisms include immune responses directed at such altered proteins. Therefore an immune response directed against cancer cells always carries a risk of cross reactive immune responses against healthy cells displaying the unaltered protein. Therefore, cancer induced autoimmune responses are a consequence of normal, healthy immune system behavior.

Animal proteins have minor differences compared to human proteins. Peptides that are identical between humans and animals are unlikely to cause any problem due to strong self tolerance. However, peptides with one amino acid residue difference produce the strongest cross reactive immune responses (11)???. They are ideally suited to induce autoimmune diseases. Injecting animal proteins results in anti-cancer immune responses because the immune system perceives animal proteins as altered human proteins. Adjuvants in the vaccine boost this anti-cancer immune response. This artificial anti-cancer response directed at thousands of APF proteins in vaccines or biologics, therefore cross react and cause numerous autoimmune disorders.

For this reason, one can predict that single amino acid residue difference (SAARD) between autoimmune disease related epitopes in the IEDB and homologous APF peptides in vaccines, would occur at a higher probability than by mere chance. We perform a BLASTP analysis to verify.

Methods

Basic local alignment search tool for proteins (BLASTP) (12)???, Universal Protein Resource (UniProt)(13)??? and the Immune Epitope Database (IEDB) (14)??? were used for bioinformatics analysis.

Specifically, the BLASTP sequence alignment of IEDB peptides was performed against bovine, chick, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes. Vaccines and biologics contain residual proteins from all these organism due to media used to grow viruses or bacteria, recombinant cells/organisms used for protein expression or as excipients.

Results

57% of IEDB peptides have a SAARD and 78% have up to two amino acid differences compared to animal, fungal or plant peptides present in vaccines.

Discussion

Could this result be a chance occurrence?

A majority of IEDB epitopes analyzed were 9-mer peptides. Five thousand 9-mer peptides were chosen at random from the human proteome. BLASTP was run using these peptides to compare against each organism???s proteome or a subset. This provides us the probability that randomly selected human peptides have an alignment providing a SAARD compared to peptides from these organisms. These are listed in table 1 under ??? Random SAARD alignment???. Given this, we can compute the probability of the actual SAARD alignment to IEDB epitopes, occurring by chance. This is listed in table 1 under ???Estimated probability of actual SAARD outcome occurring just by chance???.

For a simple coin toss example, we would perform the calculation as follows:

Computing probability of say a 7 heads, 3 tails outcome of 10 trials of a fair coin:

Probability = (0.5^7) x (0.5^3) x 10! / (7! x 3!)

Where:

0.5 is the probability of a head or tail outcome of a fair coin.

For an unfair coin, say probability of head outcome = 0.4 and tail outcome 0.6, we would have:

Probability = (0.4^7) x (0.6^3) x 10! / (7! x 3!)

For the IEDB peptide probability analysis, the outcome is for 23192 trials (peptides).

The ???head outcome??? is the ???Random SAARD alignment ??? entries in table 1. The ???tail outcome??? probability is 1-???head outcome???.

Sample calculation for Chinese Hamster:

Probability = ((889/5000)^4574) x ((4111/5000)^18618) x 23192! / (4574! x 18618!)

Probability = 1.488e-15

Where: 889*100/5000 = 17.8% is the entry in Table 1 for Chinese Hamster. BLASTP analysis shows 889 SAARD out of 5000 peptides analyzed.

And, 4574*100/23192=19.7% is the IEDB entry in Table 1 for Chinese Hamster. BLASTP analysis shows 4574 SAARD out of 23192 peptides analyzed.

So the 1.488e-15 value is the probability that we will have exactly 4574 SAARD alignments out of 23192 peptides. The probability goes down for all values > 4574. Conservatively, applying the same probability as for 4574, to all values >4574, we can calculate the probability of the chance occurrence of 4574 or greater number of SAARD alignments as 1.488e15 * 18618 = 27e-12, entry in table.

The Gnome calculator was used to perform these calculations and the results were verified using the Qalculate! calculator and WolframAlpha (15)??? since spreadsheets are unable to perform these calculations.

Table 1

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
African green monkey (*Chlorocebus aethiops*)	26 (0.5)	420 (1.8)	~1.7e-96	Probabilit is vanishi vaccines,
Cow (*Bos taurus*)	936 (18.7)	4385 (18.9)	~1	There are occurred j cow protei amount is bovine gel vaccines. tissues in other cow more likel entry belo
Cow???s Milk (*Bos taurus*)	0 (0)	12 (0.05)	0	Probabilit is 0. So th these disea
Chinese Hamster (*Cricetulus griseus*)	889 (17.8)	4574 (19.7)	~27e-12	Probabilit is vanishi vaccines,
Chicken (*Gallus gallus*)	536 (10.7)	3901 (16.8)	<1e-100	Probabilit is vanishi vaccines, porcine an embryo is proteins ca
Guinea Pig (*Cavia porcellus*)	837 (16.7)	4439 (19.1)	~1e-18	Probabilit is vanishi vaccines,
Mice (*Mus musculus*)	940 (18.8)	4467 (19.3)	~1	There are occurred j mice prote amount is

				cells are u proteins pr present in be present
Maize (*Zea mays*)	303 (6.1)	1667 (7.2)	~5e-9	Probability is vanishir vaccines,
Peanut (*Arachis hypogaea)*	223 (4.5)	1697 (7.3)	~79e-81	Probability is vanishir vaccines,
Yeast *(Saccharomyces cerevisiae)*	64 (1.3)	828 (3.6)	<1e-100	Probability is vanishir vaccines,
Sesame (*Sesamum indicum*)	155 (3.1)	1398 (6.0)	<1e-100	Probability is vanishir vaccines,
Soy (*Glycine max)*	215 (4.3)	1548 (6.7)	~86e-59	Probability is vanishir vaccines,
Pig (*Sus scrofa*)	963 (19.3)	4407 (19.0)	~1	There are occurred ju porcine pr amount is used in va present in vaccines b present. T
Wheat (*Triticum aestivum*)	138 (2.8)	977 (4.2)	~18e-33	Probability is vanishir vaccines,

The calculations make it clear that the findings cannot be merely a chance outcome and that immunization against animal/plant/fungal antigens in the vaccines do cause these autoimmune diseases in the IEDB.

Conclusion

Vaccines containing animal, plant or fungal proteins are extremely dangerous and cause numerous autoimmune diseases and cancer (16???19)???. All non-target proteins in vaccines must be immediately removed using processes such affinity chromatography (20)???.

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To: nick.whigham@verizonmedia.com[nick.whigham@verizonmedia.com];
claudia.j.chaves@lahey.org[claudia.j.chaves@lahey.org]; feedback@verywell.com[feedback@verywell.com];
press@verywell.com[press@verywell.com]; writeforus@verywell.com[writeforus@verywell.com];
joel.forman@mssm.edu[joel.forman@mssm.edu]; sgans@partners.org[sgans@partners.org]; hughesg@uw.edu[hughesg@uw.edu];
sj366@columbia.edu[sj366@columbia.edu]; info@blueberrypediatrics.com[info@blueberrypediatrics.com];
dop9054@med.cornell.edu[dop9054@med.cornell.edu]; contact@drsadaty.com[contact@drsadaty.com];
robyn.correll@gmail.com[robyn.correll@gmail.com]; ja9qr@virginia.edu[ja9qr@virginia.edu];
yshafrir@lifebridgehealth.org[yshafrir@lifebridgehealth.org]; Max.Wiznitzer@UHHospitals.org[Max.Wiznitzer@UHHospitals.org];
Lynn.Ricciardella@ihs.gov[Lynn.Ricciardella@ihs.gov]; arnaldo.caruso@unibs.it[arnaldo.caruso@unibs.it]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; zimmermand@si.edu[zimmermand@si.edu]; danielle.anderson@duke-nus.edu.sg[danielle.anderson@duke-nus.edu.sg]; pcywoo@hku.hk[pcywoo@hku.hk]; S Ahmed[ssahmed16@gmail.com];
hafiz.khan@mclaren.org[hafiz.khan@mclaren.org]; alex.ward@vox.com[alex.ward@vox.com];
julia.belluz@voxmedia.com[julia.belluz@voxmedia.com]; orthopedics@whu.edu.cn[orthopedics@whu.edu.cn];
xiemx@hust.edu.cn[xiemx@hust.edu.cn]; alexander.cohen@kcl.ac.uk[alexander.cohen@kcl.ac.uk];
Moliterno@uky.edu[Moliterno@uky.edu]; dmann@wustl.edu[dmann@wustl.edu]; 499388475@qq.com[499388475@qq.com];
2716637947@qq.com[2716637947@qq.com]; aspyropoul@northwell.edu[aspyropoul@northwell.edu];
media@chestnet.org[media@chestnet.org]; k.j.pasi@qmul.ac.uk[k.j.pasi@qmul.ac.uk];
cchumley@washingtontimes.com[cchumley@washingtontimes.com];
badams@washingtonexaminer.com[badams@washingtonexaminer.com]; david.weigel@washpost.com[david.weigel@washpost.com];
lindsey.bever@washpost.com[lindsey.bever@washpost.com]; lena.sun@washpost.com[lena.sun@washpost.com];
kristine.phillips@washpost.com[kristine.phillips@washpost.com]; ashley.halsey@washpost.com[ashley.halsey@washpost.com];
fenit.nirappil@washpost.com[fenit.nirappil@washpost.com]; marwa.eltagouri@washpost.com[marwa.eltagouri@washpost.com];
martin.baron@washpost.com[martin.baron@washpost.com]; alex.horton@washpost.com[alex.horton@washpost.com];
michaelgerson@washpost.com[michaelgerson@washpost.com]; gene.weingarten@washpost.com[gene.weingarten@washpost.com];
ejc@estherjcepeda.com[ejc@estherjcepeda.com]; cohenr@washpost.com[cohenr@washpost.com];
ejdionne@washpost.com[ejdionne@washpost.com]; kenharney@earthlink.net[kenharney@earthlink.net];
davidignatius@washpost.com[davidignatius@washpost.com]; ruthmarcus@washpost.com[ruthmarcus@washpost.com];
dana.milbank@washpost.com[dana.milbank@washpost.com]; kathleenparker@washpost.com[kathleenparker@washpost.com];
alexandra.petri@washpost.com[alexandra.petri@washpost.com]; crampell@washpost.com[crampell@washpost.com];
eugenerobinson@washpost.com[eugenerobinson@washpost.com];
michelle.singletary@washpost.com[michelle.singletary@washpost.com]; georgewill@washpost.com[georgewill@washpost.com];
fareed.zakaria.gps@turner.com[fareed.zakaria.gps@turner.com]; ben.guarino@washpost.com[ben.guarino@washpost.com];
carolyn.johnson@washpost.com[carolyn.johnson@washpost.com]; josh.rogin@washpost.com[josh.rogin@washpost.com];
andrew.freedman@washpost.com[andrew.freedman@washpost.com]; chelsea.janes@washpost.com[chelsea.janes@washpost.com];
ariana.cha@washpost.com[ariana.cha@washpost.com]; laurie.mcginley@washpost.com[laurie.mcginley@washpost.com];
josh.dawsey@washpost.com[josh.dawsey@washpost.com]; Jan.Angel@leg.wa.gov[Jan.Angel@leg.wa.gov];
Sherry.Appleton@leg.wa.gov[Sherry.Appleton@leg.wa.gov]; Barbara.Bailey@leg.wa.gov[Barbara.Bailey@leg.wa.gov];
Andrew.Barkis@leg.wa.gov[Andrew.Barkis@leg.wa.gov]; Michael.Baumgartner@leg.wa.gov[Michael.Baumgartner@leg.wa.gov];
Randi.Becker@leg.wa.gov[Randi.Becker@leg.wa.gov]; Steve.Bergquist@leg.wa.gov[Steve.Bergquist@leg.wa.gov];
Andy.Billig@leg.wa.gov[Andy.Billig@leg.wa.gov]; Brian.Blake@leg.wa.gov[Brian.Blake@leg.wa.gov];
John.Braun@leg.wa.gov[John.Braun@leg.wa.gov]; Sharon.Brown@leg.wa.gov[Sharon.Brown@leg.wa.gov];
Vincent.Buys@leg.wa.gov[Vincent.Buys@leg.wa.gov]; Michelle.Caldier@leg.wa.gov[Michelle.Caldier@leg.wa.gov];
Reuven.Carlyle@leg.wa.gov[Reuven.Carlyle@leg.wa.gov]; Bruce.Chandler@leg.wa.gov[Bruce.Chandler@leg.wa.gov];
Mike.Chapman@leg.wa.gov[Mike.Chapman@leg.wa.gov]; Maralyn.Chase@leg.wa.gov[Maralyn.Chase@leg.wa.gov];
Frank.Chopp@leg.wa.gov[Frank.Chopp@leg.wa.gov]; Annette.Cleveland@leg.wa.gov[Annette.Cleveland@leg.wa.gov];
Judy.Clibborn@leg.wa.gov[Judy.Clibborn@leg.wa.gov]; Eileen.Cody@leg.wa.gov[Eileen.Cody@leg.wa.gov];
Cary.Condotta@leg.wa.gov[Cary.Condotta@leg.wa.gov]; Steve.Conway@leg.wa.gov[Steve.Conway@leg.wa.gov];
Jeannie.Darneille@leg.wa.gov[Jeannie.Darneille@leg.wa.gov]; Richard.DeBolt@leg.wa.gov[Richard.DeBolt@leg.wa.gov];
Tom.Dent@leg.wa.gov[Tom.Dent@leg.wa.gov]; Manka.Dhingra@leg.wa.gov[Manka.Dhingra@leg.wa.gov];
Beth.Doglio@leg.wa.gov[Beth.Doglio@leg.wa.gov]; Laurie.Dolan@leg.wa.gov[Laurie.Dolan@leg.wa.gov];
Mary.Dye@leg.wa.gov[Mary.Dye@leg.wa.gov]; Doug.Ericksen@leg.wa.gov[Doug.Ericksen@leg.wa.gov];
Carolyn.Eslick@leg.wa.gov[Carolyn.Eslick@leg.wa.gov]; Joe.Fain@leg.wa.gov[Joe.Fain@leg.wa.gov];
Jake.Fey@leg.wa.gov[Jake.Fey@leg.wa.gov]; Joe.Fitzgibbon@leg.wa.gov[Joe.Fitzgibbon@leg.wa.gov];
phil.fortunato@leg.wa.gov[phil.fortunato@leg.wa.gov]; Nicole.Macri@leg.wa.gov[Nicole.Macri@leg.wa.gov];
David.Frockt@leg.wa.gov[David.Frockt@leg.wa.gov]; Roger.Goodman@leg.wa.gov[Roger.Goodman@leg.wa.gov];
Paul.Graves@leg.wa.gov[Paul.Graves@leg.wa.gov]; Mia.Gregerson@leg.wa.gov[Mia.Gregerson@leg.wa.gov];
Dan.Griffey@leg.wa.gov[Dan.Griffey@leg.wa.gov]; Larry.Haler@leg.wa.gov[Larry.Haler@leg.wa.gov];
Drew.Hansen@leg.wa.gov[Drew.Hansen@leg.wa.gov]; Mark.Hargrove@leg.wa.gov[Mark.Hargrove@leg.wa.gov];
Mark.Harmsworth@leg.wa.gov[Mark.Harmsworth@leg.wa.gov]; Paul.Harris@leg.wa.gov[Paul.Harris@leg.wa.gov];
Bob.Hasegawa@leg.wa.gov[Bob.Hasegawa@leg.wa.gov]; Brad.Hawkins@leg.wa.gov[Brad.Hawkins@leg.wa.gov];
Dave.Hayes@leg.wa.gov[Dave.Hayes@leg.wa.gov]; Steve.Hobbs@leg.wa.gov[Steve.Hobbs@leg.wa.gov];
Jeff.Holy@leg.wa.gov[Jeff.Holy@leg.wa.gov]; Jim.Honeyford@leg.wa.gov[Jim.Honeyford@leg.wa.gov];
Zack.Hudgins@leg.wa.gov[Zack.Hudgins@leg.wa.gov]; Sam.Hunt@leg.wa.gov[Sam.Hunt@leg.wa.gov];
Morgan.Irwin@leg.wa.gov[Morgan.Irwin@leg.wa.gov]; Bill.Jenkin@leg.wa.gov[Bill.Jenkin@leg.wa.gov];
Laurie.Jinkins@leg.wa.gov[Laurie.Jinkins@leg.wa.gov]; Norm.Johnson@leg.wa.gov[Norm.Johnson@leg.wa.gov];
Ruth.Kagi@leg.wa.gov[Ruth.Kagi@leg.wa.gov]; Karen.Keiser@leg.wa.gov[Karen.Keiser@leg.wa.gov];
Christine.Kilduff@leg.wa.gov[Christine.Kilduff@leg.wa.gov]; Curtis.King@leg.wa.gov[Curtis.King@leg.wa.gov];

Steve.Kirby@leg.wa.gov[Steve.Kirby@leg.wa.gov]; Brad.Klippert@leg.wa.gov[Brad.Klippert@leg.wa.gov];
Shelley.Kloba@leg.wa.gov[Shelley.Kloba@leg.wa.gov]; Vicki.Kraft@leg.wa.gov[Vicki.Kraft@leg.wa.gov];
Joel.Kretz@leg.wa.gov[Joel.Kretz@leg.wa.gov]; Dan.Kristiansen@leg.wa.gov[Dan.Kristiansen@leg.wa.gov];
Patty.Kuderer@leg.wa.gov[Patty.Kuderer@leg.wa.gov]; Marko.Liias@leg.wa.gov[Marko.Liias@leg.wa.gov];
John.Lovick@leg.wa.gov[John.Lovick@leg.wa.gov]; Kristine.Lytton@leg.wa.gov[Kristine.Lytton@leg.wa.gov];
Drew.MacEwen@leg.wa.gov[Drew.MacEwen@leg.wa.gov]; Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov];
Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov];
Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov];
John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov];
Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov];
Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov];
Terry.Nealey@leg.wa.gov[Terry.Nealey@leg.wa.gov]; Sharon.Nelson@leg.wa.gov[Sharon.Nelson@leg.wa.gov];
Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov];
Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov];
Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov];
Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov];
Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov];
Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov];
Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov];
Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov];
Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov];
Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov];
Cindy.Ryu@leg.wa.gov[Cindy.Ryu@leg.wa.gov]; Rebecca.Saldana@leg.wa.gov[Rebecca.Saldana@leg.wa.gov];
SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov];
Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov];
Mike.Sells@leg.wa.gov[Mike.Sells@leg.wa.gov]; Tana.Senn@leg.wa.gov[Tana.Senn@leg.wa.gov];
Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov];
Shelly.Short@leg.wa.gov[Shelly.Short@leg.wa.gov]; Vandana.Slatter@leg.wa.gov[Vandana.Slatter@leg.wa.gov];
Norma.Smith@leg.wa.gov[Norma.Smith@leg.wa.gov]; Larry.Springer@leg.wa.gov[Larry.Springer@leg.wa.gov];
Melanie.Stambaugh@leg.wa.gov[Melanie.Stambaugh@leg.wa.gov]; Derek.Stanford@leg.wa.gov[Derek.Stanford@leg.wa.gov];
mike.steele@leg.wa.gov[mike.steele@leg.wa.gov]; Drew.Stokesbary@leg.wa.gov[Drew.Stokesbary@leg.wa.gov];
Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov];
Dean.Takko@leg.wa.gov[Dean.Takko@leg.wa.gov]; Gael.Tarleton@leg.wa.gov[Gael.Tarleton@leg.wa.gov];
David.Taylor@leg.wa.gov[David.Taylor@leg.wa.gov]; Steve.Tharinger@leg.wa.gov[Steve.Tharinger@leg.wa.gov];
Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov];
Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov];
Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov];
Jim.Walsh@leg.wa.gov[Jim.Walsh@leg.wa.gov]; Maureen.Walsh@leg.wa.gov[Maureen.Walsh@leg.wa.gov];
Judy.Warnick@leg.wa.gov[Judy.Warnick@leg.wa.gov]; Lisa.Wellman@leg.wa.gov[Lisa.Wellman@leg.wa.gov];
JT.Wilcox@leg.wa.gov[JT.Wilcox@leg.wa.gov]; Lynda.Wilson@leg.wa.gov[Lynda.Wilson@leg.wa.gov];
Sharon.Wylie@leg.wa.gov[Sharon.Wylie@leg.wa.gov]; Jesse.Young@leg.wa.gov[Jesse.Young@leg.wa.gov];
Hans.Zeiger@leg.wa.gov[Hans.Zeiger@leg.wa.gov]; kanchanmvk@yahoo.com[kanchanmvk@yahoo.com];
ushamvk@yahoo.co.in[ushamvk@yahoo.co.in]; mike.agogliati@wfsb.com[mike.agogliati@wfsb.com];
fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com]; wjbkwebteam@foxtv.com;[wjbkwebteam@foxtv.com];
sanjay.mishra@Vanderbilt.Edu[sanjay.mishra@Vanderbilt.Edu]; kienym@who.int[kienym@who.int];
Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu]; sbaldwin@idri.org[sbaldwin@idri.org];
friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov]; Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org];
cww@austin.utexas.edu[cww@austin.utexas.edu]; henaorestrepoa@who.int[henaorestrepoa@who.int]; www.felix@konpotey-
ahulu.com[www.felix@konpotey-ahulu.com]; olin0012@umn.edu[olin0012@umn.edu];
sinabavari@comcast.net[sinabavari@comcast.net]; maryam.keshtkar@jhmi.edu[maryam.keshtkar@jhmi.edu];
corey.casper@idri.org[corey.casper@idri.org]; theiland@immunomix.com[theiland@immunomix.com];
ProjanSJ@medimmune.com[ProjanSJ@medimmune.com]; schleiss@umn.edu[schleiss@umn.edu];
mail@wired.com[mail@wired.com]; submit@wired.com[submit@wired.com];
megan_molteni@wired.com[megan_molteni@wired.com]; tyagi@ebi.ac.uk[tyagi@ebi.ac.uk];
Nick.Furnham@lshtm.ac.uk[Nick.Furnham@lshtm.ac.uk]; betsy.mckay@wsj.com[betsy.mckay@wsj.com];
spencer.macnaughton@wsj.com[spencer.macnaughton@wsj.com]; conall.jones@wsj.com[conall.jones@wsj.com];
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mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com]; lifang@umn.edu[lifang@umn.edu];
LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk]; mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk];
Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU];
jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-
muenchen.de[rothe@lrz.uni-muenchen.de]; zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn];
sanchak@gmail.com[sanchak@gmail.com]; badrishanthi@hotmail.com[badrishanthi@hotmail.com];
gmaclaren@iinet.net.au[gmaclaren@iinet.net.au]; ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com];

suoban@simm.ac.cn[suoban@simm.ac.cn]; wiv@wh.iov.cn[wiv@wh.iov.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg]; oon_tek_ng@ncid.sg[oon_tek_ng@ncid.sg]; Linfa.wang@csiro.au[Linfa.wang@csiro.au]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]
From: vinu arumugham[igesynth@yahoo.com]
Sent: Sat 10/17/2020 12:50:03 AM (UTC-05:00)
Subject: Flu shot makes COVID-19 worse, confirmed by Cleveland Clinic; Make Famotidine/Cetirizine SOC for COVID-19; COVID-19 vaccines are unsafe

"Trump had been administered a Regeneron polyclonal antibody cocktail and has been taking zinc, vitamin D, **famotidine**, melatonin and a daily aspirin."

https://www.cnn.com/2020/10/02/politics/president-donald-trump-walter-reed-coronavirus/index.html

Trump gets **famotidine** for COVID-19 but it is not "standard of care" (SOC) for you and me.

The IDSA is killing hundreds of thousands by **DENYING** them **famotidine**, a cheap, safe and effective over-the-counter drug for COVID-19.

Did the money from vaccine makers and remdesivir maker Gilead, sloshing around at IDSA, influence their decision?

https://www.idsociety.org/practice-guideline/covid-19-guideline-treatment-and-management/

"The guideline panel suggests against famotidine for the sole purpose of treating COVID-19, unless in the context of a clinical trial."

Here's what the authors collected:

KATHRYN M EDWARDS collected ~$150k from vaccine makers.

https://openpaymentsdata.cms.gov/physician/651167

Lindsey Baden collected ~$50k from Janssen Pharma (a vaccine maker).

https://openpaymentsdata.cms.gov/physician/884460

RAJESH TIM GANDHI collected ~$40k from Gilead and Merck.

https://openpaymentsdata.cms.gov/physician/1273478

WILLIAM J MULLER collected ~$140k from Astrazeneca, Merck and Janssen

https://openpaymentsdata.cms.gov/physician/613576

SHUMEL SHOHAM collected $180k from Merck, Gilead, Emergent, Jannsen

https://openpaymentsdata.cms.gov/physician/780712

Mechanistic evidence (prediction)

Proteins that contaminate influenza vaccines have high homology to SARS-CoV-2 proteins thus increasing risk of severe COVID-19 disease and mortality
https://doi.org/10.5281/zenodo.3996984

Epidemiological evidence (confirmation)

Flu shot increases risk of COVID-19 Hospitalization **240%**, ICU admission **204%**, Hospital mortality **232%**.

Safety of Influenza Vaccine during COVID-19

https://doi.org/10.1017/cts.2020.543

"Among individuals with a positive SARS-CoV-2 test, patients previously vaccinated for influenza in 2019 were more likely to be hospitalized. Once hospitalized, they were more likely to be admitted to the ICU and die during hospitalization."

From Table 1:

	Never Vaccinated (N=1,125)	Vaccinated in 2019 (N=309)
Hospitalization - no.(%)	192 (17.1)	127 (41.1)
ICU Admission - no.(%)	77 (6.8)	43 (13.9)
Hospital Mortality - no.(%)	32 (2.8)	20 (6.5)

My comment posted in the Annals of Internal Medicine

The iatrogenic cascade of illnesses

https://www.acpjournals.org/doi/full/10.7326/M20-2470#_comments

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COVID-19 vaccines are **fundamentally flawed and unsafe**. Details below:

The CanSino Biologics vaccine:

https://publons.com/r/9024531/

The Oxford vaccine:

https://publons.com/r/9015091/

The Moderna mRNA vaccine:

https://publons.com/r/9025990/

The Pfizer/BioNTech vaccine:

https://publons.com/r/9026177/

The Novavax vaccine

https://publons.com/review/9108287/

Prof. Kounis' team and I, describe the common immunological mechanisms involved in cardiac injury in COVID-19, severe dengue infection and allergic reactions/anaphylaxis (Kounis syndrome). The medications for prevention/treatment include famotidine/cetirizine.

The passepartout wayfares of Covid-19, Cytokine storm and Kounis syndrome

https://doi.org/10.5281/zenodo.3977923
Dual-Histamine Blockade with Cetirizine - Famotidine Reduces Pulmonary Symptoms in COVID-19 Patients
https://www.medrxiv.org/content/10.1101/2020.06.30.20137752v1

I predicted in **JANUARY 2020** (email below) that mast cell stabilizers and antihistamines can help in COVID-19. I notified health authorities and thousands of doctors/researchers, worldwide. Hundreds of thousands of lives could have been saved.

The **key is to understand that COVID-19 severity is a result of an allergic reaction to the virus**, a "slow rolling anaphylaxis". **WE HAVE PROVEN TREATMENTS FOR ANAPHYLAXIS. NO CLINICAL TRIALS NEEDED.**

The diagnosis and management of anaphylaxis: An updated practice parameter

https://www.jacionline.org/article/S0091-6749(05)00115-6/fulltext

"These protocols have recommended the administration of **H1 and H2 antagonists, ??-agonists, antileukotrienes, and corticosteroids**."

Cetirizine is an histamine H1 blocker or antagonist. Famotidine is an histamine H2 blocker or antagonist.

These safe, OTC drugs above can be used immediately upon COVID-19 symptoms (or even a low dose if exposure is suspected). Mast cell stabilizers, ??-agonists, antileukotrienes, and corticosteroids can be prescribed as standard of care. Hundreds of thousands of lives can be saved.

As I wrote in my comment posted in the Annals of Internal Medicine:

Please see comments section:

https://annals.org/aim/fullarticle/2764199/use-hydroxychloroquine-chloroquine-during-covid-19-pandemic-what-every-clinician

Understanding mechanisms is better than demanding clinical trials in the middle of a pandemic

More details:

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
https://www.researchsquare.com/article/rs-30934/v2

Repositioning Chromones for Early Anti-inflammatory Treatment of COVID-19

https://www.frontiersin.org/articles/10.3389/fphar.2020.00854/full

Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy??

https://pubmed.ncbi.nlm.nih.gov/32013309/

Thanks,
Vinu

-------- Forwarded Message --------
Subject: Wuhan 2019-nCoV treatment; Vaccines induce autoimmunity: Epitope database evidence; Ebola vaccine will cause rice allergy epidemic
Date: Fri, 24 Jan 2020 17:42:02 -0800
From: vinu arumugham <igesynth@yahoo.com>
To: jay.slater@fda.hhs.gov <jay.slater@fda.hhs.gov>, jane.woo@fda.hhs.gov <jane.woo@fda.hhs.gov>, maureen.hess@fda.hhs.gov <maureen.hess@fda.hhs.gov>, Richard.Forshee@fda.hhs.gov <Richard.Forshee@fda.hhs.gov>, Mark.Walderhaug@fda.hhs.gov <Mark.Walderhaug@fda.hhs.gov>, CBER OCOD Consumer Account <cberocod@fda.hhs.gov>, Destefano, Frank (CDC/OID/NCEZID) <fxd1@cdc.gov>, isq8@cdc.gov <isq8@cdc.gov>, nar5@cdc.gov <nar5@cdc.gov>, hjn0@cdc.gov <hjn0@cdc.gov>, Secretary@HHS.gov <Secretary@HHS.gov>, CommissionerFDA@fda.hhs.gov <CommissionerFDA@fda.hhs.gov>, olx1@cdc.gov <olx1@cdc.gov>, directorsincoming@cdc.gov <directorsincoming@cdc.gov>, francis.collins@nih.gov <francis.collins@nih.gov>, mrolfes1@cdc.gov <mrolfes1@cdc.gov>, xzd2@cdc.gov <xzd2@cdc.gov>, acy9@cdc.gov <acy9@cdc.gov>, dbj0@cdc.gov <dbj0@cdc.gov>, jmk9@cdc.gov <jmk9@cdc.gov>, tft9@cdc.gov <tft9@cdc.gov>, gll9@cdc.gov <gll9@cdc.gov>, sharplessne@nih.hhs.gov <sharplessne@nih.hhs.gov>, tnc4@cdc.gov <tnc4@cdc.gov>, kok4@cdc.gov <kok4@cdc.gov>, rxl3@cdc.gov <rxl3@cdc.gov>, gbq7@cdc.gov <gbq7@cdc.gov>, fwf7@cdc.gov <fwf7@cdc.gov>, megan.mcseveney@fda.hhs.gov <megan.mcseveney@fda.hhs.gov>, afauci@niaid.nih.gov <afauci@niaid.nih.gov>, Emelia.Benjamin@bmc.org <Emelia.Benjamin@bmc.org>, mjessup@leducq.com <mjessup@leducq.com>, tavori@ohsu.edu <tavori@ohsu.edu>, jessica.lilley@vanderbilt.edu <jessica.lilley@vanderbilt.edu>, web@beasleyallen.com <web@beasleyallen.com>, dr.flegg@bfwhospitals.nhs.uk <dr.flegg@bfwhospitals.nhs.uk>

IgE mediated sensitization to peptides that have homology to 2019-nCoV peptides may contribute to disease severity. In that case, antihistamines and other allergy treatments such as mast cell stabilizers may help reduce infection severity.

A BLASTP analysis of 2019-nCoV proteome against common vaccine antigens was performed. Preliminary results suggest that IgE mediated sensitization to common vaccine antigens can result in cross reactive immune responses to 2019-nCoV.

Please see details of the mechanisms here:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

https://www.quora.com/Why-was-the-flu-so-deadly-in-outbreaks-in-the-past-And-what-made-the-flu-become-less-deadly/answers/86456279

"Scientists" at the global vaccine safety summit spill the beans: There is no science behind vaccine safety claims, it's a fairy tale.

The party is over folks.

https://youtu.be/s2IujhTdCLE

ERVEBO Ebola vaccine will create a rice allergy epidemic, add to numerous autoimmune diseases, cancer and make Ebola disease even more severe. Design for safety and vaccine safety regulation remain abject failures. Incompetence or indifference?
https://doi.org/10.5281/zenodo.3595020

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

https://doi.org/10.5281/zenodo.3603480

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

Vinu Arumugham
Jan 2020
vinucubeacc@gmail.com

Lay summary

Proteins are a chain of amino acids. Proteins can have up to several hundred amino acids. Snippets of proteins (peptides), 7-15 amino acids in length are important in immunology. There are 20 types of amino acids. Each is assigned a letter (1 letter code).

Antibodies are proteins that can bind to peptides that have a specific amino acid sequence. Such a target peptide is known as an epitope.?? When an antibody binds to a peptide (which is part of a protein, which in turn may be part of a cell surface), it can trigger an immune attack on the cell. If the cell were a bacterium, the bacterium would be killed.

Humans (like all organisms) are made of numerous proteins (self proteins). So we have self-proteins, self-peptides and self-epitopes. In a healthy person, the body will not make antibodies that bind strongly to self-peptides (self-tolerance).

DNA is a chain of base-pairs. The DNA base-pair sequence determines the amino acid sequence in the protein produced. If there is a mutation that alters a single base-pair, the resulting protein will have a single amino acid that is altered. To prevent

cancer, the immune system is capable of making antibodies against such altered peptides. Such antibodies can also weakly bind (cross react) to the unaltered normal peptide thus resulting in destruction of some healthy cells.

Say a normal protein has the following peptide (10 amino acids, each represented by its 1 letter code):

ALSTLVVNKI

Say DNA in a cell mutates due to a carcinogen exposure and it alters the protein thus resulting in this peptide with a single amino acid change:

ALSTLVV**S**KI

When the immune system makes antibodies targeted at ALSTLVV**S**KI (to attack the cell with the DNA mutation), the same antibodies can weakly bind to the normal ALSTLVVNKI peptide.

ALSTLVVNKI is an epitope associated with rheumatoid arthritis (RA).

So as a result of the immune system defending against cancer, the person can develop RA.

Now consider vaccines containing animal proteins. Animal proteins are very similar to human proteins, containing only occasional amino acid differences. An animal peptide could therefore have the ALSTLVV**S**KI sequence. Such a vaccine would fool the immune system into creating an anti-cancer immune response, creating antibodies targeted at ALSTLVV**S**KI. The result is vaccine induced RA.

Therefore one can predict that analyzing epitopes associated with autoimmune diseases, such single amino acid difference compared to animal peptides present in vaccines, would occur more frequently than can be expected merely by chance. The analysis confirms that this prediction is valid.

Abstract

The National Institute of Allergy and Infectious Diseases (NIAID) sponsors the Immune Epitope Data Base (IEDB). IEDB contains epitopes identified from the medical literature and organized by diseases and categories of diseases. All epitopes (23000+) associated with 82 autoimmune diseases in humans were analyzed.

The role of animal, plant, fungal proteins contained in vaccines in the etiology of autoimmune diseases have been described in humans and animals. BLASTP was used to analyze IEDB derived epitopes for sequence alignment to animal, plant, fungal (APF) proteins present in vaccines and biologics. Specifically, the search was performed against bovine, chicken, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes.

The results show that 57% of epitopes differed by exactly one amino acid residue from an APF peptide. 78% of the epitopes differed by up to two amino acid residues from an APF peptide. The rest of the epitopes were either identical or differed by more than two amino acid residues.

A majority of IEDB epitopes analyzed were 9-mer peptides. Comparing randomly selected 9-mer human peptides with APF proteomes, the probability of single amino acid residue difference (SAARD) outcomes was derived. This was used to estimate the probability that actual IEDB SAARD alignments to APF peptides were merely a chance outcome. The estimates show that the probability that the observed IEDB alignments to APF being merely a chance outcome are vanishingly small. So the results make it absolutely clear that APF proteins in vaccines cause all these autoimmune diseases.

Introduction

Vaccines contain thousands of residual animal, plant and fungal (APF) proteins from the manufacturing process (1???6)???. 293 chicken proteins were identified in the influenza vaccine (7)???, for example. Actin and vimentin proteins were detected in the Priorix Tetra vaccine (8)???. Immunization with homologous xenogeneic antigens resulting in autoimmune diseases has been known for at least 40 years (9)???. Vaccines that contain bovine proteins caused autoimmunity in dogs (10)???. We previously described the immunological mechanism involved in autoimmunity induction by immunization with homologous xenogeneic antigens (11)???.

Cancer cells have minor differences when compared to healthy cells. Due to mutation of the DNA encoding the proteins, cancer cells can display altered proteins on their surface. Healthy cancer defense mechanisms include immune responses directed at such altered proteins. Therefore an immune response directed against cancer cells always carries a risk of cross

reactive immune responses against healthy cells displaying the unaltered protein. Therefore, cancer induced autoimmune responses are a consequence of normal, healthy immune system behavior.

Animal proteins have minor differences compared to human proteins. Peptides that are identical between humans and animals are unlikely to cause any problem due to strong self tolerance. However, peptides with one amino acid residue difference produce the strongest cross reactive immune responses (11)???. They are ideally suited to induce autoimmune diseases. Injecting animal proteins results in anti-cancer immune responses because the immune system perceives animal proteins as altered human proteins. Adjuvants in the vaccine boost this anti-cancer immune response. This artificial anti-cancer response directed at thousands of APF proteins in vaccines or biologics, therefore cross react and cause numerous autoimmune disorders.

For this reason, one can predict that single amino acid residue difference (SAARD) between autoimmune disease related epitopes in the IEDB and homologous APF peptides in vaccines, would occur at a higher probability than by mere chance. We perform a BLASTP analysis to verify.

Methods

Basic local alignment search tool for proteins (BLASTP) (12)???, Universal Protein Resource (UniProt)(13)??? and the Immune Epitope Database (IEDB) (14)??? were used for bioinformatics analysis.

Specifically, the BLASTP sequence alignment of IEDB peptides was performed against bovine, chick, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes. Vaccines and biologics contain residual proteins from all these organism due to media used to grow viruses or bacteria, recombinant cells/organisms used for protein expression or as excipients.

Results

57% of IEDB peptides have a SAARD and 78% have up to two amino acid differences compared to animal, fungal or plant peptides present in vaccines.

Discussion

Could this result be a chance occurrence?

A majority of IEDB epitopes analyzed were 9-mer peptides. Five thousand 9-mer peptides were chosen at random from the human proteome. BLASTP was run using these peptides to compare against each organism???s proteome or a subset. This provides us the probability that randomly selected human peptides have an alignment providing a SAARD compared to peptides from these organisms. These are listed in table 1 under ??? Random SAARD alignment???. Given this, we can compute the probability of the actual SAARD alignment to IEDB epitopes, occurring by chance. This is listed in table 1 under ???Estimated probability of actual SAARD outcome occurring just by chance???.

For a simple coin toss example, we would perform the calculation as follows:

Computing probability of say a 7 heads, 3 tails outcome of 10 trials of a fair coin:

Probability = (0.5^7) x (0.5^3) x 10! / (7! x 3!)

Where:

0.5 is the probability of a head or tail outcome of a fair coin.

For an unfair coin, say probability of head outcome = 0.4 and tail outcome 0.6, we would have:

Probability = (0.4^7) x (0.6^3) x 10! / (7! x 3!)

For the IEDB peptide probability analysis, the outcome is for 23192 trials (peptides). The ???head outcome??? is the ???Random SAARD alignment ??? entries in table 1. The ???tail outcome??? probability is 1-???head outcome???.

Sample calculation for Chinese Hamster:

Probability = ((889/5000)^4574) x ((4111/5000)^18618) x 23192! / (4574! x 18618!)

Probability = 1.488e-15

Where: 889*100/5000 = 17.8% is the entry in Table 1 for Chinese Hamster. BLASTP analysis shows 889 SAARD out of 5000 peptides analyzed.

And, 4574*100/23192=19.7% is the IEDB entry in Table 1 for Chinese Hamster. BLASTP analysis shows 4574 SAARD out of 23192 peptides analyzed.

So the 1.488e-15 value is the probability that we will have exactly 4574 SAARD alignments out of 23192 peptides. The probability goes down for all values > 4574. Conservatively, applying the same probability as for 4574, to all values >4574, we can calculate the probability of the chance occurrence of 4574 or greater number of SAARD alignments as 1.488e15 * 18618 = 27e-12, entry in table.

The Gnome calculator was used to perform these calculations and the results were verified using the Qalculate! calculator and WolframAlpha (15)??? since spreadsheets are unable to perform these calculations.

Table 1

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
African green monkey (*Chlorocebus aethiops*)	26 (0.5)	420 (1.8)	~1.7e-96	Probability is vanishir vaccines,
Cow (*Bos taurus*)	936 (18.7)	4385 (18.9)	~1	There are occurred ju cow protei amount is bovine gel vaccines. S tissues in t other cow more likel entry belo
Cow???s Milk (*Bos taurus*)	0 (0)	12 (0.05)	0	Probability is 0. So th these disea
Chinese Hamster (*Cricetulus griseus*)	889 (17.8)	4574 (19.7)	~27e-12	Probability is vanishir vaccines, b
Chicken (*Gallus gallus*)	536 (10.7)	3901 (16.8)	<1e-100	Probability is vanishir vaccines, porcine an embryo is proteins ca
Guinea Pig (*Cavia porcellus*)	837 (16.7)	4439 (19.1)	~1e-18	Probability is vanishir vaccines,
Mice (*Mus musculus*)	940 (18.8)	4467 (19.3)	~1	There are occurred ju mice prote amount is cells are u proteins pr present in be present
Maize (*Zea mays*)	303 (6.1)	1667 (7.2)	~5e-9	Probability is vanishir vaccines,
Peanut (*Arachis hypogaea*)	223 (4.5)	1697 (7.3)	~79e-81	Probability is vanishir vaccines,

Yeast (*Saccharomyces cerevisiae)*	64 (1.3)	828 (3.6)	<1e-100	Probabilit is vanishi vaccines,
Sesame (*Sesamum indicum*)	155 (3.1)	1398 (6.0)	<1e-100	Probabilit is vanishi vaccines,
Soy (*Glycine max)*	215 (4.3)	1548 (6.7)	~86e-59	Probabilit is vanishi vaccines,
Pig (*Sus scrofa*)	963 (19.3)	4407 (19.0)	~1	There are occurred j porcine pr amount is used in va present in vaccines b present. T
Wheat (*Triticum aestivum*)	138 (2.8)	977 (4.2)	~18e-33	Probabilit is vanishi vaccines,

The calculations make it clear that the findings cannot be merely a chance outcome and that immunization against animal/plant/fungal antigens in the vaccines do cause these autoimmune diseases in the IEDB.

Conclusion

Vaccines containing animal, plant or fungal proteins are extremely dangerous and cause numerous autoimmune diseases and cancer (16???19)???. All non-target proteins in vaccines must be immediately removed using processes such affinity chromatography (20)???.

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To: kanchanmvk@yahoo.com[kanchanmvk@yahoo.com]; ushamvk@yahoo.co.in[ushamvk@yahoo.co.in];
mike.agogliati@wfsb.com[mike.agogliati@wfsb.com]; fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com];
wjbkwebteam@foxtv.com;[wjbkwebteam@foxtv.com]; sanjay.mishra@Vanderbilt.Edu[sanjay.mishra@Vanderbilt.Edu];
kienym@who.int[kienym@who.int]; Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu];
sbaldwin@idri.org[sbaldwin@idri.org]; friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov];
Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org]; cww@austin.utexas.edu[cww@austin.utexas.edu];
henaorestrepoa@who.int[henaorestrepoa@who.int]; www.felix@konpotey-ahulu.com[www.felix@konpotey-ahulu.com];
olin0012@umn.edu[olin0012@umn.edu]; sinabavari@comcast.net[sinabavari@comcast.net];
maryam.keshtkar@jhmi.edu[maryam.keshtkar@jhmi.edu]; corey.casper@idri.org[corey.casper@idri.org];
theiland@immunomix.com[theiland@immunomix.com]; ProjanSJ@medimmune.com[ProjanSJ@medimmune.com];
schleiss@umn.edu[schleiss@umn.edu]; Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov];
Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov];
Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov];
John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov];
Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov];
Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov];
Terry.Nealey@leg.wa.gov[Terry.Nealey@leg.wa.gov]; Sharon.Nelson@leg.wa.gov[Sharon.Nelson@leg.wa.gov];
Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov];
Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov];
Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov];
Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov];
Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov];
Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov];
Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov];
Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov];
Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov];
Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov];
Cindy.Ryu@leg.wa.gov[Cindy.Ryu@leg.wa.gov]; Rebecca.Saldana@leg.wa.gov[Rebecca.Saldana@leg.wa.gov];
SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov];
Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov];
Mike.Sells@leg.wa.gov[Mike.Sells@leg.wa.gov]; Tana.Senn@leg.wa.gov[Tana.Senn@leg.wa.gov];
Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov];
Shelly.Short@leg.wa.gov[Shelly.Short@leg.wa.gov]; Vandana.Slatter@leg.wa.gov[Vandana.Slatter@leg.wa.gov];
Norma.Smith@leg.wa.gov[Norma.Smith@leg.wa.gov]; Larry.Springer@leg.wa.gov[Larry.Springer@leg.wa.gov];
Melanie.Stambaugh@leg.wa.gov[Melanie.Stambaugh@leg.wa.gov]; Derek.Stanford@leg.wa.gov[Derek.Stanford@leg.wa.gov];
mike.steele@leg.wa.gov[mike.steele@leg.wa.gov]; Drew.Stokesbary@leg.wa.gov[Drew.Stokesbary@leg.wa.gov];
Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov];
Dean.Takko@leg.wa.gov[Dean.Takko@leg.wa.gov]; Gael.Tarleton@leg.wa.gov[Gael.Tarleton@leg.wa.gov];
David.Taylor@leg.wa.gov[David.Taylor@leg.wa.gov]; Steve.Tharinger@leg.wa.gov[Steve.Tharinger@leg.wa.gov];
Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov];
Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov];
Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov];
Jim.Walsh@leg.wa.gov[Jim.Walsh@leg.wa.gov]; Maureen.Walsh@leg.wa.gov[Maureen.Walsh@leg.wa.gov];
Judy.Warnick@leg.wa.gov[Judy.Warnick@leg.wa.gov]; Lisa.Wellman@leg.wa.gov[Lisa.Wellman@leg.wa.gov];
JT.Wilcox@leg.wa.gov[JT.Wilcox@leg.wa.gov]; Lynda.Wilson@leg.wa.gov[Lynda.Wilson@leg.wa.gov];
Sharon.Wylie@leg.wa.gov[Sharon.Wylie@leg.wa.gov]; Jesse.Young@leg.wa.gov[Jesse.Young@leg.wa.gov];
Hans.Zeiger@leg.wa.gov[Hans.Zeiger@leg.wa.gov]; mail@wired.com[mail@wired.com]; submit@wired.com[submit@wired.com];
megan_molteni@wired.com[megan_molteni@wired.com]; tyagi@ebi.ac.uk[tyagi@ebi.ac.uk];
Nick.Furnham@lshtm.ac.uk[Nick.Furnham@lshtm.ac.uk]; betsy.mckay@wsj.com[betsy.mckay@wsj.com];
spencer.macnaughton@wsj.com[spencer.macnaughton@wsj.com]; conall.jones@wsj.com[conall.jones@wsj.com];
brianna.abbott@wsj.com[brianna.abbott@wsj.com]; Christopher.Weaver@wsj.com[Christopher.Weaver@wsj.com];
jared.hopkins@wsj.com[jared.hopkins@wsj.com]; Peter.Loftus@dowjones.com[Peter.Loftus@dowjones.com];
jon.kamp@wsj.com[jon.kamp@wsj.com]; Holman.Jenkins@wsj.com[Holman.Jenkins@wsj.com];
Jan.Angel@leg.wa.gov[Jan.Angel@leg.wa.gov]; Sherry.Appleton@leg.wa.gov[Sherry.Appleton@leg.wa.gov];
Barbara.Bailey@leg.wa.gov[Barbara.Bailey@leg.wa.gov]; Andrew.Barkis@leg.wa.gov[Andrew.Barkis@leg.wa.gov];
Michael.Baumgartner@leg.wa.gov[Michael.Baumgartner@leg.wa.gov]; Randi.Becker@leg.wa.gov[Randi.Becker@leg.wa.gov];
Steve.Bergquist@leg.wa.gov[Steve.Bergquist@leg.wa.gov]; Andy.Billig@leg.wa.gov[Andy.Billig@leg.wa.gov];
Brian.Blake@leg.wa.gov[Brian.Blake@leg.wa.gov]; John.Braun@leg.wa.gov[John.Braun@leg.wa.gov];
Sharon.Brown@leg.wa.gov[Sharon.Brown@leg.wa.gov]; Vincent.Buys@leg.wa.gov[Vincent.Buys@leg.wa.gov];
Michelle.Caldier@leg.wa.gov[Michelle.Caldier@leg.wa.gov]; Reuven.Carlyle@leg.wa.gov[Reuven.Carlyle@leg.wa.gov];
Bruce.Chandler@leg.wa.gov[Bruce.Chandler@leg.wa.gov]; Mike.Chapman@leg.wa.gov[Mike.Chapman@leg.wa.gov];
Maralyn.Chase@leg.wa.gov[Maralyn.Chase@leg.wa.gov]; Frank.Chopp@leg.wa.gov[Frank.Chopp@leg.wa.gov];
Annette.Cleveland@leg.wa.gov[Annette.Cleveland@leg.wa.gov]; Judy.Clibborn@leg.wa.gov[Judy.Clibborn@leg.wa.gov];
Eileen.Cody@leg.wa.gov[Eileen.Cody@leg.wa.gov]; Cary.Condotta@leg.wa.gov[Cary.Condotta@leg.wa.gov];
Steve.Conway@leg.wa.gov[Steve.Conway@leg.wa.gov]; Jeannie.Darneille@leg.wa.gov[Jeannie.Darneille@leg.wa.gov];
Richard.DeBolt@leg.wa.gov[Richard.DeBolt@leg.wa.gov]; Tom.Dent@leg.wa.gov[Tom.Dent@leg.wa.gov];
Manka.Dhingra@leg.wa.gov[Manka.Dhingra@leg.wa.gov]; Beth.Doglio@leg.wa.gov[Beth.Doglio@leg.wa.gov];

Laurie.Dolan@leg.wa.gov[Laurie.Dolan@leg.wa.gov]; Mary.Dye@leg.wa.gov[Mary.Dye@leg.wa.gov];
Doug.Ericksen@leg.wa.gov[Doug.Ericksen@leg.wa.gov]; Carolyn.Eslick@leg.wa.gov[Carolyn.Eslick@leg.wa.gov];
Joe.Fain@leg.wa.gov[Joe.Fain@leg.wa.gov]; Jake.Fey@leg.wa.gov[Jake.Fey@leg.wa.gov];
Joe.Fitzgibbon@leg.wa.gov[Joe.Fitzgibbon@leg.wa.gov]; phil.fortunato@leg.wa.gov[phil.fortunato@leg.wa.gov];
Nicole.Macri@leg.wa.gov[Nicole.Macri@leg.wa.gov]; David.Frockt@leg.wa.gov[David.Frockt@leg.wa.gov];
Roger.Goodman@leg.wa.gov[Roger.Goodman@leg.wa.gov]; Paul.Graves@leg.wa.gov[Paul.Graves@leg.wa.gov];
Mia.Gregerson@leg.wa.gov[Mia.Gregerson@leg.wa.gov]; Dan.Griffey@leg.wa.gov[Dan.Griffey@leg.wa.gov];
Larry.Haler@leg.wa.gov[Larry.Haler@leg.wa.gov]; Drew.Hansen@leg.wa.gov[Drew.Hansen@leg.wa.gov];
Mark.Hargrove@leg.wa.gov[Mark.Hargrove@leg.wa.gov]; Mark.Harmsworth@leg.wa.gov[Mark.Harmsworth@leg.wa.gov];
Paul.Harris@leg.wa.gov[Paul.Harris@leg.wa.gov]; Bob.Hasegawa@leg.wa.gov[Bob.Hasegawa@leg.wa.gov];
Brad.Hawkins@leg.wa.gov[Brad.Hawkins@leg.wa.gov]; Dave.Hayes@leg.wa.gov[Dave.Hayes@leg.wa.gov];
Steve.Hobbs@leg.wa.gov[Steve.Hobbs@leg.wa.gov]; Jeff.Holy@leg.wa.gov[Jeff.Holy@leg.wa.gov];
Jim.Honeyford@leg.wa.gov[Jim.Honeyford@leg.wa.gov]; Zack.Hudgins@leg.wa.gov[Zack.Hudgins@leg.wa.gov];
Sam.Hunt@leg.wa.gov[Sam.Hunt@leg.wa.gov]; Morgan.Irwin@leg.wa.gov[Morgan.Irwin@leg.wa.gov];
Bill.Jenkin@leg.wa.gov[Bill.Jenkin@leg.wa.gov]; Laurie.Jinkins@leg.wa.gov[Laurie.Jinkins@leg.wa.gov];
Norm.Johnson@leg.wa.gov[Norm.Johnson@leg.wa.gov]; Ruth.Kagi@leg.wa.gov[Ruth.Kagi@leg.wa.gov];
Karen.Keiser@leg.wa.gov[Karen.Keiser@leg.wa.gov]; Christine.Kilduff@leg.wa.gov[Christine.Kilduff@leg.wa.gov];
Curtis.King@leg.wa.gov[Curtis.King@leg.wa.gov]; Steve.Kirby@leg.wa.gov[Steve.Kirby@leg.wa.gov];
Brad.Klippert@leg.wa.gov[Brad.Klippert@leg.wa.gov]; Shelley.Kloba@leg.wa.gov[Shelley.Kloba@leg.wa.gov];
Vicki.Kraft@leg.wa.gov[Vicki.Kraft@leg.wa.gov]; Joel.Kretz@leg.wa.gov[Joel.Kretz@leg.wa.gov];
Dan.Kristiansen@leg.wa.gov[Dan.Kristiansen@leg.wa.gov]; Patty.Kuderer@leg.wa.gov[Patty.Kuderer@leg.wa.gov];
Marko.Liias@leg.wa.gov[Marko.Liias@leg.wa.gov]; John.Lovick@leg.wa.gov[John.Lovick@leg.wa.gov];
Kristine.Lytton@leg.wa.gov[Kristine.Lytton@leg.wa.gov]; Drew.MacEwen@leg.wa.gov[Drew.MacEwen@leg.wa.gov];
dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int];
wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com];
lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk];
mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk];
Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com];
Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de];
zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com];
badrishanthi@hotmail.com[badrishanthi@hotmail.com]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au];
ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com]; suoban@simm.ac.cn[suoban@simm.ac.cn];
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jones.j.k@wustl.edu[jones.j.k@wustl.edu]; julia.pulliam@wustl.edu[julia.pulliam@wustl.edu]; kass@wustl.edu[kass@wustl.edu];
kdohrman@wustl.edu[kdohrman@wustl.edu]; kefalov@wustl.edu[kefalov@wustl.edu];
kerschensteinerd@wustl.edu[kerschensteinerd@wustl.edu]; lhassman@wustl.edu[lhassman@wustl.edu];
lueder@wustl.edu[lueder@wustl.edu]; lukasiewicz@wustl.edu[lukasiewicz@wustl.edu]; maamarir@wustl.edu[maamarir@wustl.edu];
mae@wustl.edu[mae@wustl.edu]; margaret.reynolds@wustl.edu[margaret.reynolds@wustl.edu];
margolist@wustl.edu[margolist@wustl.edu]; markbarlow@wustl.edu[markbarlow@wustl.edu]; mblatt@wustl.edu[mblatt@wustl.edu];
migneco@wustl.edu[migneco@wustl.edu]; montanac@wustl.edu[montanac@wustl.edu];
mortonsmith@wustl.edu[mortonsmith@wustl.edu]; nathantuttle@wustl.edu[nathantuttle@wustl.edu];
nicklasa@wustl.edu[nicklasa@wustl.edu]; njamin@email.wustl.edu[njamin@email.wustl.edu];
obrienm@wustl.edu[obrienm@wustl.edu]; piggottk@wustl.edu[piggottk@wustl.edu]; p.ruzycki@wustl.edu[p.ruzycki@wustl.edu];
prwillia@wustl.edu[prwillia@wustl.edu]; rajagopalr@wustl.edu[rajagopalr@wustl.edu]; rallo@wustl.edu[rallo@wustl.edu];
raopk@wustl.edu[raopk@wustl.edu]; ravi@wustl.edu[ravi@wustl.edu]; sarahgore@wustl.edu[sarahgore@wustl.edu];
shepherd@wustl.edu[shepherd@wustl.edu]; sheybaniar@wustl.edu[sheybaniar@wustl.edu]; shiels@wustl.edu[shiels@wustl.edu];
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steskaJ@wustl.edu[steskaJ@wustl.edu]; stunkell@wustl.edu[stunkell@wustl.edu]; tsai@wustl.edu[tsai@wustl.edu];
tychsen@wustl.edu[tychsen@wustl.edu]; vanstaverng@wustl.edu[vanstaverng@wustl.edu];
vollmanD@wustl.edu[vollmanD@wustl.edu]; wieder@wustl.edu[wieder@wustl.edu]
From: Vinu Arumugham[vaccine.safety@aol.com]
Sent: Fri 11/20/2020 10:13:10 PM (UTC-06:00)
Subject: Verizon is killing my family using 5G cellular radiation. Your family is next.

Verizon is installing 5G antennas on light poles next to my house to kill my family by causing cancer. Your family comes next.

Studies have repeatedly shown that cell phone radiation is unsafe and causes cancer. Big Telecom is corrupting the science to lie and kill for profit.

Google appropriately displays an ad showing a cancer-stricken child at St.Jude hospital, above an article on cell phone antennas on light/telephone poles.

Eve

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Opinion

OP-ED CONTRIBUT

Why Do
Telepho

By Sam Liccardo

Oct. 3, 2017

https://time.com/5069317/california-mobile-phone-radiation/

https://www.cdph.ca.gov/Programs/CCDPHP/DEODC/EHIB/CDPH%20Document%20Library/Cell-Phone-Guidance.pdf

Report of final results regarding brain and heart tumors in Sprague-Dawley rats exposed from prenatal life until natural death to mobile phone radio frequency field representative of a 1.8 GHz GSM base station environmental emission.
https://www.ncbi.nlm.nih.gov/pubmed/29530389

CONCLUSIONS:
The RI findings on far field exposure to RFR are consistent with and reinforce the results of the NTP study on near field exposure, as both reported an increase in the incidence of tumors of the brain and heart in RFR-exposed Sprague-Dawley rats. These tumors are of the same histotype of those observed in some epidemiological studies on cell phone users. These experimental studies provide sufficient evidence to call for the re-evaluation of IARC conclusions regarding the carcinogenic potential of RFR in humans.

National Institute of Environmental Health Sciences (NIEHS)/National Toxicology Program (NTP)

High Exposure to Radio Frequency Radiation Associated With Cancer in Male Rats

https://www.niehs.nih.gov/news/newsroom/releases/2018/november1/index.cfm

"We believe that the link between radio frequency radiation and tumors in male rats is real, and the external experts agreed," said Bucher.

The carcinogenic potential of non-ionizing radiations: The cases of S-50 Hz MF and 1.8 GHz GSM radio frequency radiation.

https://www.ncbi.nlm.nih.gov/pubmed/30801980

Association between vestibular schwannomas and mobile phone use

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3907669/

FCC's fake science meets reality

WHO

https://www.iarc.fr/wp-content/uploads/2018/07/pr208_E.pdf

"The WHO/International Agency for Research on Cancer (IARC) has classified radiofrequency electromagnetic fields as possibly carcinogenic to humans (Group 2B),based on an increased risk for glioma, a malignant type of brain cancer, associated with wireless phone use."

FCC

The following FCC site says:

https://www.fcc.gov/engineering-technology/electromagnetic-compatibility-division/radio-frequency-safety/faq/rf-safety#Q5

"It is generally agreed that further research is needed to determine the generality of such effects and their possible relevance, if any, to human health."

"research is continuing"

"The FDA, which has primary jurisdiction for investigating mobile phone safety, has stated that it cannot rule

out the possibility of risk, but if such a risk exists, "it is probably small." "

That's called speculation, not science, from the same corrupted FDA.

"Further, it has stated that, while there is no proof that cellular telephones can be harmful, concerned individuals can take various precautionary actions, including limiting conversations on hand-held cellular telephones and making greater use of telephones with hands-free kits where there is a greater separation distance between the user and the radiating antenna."

"no proof that cellular telephones can be harmful"? That is **UNACCEPTABLE NONSENSE**. We want proof that cellular telephones/antennas **ARE HARMLESS** before **ANY DEPLOYMENT**.

Taking that advise from the FDA we demand that such "small cell" antennas NOT be installed, so we can get a greater separation distance between the user and the radiating antenna.

"The Government Accountability Office (GAO) prepared a report of its investigation into safety concerns related to mobile phones.
The report concluded that further research is needed to confirm whether mobile phones are completely safe for the user."

The **SAFETY SCIENCE SIMPLY DOES NOT EXIST**. Without the science, you CANNOT create a safety specification. So the current "specifications" are ridiculous, arbitrary, PROVEN TO BE DANGEROUS and ABSOLUTELY UNACCEPTABLE.

The corrupted, incompetent FCC should STOP LYING about RF safety. We have to demand that all such cell installations be IMMEDIATELY BANNED AND TORN DOWN until the UNCORRUPTED SCIENCE is completed.

Reality

After several childhood cancer cases at one school, parents question radiation from cell tower

https://www.cbsnews.com/news/cell-tower-shut-down-some-california-parents-link-to-several-cases-of-childhood-cancer/

Firefighters suffer neurological disorders

https://www.iaff.org/om/cell-tower-radiation-health-effects/

How much abuse can the human body take? Pesticide-laden food, rocket fuel in drinking water, polluted air, dirty, contaminated vaccines, carcinogen-laden pharmaceuticals, power line radiation and now 5G on top of 2/3/4G radiation.

FAA/Boeing lied. 346 died due to the 737 MAX. FDA/Pharma lie. Vaccines maim and kill millions. FCC/Telecom lie. Cellular radiation maims and kills millions.

Corruption kills. COVID or not.

Covid-19: politicisation, "corruption," and suppression of science
https://www.bmj.com/content/371/bmj.m4425

Thanks,

Vinu

To: kanchanmvk@yahoo.com[kanchanmvk@yahoo.com]; ushamvk@yahoo.co.in[ushamvk@yahoo.co.in]; mike.agogliati@wfsb.com[mike.agogliati@wfsb.com]; kienym@who.int[kienym@who.int]; Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu]; sbaldwin@idri.org[sbaldwin@idri.org]; friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov]; Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org]; cww@austin.utexas.edu[cww@austin.utexas.edu]; mail@wired.com[mail@wired.com]; submit@wired.com[submit@wired.com]; megan_molteni@wired.com[megan_molteni@wired.com]; wjbkwebteam@foxtv.com;[wjbkwebteam@foxtv.com]; fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com]; tyagi@ebi.ac.uk[tyagi@ebi.ac.uk]; Nick.Furnham@lshtm.ac.uk[Nick.Furnham@lshtm.ac.uk]; betsy.mckay@wsj.com[betsy.mckay@wsj.com]; spencer.macnaughton@wsj.com[spencer.macnaughton@wsj.com]; conall.jones@wsj.com[conall.jones@wsj.com]; brianna.abbott@wsj.com[brianna.abbott@wsj.com]; Christopher.Weaver@wsj.com[Christopher.Weaver@wsj.com]; dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int]; wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com]; lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk]; mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de]; zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com]; badrishanthi@hotmail.com[badrishanthi@hotmail.com]; ljli@zju.edu.cn[ljli@zju.edu.cn]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au]; wiv@wh.iov.cn[wiv@wh.iov.cn]; suoban@simm.ac.cn[suoban@simm.ac.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; sunguibo@126.com[sunguibo@126.com]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg]; oon_tek_ng@ncid.sg[oon_tek_ng@ncid.sg]; david.szymkowski@xencor.com[david.szymkowski@xencor.com]; media.relations@roche.com[media.relations@roche.com]; murthy.aditya@gene.com[murthy.aditya@gene.com]; joshua.wallach@yale.edu[joshua.wallach@yale.edu]; alexander.egilman@yale.edu[alexander.egilman@yale.edu]; margaret.e.mccarthy@yale.edu[margaret.e.mccarthy@yale.edu]; jennifer.miller@nyumc.org[jennifer.miller@nyumc.org]; steven.woloshin@dartmouth.edu[steven.woloshin@dartmouth.edu]; lisa.schwartz@dartmouth.edu[lisa.schwartz@dartmouth.edu]; joseph.ross@yale.edu[joseph.ross@yale.edu]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Linfa.wang@csiro.au[Linfa.wang@csiro.au]
From: vinu arumugham[vaccine.safety@aol.com]
Sent: Sat 6/13/2020 12:17:01 AM (UTC-05:00)
Subject: Fwd: Re: Confirmation of my predictions on the role of mast cells, histamine in COVID-19

COVID-19 severity is caused by an allergic reaction to the coronavirus involving mast cell degranulation and histamine release (elicitation). The development of this allergy (sensitization) was caused by vaccine components that are similar to coronavirus proteins.

Sharing with permission.

-------- Forwarded Message --------
Subject: Re: Confirmation of my predictions on the role of mast cells, histamine in COVID-19
Date: Sun, 7 Jun 2020 04:07:28 +0000
From: Lawrence Steinman <steiny@stanford.edu>
To:vinu arumugham <vaccine.safety@aol.com>

Dear Vinu,

All very interesting.
Congratulations to you for being correct, on point and prescient!
Thanks for sharing
Larry

Prof. Lawrence Steinman
Zimmermann Professor of Pediatrics, Neurology and Neurological Sciences

Beckman Center for Molecular Medicine
279 Campus Drive
Stanford, CA 94305-5316

From: vinu arumugham <vaccine.safety@aol.com>
Sent: Saturday, June 6, 2020 5:44 PM
To: Lawrence Steinman <steiny@stanford.edu>
Subject: Confirmation of my predictions on the role of mast cells, histamine in COVID-19
ï¿½

Prof. Steinman,

Thought this may be of interest:

I have been predicting for 4 months now that mast cell stabilizers and antihistamines (like H1/H2 blockers) can help in COVID-19.

I described the details, connecting mast cells, histamine, COVID-19 and dengue in my article below (uploaded Apr 11'20):

Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

As you may have read, famotidine (an antihistamine, H2 blocker) has been found to help in COVID-19, just like I predicted.

A large group of experts with expertise covering drug discovery, vaccines, pathology etc. recently (May 24'20 report) hypothesized and investigated numerous potential mechanisms involved in famotidine's beneficial effect in COVID-19. The study was funded by the "Department of Defense (DoD), Defense Threat Reduction Agency (DTRA), and the Joint Science and Technology Office (JSTO) of the Chemical and Biological Defense Program (CBDP) for funding under the Discovery of Medical countermeasures Against Novel Entities (DOMANE) initiative."

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
www.researchsquare.com/article/rs-30934/v1

They conclude: "We propose that the principal famotidine mechanism of action for COVID-19 involves on-target histamine receptor H2 activity, and that development of clinical COVID-19 involves dysfunctional mast cell activation and histamine release."

They write: " ... COVID-19 disease progression could share an immunologic basis with Dengue hemorrhagic fever" and

"This model is also supported by the significant overlap in the clinical signs and symptoms of the initial phase of COVID-19 disease and those of mast cell activation syndrome (MCAS) 89-92 as well similarities to Dengue hemorrhagic fever and shock syndrome (including T cell depletion) during the later phase of COVID-19"

"If COVID-19 is partially driven by dysfunctional mast cell degranulation, then a variety of medical interventions employing

marketed drugs useful for treating mast cell-related disorders may help to reduce death and disease associated with SARS-CoV-2 infection. Examples include drugs with mast cell stabilizing activity, other histamine antagonists (for example H1 and H4 types), leukotriene antagonists and leukotriene receptor antagonists"

In other words, their findings are in perfect agreement with my prediction and analysis.

Thanks,

Vinu

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Sun 6/14/2020 6:08:38 AM (UTC-05:00)
Subject: Questions - reply requested

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April?

Look forward to hearing from you.

best wishes
Marcus Williamson

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=02%7C01%7Cvimenach%40utmb.edu%7C5d7f1c89b0a2466dc2d408d810537f59%7C7bef256d85db4526a72d31aea2546852%7C0%7C1%7C637277298089224467&sdata=LKjNwoACjfbifwfhDQtkvbWHHEdw%2F2%2BQMydkOdIGOC0%3D&reserved=0

which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Leist, Sarah Rebecca[leist@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Lisa Gralinski[lgralins@email.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Gabrielle Choonoo[gchoonoo@gmail.com]; Sophia Jeng[jengs@ohsu.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Shannon McWeeney[mcweeney@ohsu.edu]; mtferris[mtferris@email.unc.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]
Cc: Graham PhD, Jessica B[jgraham@fredhutch.org]; Swarts, Jessica L[jswarts@fredhutch.org]
From: Lund PhD, Jennifer[jlund@fredhutch.org]
Sent: Thur 9/10/2020 1:01:12 PM (UTC-05:00)
Subject: Co-authored CC/SARS manuscript
SARS_SpleenBaselineMs.docx
Figuresv2.pdf

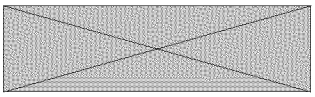
Hi everyone,

As promised, here is a manuscript describing pre-infection T cell correlates of virologic and clinical outcomes following SARS-CoV infection using data from the screen. I'd love to get everyone's feedback as soon as you can so that we can submit while the field is still hot. I'd also welcome journal suggestions, as I'm not sure of the best place to submit. Oh, and let me know if I've left authors off the list – it wasn't intentional, I just don't always know who worked on the screen!

As usual, even if you don't have any comments, please send me your approval to submit at the very least.

Hope everyone is hanging in there!
Jenny

Jennifer M. Lund
Associate Professor
Vaccine and Infectious Disease Division
O 206.667.2217
F 206.667.7767
jlund@fredhutch.org



Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Mail Stop E5-110
Seattle, WA 98109
fredhutch.org

To: dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int]; wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com]; lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk]; mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de]; zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com]; badrishanthi@hotmail.com[badrishanthi@hotmail.com]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au]; ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com]; suoban@simm.ac.cn[suoban@simm.ac.cn]; wiv@wh.iov.cn[wiv@wh.iov.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg]; oon_tek_ng@ncid.sg[oon_tek_ng@ncid.sg]; Linfa.wang@csiro.au[Linfa.wang@csiro.au]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; david.szymkowski@xencor.com[david.szymkowski@xencor.com]; media.relations@roche.com[media.relations@roche.com]; murthy.aditya@gene.com[murthy.aditya@gene.com]; joshua.wallach@yale.edu[joshua.wallach@yale.edu]; alexander.egilman@yale.edu[alexander.egilman@yale.edu]; margaret.e.mccarthy@yale.edu[margaret.e.mccarthy@yale.edu]; jennifer.miller@nyumc.org[jennifer.miller@nyumc.org]; steven.woloshin@dartmouth.edu[steven.woloshin@dartmouth.edu]; lisa.schwartz@dartmouth.edu[lisa.schwartz@dartmouth.edu]; joseph.ross@yale.edu[joseph.ross@yale.edu]; johan.neyts@kuleuven.be[johan.neyts@kuleuven.be]; kai.dallmeier@kuleuven.be[kai.dallmeier@kuleuven.be]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; manjunath.k@zyduscadila.com[manjunath.k@zyduscadila.com]; rajeshbahekar@zyduscadila.com[rajeshbahekar@zyduscadila.com]; 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alex.blaise@csus.edu[alex.blaise@csus.edu]; alexgoelzer@csus.edu[alexgoelzer@csus.edu];
alexg@saclink.csus.edu[alexg@saclink.csus.edu]; alexisgamez@csus.edu[alexisgamez@csus.edu];
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alharsami@csus.edu[alharsami@csus.edu]; alice.t.peralta@csus.edu[alice.t.peralta@csus.edu];
aliciabarros@csus.edu[aliciabarros@csus.edu]; alicias@csus.edu[alicias@csus.edu]; alino@csus.edu[alino@csus.edu];
alisa.patterson@csus.edu[alisa.patterson@csus.edu]; alisa.vanderkar@saclink.csus.edu[alisa.vanderkar@saclink.csus.edu];
alisharedhouse@csus.edu[alisharedhouse@csus.edu]; alisher.abdul@csus.edu[alisher.abdul@csus.edu];
alison.beug@saclink.csus.edu[alison.beug@saclink.csus.edu]; alison.morgan@csus.edu[alison.morgan@csus.edu];
alivia.gok@csus.edu[alivia.gok@csus.edu]; allamj@saclink.csus.edu[allamj@saclink.csus.edu];
allan.crow@csus.edu[allan.crow@csus.edu]
From: Vinu Arumugham[vaccine.safety@aol.com]
Sent: Fri 11/13/2020 2:02:39 PM (UTC-06:00)
Subject: How dirty vaccines turned COVID-19 into a killer; Make Famotidine/Cetirizine standard of care for COVID-19; COVID-19 vaccines are unsafe

Immunological mechanisms explaining the role of vaccines, IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines: Predictions and confirmations

https://doi.org/10.5281/zenodo.4100663

"Trump had been administered a Regeneron polyclonal antibody cocktail and has been taking zinc, vitamin D, **famotidine**, melatonin and a daily aspirin."

https://www.cnn.com/2020/10/02/politics/president-donald-trump-walter-reed-coronavirus/index.html

Trump gets **famotidine** for COVID-19 but it is not "standard of care" (SOC) for you and me.

The IDSA is killing hundreds of thousands by **DENYING** them **famotidine**, a cheap, safe and effective over-the-counter drug for COVID-19.

Did the money from vaccine makers and remdesivir maker Gilead, sloshing around at IDSA, influence their decision?

https://www.idsociety.org/practice-guideline/covid-19-guideline-treatment-and-management/

"The guideline panel suggests against famotidine for the sole purpose of treating COVID-19, unless in the context of a clinical trial."

Here's what the authors collected:

KATHRYN M EDWARDS collected ~$150k from vaccine makers.

https://openpaymentsdata.cms.gov/physician/651167

Lindsey Baden collected ~$50k from Janssen Pharma (a vaccine maker).

https://openpaymentsdata.cms.gov/physician/884460

RAJESH TIM GANDHI collected ~$40k from Gilead and Merck.

https://openpaymentsdata.cms.gov/physician/1273478

WILLIAM J MULLER collected ~$140k from Astrazeneca, Merck and Janssen

https://openpaymentsdata.cms.gov/physician/613576

SHUMEL SHOHAM collected $180k from Merck, Gilead, Emergent, Jannsen

https://openpaymentsdata.cms.gov/physician/780712

Mechanistic evidence (prediction)

Proteins that contaminate influenza vaccines have high homology to SARS-CoV-2 proteins thus increasing risk of severe COVID-19 disease and mortality
https://doi.org/10.5281/zenodo.3996984

Epidemiological evidence (confirmation)

Flu shot increases risk of COVID-19 Hospitalization **240%**, ICU admission **204%**, Hospital mortality **232%**.

Safety of Influenza Vaccine during COVID-19

https://doi.org/10.1017/cts.2020.543

"Among individuals with a positive SARS-CoV-2 test, patients previously vaccinated for influenza in 2019 were more likely to be hospitalized. Once hospitalized, they were more likely to be admitted to the ICU and die during hospitalization."

From Table 1:

	Never Vaccinated (N=1,125)	Vaccinated in 2019 (N=309)
Hospitalization - no.(%)	192 (17.1)	127 (41.1)
ICU Admission - no.(%)	77 (6.8)	43 (13.9)
Hospital Mortality - no.(%)	32 (2.8)	20 (6.5)

My comment posted in the Annals of Internal Medicine
The iatrogenic cascade of illnesses

https://www.acpjournals.org/doi/full/10.7326/M20-2470#_comments

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COVID-19 vaccines are **fundamentally flawed and unsafe**. Details below:

The CanSino Biologics vaccine:

https://publons.com/r/9024531/

The Oxford vaccine:

https://publons.com/r/9015091/

The Moderna mRNA vaccine:

https://publons.com/r/9025990/

The Pfizer/BioNTech vaccine:

https://publons.com/r/9026177/

The Novavax vaccine

https://publons.com/review/9108287/

Prof. Kounis' team and I, describe the common immunological mechanisms involved in cardiac injury in COVID-19, severe dengue infection and allergic reactions/anaphylaxis (Kounis syndrome). The medications for prevention/treatment include famotidine/cetirizine.

The passepartout wayfares of Covid-19, Cytokine storm and Kounis syndrome

https://doi.org/10.5281/zenodo.3977923
Dual-Histamine Blockade with Cetirizine - Famotidine Reduces Pulmonary Symptoms in COVID-19 Patients
https://www.medrxiv.org/content/10.1101/2020.06.30.20137752v1

I predicted in **JANUARY 2020** (email below) that mast cell stabilizers and antihistamines can help in COVID-19. I notified health authorities and thousands of doctors/researchers, worldwide. Hundreds of thousands of lives could have been saved.

The **key is to understand that COVID-19 severity is a result of an allergic reaction to the virus**, a "slow rolling anaphylaxis". **WE HAVE PROVEN TREATMENTS FOR ANAPHYLAXIS. NO CLINICAL TRIALS NEEDED.**

The diagnosis and management of anaphylaxis: An updated practice parameter

https://www.jacionline.org/article/S0091-6749(05)00115-6/fulltext

"These protocols have recommended the administration of **H1 and H2 antagonists, ??-agonists, antileukotrienes, and corticosteroids**."

Cetirizine is an histamine H1 blocker or antagonist. Famotidine is an histamine H2 blocker or antagonist.

These safe, OTC drugs above can be used immediately upon COVID-19 symptoms (or even a low dose if exposure is suspected). Mast cell stabilizers, ??-agonists, antileukotrienes, and corticosteroids can be prescribed as standard of care. Hundreds of thousands of lives can be saved.

As I wrote in my comment posted in the Annals of Internal Medicine:
Please see comments section:

https://annals.org/aim/fullarticle/2764199/use-hydroxychloroquine-chloroquine-during-covid-19-pandemic-what-every-clinician

Understanding mechanisms is better than demanding clinical trials in the middle of a pandemic

More details:
Immunological mechanisms explaining the role of IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines, Vitamin C, hydroxychloroquine, ivermectin and azithromycin
https://doi.org/10.5281/zenodo.3748303

COVID-19: Famotidine, Histamine, Mast Cells, and Mechanisms
https://www.researchsquare.com/article/rs-30934/v2

Repositioning Chromones for Early Anti-inflammatory Treatment of COVID-19

https://www.frontiersin.org/articles/10.3389/fphar.2020.00854/full

Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy??

https://pubmed.ncbi.nlm.nih.gov/32013309/

Thanks,
Vinu

-------- Forwarded Message --------

Subject: Wuhan 2019-nCoV treatment; Vaccines induce autoimmunity: Epitope database evidence; Ebola vaccine will cause rice allergy epidemic

Date: Fri, 24 Jan 2020 17:42:02 -0800

From: vinu arumugham <igesynth@yahoo.com>

To: jay.slater@fda.hhs.gov <jay.slater@fda.hhs.gov>, jane.woo@fda.hhs.gov <jane.woo@fda.hhs.gov>, maureen.hess@fda.hhs.gov <maureen.hess@fda.hhs.gov>, Richard.Forshee@fda.hhs.gov <Richard.Forshee@fda.hhs.gov>, Mark.Walderhaug@fda.hhs.gov <Mark.Walderhaug@fda.hhs.gov>, CBER OCOD Consumer Account <cberocod@fda.hhs.gov>, Destefano, Frank (CDC/OID/NCEZID) <fxd1@cdc.gov>, isq8@cdc.gov <isq8@cdc.gov>, nar5@cdc.gov <nar5@cdc.gov>, hjn0@cdc.gov <hjn0@cdc.gov>, Secretary@HHS.gov <Secretary@HHS.gov>, CommissionerFDA@fda.hhs.gov <CommissionerFDA@fda.hhs.gov>, olx1@cdc.gov <olx1@cdc.gov>, directorsincoming@cdc.gov <directorsincoming@cdc.gov>, francis.collins@nih.gov <francis.collins@nih.gov>, mrolfes1@cdc.gov <mrolfes1@cdc.gov>, xzd2@cdc.gov <xzd2@cdc.gov>, acy9@cdc.gov <acy9@cdc.gov>, dbj0@cdc.gov <dbj0@cdc.gov>, jmk9@cdc.gov <jmk9@cdc.gov>, tft9@cdc.gov <tft9@cdc.gov>, gll9@cdc.gov <gll9@cdc.gov>, sharplessne@nih.hhs.gov <sharplessne@nih.hhs.gov>, tnc4@cdc.gov <tnc4@cdc.gov>, kok4@cdc.gov <kok4@cdc.gov>, rxl3@cdc.gov <rxl3@cdc.gov>, gbq7@cdc.gov <gbq7@cdc.gov>, fwf7@cdc.gov <fwf7@cdc.gov>, megan.mcseveney@fda.hhs.gov <megan.mcseveney@fda.hhs.gov>, afauci@niaid.nih.gov <afauci@niaid.nih.gov>, Emelia.Benjamin@bmc.org <Emelia.Benjamin@bmc.org>, mjessup@leducq.com <mjessup@leducq.com>, tavori@ohsu.edu <tavori@ohsu.edu>, jessica.lilley@vanderbilt.edu <jessica.lilley@vanderbilt.edu>, web@beasleyallen.com <web@beasleyallen.com>, dr.flegg@bfwhospitals.nhs.uk <dr.flegg@bfwhospitals.nhs.uk>

IgE mediated sensitization to peptides that have homology to 2019-nCoV peptides may contribute to disease severity. In that case, antihistamines and other allergy treatments such as mast cell stabilizers may help reduce infection severity.

A BLASTP analysis of 2019-nCoV proteome against common vaccine antigens was performed. Preliminary results suggest that IgE mediated sensitization to common vaccine antigens can result in cross reactive immune responses to 2019-nCoV.

Please see details of the mechanisms here:

Influenza vaccines and dengue-like disease

https://www.bmj.com/content/360/bmj.k1378/rr-15

https://www.quora.com/Why-was-the-flu-so-deadly-in-outbreaks-in-the-past-And-what-made-the-flu-become-less-deadly/answers/86456279

"Scientists" at the global vaccine safety summit spill the beans: There is no science behind vaccine safety claims, it's a fairy tale.

The party is over folks.

https://youtu.be/s2IujhTdCLE

ERVEBO Ebola vaccine will create a rice allergy epidemic, add to numerous autoimmune diseases, cancer and make Ebola disease even more severe. Design for safety and vaccine safety regulation remain abject failures. Incompetence or indifference?
https://doi.org/10.5281/zenodo.3595020

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

https://doi.org/10.5281/zenodo.3603480

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies

Vinu Arumugham
Jan 2020
vinucubeacc@gmail.com

Lay summary

Proteins are a chain of amino acids. Proteins can have up to several hundred amino acids. Snippets of proteins (peptides), 7-15 amino acids in length are important in immunology. There are 20 types of amino acids. Each is assigned a letter (1 letter code).

Antibodies are proteins that can bind to peptides that have a specific amino acid sequence. Such a target peptide is known as an epitope.?? When an antibody binds to a peptide (which is part of a protein, which in turn may be part of a cell surface), it can trigger an immune attack on the cell. If the cell were a bacterium, the bacterium would be killed.

Humans (like all organisms) are made of numerous proteins (self proteins). So we have self-proteins, self-peptides and self-epitopes. In a healthy person, the body will not make antibodies that bind strongly to self-peptides (self-tolerance).

DNA is a chain of base-pairs. The DNA base-pair sequence determines the amino acid sequence in the protein produced. If there is a mutation that alters a single base-pair, the resulting protein will have a single amino acid that is altered. To prevent cancer, the immune system is capable of making antibodies against such altered peptides. Such antibodies can also weakly bind (cross react) to the unaltered normal peptide thus resulting in destruction of some healthy cells.

Say a normal protein has the following peptide (10 amino acids, each represented by its 1 letter code):

ALSTLVVNKI

Say DNA in a cell mutates due to a carcinogen exposure and it alters the protein thus resulting in this peptide with a single amino acid change:

ALSTLVV**S**KI

When the immune system makes antibodies targeted at ALSTLVV**S**KI (to attack the cell with the DNA mutation), the same antibodies can weakly bind to the normal ALSTLVVNKI peptide.

ALSTLVVNKI is an epitope associated with rheumatoid arthritis (RA).

So as a result of the immune system defending against cancer, the person can develop RA.

Now consider vaccines containing animal proteins. Animal proteins are very similar to human proteins, containing only occasional amino acid differences. An animal peptide could therefore have the ALSTLVV**S**KI sequence. Such a vaccine

would fool the immune system into creating an anti-cancer immune response, creating antibodies targeted at ALSTLVV**S**KI. The result is vaccine induced RA.

Therefore one can predict that analyzing epitopes associated with autoimmune diseases, such single amino acid difference compared to animal peptides present in vaccines, would occur more frequently than can be expected merely by chance. The analysis confirms that this prediction is valid.

Abstract

The National Institute of Allergy and Infectious Diseases (NIAID) sponsors the Immune Epitope Data Base (IEDB). IEDB contains epitopes identified from the medical literature and organized by diseases and categories of diseases. All epitopes (23000+) associated with 82 autoimmune diseases in humans were analyzed.

The role of animal, plant, fungal proteins contained in vaccines in the etiology of autoimmune diseases have been described in humans and animals. BLASTP was used to analyze IEDB derived epitopes for sequence alignment to animal, plant, fungal (APF) proteins present in vaccines and biologics. Specifically, the search was performed against bovine, chicken, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes.

The results show that 57% of epitopes differed by exactly one amino acid residue from an APF peptide. 78% of the epitopes differed by up to two amino acid residues from an APF peptide. The rest of the epitopes were either identical or differed by more than two amino acid residues.

A majority of IEDB epitopes analyzed were 9-mer peptides. Comparing randomly selected 9-mer human peptides with APF proteomes, the probability of single amino acid residue difference (SAARD) outcomes was derived. This was used to estimate the probability that actual IEDB SAARD alignments to APF peptides were merely a chance outcome. The estimates show that the probability that the observed IEDB alignments to APF being merely a chance outcome are vanishingly small. So the results make it absolutely clear that APF proteins in vaccines cause all these autoimmune diseases.

Introduction

Vaccines contain thousands of residual animal, plant and fungal (APF) proteins from the manufacturing process (1???6)???. 293 chicken proteins were identified in the influenza vaccine (7)???, for example. Actin and vimentin proteins were detected in the Priorix Tetra vaccine (8)???. Immunization with homologous xenogeneic antigens resulting in autoimmune diseases has been known for at least 40 years (9)???. Vaccines that contain bovine proteins caused autoimmunity in dogs (10)???. We previously described the immunological mechanism involved in autoimmunity induction by immunization with homologous xenogeneic antigens (11)???.

Cancer cells have minor differences when compared to healthy cells. Due to mutation of the DNA encoding the proteins, cancer cells can display altered proteins on their surface. Healthy cancer defense mechanisms include immune responses directed at such altered proteins. Therefore an immune response directed against cancer cells always carries a risk of cross reactive immune responses against healthy cells displaying the unaltered protein. Therefore, cancer induced autoimmune responses are a consequence of normal, healthy immune system behavior.

Animal proteins have minor differences compared to human proteins. Peptides that are identical between humans and animals are unlikely to cause any problem due to strong self tolerance. However, peptides with one amino acid residue difference produce the strongest cross reactive immune responses (11)???. They are ideally suited to induce autoimmune diseases. Injecting animal proteins results in anti-cancer immune responses because the immune system perceives animal proteins as altered human proteins. Adjuvants in the vaccine boost this anti-cancer immune response. This artificial anti-cancer response directed at thousands of APF proteins in vaccines or biologics, therefore cross react and cause numerous autoimmune disorders.

For this reason, one can predict that single amino acid residue difference (SAARD) between autoimmune disease related epitopes in the IEDB and homologous APF peptides in vaccines, would occur at a higher probability than by mere chance. We perform a BLASTP analysis to verify.

Methods

Basic local alignment search tool for proteins (BLASTP) (12)???, Universal Protein Resource (UniProt)(13)??? and the Immune Epitope Database (IEDB) (14)??? were used for bioinformatics analysis.

Specifically, the BLASTP sequence alignment of IEDB peptides was performed against bovine, chick, porcine, guinea pig, African green monkey, Chinese hamster, murine, peanut, soy, wheat, corn, sesame and *Saccharomyces cerevisiae* proteomes. Vaccines and biologics contain residual proteins from all these organism due to media used to grow viruses or bacteria, recombinant cells/organisms used for protein expression or as excipients.

Results

57% of IEDB peptides have a SAARD and 78% have up to two amino acid differences compared to animal, fungal or plant peptides present in vaccines.

Discussion

Could this result be a chance occurrence?

A majority of IEDB epitopes analyzed were 9-mer peptides. Five thousand 9-mer peptides were chosen at random from the human proteome. BLASTP was run using these peptides to compare against each organism???s proteome or a subset. This provides us the probability that randomly selected human peptides have an alignment providing a SAARD compared to peptides from these organisms. These are listed in table 1 under ??? Random SAARD alignment???. Given this, we can compute the probability of the actual SAARD alignment to IEDB epitopes, occurring by chance. This is listed in table 1 under ???Estimated probability of actual SAARD outcome occurring just by chance???.

For a simple coin toss example, we would perform the calculation as follows:

Computing probability of say a 7 heads, 3 tails outcome of 10 trials of a fair coin:

Probability = (0.5^7) x (0.5^3) x 10! / (7! x 3!)

Where:

0.5 is the probability of a head or tail outcome of a fair coin.

For an unfair coin, say probability of head outcome = 0.4 and tail outcome 0.6, we would have:

Probability = (0.4^7) x (0.6^3) x 10! / (7! x 3!)

For the IEDB peptide probability analysis, the outcome is for 23192 trials (peptides).

The ???head outcome??? is the ???Random SAARD alignment ??? entries in table 1. The ???tail outcome??? probability is 1-???head outcome???.

Sample calculation for Chinese Hamster:

Probability = ((889/5000)^4574) x ((4111/5000)^18618) x 23192! / (4574! x 18618!)

Probability = 1.488e-15

Where: 889*100/5000 = 17.8% is the entry in Table 1 for Chinese Hamster. BLASTP analysis shows 889 SAARD out of 5000 peptides analyzed.

And, 4574*100/23192=19.7% is the IEDB entry in Table 1 for Chinese Hamster. BLASTP analysis shows 4574 SAARD out of 23192 peptides analyzed.

So the 1.488e-15 value is the probability that we will have exactly 4574 SAARD alignments out of 23192 peptides. The probability goes down for all values > 4574. Conservatively, applying the same probability as for 4574, to all values >4574, we can calculate the probability of the chance occurrence of 4574 or greater number of SAARD alignments as 1.488e15 * 18618 = 27e-12, entry in table.

The Gnome calculator was used to perform these calculations and the results were verified using the Qalculate! calculator and WolframAlpha (15)??? since spreadsheets are unable to perform these calculations.

Table 1

Organism	Random SAARD alignment Number of Peptides(%)	Actual (IEDB) SAARD alignment Number of Peptides (%)	Estimated probability of actual SAARD outcome occurring just by chance	Remarks
African green monkey (*Chlorocebus aethiops*)	26 (0.5)	420 (1.8)	~1.7e-96	Probabilit is vanishi vaccines,
Cow (*Bos taurus*)	936 (18.7)	4385 (18.9)	~1	There are occurred j cow protei amount is bovine gel vaccines. tissues in other cow more likel

				entry belo
Cow???s Milk (*Bos taurus*)	0 (0)	12 (0.05)	0	Probability is 0. So th these disea
Chinese Hamster (*Cricetulus griseus*)	889 (17.8)	4574 (19.7)	~27e-12	Probability is vanishi vaccines,
Chicken (*Gallus gallus*)	536 (10.7)	3901 (16.8)	<1e-100	Probability is vanishi vaccines, porcine an embryo is proteins ca
Guinea Pig (*Cavia porcellus*)	837 (16.7)	4439 (19.1)	~1e-18	Probability is vanishi vaccines,
Mice (*Mus musculus*)	940 (18.8)	4467 (19.3)	~1	There are occurred j mice prote amount is cells are u proteins p present in be present
Maize (*Zea mays*)	303 (6.1)	1667 (7.2)	~5e-9	Probability is vanishi vaccines,
Peanut (*Arachis hypogaea*)	223 (4.5)	1697 (7.3)	~79e-81	Probability is vanishi vaccines,
Yeast (*Saccharomyces cerevisiae*)	64 (1.3)	828 (3.6)	<1e-100	Probability is vanishi vaccines,
Sesame (*Sesamum indicum*)	155 (3.1)	1398 (6.0)	<1e-100	Probability is vanishi vaccines,

Soy (*Glycine max)*	215 (4.3)	1548 (6.7)	~86e-59	Probability is vanishir vaccines,
Pig (*Sus scrofa*)	963 (19.3)	4407 (19.0)	~1	There are occurred j porcine pr amount is used in va present in vaccines b present. T
Wheat (*Triticum aestivum*)	138 (2.8)	977 (4.2)	~18e-33	Probability is vanishir vaccines,

The calculations make it clear that the findings cannot be merely a chance outcome and that immunization against animal/plant/fungal antigens in the vaccines do cause these autoimmune diseases in the IEDB.

Conclusion

Vaccines containing animal, plant or fungal proteins are extremely dangerous and cause numerous autoimmune diseases and cancer (16???19)???. All non-target proteins in vaccines must be immediately removed using processes such affinity chromatography (20)???.

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To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Mon 11/16/2020 4:25:32 AM (UTC-06:00)
Subject: Questions - reply requested

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April?

Look forward to hearing from you.

best wishes
Marcus Williamson

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

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which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Thur 12/3/2020 7:06:17 PM (UTC-06:00)
Subject: Questions - reply requested

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Cc: kevin.guskiewicz@unc.edu[kevin.guskiewicz@unc.edu]; braimer@utmb.edu[braimer@utmb.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Sun 1/10/2021 10:16:08 AM (UTC-06:00)
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Can you please reply to this email of 14 April 2020, shown below?

I have copied the UNC Chancellor and UTMB President, so that they can be aware of this apparent lack of responsiveness and openness of their staff.

Please respond openly and honestly to my questions.

I look forward to hearing from you, without further delay.

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Marcus Williamson
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To: Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov];
Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov];
Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov];
John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov];
Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov];
Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov];
Terry.Nealey@leg.wa.gov[Terry.Nealey@leg.wa.gov]; Sharon.Nelson@leg.wa.gov[Sharon.Nelson@leg.wa.gov];
Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov];
Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov];
Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov];
Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov];
Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov];
Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov];
Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov];
Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov];
Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov];
Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov];
Cindy.Ryu@leg.wa.gov[Cindy.Ryu@leg.wa.gov]; Rebecca.Saldana@leg.wa.gov[Rebecca.Saldana@leg.wa.gov];
SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov];
Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov];
Mike.Sells@leg.wa.gov[Mike.Sells@leg.wa.gov]; Tana.Senn@leg.wa.gov[Tana.Senn@leg.wa.gov];
Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov];
Shelly.Short@leg.wa.gov[Shelly.Short@leg.wa.gov]; Vandana.Slatter@leg.wa.gov[Vandana.Slatter@leg.wa.gov];
Norma.Smith@leg.wa.gov[Norma.Smith@leg.wa.gov]; Larry.Springer@leg.wa.gov[Larry.Springer@leg.wa.gov];
Melanie.Stambaugh@leg.wa.gov[Melanie.Stambaugh@leg.wa.gov]; Derek.Stanford@leg.wa.gov[Derek.Stanford@leg.wa.gov];
mike.steele@leg.wa.gov[mike.steele@leg.wa.gov]; Drew.Stokesbary@leg.wa.gov[Drew.Stokesbary@leg.wa.gov];
Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov];
Dean.Takko@leg.wa.gov[Dean.Takko@leg.wa.gov]; Gael.Tarleton@leg.wa.gov[Gael.Tarleton@leg.wa.gov];
David.Taylor@leg.wa.gov[David.Taylor@leg.wa.gov]; Steve.Tharinger@leg.wa.gov[Steve.Tharinger@leg.wa.gov];
Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov];
Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov];
Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov];
Jim.Walsh@leg.wa.gov[Jim.Walsh@leg.wa.gov]; Maureen.Walsh@leg.wa.gov[Maureen.Walsh@leg.wa.gov];
Judy.Warnick@leg.wa.gov[Judy.Warnick@leg.wa.gov]; Lisa.Wellman@leg.wa.gov[Lisa.Wellman@leg.wa.gov];
JT.Wilcox@leg.wa.gov[JT.Wilcox@leg.wa.gov]; Lynda.Wilson@leg.wa.gov[Lynda.Wilson@leg.wa.gov];
Sharon.Wylie@leg.wa.gov[Sharon.Wylie@leg.wa.gov]; Jesse.Young@leg.wa.gov[Jesse.Young@leg.wa.gov];
Hans.Zeiger@leg.wa.gov[Hans.Zeiger@leg.wa.gov]; Jan.Angel@leg.wa.gov[Jan.Angel@leg.wa.gov];
Sherry.Appleton@leg.wa.gov[Sherry.Appleton@leg.wa.gov]; Barbara.Bailey@leg.wa.gov[Barbara.Bailey@leg.wa.gov];
Andrew.Barkis@leg.wa.gov[Andrew.Barkis@leg.wa.gov]; Michael.Baumgartner@leg.wa.gov[Michael.Baumgartner@leg.wa.gov];
Randi.Becker@leg.wa.gov[Randi.Becker@leg.wa.gov]; Steve.Bergquist@leg.wa.gov[Steve.Bergquist@leg.wa.gov];
Andy.Billig@leg.wa.gov[Andy.Billig@leg.wa.gov]; Brian.Blake@leg.wa.gov[Brian.Blake@leg.wa.gov];
John.Braun@leg.wa.gov[John.Braun@leg.wa.gov]; Sharon.Brown@leg.wa.gov[Sharon.Brown@leg.wa.gov];
Vincent.Buys@leg.wa.gov[Vincent.Buys@leg.wa.gov]; Michelle.Caldier@leg.wa.gov[Michelle.Caldier@leg.wa.gov];
Reuven.Carlyle@leg.wa.gov[Reuven.Carlyle@leg.wa.gov]; Bruce.Chandler@leg.wa.gov[Bruce.Chandler@leg.wa.gov];
Mike.Chapman@leg.wa.gov[Mike.Chapman@leg.wa.gov]; Maralyn.Chase@leg.wa.gov[Maralyn.Chase@leg.wa.gov];
Frank.Chopp@leg.wa.gov[Frank.Chopp@leg.wa.gov]; Annette.Cleveland@leg.wa.gov[Annette.Cleveland@leg.wa.gov];
Judy.Clibborn@leg.wa.gov[Judy.Clibborn@leg.wa.gov]; Eileen.Cody@leg.wa.gov[Eileen.Cody@leg.wa.gov];
Cary.Condotta@leg.wa.gov[Cary.Condotta@leg.wa.gov]; Steve.Conway@leg.wa.gov[Steve.Conway@leg.wa.gov];
Jeannie.Darneille@leg.wa.gov[Jeannie.Darneille@leg.wa.gov]; Richard.DeBolt@leg.wa.gov[Richard.DeBolt@leg.wa.gov];
Tom.Dent@leg.wa.gov[Tom.Dent@leg.wa.gov]; Manka.Dhingra@leg.wa.gov[Manka.Dhingra@leg.wa.gov];
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Carolyn.Eslick@leg.wa.gov[Carolyn.Eslick@leg.wa.gov]; Joe.Fain@leg.wa.gov[Joe.Fain@leg.wa.gov];
Jake.Fey@leg.wa.gov[Jake.Fey@leg.wa.gov]; Joe.Fitzgibbon@leg.wa.gov[Joe.Fitzgibbon@leg.wa.gov];
phil.fortunato@leg.wa.gov[phil.fortunato@leg.wa.gov]; Nicole.Macri@leg.wa.gov[Nicole.Macri@leg.wa.gov];
David.Frockt@leg.wa.gov[David.Frockt@leg.wa.gov]; Roger.Goodman@leg.wa.gov[Roger.Goodman@leg.wa.gov];
Paul.Graves@leg.wa.gov[Paul.Graves@leg.wa.gov]; Mia.Gregerson@leg.wa.gov[Mia.Gregerson@leg.wa.gov];
Dan.Griffey@leg.wa.gov[Dan.Griffey@leg.wa.gov]; Larry.Haler@leg.wa.gov[Larry.Haler@leg.wa.gov];
Drew.Hansen@leg.wa.gov[Drew.Hansen@leg.wa.gov]; Mark.Hargrove@leg.wa.gov[Mark.Hargrove@leg.wa.gov];
Mark.Harmsworth@leg.wa.gov[Mark.Harmsworth@leg.wa.gov]; Paul.Harris@leg.wa.gov[Paul.Harris@leg.wa.gov];
Bob.Hasegawa@leg.wa.gov[Bob.Hasegawa@leg.wa.gov]; Brad.Hawkins@leg.wa.gov[Brad.Hawkins@leg.wa.gov];
Dave.Hayes@leg.wa.gov[Dave.Hayes@leg.wa.gov]; Steve.Hobbs@leg.wa.gov[Steve.Hobbs@leg.wa.gov];
Jeff.Holy@leg.wa.gov[Jeff.Holy@leg.wa.gov]; Jim.Honeyford@leg.wa.gov[Jim.Honeyford@leg.wa.gov];
Zack.Hudgins@leg.wa.gov[Zack.Hudgins@leg.wa.gov]; Sam.Hunt@leg.wa.gov[Sam.Hunt@leg.wa.gov];
Morgan.Irwin@leg.wa.gov[Morgan.Irwin@leg.wa.gov]; Bill.Jenkin@leg.wa.gov[Bill.Jenkin@leg.wa.gov];
Laurie.Jinkins@leg.wa.gov[Laurie.Jinkins@leg.wa.gov]; Norm.Johnson@leg.wa.gov[Norm.Johnson@leg.wa.gov];
Ruth.Kagi@leg.wa.gov[Ruth.Kagi@leg.wa.gov]; Karen.Keiser@leg.wa.gov[Karen.Keiser@leg.wa.gov];

Christine.Kilduff@leg.wa.gov[Christine.Kilduff@leg.wa.gov]; Curtis.King@leg.wa.gov[Curtis.King@leg.wa.gov]; Steve.Kirby@leg.wa.gov[Steve.Kirby@leg.wa.gov]; Brad.Klippert@leg.wa.gov[Brad.Klippert@leg.wa.gov]; Shelley.Kloba@leg.wa.gov[Shelley.Kloba@leg.wa.gov]; Vicki.Kraft@leg.wa.gov[Vicki.Kraft@leg.wa.gov]; Joel.Kretz@leg.wa.gov[Joel.Kretz@leg.wa.gov]; Dan.Kristiansen@leg.wa.gov[Dan.Kristiansen@leg.wa.gov]; Patty.Kuderer@leg.wa.gov[Patty.Kuderer@leg.wa.gov]; Marko.Liias@leg.wa.gov[Marko.Liias@leg.wa.gov]; John.Lovick@leg.wa.gov[John.Lovick@leg.wa.gov]; Kristine.Lytton@leg.wa.gov[Kristine.Lytton@leg.wa.gov]; Drew.MacEwen@leg.wa.gov[Drew.MacEwen@leg.wa.gov]; kanchanmvk@yahoo.com[kanchanmvk@yahoo.com]; ushamvk@yahoo.co.in[ushamvk@yahoo.co.in]; mike.agogliati@wfsb.com[mike.agogliati@wfsb.com]; fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com]; wjbkwebteam@foxtv.com;[wjbkwebteam@foxtv.com]; sanjay.mishra@Vanderbilt.Edu[sanjay.mishra@Vanderbilt.Edu]; kienym@who.int[kienym@who.int]; Pasi.Penttinen@ecdc.europa.eu[Pasi.Penttinen@ecdc.europa.eu]; sbaldwin@idri.org[sbaldwin@idri.org]; friedem@who.int[friedem@who.int]; angela.shen@hhs.gov[angela.shen@hhs.gov]; Bruce.Gellin@sabin.org[Bruce.Gellin@sabin.org]; cww@austin.utexas.edu[cww@austin.utexas.edu]; henaorestrepoa@who.int[henaorestrepoa@who.int]; www.felix@konpotey-ahulu.com[www.felix@konpotey-ahulu.com]; olin0012@umn.edu[olin0012@umn.edu]; sinabavari@comcast.net[sinabavari@comcast.net]; maryam.keshtkar@jhmi.edu[maryam.keshtkar@jhmi.edu]; corey.casper@idri.org[corey.casper@idri.org]; theiland@immunomix.com[theiland@immunomix.com]; ProjanSJ@medimmune.com[ProjanSJ@medimmune.com]; schleiss@umn.edu[schleiss@umn.edu]; mail@wired.com[mail@wired.com]; submit@wired.com[submit@wired.com]; megan_molteni@wired.com[megan_molteni@wired.com]; tyagi@ebi.ac.uk[tyagi@ebi.ac.uk]; Nick.Furnham@lshtm.ac.uk[Nick.Furnham@lshtm.ac.uk]; dschui@cuhk.edu.hk[dschui@cuhk.edu.hk]; wpchnwr@who.int[wpchnwr@who.int]; wpchnmedia@who.int[wpchnmedia@who.int]; wprocom@who.int[wprocom@who.int]; mediainquiries@who.int[mediainquiries@who.int]; 13698665@qq.com[13698665@qq.com]; lifang@umn.edu[lifang@umn.edu]; LDu@nybc.org[LDu@nybc.org]; kyyuen@hku.hk[kyyuen@hku.hk]; mark.woolhouse@ed.ac.uk[mark.woolhouse@ed.ac.uk]; Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU]; jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-muenchen.de[rothe@lrz.uni-muenchen.de]; zhangyongzhen@shphc.org.cn[zhangyongzhen@shphc.org.cn]; sanchak@gmail.com[sanchak@gmail.com]; badrishanthi@hotmail.com[badrishanthi@hotmail.com]; gmaclaren@iinet.net.au[gmaclaren@iinet.net.au]; ljli@zju.edu.cn[ljli@zju.edu.cn]; sunguibo@126.com[sunguibo@126.com]; suoban@simm.ac.cn[suoban@simm.ac.cn]; wiv@wh.iov.cn[wiv@wh.iov.cn]; yqi@implad.ac.cn[yqi@implad.ac.cn]; kalisvar_marimuthu@ncid.sg[kalisvar_marimuthu@ncid.sg]; oon_tek_ng@ncid.sg[oon_tek_ng@ncid.sg]; Linfa.wang@csiro.au[Linfa.wang@csiro.au]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; ahong22@wustl.edu[ahong22@wustl.edu]; andley@wustl.edu[andley@wustl.edu]; apte@wustl.edu[apte@wustl.edu]; arlee@wustl.edu[arlee@wustl.edu]; bassnett@wustl.edu[bassnett@wustl.edu]; bhorade@wustl.edu[bhorade@wustl.edu]; brian.s.clark@wustl.edu[brian.s.clark@wustl.edu]; brosenthal@wustl.edu[brosenthal@wustl.edu]; chenshiming@wustl.edu[chenshiming@wustl.edu]; couchS@wustl.edu[couchS@wustl.edu]; custer@wustl.edu[custer@wustl.edu]; demetruliasa@wustl.edu[demetruliasa@wustl.edu]; eric.harris@wustl.edu[eric.harris@wustl.edu]; erin.sieck@wustl.edu[erin.sieck@wustl.edu]; ferguson@wustl.edu[ferguson@wustl.edu]; harocopos@wustl.edu[harocopos@wustl.edu]; hoekel@wustl.edu[hoekel@wustl.edu]; huangandrew@wustl.edu[huangandrew@wustl.edu]; jlmorgan@wustl.edu[jlmorgan@wustl.edu]; jones.j.k@wustl.edu[jones.j.k@wustl.edu]; julia.pulliam@wustl.edu[julia.pulliam@wustl.edu]; kass@wustl.edu[kass@wustl.edu]; kdohrman@wustl.edu[kdohrman@wustl.edu]; kefalov@wustl.edu[kefalov@wustl.edu]; kerschensteinerd@wustl.edu[kerschensteinerd@wustl.edu]; lhassman@wustl.edu[lhassman@wustl.edu]; lueder@wustl.edu[lueder@wustl.edu]; lukasiewicz@wustl.edu[lukasiewicz@wustl.edu]; maamarir@wustl.edu[maamarir@wustl.edu]; mae@wustl.edu[mae@wustl.edu]; margaret.reynolds@wustl.edu[margaret.reynolds@wustl.edu]; margolist@wustl.edu[margolist@wustl.edu]; markbarlow@wustl.edu[markbarlow@wustl.edu]; mblatt@wustl.edu[mblatt@wustl.edu]; migneco@wustl.edu[migneco@wustl.edu]; montanac@wustl.edu[montanac@wustl.edu]; mortonsmith@wustl.edu[mortonsmith@wustl.edu]; nathantuttle@wustl.edu[nathantuttle@wustl.edu]; nicklasa@wustl.edu[nicklasa@wustl.edu]; njamin@email.wustl.edu[njamin@email.wustl.edu]; obrienm@wustl.edu[obrienm@wustl.edu]; piggottk@wustl.edu[piggottk@wustl.edu]; p.ruzycki@wustl.edu[p.ruzycki@wustl.edu]; prwillia@wustl.edu[prwillia@wustl.edu]; rajagopalr@wustl.edu[rajagopalr@wustl.edu]; rallo@wustl.edu[rallo@wustl.edu]; raopk@wustl.edu[raopk@wustl.edu]; ravi@wustl.edu[ravi@wustl.edu]; sarahgore@wustl.edu[sarahgore@wustl.edu]; shepherd@wustl.edu[shepherd@wustl.edu]; sheybaniar@wustl.edu[sheybaniar@wustl.edu]; 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From: Vinu Arumugham[vaccine.safety@aol.com]
Sent: Thur 1/28/2021 1:17:35 PM (UTC-06:00)
Subject: COVID-19 vaccine dangers; CDC's "Vaccines do not cause autism" lie, taken down; NH commission exposes FCC corruption, cellular radiation dangers

Vaccines absolutely do cause autism

The CDC has flip-flopped twice in ~5 months on the fraudulent claim that "Vaccines do not cause autism", on their website. It suggests that the CDC's vaccine/autism claims are based on the conjunction of Jupiter and Saturn, not science.

They were forced to take the false claim down because ICAN demonstrated there was **ZERO** science behind that claim.

The CDC Finally Capitulated To ICAN's Legal Demands and Removed the Claim that "Vaccines Do Not Cause Autism" From Its Website!

https://www.icandecide.org/ican_press/the-cdc-finally-capitulated-to-icans-legal-demands-and-removed-the-claim-that-vaccines-do-not-cause-autism-from-its-website/

THE CDC JUST SOLIDIFIED THAT ITS DECISIONS ARE NOT DRIVEN BY SCIENCE

https://www.icandecide.org/ican_press/the-cdc-just-solidified-that-its-decisions-are-not-driven-by-science/

FACT: Milk protein contaminated vaccines (DTap/Tdap/Prevnar 13/ActHiB) cause at least 75% of autism cases.

Autism pathogenesis: Piecing it all together, from end to beginning ...
https://doi.org/10.5281/zenodo.1477515

NOTICE!

By authority of the Nuremberg Code on Medical Experimentation, I do hereby exercise my right to refuse to submit to or to administer the Covid-19 vaccine. The United States Government has prosecuted, convicted and executed Medical Doctors who have violated the Nuremberg Code on Medical Experimentation. Aiders and abettors of Nuremberg Crimes are equally guilty and have also been prosecuted, convicted, and executed.

Francis A. Boyle
Professor of Law.

My comment in the Annals of Internal Medicine, against Fauci's "SARS-CoV-2 Vaccines: Much Accomplished, Much to Learn"

https://www.acpjournals.org/doi/10.7326/M21-0111

Vinu Arumugham Independent 18 January 2021
These vaccines are unsafe, unnecessary and must be immediately withdrawn

The vaccine safety claims made by the authors are unsupported by evidence. Vaccines must be designed for safety. These vaccines were not designed at all. So they are unsafe by definition. I predicted the allergic sensitization and autoimmunity risks with these vaccines which have now been confirmed.

The Pfizer/BioNTech vaccine is unnecessary, unsafe and should not be authorized.

https://www.regulations.gov/document?D=FDA-2020-N-1898-0039

Robert F Kennedy Jr. warned the FDA months back about the risk of allergic reactions due to the use of polyethylene glycol (PEG) in the vaccines.
https://childrenshealthdefense.org/defender/pfizer-covid-vaccine-allergic-reactions/

The FDA/VRBPAC ignored us and authorized these horrendously dangerous vaccines.

Recently, Dr. Peter Marks of the FDA admitted that the population was sensitized by PEG-containing pharmaceutical preparations (that include other vaccines/injections).

https://www.wsj.com/articles/scientists-eye-potential-culprit-for-covid-19-vaccine-allergic-reactions-11608901200?mod=hp_lead_pos2

“What we’re learning now is that those **allergic reactions could be somewhat more common** than the highly uncommon that we thought they were **because people do get exposed to polyethylene glycol in various pharmaceutical preparations,**” - Peter Marks, Director, CBER,FDA.

We of course already knew that any vaccine/injection that has enough allergen to cause a reaction, has more than enough allergen to guarantee sensitization/priming (causing the development of new allergy).

Evidence that Food Proteins in Vaccines Cause the Development of Food Allergies and Its Implications for Vaccine Policy

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3571073

www.sciencemag.org/news/2020/12/suspicions-grow-nanoparticles-pfizer-s-covid-19-vaccine-trigger-rare-allergic-reactions

"he worries anti-PEG antibodies triggered by the first shot could increase the risk of an allergic reaction to the second or to PEGylated drugs."

- Janos Szebeni, an immunologist at Semmelweis University

So now, these vaccines have sensitized millions to PEG. The goal is to sensitize/boost PEG allergy in a 100 million more in the next 100 days.

PEG is contaminated with 1,4-dioxane, a carcinogen.

https://www.fda.gov/cosmetics/potential-contaminants-cosmetics/14-dioxane-cosmetics-manufacturing-byproduct

As predicted, Pfizer COVID-19 vaccine induced autoimmunity (thrombocytopenia) killed a Florida doctor. This is just the tip of the iceberg. Thousands of cases of vaccine induced autoimmune diseases may take months/years to be diagnosed and will be dismissed as unrelated to the vaccine.

https://www.nytimes.com/2021/01/12/health/covid-vaccine-death.html

Only a few lots were tested in the trial. No one has a clue what other lots will do. 100-fold variation of contaminants in vaccines makes trials and epidemiological studies worthless as I detailed in my comments in the Annals of Internal Medicine before. Vaccine safety remains an oxymoron.

https://www.acpjournals.org/doi/10.7326/m18-2101

California calls for pause of 330,000 doses, investigation after allergic reactions to Moderna vaccine batch

https://www.mercurynews.com/2021/01/18/coronavirus-california-calls-for-pause-investigation-after-allergic-reactions-to-moderna-vaccine-batch/

What's worse? Effective, life-saving, cheap, safe medicines such as famotidine/cetirizine/ivermectin are being ignored in this blind race to vaccinate at any cost.

Immunological mechanisms explaining the role of vaccines, IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines: Predictions and confirmations

https://europepmc.org/article/PPR/PPR241819

Big picture of the damage vaccines do:

Vaccines and Biologics injury table based on mechanistic evidence – Feb 2020

Covering over 125 conditionshttps://zenodo.org/record/3647593/files/vbitr2_final.pdf?download=1

The New Hampshire Commission report below has ripped FCC's 5G (and all other cellular) RF safety claims:

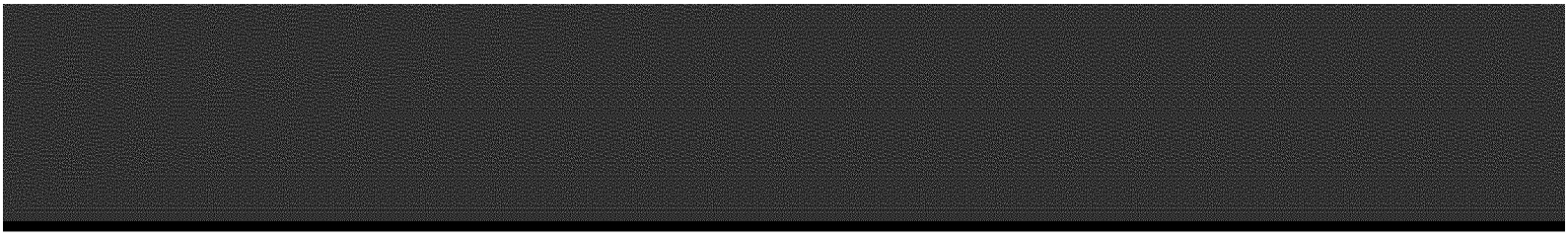
Final Report of the Commission to Study The Environmental and Health Effects of Evolving 5G Technology

http://www.gencourt.state.nh.us/statstudcomm/committees/1474/reports/5G%20final%20report.pdf

"RECOMMENDATION 1- Propose a resolution of the House to the US Congress and Executive Branch to **require the Federal Communication Commission (FCC) to commission an independent review** of the current radiofrequency (RF) standards of the electromagnetic radiation in the 300MHz to 300GHz microwave spectrum as well as a health study to assess and recommend mitigation for the health risks associated with the use of cellular communications and data transmittal."

"A likely explanation as to why **regulatory agencies have opted to ignore the body of scientific evidence demonstrating the negative impact of cellphone radiation** is that **those agencies are "captured"** (see Harvard University publication entitled, "Captured Agency: How the Federal Communications Commission Is Dominated by the Industries It Presumably Regulates" linked in Appendix G). This report documents how **the leadership roles in some agencies (the FCC in particular) are filled by individuals with strong industry ties** and hence are more **focused on**

industry interests than the health of citizens"



Read Today's Press Release

Visit the New Tahoe Safe Tech Website

Support the Landmark Litigation

Read the News

Listen to Recording of the Oral Arguments

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Contribute to 5G Crisis

Share

Forward

Thanks,

Vinu

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
Cc: kevin.guskiewicz@unc.edu[kevin.guskiewicz@unc.edu]; braimer@utmb.edu[braimer@utmb.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Mon 2/15/2021 11:42:53 AM (UTC-06:00)
Subject: Questions - reply requested

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions - reply requested
From: Marcus Williamson <marcus@connectotel.com>
Date: Sun, 10 Jan 2021 16:16:08 +0000
Cc: kevin.guskiewicz@unc.edu, braimer@utmb.edu

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April 2020, shown below?

I have copied the UNC Chancellor and UTMB President, so that they can be aware of this apparent lack of responsiveness and openness of their staff.

Please respond openly and honestly to my questions.

I look forward to hearing from you, without further delay.

best wishes
Marcus Williamson
Editor
https://nam11.safelinks.protection.outlook.com/?url=http%3A%2F%2Fwww.ceoemail.com%2F&data=04%7C01%7Cvimenach%40utmb.edu%7Cecda36bd6e614901bc2308d8d1d9312a%7C7bef256d85db4526a72d31aea2546852%7C0%7C1%7C637490078059897547%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C2000&sdata=6YDFySw25BLSK3tEUPc38vKefhpXN1hQ%2B9eqbgG1BqI%3D&reserved=0

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=04%7C01%7Cvimenach%40utmb.edu%7Cecda36bd6e614901bc2308d8d1d9312a%7C7bef256d85db4526a72d31aea2546852%7C0%7C1%7C637490078059902533%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C2000&sdata=VBUI2N5G%2FZFTWqyTydTr8IEZnWDsYUj3IKMIE6pUkMI%3D&reserved=0

which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

From: Virologica Sinica [virologicasinica@wh.iov.cn]
Sent: 2/22/2021 10:29:10 PM
To: Menachery, Vineet [vimenach@UTMB.EDU]
Subject: To Dr.Menachery - Virologica Sinica, Volume 35, Special Issue on SARS-CoV-2 and COVID-19 (II)

The linked image cannot be display

Dear Dr. Menachery,

It is my pleasure to present you the Special Issue on **SARS-CoV-2 and COVID-19 (II)** recently published in *Virologica Sinica*.

Your suggestions are welcome!

Zheng-Li Shi, Ph.D.
Editor-in-Chief, *Virologica Sinica*

Browse the website www.virosin.org for more information

Enjoy **rapid** & **free** publication in *Virologica Sinica*

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Virologica Sinica is an academic journal which aims at presenting the cutting-edge research on viruses. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including research on animal, plant and microbe viruses. The journal welcomes articles on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related biotechniques. *Virologica Sinica*, the official journal of the Chinese Society for Microbiology, will serve as a platform for the communication and exchange of academic information and ideas in an international context.

The journal is indexed by: Science Citation Index (SCI), Journal Citation Reports (JCR), PubMed/Medline, Pubmed Central, Scopus, BIOSIS, Google Scholar.

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Special Issue: SARS-CoV-2 and COVID-19 (II)
Issue Editor: Zheng-Li Shi, PhD, Wuhan Institute of Virology, Chinese Academy of Sciences

By the end of November 2020, SARS-CoV-2—the new coronavirus behind the disease COVID-19— has infected over 60 million people around the world and caused about one and a half million deaths. Facing the biggest global pandemic of the century, doctors, scientists and the scientific community have been working hard to uncover the pathogenesis and search for effective scientific solutions. *Virologica Sinica* has online published a series of original articles and reviews on SARS-CoV-2 and COVID-19, covering topics on clinical cohorts /cases and disease features, virus characterization and surveillance, diagnosis and improved methods, antiviral agents and therapeutic treatment, and etc, and they are collectively presented in this special issue. Those researches have greatly advanced our understandings of and empowered our strength to combat the disease. The cover depicts the SARS-CoV-2 virus particle, surrounded by human blood cells.

2020, Vol. 35, Issue 6

Review

A Crowned Killer's Résumé: Genome, Structure, Receptors, and Origin of SARS-CoV-2

Free Full Text (HTML) *Free* Full Text (PDF)

Shichuan Wang, Mirko Trilling, Kathrin Sutter, Ulf Dittmer, Mengji Lu, Xin Zheng, Dongliang Yang, Jia Liu

The recent emergence and rapid global spread of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pose an unprecedented medical and socioeconomic crisis, and the disease caused by it, Coronavirus disease 2019 (COVID-19), was declared a pandemic by the World Health Organization (WHO) on March 11, 2020. Chinese scientists and physicians rapidly identified the causative pathogen, which turned out to be a novel betacoronavirus with high sequence similarities to bat and pangolin coronaviruses. The scientific community has ignited tremendous efforts to unravel the biological underpinning of SARS-CoV-2, which constitutes the foundation for therapy and vaccine development strategies. Here, we summarize the current state of knowledge on the genome, structure, receptor, and origin of SARS-CoV-2.

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Review

COVID-19: Antiviral Agents, Antibody Development and Traditional Chinese Medicine

Free Full Text (HTML) *Free* Full Text (PDF)

Wenyi Guan, Wendong Lan, Jing Zhang, Shan Zhao, Junxian Ou, Xiaowei Wu, Yuqian Yan, Jianguo Wu, Qiwei Zhang

The World Health Organization (WHO) has declared coronavirus disease 2019 (COVID-19) is the first pandemic caused by coronavirus named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Currently, there is no effective anti-SARS-CoV-2 drug approved worldwide for treatment of patients with COVID-19. Therapeutic options in response to the COVID-19 outbreak are urgently needed. To facilitate the better and faster development of therapeutic COVID-19 drugs, we present an overview of the global promising therapeutic drugs, including repurposing existing antiviral agents, network-based pharmacology research, antibody development and traditional Chinese medicine. Among all these drugs, we focus on the most promising drugs (such as favipiravir, tocilizumab, SARS-CoV-2 convalescent plasma, hydroxychloroquine, Lianhua Qingwen, interferon beta-1a, remdesivir, etc.) that have or will enter the final stage of human testing—phase III–IV clinical trials.

Review

Summary of the Detection Kits for SARS-CoV-2 Approved by the National Medical Products Administration of China and Their Application for Diagnosis of COVID-19

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Ruhan A, Huijuan Wang, Wenling Wang, Wenjie Tan

The on-going global pandemic of coronavirus disease 2019 (COVID-19) caused by a novel coronavirus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been underway for about 11 months. Through November 20,2020,51 detection kits for SARS-CoV-2 nucleic acids (24 kits), antibodies (25 kits), or antigens (2 kits) have been approved by the National Medical Products Administration of China (NMPA). Convenient and reliable SARS-CoV-2 detection assays are urgently needed worldwide for strategic control of the pandemic. In this review, the detection kits approved in China are summarised and the three types of tests, namely nucleic acid, serological and antigen detection, which are available for the detection of COVID-19 are discussed in detail. The development of novel detection kits will lay the foundation for the control and prevention of the COVID-19 pandemic globally.

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Review

Human Monoclonal Antibodies: On the Menu of Targeted Therapeutics Against COVID-19

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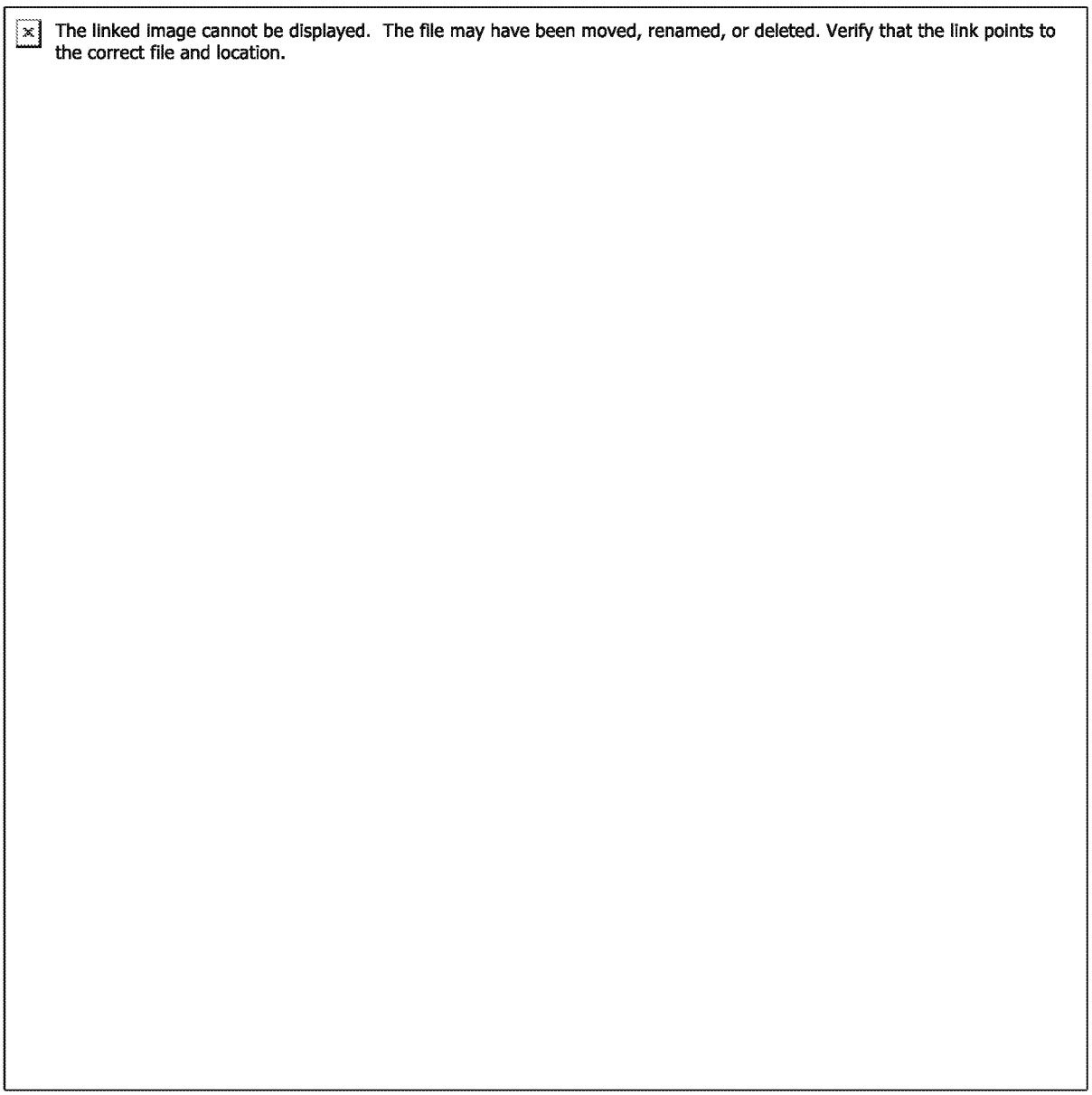
Junsen Chen, Rui Huang, Yiwen Nie, Xinyue Wen, Ying Wu

Coronavirus disease 2019 (COVID-19), reminiscent of the severe acute respiratory syndrome (SARS) outbreak in 2003, has been a tragic disaster to people all over the world. As there is no specific drug for COVID-19, neutralizing antibodies are attracting more and more attention as one of the most effective means to combat the pandemic. Here, we introduced the etiological and serological characteristics of COVID-19, discussed the current stage of development of human monoclonal antibodies against SARS-CoV-2 and summarized the antigenic epitopes in the S glycoprotein, which may deepen the understanding of the profile of immune recognition and response against SARS-CoV-2 and provide insight for the design of effective vaccines and antibody-based therapies.



Research Article

A Small-Scale Medication of Leflunomide as a Treatment of COVID-19 in an Open-Label Blank-Controlled Clinical Trial

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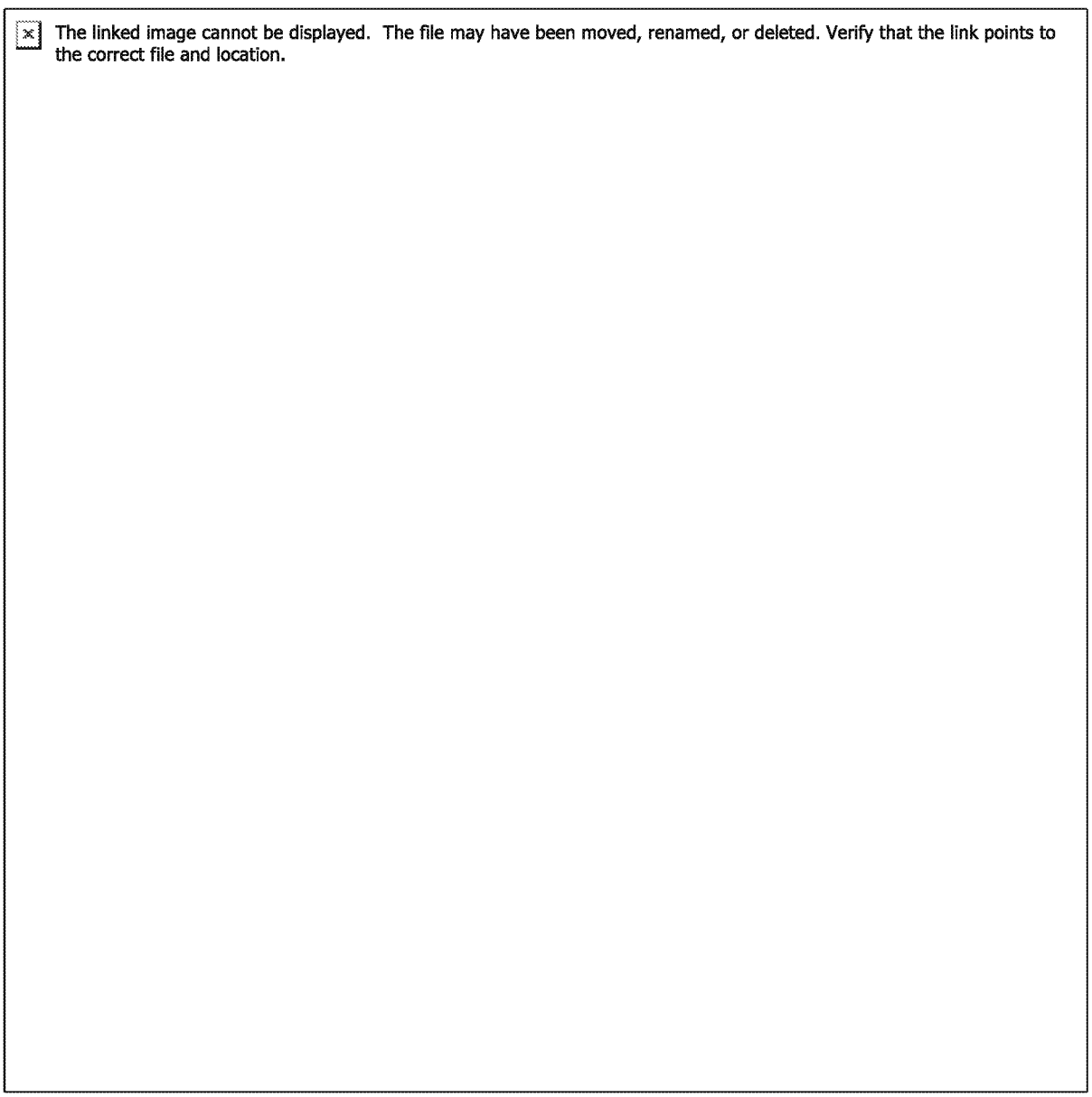
Ke Hu, Mengmei Wang, Yang Zhao, Yunting Zheng, Tao Wang, Zhishui Zheng, Xiaochen Li, Shaolin Zeng, Dong Zhao, Honglin Li, Ke Xu, Ke Lan

We recently reported that inhibitors against human dihydroorotate dehydrogenase (DHODH) have broad-spectrum antiviral activities including their inhibitory efficacies on SARS-CoV-2 replication in infected cells. However, there are limited data from clinical studies to prove the application of DHODH inhibitors in Coronavirus disease 2019 (COVID-19) patients. In the present study, we evaluated Leflunomide, an approved DHODH inhibitor widely used as a modest immune regulator to treat autoimmune diseases, in treating COVID-19 disease with a small-scale of patients. Cases of 10 laboratory-confirmed COVID-19 patients of moderate type with obvious opacity in the lung were included. Five of the patients were treated with Leflunomide, and another five were treated as blank controls without a placebo. All the patients accepted standard supportive treatment for COVID-19. The patients given Leflunomide had a shorter viral shedding time (median of 5 days) than the controls (median of 11 days, P=0.046). The patients given Leflunomide also showed a significant reduction in C-reactive protein levels, indicating that immunopathological inflammation was well controlled. No obvious adverse effects were observed in Leflunomide-treated patients, and they all discharged from the hospital faster than controls. This preliminary study on a small-scale compassionate use of Leflunomide provides clues for further understanding of Leflunomide as a potential antiviral drug against COVID-19.



Research Article

Mild Cytokine Elevation, Moderate $CD4^+$ T Cell Response and Abundant Antibody Production in Children with COVID-19

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Ran Jia, Xiangshi Wang, Pengcheng Liu, Xiaozhen Liang, Yanling Ge, He Tian, Hailing Chang, Hao Zhou, Mei Zeng, Jin Xu

Children with Coronavirus Disease 2019 (COVID-19) were reported to show milder symptoms and better prognosis than their adult counterparts, but the difference of immune response against SARS-CoV-2 between children and adults hasn't been reported. Therefore we initiated this study to figure out the features of immune response in children with COVID-19. Sera and whole blood cells from 19 children with COVID-19 during different phases after disease onset were collected. The cytokine concentrations, SARS-CoV-2 S-RBD or N-specific antibodies and T cell immune responses were detected respectively. In children with COVID-19, only 3 of 12 cytokines were increased in acute sera, including interferon (IFN)-γ-induced protein 10 (IP10), interleukin (IL)-10 and IL-16. We observed an increase in T helper (Th)-2 cells and a suppression in regulatory T cells (Treg) in patients during acute phase, but no significant response was found in the IFN-γ-producing or tumor necrosis factor (TNF)-α-producing $CD8^+$ T cells in patients. S-RBD and N IgM showed an early induction, while S-RBD and N IgG were prominently induced later in convalescent phase. Potent S-RBD IgA response was observed but N IgA seemed to be inconspicuous. Children with COVID-19 displayed an immunophenotype that is less inflammatory than adults, including unremarkable cytokine elevation, moderate $CD4^+$ T cell response and inactive $CD8^+$ T cell response, but their humoral immunity against SARS-CoV-2 were as strong as adults. Our finding presented immunological characteristics of children with COVID-19 and might give some clues as to why children develop less severe disease than adults.

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Research Article

Dynamic Changes of Antibodies to SARS-CoV-2 in COVID-19 Patients at Early Stage of Outbreak

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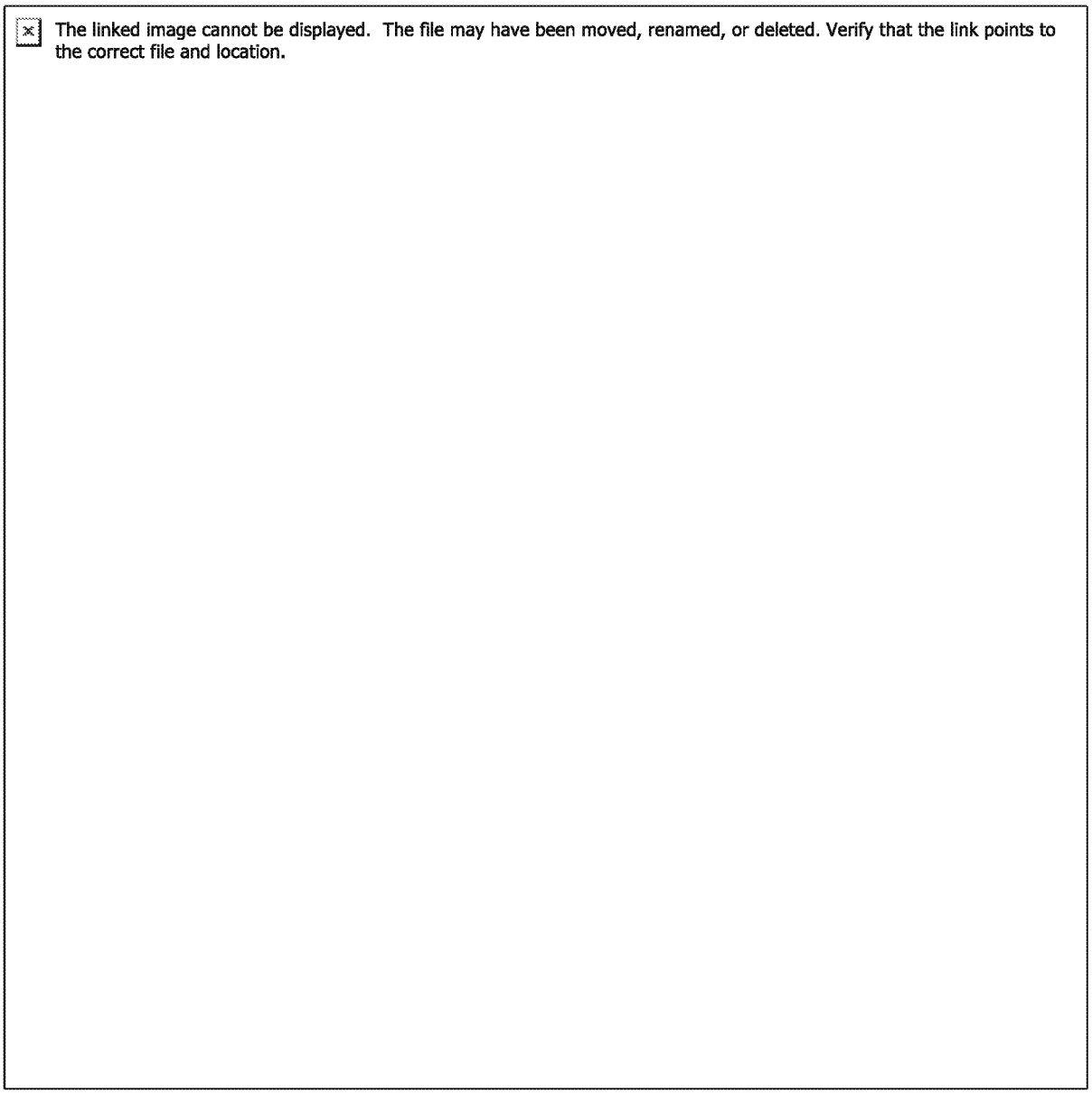
Huaqing Shu, Shuzhen Wang, Shunan Ruan, Yaxin Wang, Jiancheng Zhang, Yin Yuan, Hong Liu, Yongran Wu, Ruiting Li, Shangwen Pan, Yaqi Ouyang, Shiying Yuan, Peng Zhou, You Shang

The coronavirus disease 2019 (COVID-19), caused by SARS-CoV-2, has spread around the world with high mortality. To diagnose promptly and accurately is the vital step to effectively control its pandemic. Dynamic characteristics of SARS-CoV-2-specific antibodies which are important for diagnosis of infection have not been fully demonstrated. In this retrospective, single-center, observational study, we enrolled the initial 131 confirmed cases of COVID-19 at Jin-Yin-Tan Hospital who had at least one-time antibody tested during their hospitalization. The dynamic changes of IgM and IgG antibodies to SARS-CoV-2 nucleocapsid protein in 226 serum samples were detected by ELISA. The sensitivities of IgM and IgG ELISA detection were analyzed. Result showed that the sensitivity of the IgG ELISA detection (92.5%) was significantly higher than that of the IgM (70.8%) ($P < 0.001$). The meantimes of seroconversion for IgM and IgG were 6 days and 3 days, respectively. The IgM and IgG antibody levels peaked at around 18 days and 23 days, and then IgM fell to below the baseline level at about day 36, whereas IgG maintained at a relatively high level. In conclusion,

antibodies should be detected to aid in diagnosis of COVID-19 infection. IgG could be a sensitive indicator for retrospective diagnosis and contact tracing, while IgM could be an indicator of early infection.



Research Article

Serologic Response to SARS-CoV-2 in COVID-19 Patients with Different Severity

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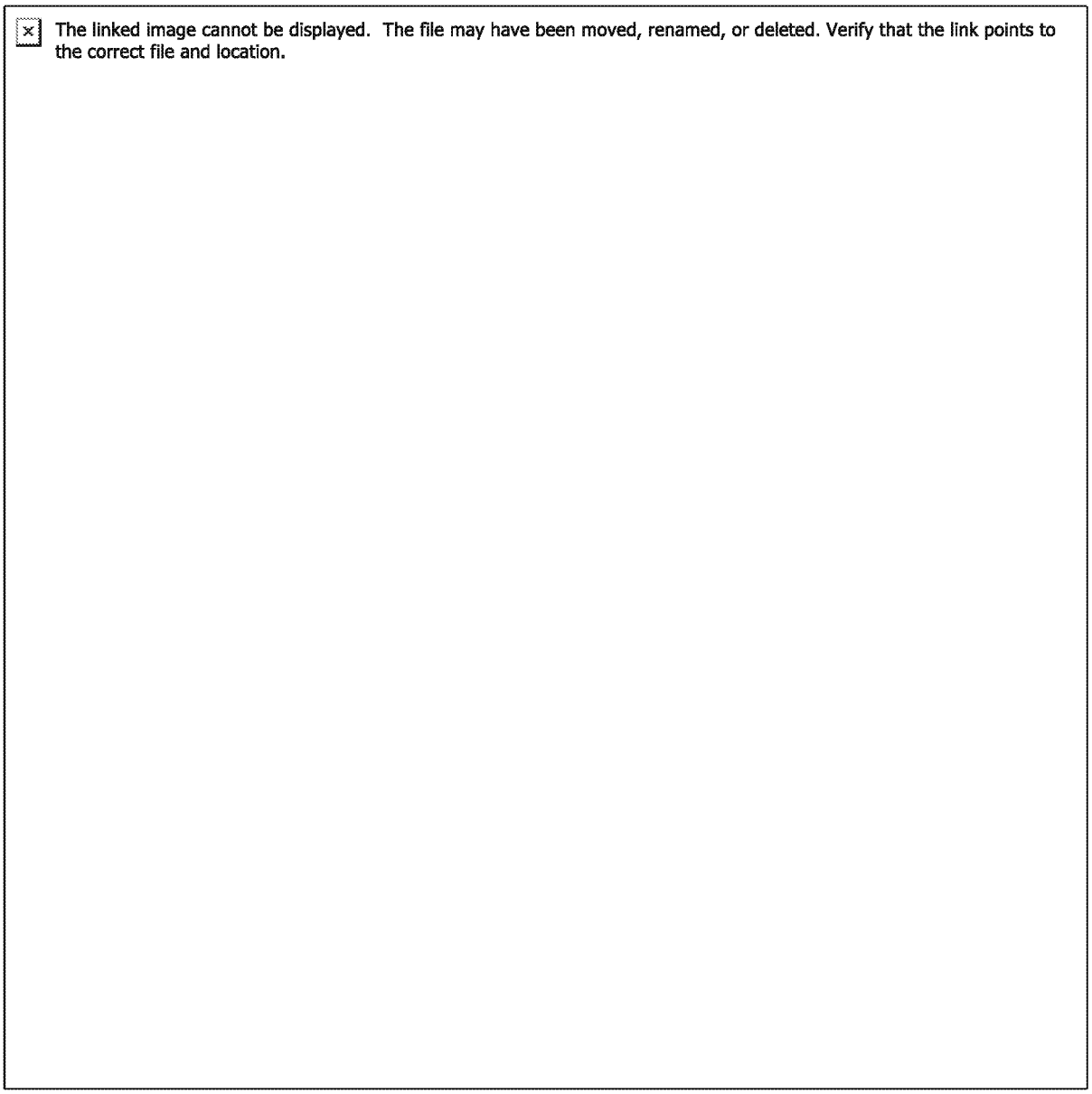
Wen-Hua Kong, Rong Zhao, Jun-Bo Zhou, Fang Wang, De-Guang Kong, Jian-Bin Sun, Qiong-Fang Ruan, Man-Qing Liu

The immense patient number caused by coronavirus disease 2019 (COVID-19) global pandemic brings the urge for more knowledge about its immunological features, including the profile of basic immune parameters. In this study, eighty-eight reported COVID-19 patients in Wuhan were recruited from January to February, 2020, including 32 severe/critical cases and 56 mild/moderate cases. Their mean age was 56.43 years (range 17-83) and gender ratio (male/female) was 43:45. We tested SARS-CoV-2 RNA with commercial kits, investigated the level of serologic IgM and IgG antibodies against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) using magnetic particle chemiluminescence immunoassays, and compared the results of serologic tests and nucleic acid test (NAT). Among 88 patients, 95.45% were confirmed as positive by the combination of NAT and antibody test, which was significantly higher ($P < 0.001$) than by single nucleic

acid test (73.86%) or serologic test (65.91%). Then the correlation between temporal profile and the level of antibody response was analyzed. It showed that seroconversion started on day 5 after disease onset and IgG level was rose earlier than IgM. Comparison between patients with different disease severity suggested early seroconversion and high antibody titer were linked with less severe clinical symptoms. These results supported the combination of serologic testing and NAT in routine COVID-19 diagnosis and provided evidence on the temporal profile of antibody response in patients with different disease severity.



Research Article

Discrimination of False Negative Results in RT-PCR Detection of SARS-CoV-2 RNAs in Clinical Specimens by Using an Internal Reference

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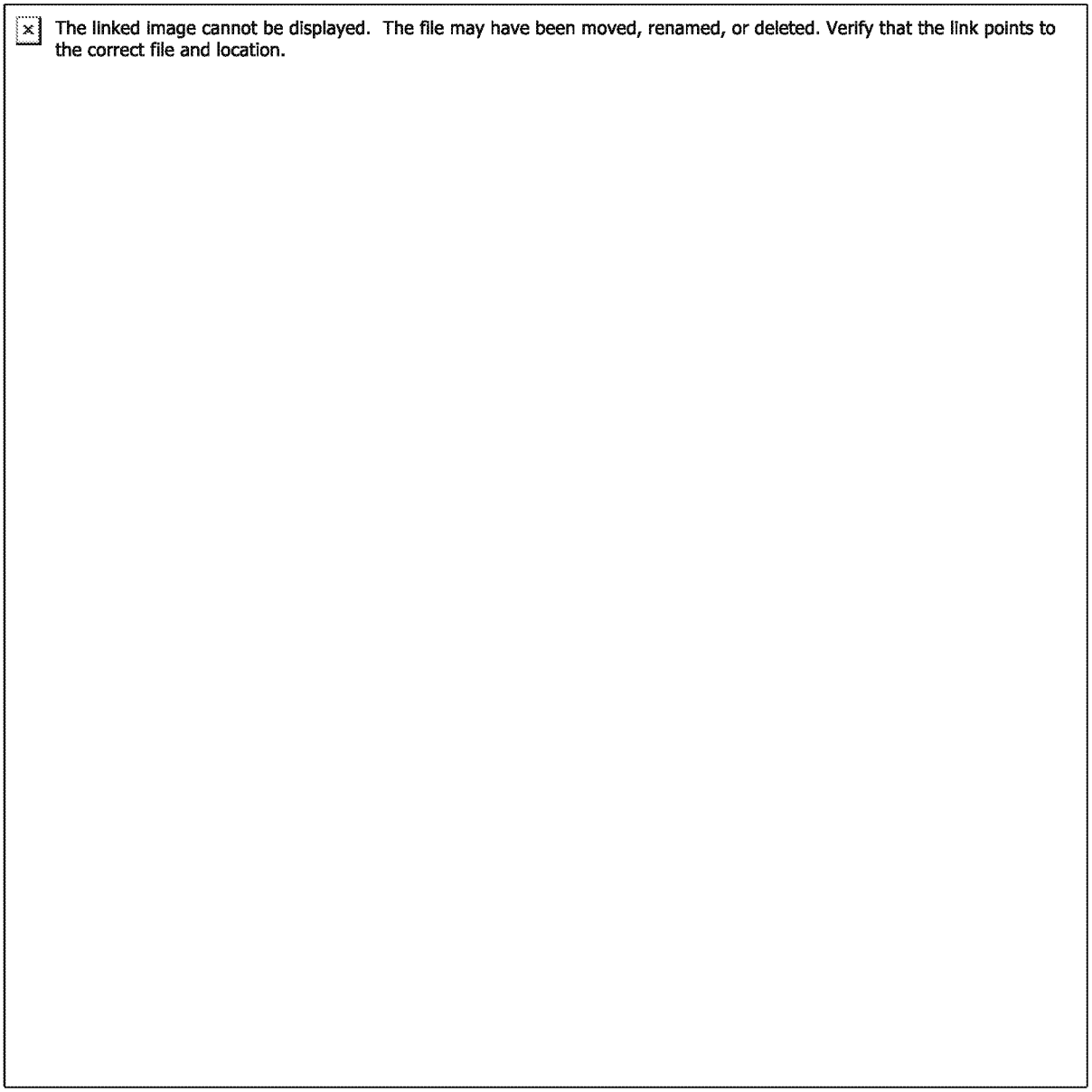
Yefei Zhang, Changtai Wang, Mingfeng Han, Jun Ye, Yong Gao, Zhongping Liu, Tengfei He, Tuantuan Li, Mengyuan Xu, Luping Zhou, Guizhou Zou, Mengji Lu, Zhenhua Zhang

Reverse transcription-polymerase chain reaction (RT-PCR) is an essential method for specific diagnosis of SARS-CoV-2 infection. Unfortunately, false negative test results are often reported. In this study, we attempted to determine the principal causes leading to false negative results of RT-PCR detection of SARS-CoV-2 RNAs in respiratory tract specimens. Multiple sputum and throat swab specimens from 161 confirmed

COVID-19 patients were tested with a commercial fluorescent RT-PCR kit targeting the *ORF1ab* and *N* regions of SARS-CoV-2 genome. The RNA level of a cellular housekeeping gene ribonuclease P/MRP subunit p30 (*RPP30*) in these specimens was also assessed by RT-PCR. Data for a total of 1052 samples were retrospectively re-analyzed and a strong association between positive results in SARS-CoV-2 RNA tests and high level of *RPP30* RNA in respiratory tract specimens was revealed. By using the ROC-AUC analysis, we identified Ct cutoff values for *RPP30* RT-PCR which predicted false negative results for SARS-CoV-2 RT-PCR with high sensitivity (95.03%–95.26%) and specificity (83.72%–98.55%) for respective combination of specimen type and amplification reaction. Using these Ct cutoff values, false negative results could be reliably identified. Therefore, the presence of cellular materials, likely infected host cells, are essential for correct SARS-CoV-2 RNA detection by RT-PCR in patient specimens. *RPP30* could serve as an indicator for cellular content, or a surrogate indicator for specimen quality. In addition, our results demonstrated that false negativity accounted for a vast majority of contradicting results in SARS-CoV-2 RNA test by RT-PCR.



Research Article

Patients with Prolonged Positivity of SARS-CoV-2 RNA Benefit from Convalescent Plasma Therapy: A Retrospective Study

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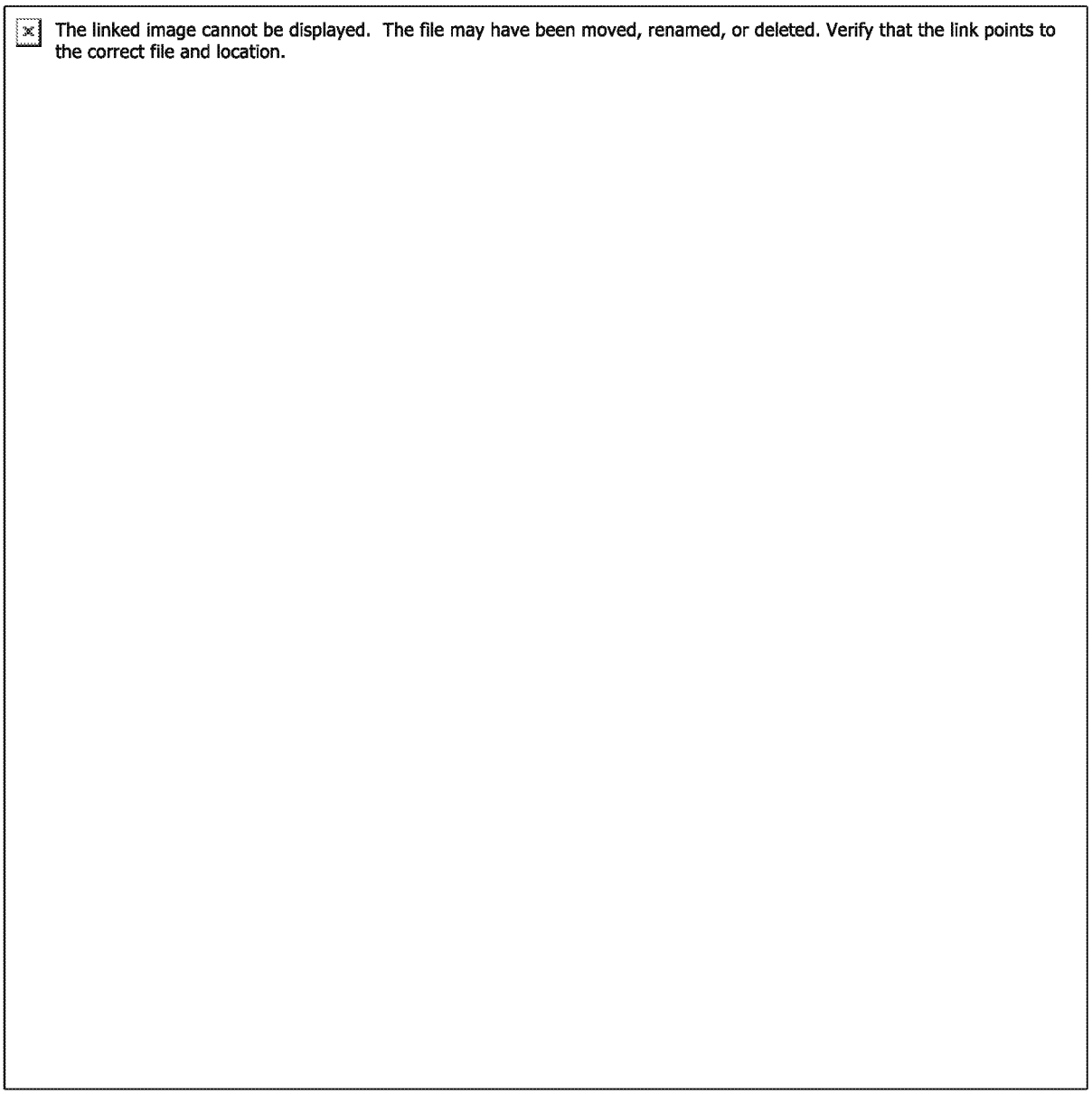
Yongran Wu, Ke Hong, Lianguo Ruan, Xiaobo Yang, Jiancheng Zhang, Jiqian Xu, Shangwen Pan, Lehao Ren, Lu Chen, Chaolin Huang, You Shang

Convalescent plasma therapy has been implemented in a few cases of severe coronavirus disease 2019. No report about convalescent plasma therapy in treating patients with prolonged positivity of SARS-CoV-2 RNA has been published. In this study, we conducted a retrospective observational study in 27 patients with prolonged positivity of SARS-CoV-2 RNA, the clinical benefit of convalescent plasma therapy were analyzed. qRT-PCR test of SARS-CoV-2 RNA turned negative (≤ 7 days) in a part of patients (early negative group, n = 15) after therapy, others (late negative group, n = 12) turned negative in more than 7 days. Pulmonary imaging improvement was confirmed in 7 patients in early negative group and 8 in late negative group after CP therapy. Viral load decreased in early negative group compared with late negative group at day 3, 5, 7 after implementing convalescent plasma therapy. Patients in early negative group had a shorter median length of hospital stay. In conclusion, convalescent plasma therapy might help eliminate virus and shorten length of hospital stay in patients with prolonged positivity of SARS-CoV-2 RNA.



Research Article

Comparative Antiviral Efficacy of Viral Protease Inhibitors against the Novel SARS-CoV-2 *In Vitro*

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Leike Zhang, Jia Liu, Ruiyuan Cao, Mingyue Xu, Yan Wu, Weijuan Shang, Xi Wang, Huanyu Zhang, Xiaming Jiang, Yuan Sun, Hengrui Hu, Yufeng Li, Gang Zou, Min Zhang, Lei Zhao, Wei Li, Xiaojia Guo, Xiaomei Zhuang, Xing-Lou Yang, Zheng-Li Shi, Fei Deng, Zhihong Hu, Gengfu Xiao, Manli Wang, Wu Zhong

The recent outbreak of novel coronavirus pneumonia (COVID-19) caused by a new coronavirus has posed a great threat to public health. Identifying safe and effective antivirals is of urgent demand to cure the huge number of patients. Virus-encoded proteases are considered potential drug targets. The human immunodeficiency virus protease inhibitors (lopinavir/ritonavir) has been recommended in the global Solidarity Trial in March launched by World Health Organization. However, there is currently no experimental evidence to support or against its clinical use. We evaluated the antiviral efficacy of lopinavir/ritonavir along with other two viral protease inhibitors *in vitro*, and discussed the possible inhibitory mechanism *in silico*. The *in vitro* to *in vivo* extrapolation was carried out to assess whether lopinavir/ritonavir could be effective in clinical. Among the four tested compounds, lopinavir showed the best inhibitory effect against the novel coronavirus infection. However, further *in vitro* to *in vivo* extrapolation of pharmacokinetics suggested that lopinavir/ritonavir could not reach effective concentration under standard dosing regimen [marketed as Kaletra®, contained lopinavir/ritonavir (200 mg/50 mg) tablets, recommended dosage is 400 mg/10 mg (2 tablets) twice daily]. This research concluded that lopinavir/ritonavir should be stopped for clinical use due to the huge gap between *in vitro* IC_{50} and free plasma concentration. Nevertheless, the structure–activity relationship analysis of the four inhibitors provided further information for *de novel* design of future viral protease inhibitors of SARS-CoV-2.

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Research Article

Identifying the Risk of SARS-CoV-2 Infection and Environmental Monitoring in Airborne Infectious Isolation Rooms (AIIRs)

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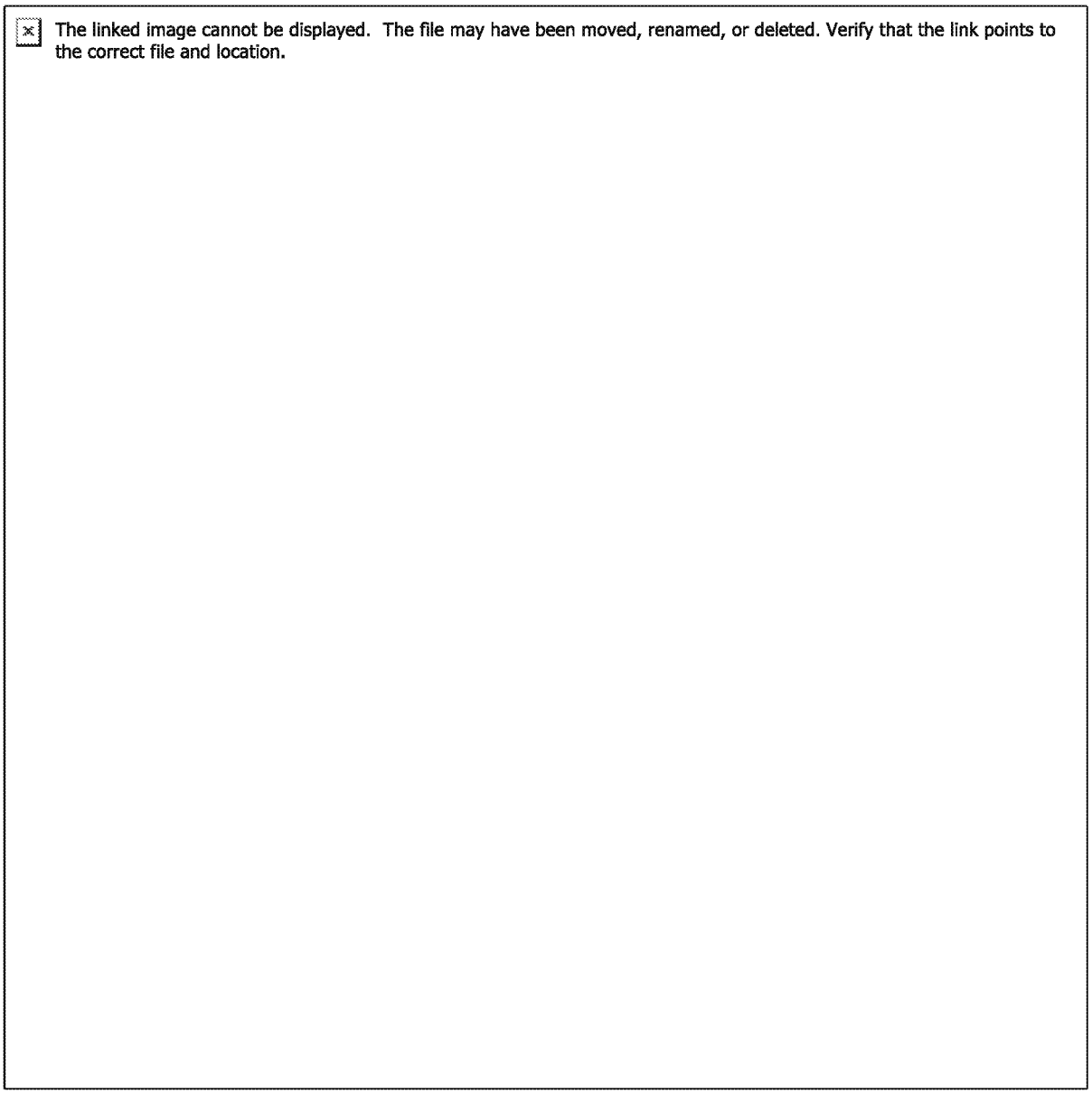
Zhi-Gang Song, Yan-Mei Chen, Fan Wu, Lin Xu, Bang-Fang Wang, Lei Shi, Xiao Chen, Fa-Hui Dai, Jia-Lei She, Jian-Min Chen, Edward C. Holmes, Tong-Yu Zhu, Yong-Zhen Zhang

Healthcare workers (HCWs) are at high risk of occupational exposure to the new pandemic human coronavirus, SARS-CoV-2, and are a source of nosocomial transmission in airborne infectious isolation rooms (AIIRs). Here, we performed comprehensive environmental contamination surveillance to evaluate the risk of viral transmission in AIIRs with 115 rooms in three buildings at the Shanghai Public Health Clinical Center, Shanghai, during the treatment of 334 patients infected with SARS-CoV-2. The results showed that the risk of airborne transmission of SARS-CoV-2 in AIIRs was low (1.62%, 25/1544) due to the directional airflow and strong environmental hygiene procedures. However, we detected viral RNA on the surface of foot-operated openers and bathroom sinks in AIIRs (viral load: 55.00–3154.50 copies/mL). This might be a source of contamination to connecting corridors and object surfaces through the footwear and gloves used by HCWs. The risk of infection was eliminated by the use of disposable footwear covers and the application of more effective environmental and personal hygiene measures. With the help of effective infection control

procedures, none of 290 HCWs was infected when working in the AIIRs at this hospital. This study has provided information pertinent for infection control in AIIRs during the treatment of COVID-19 patients.



Research Article

Long-Term Existence of SARS-CoV-2 in COVID-19 Patients: Host Immunity, Viral Virulence, and Transmissibility

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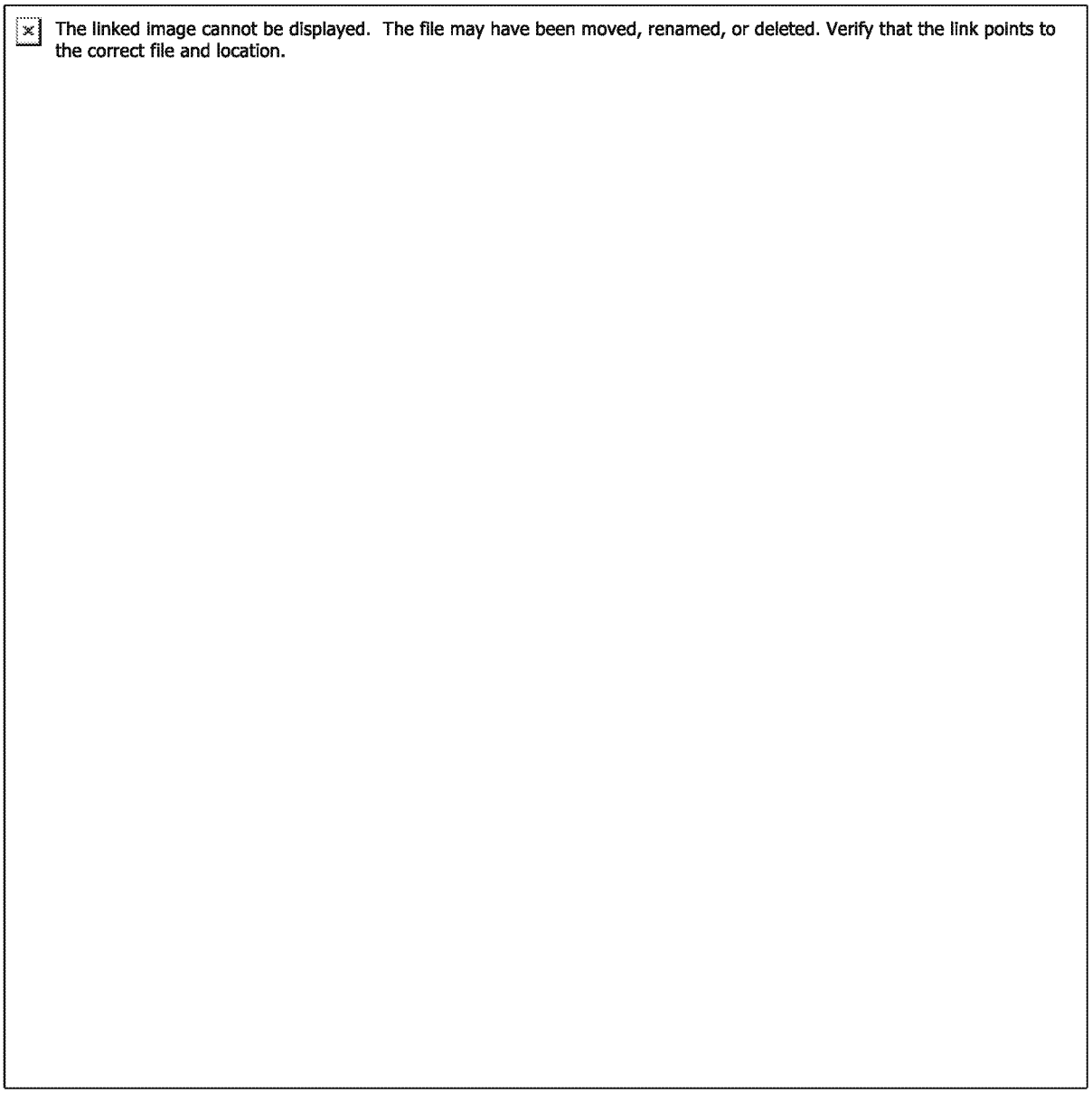
Xingyu Wang, Kun Huang, Haini Jiang, Lijuan Hua, Weiwei Yu, Dan Ding, Ke Wang, Xiaopan Li, Zhong Zou, Meilin Jin, Shuyun Xu

COVID-19 patients can recover with a median SARS-CoV-2 clearance of 20 days post initial symptoms (PIS). However, we observed some COVID-19 patients with existing SARS-CoV-2 for more than 50 days PIS. This study aimed to investigate the cause of viral clearance delay and the infectivity in these patients. Demographic data and clinical characteristics of 22 long-term COVID-19 patients were collected. The median age of the studied cohort was 59.83 ± 12.94 years. All patients were clinically cured after long-term SARS-CoV-2 infection ranging from 53 to 112 days PIS. Peripheral lymphocytes counts were normal. The ratios of interferon gamma (IFN-γ)-secreting cells to total $CD4^+$ and $CD8^+$ cells were normal as 24.68% ± 9.60% and 66.41% ± 14.87% respectively. However, the number of IFN-γ-secreting NK cells diminished (58.03% ±

11.78%). All patients presented detectable IgG, which positively correlated with mild neutralizing activity (Mean value neutralisation antibodies titers = 157.2, *P*= 0.05). No SARS-CoV-2 virus was isolated in Vero E6 cells inoculated with nasopharyngeal swab samples from all patients 50 days PIS, and the cytopathic effect was lacking. But one sample was positive for SARS-CoV-2 nucleic acid test in cell supernatants after two passages. Genome sequencing revealed that only three synonymous variants were identified in spike protein coding regions. In conclusion, decreased IFN-γ production by NK cells and low neutralizing antibodies might favor SARS-CoV-2 long-term existence. Further, low viral load and weak viral pathogenicity were observed in COVID-19 patients with long-term SARS-CoV-2 infection.



Research Article

Comparison of Clinical and Epidemiological Characteristics of Asymptomatic and Symptomatic SARS-CoV-2 Infection in Children

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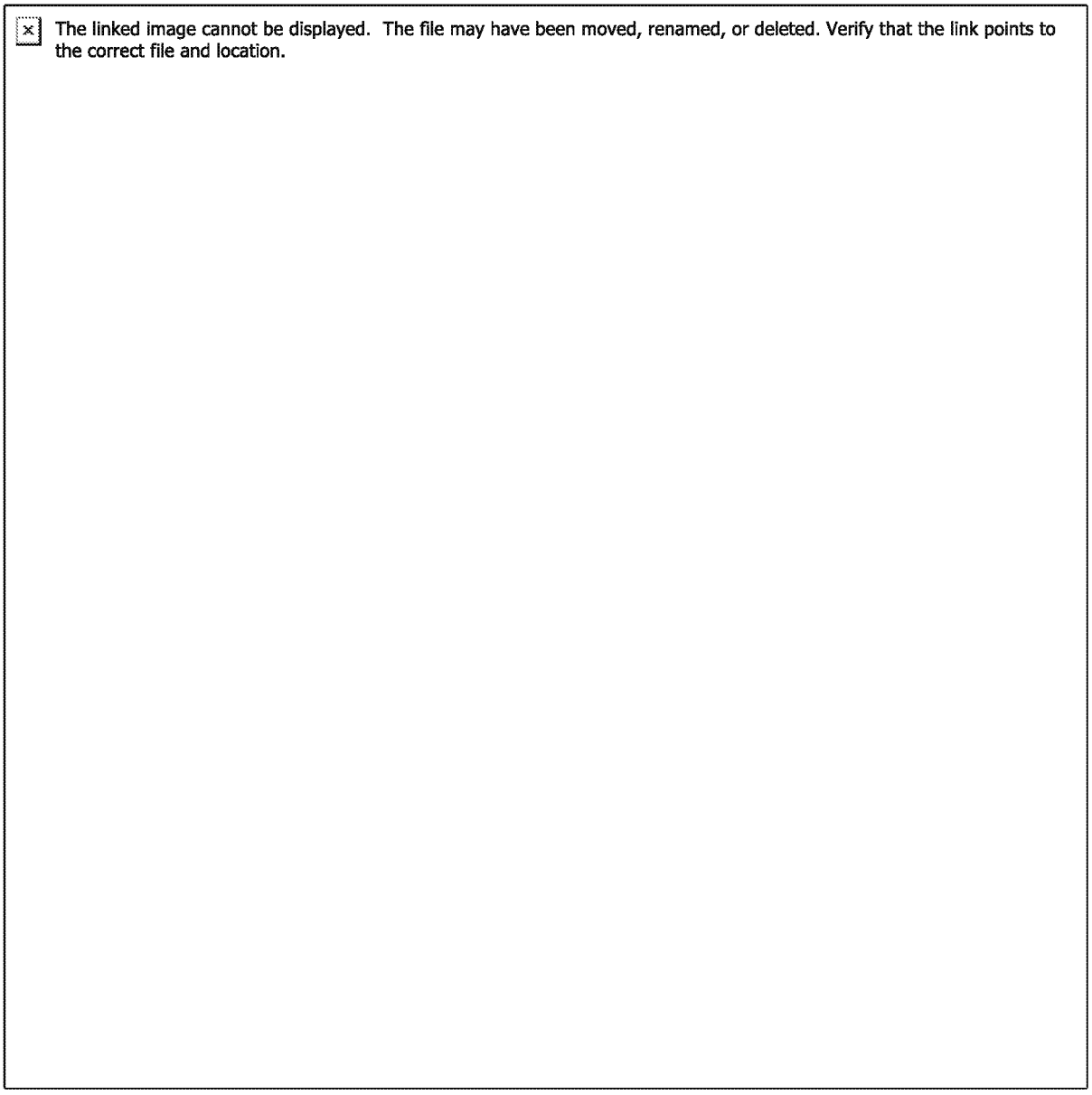
Jiehao Cai, Xiangshi Wang, Jun Zhao, Yanling Ge, Jin Xu, He Tian, Hailing Chang, Aimei Xia, Jiali Wang, Jinqiang Zhang, Zhongqiu Wei, Jingjing Li, Chuning Wang, Jianshe Wang, Qirong Zhu, Xiaowen Zhai, Mei Zeng

To understand the epidemiological and clinical features of the symptomatic and asymptomatic pediatric cases

of COVID-19, we carried out a prospective study in Shanghai during the period of January 19 to April 30, 2020. A total of 49 children (mean age 11.5 ± 5.12 years) confirmed with SARS-CoV-2 infection were enrolled in the study, including 11 (22.4%) domestic cases and 38 (77.6%) imported cases. Nine (81.8%) local cases and 12 (31.6%) imported cases had a definitive epidemiological exposure. Twenty-eight (57.1%) were symptomatic and 21 (42.9%) were asymptomatic. Neither asymptomatic nor symptomatic cases progressed to severe diseases. The mean duration of viral shedding for SARS-CoV-2 in upper respiratory tract was 14.1 ± 6.4 days in asymptomatic cases and 14.8 ± 8.4 days in symptomatic cases ($P > 0.05$). Forty-five (91.8%) cases had viral RNA detected in stool. The mean duration of viral shedding in stool was 28.1 ± 13.3 days in asymptomatic cases and 30.8 ± 18.6 days in symptomatic participants ($P > 0.05$). Children < 7 years shed viral RNA in stool for a longer duration than school-aged children ($P < 0.05$). Forty-three (87.8%) cases had seropositivity for antibodies against SARS-CoV-2 within 1–3 weeks after confirmation with infection. In conclusion, asymptomatic SARS-CoV-2 infection may be common in children in the community during the COVID-19 pandemic wave. Asymptomatic cases shed viral RNA in a similar pattern as symptomatic cases do. It is of particular concern that asymptomatic individuals are potentially seed transmission of SARS-CoV-2 and pose a challenge to disease control.



Research Article

A Prognostic Model to Predict Recovery of COVID-19 Patients Based on Longitudinal Laboratory Findings

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Suyan Tian, Xuetong Zhu, Xuejuan Sun, Jinmei Wang, Qi Zhou, Chi Wang, Li Chen, Shanji Li, Jiancheng Xu

The temporal change patterns of laboratory data may provide insightful clues into the whole course of COVID-19. This study aimed to evaluate longitudinal change patterns of key laboratory tests in patients with COVID-19, and identify independent prognostic factors by examining the associations between laboratory findings and outcomes of patients. This multicenter study included 56 patients with COVID-19 treated in Jilin Province, China, from January 21, 2020 to March 5, 2020. The laboratory findings, epidemiological characteristics and demographic data were extracted from electronic medical records. The average value of eosinophils and carbon dioxide combining power continued to significantly increase, while the average value of cardiac troponin I and mean platelet volume decreased throughout the course of the disease. The average value of lymphocytes approached the lower limit of the reference interval for the first 5 days and then rose slowly thereafter. The average value of thrombocytocrit peaked on day 7 and slowly declined thereafter. The average value of mean corpuscular volume and serum sodium showed an upward trend from day 8 and day 15, respectively. Age, sex, lactate dehydrogenase, platelet count and globulin level were included in the final model to predict the probability of recovery. The above parameters were verified in 24 patients with COVID-19 in another area of Jilin Province. The risk stratification and management of patients with COVID-19 could be improved according to the temporal trajectories of laboratory tests.

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Research Article

Viral and Antibody Kinetics of COVID-19 Patients with Different Disease Severities in Acute and Convalescent Phases: A 6-Month Follow-Up Study

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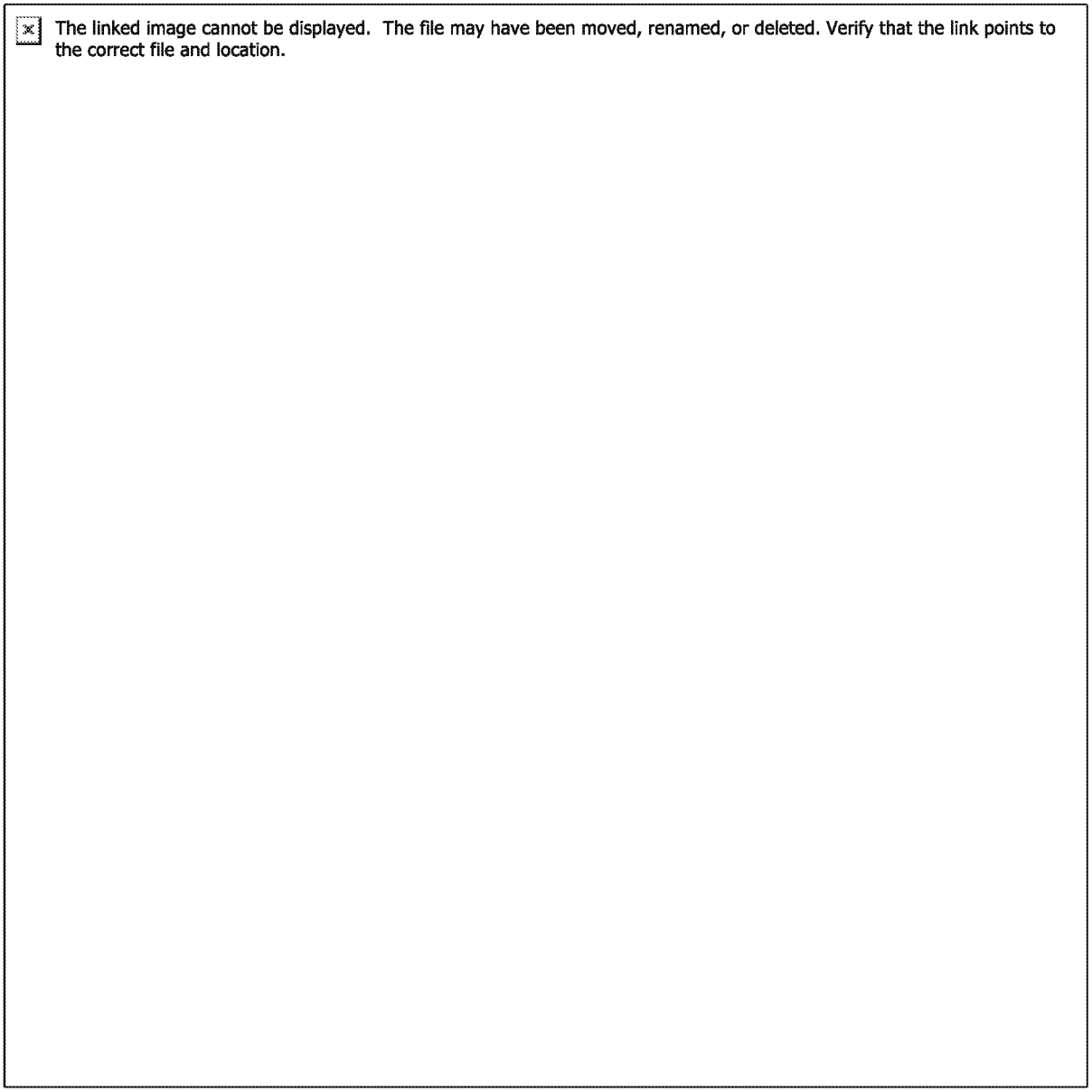
Xiaoyong Zhang, Suwen Lu, Hui Li, Yi Wang, Zhen Lu, Zhihong Liu, Qingtao Lai, Yali Ji, Xuan Huang, Yongyin Li, Jian Sun, Yingsong Wu, Xiaoning Xu, Jinlin Hou

Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has spread rapidly around the world, posing a major threat to human health and the economy. Currently, long-term data on viral shedding and the serum antibody responses in COVID-19 patients are still limited. Herein, we report the clinical features, viral RNA loads, and serum antibody levels in a cohort of 112 COVID-19 patients admitted to the Honghu People's Hospital, Hubei Province, China. Overall, 5.36% (6/112) of patients showed persistent viral RNA shedding (> 45 days). The peak viral load was higher in the severe disease group than in the mild group (median cycle threshold value, 36.4 versus 31.5; $P = 0.002$). For most patients the disappearance of IgM antibodies occurred approximately 4-6 weeks after symptoms onset, while IgG persisted for over 194 days after the onset of symptoms, although patients showed a 46% reduction in antibodies titres against SARS-CoV-2 nucleocapsid protein compared with the acute phase. We also studied 18 asymptomatic individuals with RT-qPCR confirmed SARS-CoV-2 infection together with 17 symptomatic

patients, and the asymptomatic individuals were the close contacts of these symptomatic cases. Delayed IgG seroconversion and lower IgM seropositive rates were observed in asymptomatic individuals. These data indicate that higher viral loads and stronger antibody responses are related to more severe disease status in patients with SARS-CoV-2 infection, and the antibodies persisted in the recovered patient for more than 6 months so that the vaccine may provide protection against SARS-CoV-2 infection.



Letter

Feasibility Study of Mixing Throat Swab Samples for Severe Acute Respiratory Syndrome Coronavirus-2 Screening

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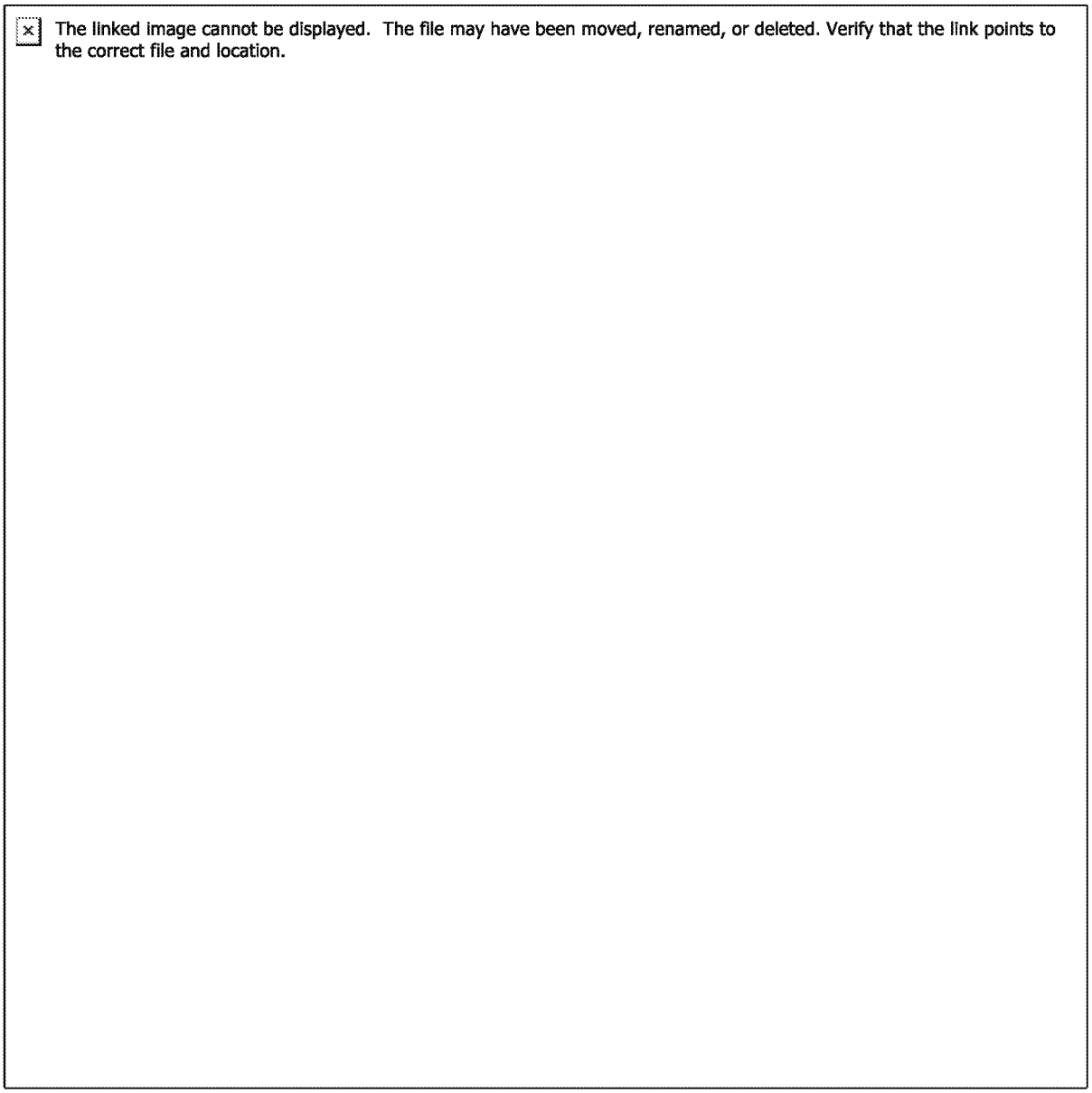
Yang Han, Qingyu Yang, Ying Liu, Ting Shu, Li Yue, Ting Xiao, Qin Zeng, Ying Wu, Xi Zhou, Dingyu Zhang

At present, viral nucleic acids are generally sampled using throat swabs and detected by quantitative real-time reverse transcription polymerase chain reaction (qRT-PCR). However, the capacity for SARS-CoV-2 nucleic acid detection is largely limited by the number of instruments, kits, and experienced laboratory personnel available. These limitations have caused low screening efficiency, which leads to a lag in identifying potential infections and may then exacerbate the spread of COVID-19 (Carter *et al*. 2020). Therefore, novel qRT-PCR approaches for nucleic acid detection are required to enhance testing efficiency.In

this study, we aimed to explore a practical method and procedure for SARS-CoV-2 qRT-PCR detection in 96-well plates using pooled throat swab samples. This method may reduce the cost of testing and increase the screening capacity for SARS-CoV-2 using existing instrument and kits, consequently facilitating the containment of COVID-19 worldwide.



Letter

Patterns of Gustatory Recovery in Patients Affected by the COVID-19 Outbreak

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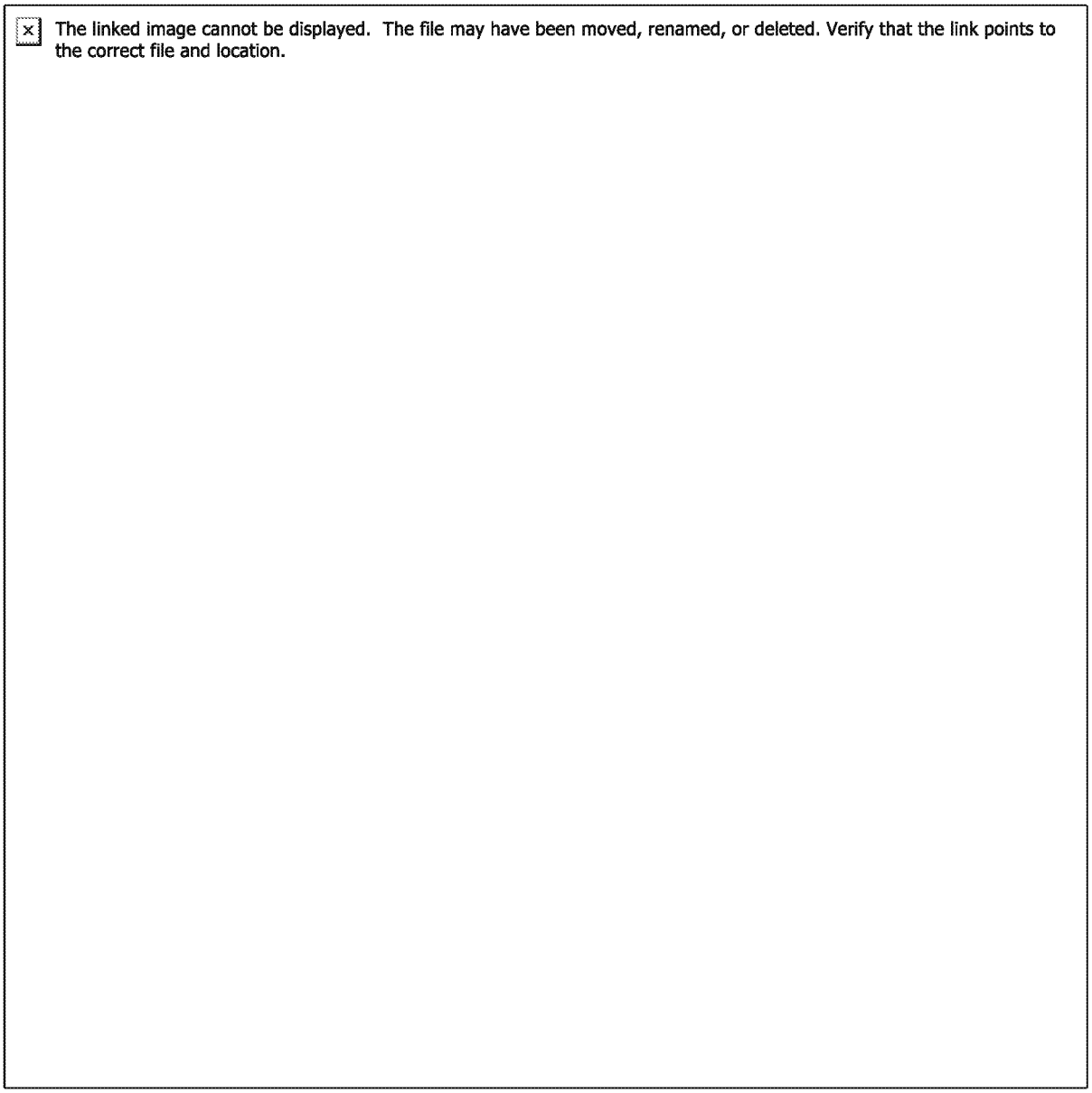
Carlos M. Chiesa-Estomba, Jerome R. Lechien, Maria R. Barillari, Sven Saussez

Coronavirus disease 2019 (COVID-19) is a viral infection caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). From March 2020, several studies indicate that many subjects affected by mild-to-moderate COVID-19 presented olfactory/gustatory dysfunction (OD/GD) that appeared strongly correlated between them but not with the other symptoms suggestive of upper airway infectionIn order to evaluate patterns of gustatoy recovery, data from patients with confirmed COVID-19 were collected prospectively from 4 University Hospitals. At this relatively early point in the pandemic, the authors considered that subjective patterns of recovery of olfactory disfunction in COVID-19 patients are valuable for our patients, for hypothesis

generation and treatment development.



Letter

Longitudinal Characteristics of T Cell Responses in Asymptomatic SARS-CoV-2 Infection

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Jingyi Yang, Ejuan Zhang, Maohua Zhong, Qingyu Yang, Ke Hong, Ting Shu, Dihan Zhou, Jie Xiang, Jianbo Xia, Xi Zhou, Dingyu Zhang, Chaolin Huang, You Shang, Huimin Yan

SARS-CoV-2 causes a spectrum of illness, ranging from an asymptomatic state to life-threatening multi-organ failure, and imposes a high socioeconomic burden on its sufferers and on society (Chen et al. 2020; Pan et al. 2020). Asymptomatic SARS-CoV-2 infection, confirmed by assay with quantitative real-time reverse transcription PCR (qRT-PCR), presented neither clinical symptom nor radiographic abnormality (Pan et al. 2020). While T cell responses are crucial for viral control, viral infection also induces significant count decrease and function impairment of T cells (Chen et al. 2020; Qin et al. 2020). Despite high rate of SARS-CoV-2 asymptomatic infections (Black et al. 2020), T cell responses of this population are still largely unknown. Here, we reported the kinetics of CD4+ and CD8+ T cell responses in an asymptomatic SARS-CoV-2 infected case.

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Letter

Clinical Characteristics of Hospitalized Patients with SARS-CoV-2 and Hepatitis B Virus Co-infection

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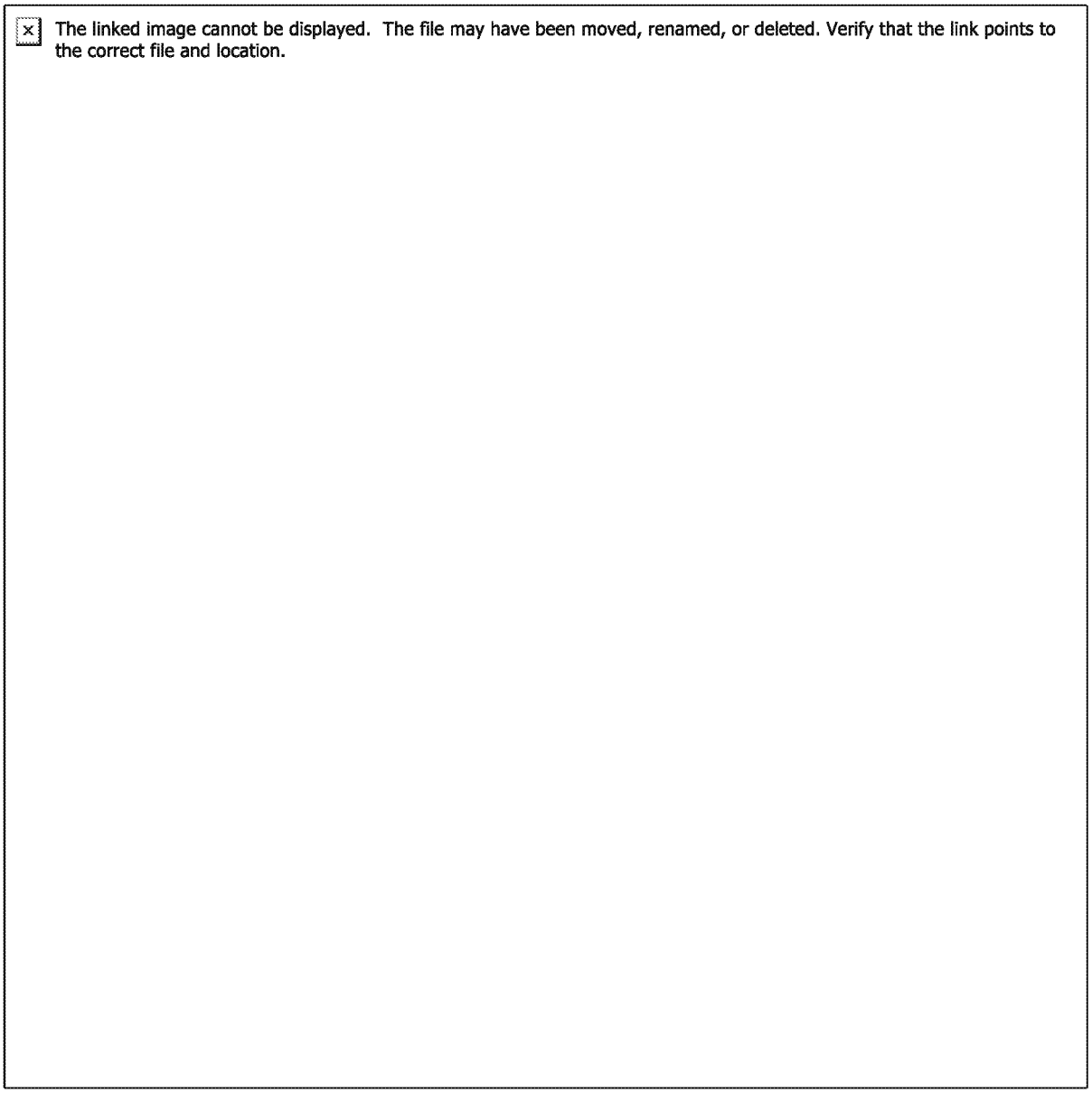
Xiaoping Chen, Qunqun Jiang, Zhiyong Ma, Jiaxin Ling, Wenjia Hu, Qian Cao, Pingzheng Mo, Lei Yao, Rongrong Yang, Shicheng Gao, Xien Gui, Wei Hou, Yong Xiong, Jinlin Li, Yongxi Zhang

In addition to the recent emerged SARS-CoV-2, hepatitis B virus (HBV) is one of the viruses which cause a global infection and threat public health. In worldwide, the prevalence of HBsAg is about 3.9% (Polaris Observatory 2018). According to a nationwide epidemiological survey of population whose ages range from 1 to 59 years in China, 2006, the prevalence of HBsAg was 7.2% (Liang *et al*. 2009). As SARS-CoV-2 and HBV both can cause liver damage (Fan *et al*. 2020), further understanding of the risk of SARS-CoV-2 on patients with HBV infection is urgently required in order to design an optimized treatment strategy. However, the impacts of SARS-CoV-2 infection on HBV patients are still not clear. For example, we do not yet know whether the SARS-CoV-2 infection is more severe in HBV patients and we also do not have much knowledge about the impact of SARS-CoV-2 on the course of HBV infection. In this retrospective study, we investigated the clinical characterizes of the patients coinfected with SARS-CoV-2 and HBV by analyzing the clinical records and laboratory tests of 123 COVID-19 patients admitted to Zhongnan Hospital of Wuhan University,

Wuhan, China, from January 5 to February 20, 2020.



Letter

SARS-CoV-2 Serological Survey of Cats in China before and after the Pandemic

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Junhua Deng, Yuxiu Liu, Chunyan Sun, Jingjing Bai, Jie Sun, Liying Hao, Xiangdong Li, Kegong Tian

The high percentage of seropositivity of cats in Wuhan, the epicentre of the SARS-CoV-2 epidemic, could be due to the large number of infected human cases (more than 14 folds than that in other cities) (Table 1) where cats may have been more frequently exposed to SARS-CoV-2 patients or contaminated environment. As yet, SARS-CoV-2 serological prevalence of cats in other Chinese cities remains unknown. Therefore, a serological survey including more cities with numbers of SARS-CoV-2 human cases in China will be valuable for elucidating the role of cats in transmission of the viruses and relieve public concerns. In this study, 630 cat serum samples collected before November 2019 and 423 cat serum samples collected during SARS-CoV-2 outbreak (from February 2020 to April 2020) in 20 cities in China for detecting the prevalence of SARS-CoV-2 specific antibodies.

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Letter

A Study of Two Cases Co-Infected with SARS-CoV-2 and Human Immunodeficiency Virus

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Rong Zhang, Xiaohua Chen, Yuqing Huang, Qi Zhang, Yan Cheng, Nan Zhang, Haibo Zhang, Bo Yang, Fang Liu, Yingle Liu, Ke Lan

Since December 2019, A new type of coronavirus pneumonia (coronavirus disease 2019, COVID-19) has become endemic in Wuhan, China. So far, COVID-19 has developed into a global epidemic. The body's immune system plays an important role in the fight against COVID-19. Here, we followed up the clinical data and treatment of two COVID-19 patients diagnosed with acquired immunodeficiency syndrome (AIDS), hoping to be helpful for the subsequent diagnosis and treatment of patients with related diseases.

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Letter

Different Laboratory Abnormalities in COVID-19 Patients with Hypertension or Diabetes

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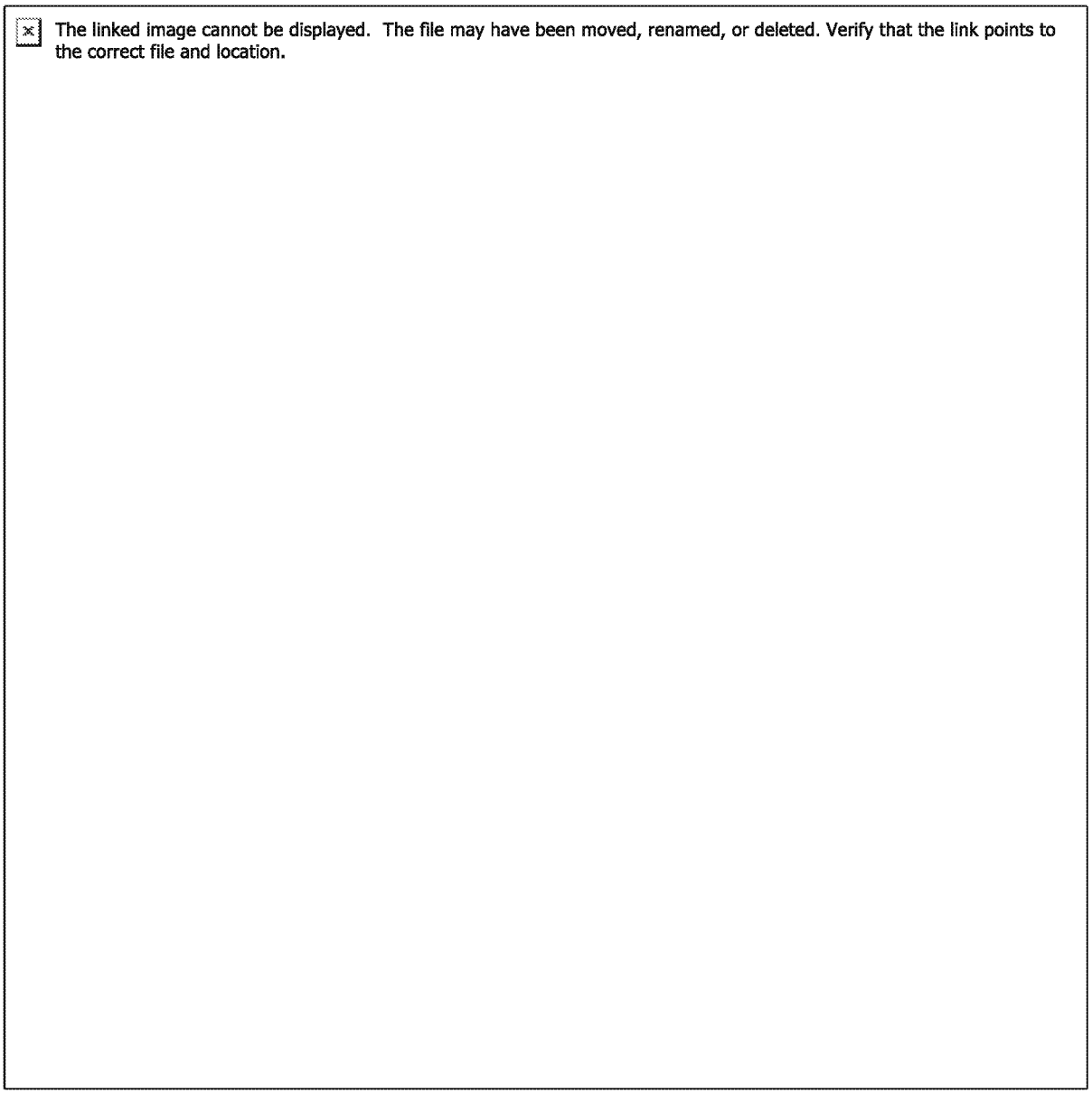
Xiaojun Wu, Tong Wang, Yilu Zhou, Xiaofan Liu, Hong Zhou, Yang Lu, Weijun Tan, Mingli Yuan, Xuhong Ding, Jinjing Zou, Ruiyun Li, Hailing Liu, Rob M. Ewing, Yi Hu, Henxiang Nie, Yihua Wang

We reported recently that hypertension is a risk factor for severe cases of COVID-19, independent of age and other variables (Liu *et al*. 2020a). An important question is why patients with hypertension and diabetes yield poorer clinical outcomes than those without. Human pathogenic coronavirus SARS-CoV-2 utilizes angiotensin-converting enzyme 2 (ACE2) as a receptor for viral cell entry. Since the levels of ACE2 are substantially increased in patients with hypertension or diabetes, who are treated with ACE inhibitors (ACEIs) and angiotensin Ⅱ type-Ⅰ receptor blockers (ARBs) (Ferrario *et al*. 2005), Fang and colleagues hypothesized that ACE2-stimulating drugs could potentially increase the risk of developing severe COVID-19 (Fang *et al*. 2020). This was not supported by a recent study led by Dr. Reynolds (Reynolds *et al*. 2020), whose analysis showed no positive association for ACEIs or ARBs for either the risk of SARS-CoV-2 infection or severe illness (Reynolds *et al*. 2020). What else might explain the poorer clinical outcomes of COVID-19 patients with hypertension or diabetes? To explore this question, we re-analysed the same cohort of 99

COVID-19 patients discharged from the general wards of Renmin Hospital of Wuhan University between 5 February 2020 and 14 March 2020 (Ethics approval No: WDRY2020-K124) (Liu *et al*. 2020a, b).



Letter

Griffithsin with A Broad-Spectrum Antiviral Activity by Binding Glycans in Viral Glycoprotein Exhibits Strong Synergistic Effect in Combination with A Pan-Coronavirus Fusion Inhibitor Targeting SARS-CoV-2 Spike S2 Subunit

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Yanxing Cai, Wei Xu, Chenjian Gu, Xia Cai, Di Qu, Lu Lu, Youhua Xie, Shibo Jiang

In this study, we tested the *in vitro* inhibitory activity of griffithsin (GRFT) against infection of pseudotyped and live SARS-CoV-2 infection, in order to repurpose the application of GRFT as a potential prophylactic or therapeutic to prevent or treat COVID-19.

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Letter

Epidemiological, Clinical and Serological Characteristics of Children with Coronavirus Disease 2019 in Wuhan: A Single-centered, Retrospective Study

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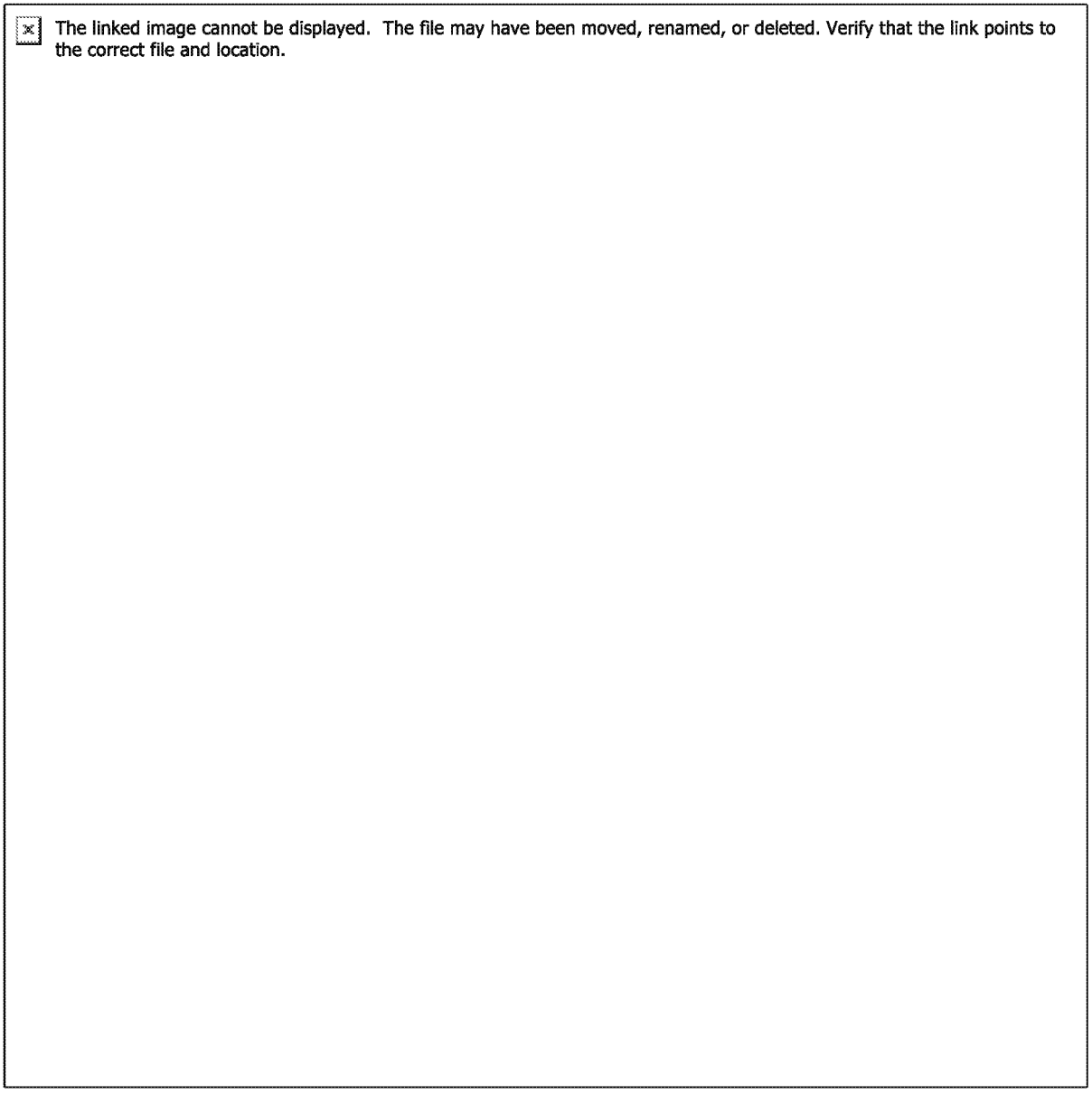
Dan Luo, Zhi Xia, Heng Li, Danna Tu, Ting Wang, Wei Zhang, Lu Peng, Wenfu Yi, Sai Zhang, Junhua Shu, Hui Xu, Yong Li, Buyun Shi, Chengjiao Huang, Wen Tang, Shuna Xiao, Xiaolan Shu, Yan Liu, Yuan Zhang, Shan Guo, Zhi Yu, Baoxiang Wang, Yuan Gao, Qinxue Hu, Hanzhong Wang, Xiaohui Song, Hong Mei, Xiaoqin Zhou, Zhenhua Zheng

In December 2019, SARS-CoV-2 was first detected in the samples obtained from three adult patients who suffered from an unknown viral pneumonia in Wuhan (Li *et al.* 2020). This unknown viral pneumonia is further named as coronavirus disease 2019 (COVID-19) by the World Health Organization. To date, the number of new COVID-19 cases has continued to skyrocket and the impact of SARS-CoV-2 on humans is far greater than any pathogen of this century in both breadth and depth. Previous studies have shown that adults with COVID-19 have symptoms of fever, dry cough, dyspnea, fatigue and lymphocytopenia. Moreover, COVID-19 is more likely to cause death in the elderly, especially those with chronic comorbidities (Huang *et al.* 2020). In Wuhan, more than 50,000 COVID-19 cases have been confirmed, including over 780 pediatric patients, and only one child death case (Lu *et al.* 2020). Although the number of children cases was far fewer than that of

adults, COVID-19 might endanger children's health and the information on children remains limited, especially in serological study. In the retrospective study, the investigators analyzed the epidemiological, clinical and serological characteristics of children with COVID-19 in Wuhan in the early stages of the outbreak, which might provide theoretical and practical help in controlling COVID-19 and similar emerging infectious diseases in the future.



Perspective

Inception of the Modern Public Health System in China and Perspectives for Effective Control of Emerging Infectious Diseases: In Commemoration of the 140th Anniversary of the Birth of the Plague Fighter Dr. Wu Lien-Teh

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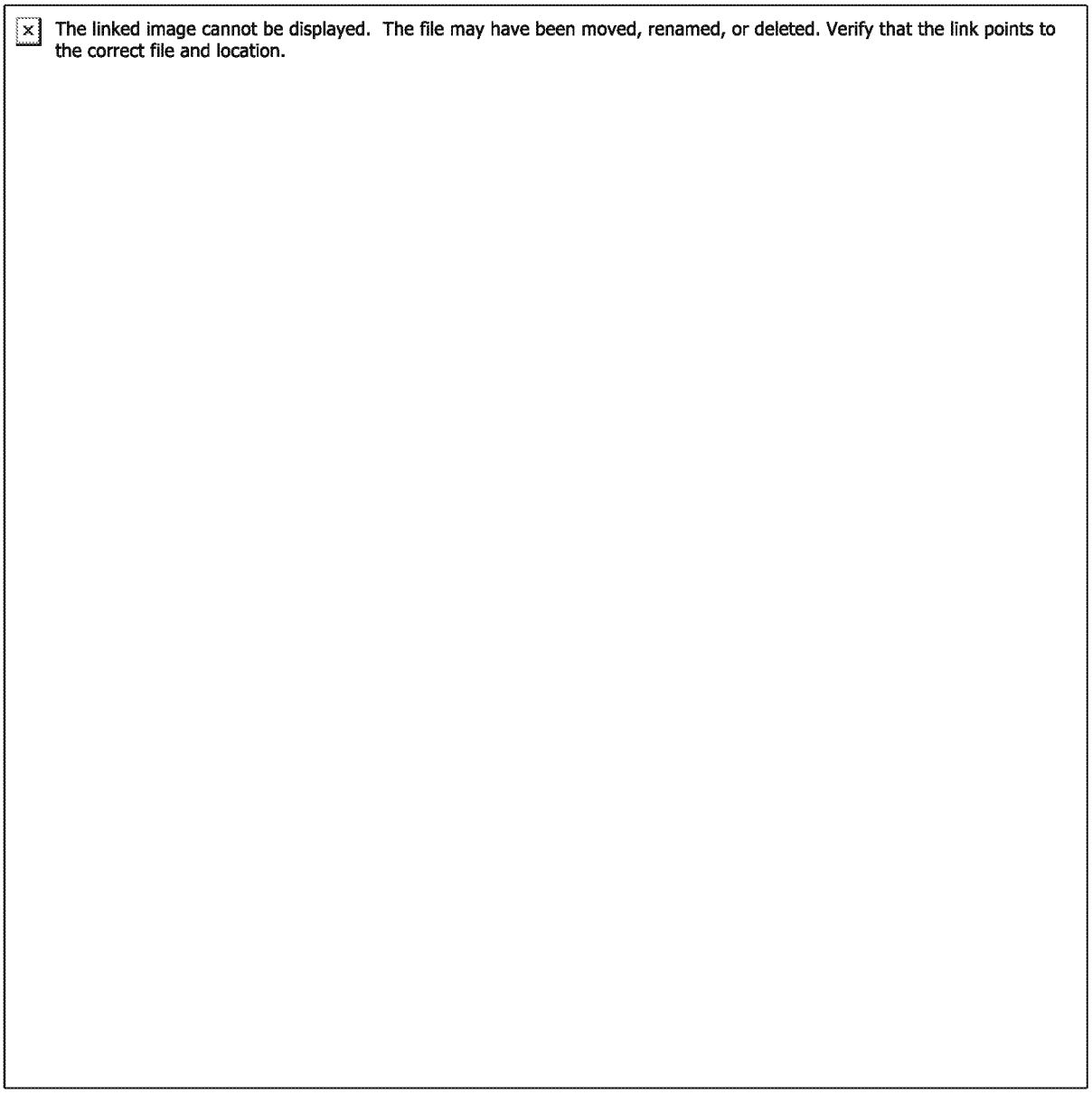
Qingmeng Zhang, Ahmed Niaz, George F. Gao, Fengmin Zhang

In this article, we systematically review Dr. Wu Lien-Teh's academic achievements and outstanding contributions in the prevention and control of the plague epidemic in northeast China and introduce the development of the earliest public health epidemic prevention system in China in order to commemorate the 140th anniversary of Dr. Wu Lien-Teh's birth. We hope that this article will provide insights into the effective prevention and control of emerging infectious diseases as well as the current worldwide pandemic of COVID-

19, facilitating the improvement and development of public health systems in China and around the globe.



Perspective

Coping with COVID-19 in Sub-Saharan Africa: What Might the Future Hold?

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Franck J. D. Mennechet, Guy R. Takoudjou Dzomo

Sub-Saharan countries are sadly linked with similar poor indicators, such as high poverty and mortality rates, the burden of disease, fragile health systems and poorly developed infrastructure. Along with the rest of the world, Sub-Saharan countries are facing this new coronavirus outbreak. Nevertheless, chaotic predictions of a particularly destructive epidemic in Africa do not seem to be borne out, at least for the time being. But uncertainties remain, such as how the virus is spreading in countries with low incomes, informal economies, high HIV/tuberculosis prevalence, extremely low median age, or warm/dry climates and for which containments are almost impossible to enforce? Not even 8 months after the first reported case in China, parts of the world are already showing post-lockdown twilight measures. Yet, the war is certainly far from over, because the virus is gaining ground in the sub-Saharan zone. This viewpoint attempts to describe the COVID-19 crisis in a sub-Saharan perspective, in particular in the Republic of Chad, from both, distant

perception and by living it on a daily basis.

To: Matt.Manweller@leg.wa.gov[Matt.Manweller@leg.wa.gov];
Jacquelin.Maycumber@leg.wa.gov[Jacquelin.Maycumber@leg.wa.gov]; Joan.McBride@leg.wa.gov[Joan.McBride@leg.wa.gov];
Gina.McCabe@leg.wa.gov[Gina.McCabe@leg.wa.gov]; Bob.McCaslin@leg.wa.gov[Bob.McCaslin@leg.wa.gov];
John.McCoy@leg.wa.gov[John.McCoy@leg.wa.gov]; Joyce.McDonald@leg.wa.gov[Joyce.McDonald@leg.wa.gov];
Mark.Miloscia@leg.wa.gov[Mark.Miloscia@leg.wa.gov]; Jeff.Morris@leg.wa.gov[Jeff.Morris@leg.wa.gov];
Mark.Mullet@leg.wa.gov[Mark.Mullet@leg.wa.gov]; Dick.Muri@leg.wa.gov[Dick.Muri@leg.wa.gov];
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Steve.OBan@leg.wa.gov[Steve.OBan@leg.wa.gov]; Ed.Orcutt@leg.wa.gov[Ed.Orcutt@leg.wa.gov];
Timm.Ormsby@leg.wa.gov[Timm.Ormsby@leg.wa.gov]; Lillian.Ortiz-Self@leg.wa.gov[Lillian.Ortiz-Self@leg.wa.gov];
Tina.Orwall@leg.wa.gov[Tina.Orwall@leg.wa.gov]; Mike.Padden@leg.wa.gov[Mike.Padden@leg.wa.gov];
Guy.Palumbo@leg.wa.gov[Guy.Palumbo@leg.wa.gov]; Jamie.Pedersen@leg.wa.gov[Jamie.Pedersen@leg.wa.gov];
Mike.Pellicciotti@leg.wa.gov[Mike.Pellicciotti@leg.wa.gov]; Strom.Peterson@leg.wa.gov[Strom.Peterson@leg.wa.gov];
Eric.Pettigrew@leg.wa.gov[Eric.Pettigrew@leg.wa.gov]; Liz.Pike@leg.wa.gov[Liz.Pike@leg.wa.gov];
Gerry.Pollet@leg.wa.gov[Gerry.Pollet@leg.wa.gov]; Kevin.Ranker@leg.wa.gov[Kevin.Ranker@leg.wa.gov];
Kristine.Reeves@leg.wa.gov[Kristine.Reeves@leg.wa.gov]; Marcus.Riccelli@leg.wa.gov[Marcus.Riccelli@leg.wa.gov];
Ann.Rivers@leg.wa.gov[Ann.Rivers@leg.wa.gov]; June.Robinson@leg.wa.gov[June.Robinson@leg.wa.gov];
Jay.Rodne@leg.wa.gov[Jay.Rodne@leg.wa.gov]; Christine.Rolfes@leg.wa.gov[Christine.Rolfes@leg.wa.gov];
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SharonTomiko.Santos@leg.wa.gov[SharonTomiko.Santos@leg.wa.gov]; David.Sawyer@leg.wa.gov[David.Sawyer@leg.wa.gov];
Joe.Schmick@leg.wa.gov[Joe.Schmick@leg.wa.gov]; Mark.Schoesler@leg.wa.gov[Mark.Schoesler@leg.wa.gov];
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Matt.Shea@leg.wa.gov[Matt.Shea@leg.wa.gov]; Timothy.Sheldon@leg.wa.gov[Timothy.Sheldon@leg.wa.gov];
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Monica.Stonier@leg.wa.gov[Monica.Stonier@leg.wa.gov]; Pat.Sullivan@leg.wa.gov[Pat.Sullivan@leg.wa.gov];
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Javier.Valdez@leg.wa.gov[Javier.Valdez@leg.wa.gov]; Kevin.VanDeWege@leg.wa.gov[Kevin.VanDeWege@leg.wa.gov];
Luanne.VanWerven@leg.wa.gov[Luanne.VanWerven@leg.wa.gov]; Brandon.Vick@leg.wa.gov[Brandon.Vick@leg.wa.gov];
Mike.Volz@leg.wa.gov[Mike.Volz@leg.wa.gov]; Keith.Wagoner@leg.wa.gov[Keith.Wagoner@leg.wa.gov];
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Christopher.Whitty@lshtm.ac.uk[Christopher.Whitty@lshtm.ac.uk]; Menachery, Vineet[vimenach@UTMB.EDU];
jiwei_yunlong@126.com[jiwei_yunlong@126.com]; Jennifer.Layden@Illinois.gov[Jennifer.Layden@Illinois.gov]; rothe@lrz.uni-
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njamin@email.wustl.edu[njamin@email.wustl.edu]; obrienm@wustl.edu[obrienm@wustl.edu]; piggottk@wustl.edu[piggottk@wustl.edu]; p.ruzycki@wustl.edu[p.ruzycki@wustl.edu]; prwillia@wustl.edu[prwillia@wustl.edu]; rajagopalr@wustl.edu[rajagopalr@wustl.edu]; rallo@wustl.edu[rallo@wustl.edu]; raopk@wustl.edu[raopk@wustl.edu]; ravi@wustl.edu[ravi@wustl.edu]; sarahgore@wustl.edu[sarahgore@wustl.edu]; shepherd@wustl.edu[shepherd@wustl.edu]; sheybaniar@wustl.edu[sheybaniar@wustl.edu]; shiels@wustl.edu[shiels@wustl.edu]; siegfried@wustl.edu[siegfried@wustl.edu]; smith.robert.e@wustl.edu[smith.robert.e@wustl.edu]; sotof@wustl.edu[sotof@wustl.edu]; steskaJ@wustl.edu[steskaJ@wustl.edu]; stunkell@wustl.edu[stunkell@wustl.edu]; tsai@wustl.edu[tsai@wustl.edu]; tychsen@wustl.edu[tychsen@wustl.edu]; vanstaverng@wustl.edu[vanstaverng@wustl.edu]; vollmanD@wustl.edu[vollmanD@wustl.edu]; wieder@wustl.edu[wieder@wustl.edu]; david.szymkowski@xencor.com[david.szymkowski@xencor.com]; virgil.schijns@wur.nl[virgil.schijns@wur.nl]; valerijus.ostapenko@vuoi.lt[valerijus.ostapenko@vuoi.lt]; agata.mlynska@vuoi.lt[agata.mlynska@vuoi.lt]; vita.pasukoniene@vuoi.lt[vita.pasukoniene@vuoi.lt]; adas@arbata.lt[adas@arbata.lt]; strioga@gmail.com[strioga@gmail.com]; marius.strioga@vuoi.lt[marius.strioga@vuoi.lt]; media.relations@roche.com[media.relations@roche.com]; murthy.aditya@gene.com[murthy.aditya@gene.com]; joshua.wallach@yale.edu[joshua.wallach@yale.edu]; alexander.egilman@yale.edu[alexander.egilman@yale.edu]; margaret.e.mccarthy@yale.edu[margaret.e.mccarthy@yale.edu]; jennifer.miller@nyumc.org[jennifer.miller@nyumc.org]; steven.woloshin@dartmouth.edu[steven.woloshin@dartmouth.edu]; lisa.schwartz@dartmouth.edu[lisa.schwartz@dartmouth.edu]; joseph.ross@yale.edu[joseph.ross@yale.edu]; karen.peart@yale.edu[karen.peart@yale.edu]; lacevedo@jbrpt.org[lacevedo@jbrpt.org]; johan.neyts@kuleuven.be[johan.neyts@kuleuven.be]; kai.dallmeier@kuleuven.be[kai.dallmeier@kuleuven.be]; hendrikjan.thibaut@kuleuven.be[hendrikjan.thibaut@kuleuven.be]; manjunath.k@zyduscadila.com[manjunath.k@zyduscadila.com]; rajeshbahekar@zyduscadila.com[rajeshbahekar@zyduscadila.com]; ashokd.jaiswal@zyduscadila.com[ashokd.jaiswal@zyduscadila.com]; kevinkumarkansagra@zyduscadila.com[kevinkumarkansagra@zyduscadila.com]; poonamgiri@zyduscadila.com[poonamgiri@zyduscadila.com]; mukul.jain@zyduscadila.com[mukul.jain@zyduscadila.com]; abhijitchatterjee@zyduscadila.com[abhijitchatterjee@zyduscadila.com]; amitjoharapurkar@zyduscadila.com[amitjoharapurkar@zyduscadila.com]; nuggehally.srinivas@zyduscadila.com[nuggehally.srinivas@zyduscadila.com]; sameeragarwal@zyduscadila.com[sameeragarwal@zyduscadila.com]; Deven.Parmar@zyduscadila.com[Deven.Parmar@zyduscadila.com]; maulikr.patel@zyduscadila.com[maulikr.patel@zyduscadila.com]; gattinoniluciano@gmail.com[gattinoniluciano@gmail.com]; sapna@jhmi.edu[sapna@jhmi.edu]; aluks@uw.edu[aluks@uw.edu]; hooman.poor@mssm.edu[hooman.poor@mssm.edu]; christoph.steininger@meduniwien.ac.at[christoph.steininger@meduniwien.ac.at]

From: Vinu Arumugham[igesynth1@yahoo.com]
Sent: Sun 4/11/2021 12:36:34 PM (UTC-05:00)
Subject: Plant protein contaminated COVID-19 vaccines cause clotting; It's a lab virus; Unstable mRNA ; Judge to FCC on radiation danger: 'I am Inclined to Rule Against You'

SARS-CoV-2 vaccines and clotting disorders

Plant proteins that contaminate SARS-CoV-2 vaccines, excipients have high protein sequence homology to IEDB listed thrombocytopenia related platelet factor 4 epitopes thus explaining induction of autoimmune bleeding disorders

https://doi.org/10.5281/zenodo.4641692

Heparin induced thrombocytopenia (HIT) is due to animal protein contamination

Heparin is derived from porcine and bovine sources and is thus contaminated with porcine/bovine proteins. As detailed below, with just a few amino acid residue differences compared to Platelet Factor 4 (PF4) epitopes involved in thrombocytopenia, porcine and bovine antigens are ideally suited for heparin induced thrombocytopenia.

Analyzing 23000+ epitopes covering 82 autoimmune diseases in the Immune Epitope Database, 57% have only one and 78% have up to two amino acid residue differences compared to animal, fungal or plant peptides present in vaccines; an unmistakable signature of the role of vaccines in their etiologies
https://doi.org/10.5281/zenodo.3603480

The BLASTP match scores for bovine/porcine antigens compared to PF4 epitopes ranges from 26-46 compared to 19.7 BLASTP match score for the epitope that resulted in Pandemrix induced narcolepsy. Higher scores mean higher probability of cross-reaction.

Same problem as Pandemrix-induced narcolepsy, different contaminants.

How the FDA squashed any discussion of safety and rushed to authorize the Pfilthy Pfizer vaccine:

Hearing Without Listening

www.pogo.org/analysis/2020/12/hearing-without-listening/

"Truncated and modified mRNA species" in the Pfizer/Moderna vaccines will cause autoimmunity, allergies, asthma, etc.

People forget the old saying **"If it sounds too good to be true, it probably is".**

Traditional vaccines took a decade to develop and they were ineffective and unsafe in most cases**.** Now they want us to believe that they magically created "safe and effective" vaccines based on never-used-before mRNA technology, in just months. That's like winning the lottery. Twice. The Pharma CEOs certainly won the lottery but now Pfizer's Pfilth is being exposed.

"Cyberattackers" exposed the cover up by our corrupted regulators**.**

The EMA covid-19 data leak, and what it tells us about mRNA instability
https://www.bmj.com/content/372/bmj.n627

On a good day at the vaccine plant, as much as 30% of the mRNA in the vaccine can be "truncated and modified" due to instability. That means instead of producing the target spike protein, this mRNA will direct the cell to produce RANDOM proteins with RANDOM peptides that can have high homology to ANYTHING. These random proteins can have peptides that have high homology to peptides in self-proteins, food proteins, aeroallergen proteins, etc. The result is the immune system is being trained to attack self-proteins (autoimmunity), food proteins (food allergy), aeroallergen (asthma) etc. These mRNA vaccines come with a powerful lipid-in-water-emulsion adjuvant that boosts all the above diseases.

So this is an ALL-diseases-in-one, shot. Making them Pharma's most sickening vaccines yet. With **85 millions doses, the vaccines have killed AT LEAST 1500 people** by VAERS documentation alone.

We have not even started to count how many will be maimed for life. **CORRUPTED SCIENCE KILLS EFFICIENTLY**.

SARS-CoV-2 originated in a lab

In a world of conspiring criminals, it takes "conspiracy theorists" to expose the truth ...

A Bayesian analysis concludes beyond a reasonable doubt that SARS-CoV-2 is not a natural zoonosis but instead is laboratory derived
https://doi.org/10.5281/zenodo.4470232

FDA/CDC's Bell's palsy lie exposed. What else are they lying about? Plenty.

www.cdc.gov/vaccines/covid-19/info-by-product/clinical-considerations.html

"Cases of Bell's palsy were reported following vaccination in participants in both the Pfizer-BioNTech and Moderna COVID-19 vaccines clinical trials. However, the FDA does not consider these to be above the frequency expected in the general population and has not concluded that these cases were causally related to vaccination."

I exposed the FDA/CDC lie above back in Dec 2020 and now a team has exposed the lie again in the Lancet Infectious Disease journal.

Bell's palsy and SARS-CoV-2 vaccines
www.thelancet.com/journals/laninf/article/PIIS1473-3099(21)00076-1/fulltext#%20

"Therefore, the observed incidence of Bell's palsy in the vaccine arms is between 3·5-times and 7-times higher than would be expected in the general population. This finding signals a potential safety phenomenon and suggests inaccurate reporting of basic epidemiological context to the public."

www.statnews.com/2020/12/28/chance-illnesses-after-covid-19-vaccinations-could-test-public-confidence-even-if-the-problems-are-unrelated/

Article above says: "Eight people in the Pfizer and Moderna trials, which enrolled nearly 74,000 participants in total, were diagnosed with the condition — seven in the vaccine arms and one in the placebo arm of the Moderna trial. The jury is still out on whether Bell's palsy, which afflicts about 40,000 people a year in the U.S., is an occasional side effect of taking a Covid-19 vaccine."

So about 1 in 8250 (330,000,000/40,000) will develop Bell's palsy each year in the US. Say the trial ran for 3 months. That makes it 1 in 33,000 probability of occurrence during the trial. One case in the placebo arms consisting of 37000 people is therefore as expected.

What's the probability of 7 cases of Bell's palsy occurring merely by chance, in the vaccine arms?

(((32999÷33000)^36993)×((1÷33000)^7)×(37000!))÷(36993!×7!) = 0.00014

1 in ~7,000. Why is "the jury still out"? The vaccine caused the Bell's palsy cases.

VAERS shows >1000 deaths after COVID-19 vaccines. Clustering of deaths on days post-vaccination and comparing with

the same data following flu vaccines, makes it clear that most of these deaths were CAUSED by the COVID-19 vaccines.

https://childrenshealthdefense.org/defender/facebook-posts-vaers-link-covid-vaccines-injuries-death

https://childrenshealthdefense.org/defender/latest-data-cdc-vaers/

"Misinformation" and censorship

Facebook censors were wrong 80% of the time.

https://businessinsider.com/facebook-supreme-court-oversight-board-overturns-4-of-5-cases-2021-1

People don't trust BigTech, mainstream media and the government.

Fauci's no mask needed, then wear a mask, then wear TWO now, does not earn him any trust. Fauci admitted lying about vaccine-related herd immunity targets.

Should Leaders Tell Noble Lies? - Strategic Leaders Academy

https://strategicleadersacademy.com/should-leaders-tell-noble-lies/

Then Fauci admitted that injected vaccines do not offer herd Immunity at all.

"Administration of parenterally administered vaccines alone typically does not result in potent mucosal immunity that might interrupt infection or transmission"

http://acpjournals.org/doi/10.7326/M21-0111

The WHO flip-flopped on COVID-19 vaccine safety in pregnancy.

Moderna's COVID-19 vaccine now recommended for pregnant women, WHO says in guidance reversal

www.foxnews.com/health/moderna-covid-vaccine-pregnant-women-who-guidance-reversal

So the "authorities", mainstream media and BigTech are not even trying to EARN trust because they spread **"OFFICIAL" MISINFORMATION**. With censorship and fraudulent "fact-checking", they are only **REAFFIRMING** that they all have plenty to hide.

Even the Wall Street Journal and MEDPAGETODAY have become victims of the "fact-check" mafia.

https://www.wsj.com/articles/fact-checking-facebooks-fact-checkers-11614987375

Vaccines absolutely do cause autism

The CDC has flip-flopped twice in ~5 months on the fraudulent claim that "Vaccines do not cause autism", on their website. It suggests that the CDC's vaccine/autism claims are based on the conjunction of Jupiter and Saturn, not science.

They were forced to take the false claim down because ICAN demonstrated there was **ZERO** science behind that claim.

The CDC Finally Capitulated To ICAN's Legal Demands and Removed the Claim that "Vaccines Do Not Cause Autism"

From Its Website!

https://www.icandecide.org/ican_press/the-cdc-finally-capitulated-to-icans-legal-demands-and-removed-the-claim-that-vaccines-do-not-cause-autism-from-its-website/

THE CDC JUST SOLIDIFIED THAT ITS DECISIONS ARE NOT DRIVEN BY SCIENCE

https://www.icandecide.org/ican_press/the-cdc-just-solidified-that-its-decisions-are-not-driven-by-science/

FACT: Milk protein contaminated vaccines (DTap/Tdap/Prevnar 13/ActHiB) cause at least 75% of autism cases.

Autism pathogenesis: Piecing it all together, from end to beginning ...
https://doi.org/10.5281/zenodo.1477515

CDC caught lying, again about the COVID-19 vaccine this time.

CDC Investigation

http://fullmeasure.news/news/cover-story/cdc-investigation

Vaccine mandates are based on a lie; Repeal all mandates immediately; Try the corrupted liars who created mandates, for CRIMES AGAINST HUMANITY

"Administration of parenterally administered vaccines alone typically does not result in potent mucosal immunity that might interrupt infection or transmission"

SARS-CoV-2 Vaccines: Much Accomplished, Much to Learn

www.acpjournals.org/doi/10.7326/M21-0111

So Fauci admits now that **ALL** injected vaccines are for individual protection only. **No herd/community immunity.** So no vaccine mandates are justifiable for **ANY** injected vaccine.

And of course this also means the vaccinated can become infected super-spreaders as occurs with the failed flu shot and failed pertussis vaccines.

Yan J, Grantham M, Pantelic J, de Mesquita PJ, Albert B, Liu F, et al. Infectious virus in exhaled breath of symptomatic seasonal influenza cases from a college community. Adamson W, Beato-Arribas B, Bischoff W, Booth W, Cauchemez S, Ehrman S, et al., editors. Proc Natl Acad Sci. National Academy of Sciences; 2018;

The potential role of subclinical Bordetella Pertussis colonization in the etiology of multiple sclerosis
pubmed.ncbi.nlm.nih.gov/26724970/

This is the consequence of **insanely injecting** antigens of pathogens whose natural routes of exposure are mucosal surfaces in the nose, mouth or eyes.

Discrimination on the basis of vaccination status (is inherently wrong)
blogs.bmj.com/medical-ethics/2021/03/01/discrimination-on-the-basis-of-vaccination-status-is-inherently-wrong/

"In practical terms, **vaccine mandates imply that all humans are born in a defective, inherently harmful state; a repugnant conclusion**."

NOTICE!

By authority of the Nuremberg Code on Medical Experimentation, I do hereby exercise my right to refuse to submit to or to administer the Covid-19 vaccine. The United States Government has prosecuted, convicted and executed Medical Doctors who have violated the Nuremberg Code on Medical Experimentation. Aiders and abettors of Nuremberg Crimes are equally guilty and have also been prosecuted, convicted, and executed.

Francis A. Boyle
Professor of Law.

My comment in the Annals of Internal Medicine, against Fauci's "SARS-CoV-2 Vaccines: Much Accomplished, Much to Learn"

https://www.acpjournals.org/doi/10.7326/M21-0111

Vinu Arumugham Independent 18 January 2021
These vaccines are unsafe, unnecessary and must be immediately withdrawn

The vaccine safety claims made by the authors are unsupported by evidence. Vaccines must be designed for safety. These vaccines were not designed at all. So they are unsafe by definition. I predicted the allergic sensitization and autoimmunity risks with these vaccines which have now been confirmed.

The Pfizer/BioNTech vaccine is unnecessary, unsafe and should not be authorized.

https://www.regulations.gov/document?D=FDA-2020-N-1898-0039

Robert F Kennedy Jr. warned the FDA months back about the risk of allergic reactions due to the use of polyethylene glycol (PEG) in the vaccines.
https://childrenshealthdefense.org/defender/pfizer-covid-vaccine-allergic-reactions/

The FDA/VRBPAC ignored us and authorized these horrendously dangerous vaccines.

Recently, Dr. Peter Marks of the FDA admitted that the population was sensitized by PEG-containing pharmaceutical preparations (that include other vaccines/injections).

https://www.wsj.com/articles/scientists-eye-potential-culprit-for-covid-19-vaccine-allergic-reactions-11608901200?mod=hp_lead_pos2

"What we're learning now is that those **allergic reactions could be somewhat more common** than the highly uncommon that we thought they were **because people do get exposed to polyethylene glycol in various pharmaceutical preparations,**" - Peter Marks, Director, CBER,FDA.

We of course already knew that any vaccine/injection that has enough allergen to cause a reaction, has more than enough allergen to guarantee sensitization/priming (causing the development of new allergy).

Evidence that Food Proteins in Vaccines Cause the Development of Food Allergies and Its Implications for

Vaccine Policy

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3571073

www.sciencemag.org/news/2020/12/suspicions-grow-nanoparticles-pfizer-s-covid-19-vaccine-trigger-rare-allergic-reactions

"he worries anti-PEG antibodies triggered by the first shot could increase the risk of an allergic reaction to the second or to PEGylated drugs."

- Janos Szebeni, an immunologist at Semmelweis University

So now, these vaccines have sensitized millions to PEG. The goal is to sensitize/boost PEG allergy in a 100 million more in the next 100 days.

PEG is contaminated with 1,4-dioxane, a carcinogen.

https://www.fda.gov/cosmetics/potential-contaminants-cosmetics/14-dioxane-cosmetics-manufacturing-byproduct

As predicted, Pfizer COVID-19 vaccine induced autoimmunity (thrombocytopenia) killed a Florida doctor. This is just the tip of the iceberg. Thousands of cases of vaccine induced autoimmune diseases may take months/years to be diagnosed and will be dismissed as unrelated to the vaccine.

https://www.nytimes.com/2021/01/12/health/covid-vaccine-death.html

Only a few lots were tested in the trial. No one has a clue what other lots will do. 100-fold variation of contaminants in vaccines makes trials and epidemiological studies worthless as I detailed in my comments in the Annals of Internal Medicine before. Vaccine safety remains an oxymoron.

https://www.acpjournals.org/doi/10.7326/m18-2101

California calls for pause of 330,000 doses, investigation after allergic reactions to Moderna vaccine batch

https://www.mercurynews.com/2021/01/18/coronavirus-california-calls-for-pause-investigation-after-allergic-reactions-to-moderna-vaccine-batch/

What's worse? Effective, life-saving, cheap, safe medicines such as famotidine/cetirizine/ivermectin are being ignored in this blind race to vaccinate at any cost.

Immunological mechanisms explaining the role of vaccines, IgE, mast cells, histamine, elevating ferritin, IL-6, D-dimer, VEGF levels in COVID-19 and dengue, potential treatments such as mast cell stabilizers, antihistamines: Predictions and confirmations

https://europepmc.org/article/PPR/PPR241819

Big picture of the damage vaccines do:

Vaccines and Biologics injury table based on mechanistic evidence – Feb 2020

Covering over 125 conditionshttps://zenodo.org/record/3647593/files/vbitr2_final.pdf?download=1

The organized suppression of vaccine safety science:

Retraction of scientific papers: the case of vaccine research
https://www.tandfonline.com/doi/full/10.1080/09581596.2021.1878109

The WHO's flip-flopping "science" competes with CDC's incompetence

WHO Recommends Against Moderna, Pfizer Vaccines for Most Pregnant Women

https://www.wsj.com/articles/who-recommends-against-moderna-pfizer-vaccines-for-most-pregnant-women-11611775138

Pregnant Women May Receive Covid Vaccines Safely, W.H.O. Says
https://www.nytimes.com/2021/01/29/health/covid-vaccine-pregnancy.html

Moderna's COVID-19 vaccine now recommended for pregnant women, WHO says in guidance reversal

https://www.foxnews.com/health/moderna-covid-vaccine-pregnant-women-who-guidance-reversal

Not to be outdone by the flip-flopping CDC, WHO did a flip-flop on COVID-19 vaccine during pregnancy.

Latest evidence that there is ZERO science behind vaccines or vaccine safety. They just pull their "science" out of a hat. Follow the money.

These flip-flopping, lying, organized criminals at the CDC/WHO, are the "reputable sources" for your "fact-checkers".

Judge to FCC: 'I am Inclined to Rule Against You'

https://childrenshealthdefense.org/defender/judge-to-fcc-i-am-inclined-to-rule-against-you/

The New Hampshire Commission report below has ripped FCC's 5G (and all other cellular) RF safety claims:

Final Report of the Commission to Study The Environmental and Health Effects of Evolving 5G Technology

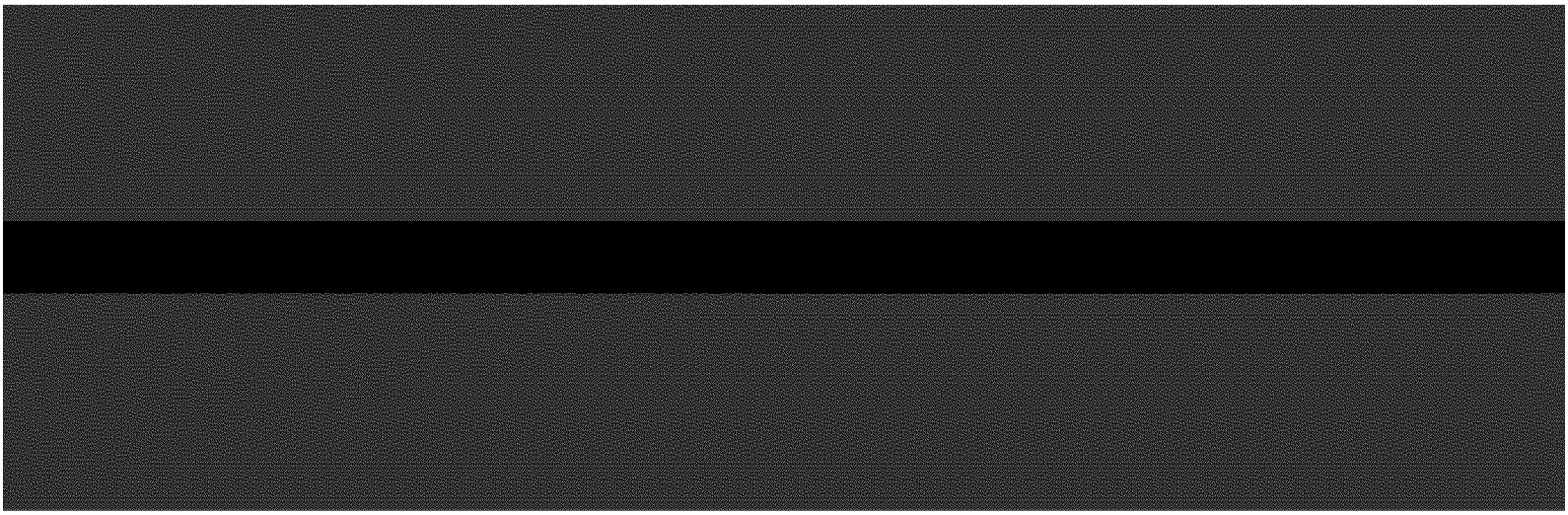
http://www.gencourt.state.nh.us/statstudcomm/committees/1474/reports/5G%20final%20report.pdf

"RECOMMENDATION 1- Propose a resolution of the House to the US Congress and Executive Branch to **require the Federal Communication Commission (FCC) to commission an independent review** of the current radiofrequency (RF) standards of the electromagnetic radiation in the 300MHz to 300GHz microwave

spectrum as well as a health study to assess and recommend mitigation for the health risks associated with the use of cellular communications and data transmittal."

"A likely explanation as to why **regulatory agencies have opted to ignore the body of scientific evidence demonstrating the negative impact of cellphone radiation** is that **those agencies are "captured"** (see Harvard University publication entitled, "Captured Agency: How the Federal Communications Commission Is Dominated by the Industries It Presumably Regulates" linked in Appendix G). This report documents how **the leadership roles in some agencies (the FCC in particular) are filled by individuals with strong industry ties** and hence are more **focused on**

industry interests than the health of citizens"



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Contact us:

Email report@5gcrisis.com

Call 516-883-0887

Thanks,

Vinu

To: Menachery, Vineet[vimenach@UTMB.EDU]; rbaric@email.unc.edu[rbaric@email.unc.edu]
Cc: kevin.guskiewicz@unc.edu[kevin.guskiewicz@unc.edu]; braimer@utmb.edu[braimer@utmb.edu]
From: Marcus Williamson[marcus@connectotel.com]
Sent: Sat 5/8/2021 7:22:36 AM (UTC-05:00)
Subject: Questions - reply requested

Can you please reply to this email of 14 April 2020, and the reminder of 10 January 2021, as shown below?

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions - reply requested
From: Marcus Williamson <marcus@connectotel.com>
Date: Sun, 10 Jan 2021 16:16:08 +0000
Cc: kevin.guskiewicz@unc.edu, braimer@utmb.edu

Dr Menachery and Professor Baric

Can you please reply to this email of 14 April 2020, shown below?

I have copied the UNC Chancellor and UTMB President, so that they can be aware of this apparent lack of responsiveness and openness of their staff.

Please respond openly and honestly to my questions.

I look forward to hearing from you, without further delay.

best wishes
Marcus Williamson
Editor
https://nam11.safelinks.protection.outlook.com/?url=http%3A%2F%2Fwww.ceoemail.com%2F&data=04%7C01%7Cvimenach%40utmb.edu%7C0cddf98e17914e6b046c08d9121bfa23%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637560733637532091%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=b26CmZtvq5dOcUSkvvhuwPQVwOR4n0k7b6Oxemaq3Ic%3D&reserved=0

To: vimenach@utmb.edu, rbaric@email.unc.edu
Subject: Questions
From: Marcus Williamson <marcus@connectotel.com>
Date: Tue, 14 Apr 2020 23:50:14 +0100

Dr Menachery and Professor Baric

I've just read this article:

https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nature.com%2Farticles%2Fnm.3985%23ref-CR2&data=04%7C01%7Cvimenach%40utmb.edu%7C0cddf98e17914e6b046c08d9121bfa23%7C7

bef256d85db4526a72d31aea2546852%7C0%7C0%7C637560733637532091%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=SPcuOovtOgc6hBnkWi50dqY593aJM%2FyKFhWedUi%2FZCQ%3D&reserved=0

which says:

"Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis."

Did you and your group, deliberately or inadvertantly, create the virus now known as COVID-19?

Was that virus then somehow released into the environment in Wuhan, deliberately or accidentally, by one or more of your co-authors, who live and work there?

Please respond openly and honestly, thank you.

Look forward to hearing from you.

best wishes
Marcus Williamson

To: Shi, Pei yong[peshi@UTMB.EDU]; Xie, Xuping[xuxie@UTMB.EDU]; shanchao@wh.iov.cn[shanchao@wh.iov.cn]
Sent: Thur 12/3/2020 10:40:23 PM (UTC-06:00)
Subject: [Signature Required] - SHI-PY-17C
SHI-PY-17C - Declarations - Unsigned.PDF

Hello Inventors,

Attached is a Declaration form for the patent application entitled "LIVE ATTENTUATED ZIKA VIRUS WITH 3'UTR DELETION, VACCINE CONTAINING AND USE THEREOF" a copy of which is also attached.

You all are listed as inventors of this technology and as such it is required to sign the attached form to file with the US patent office, the form affirms that you are an inventor of this technology and you have allowed UTMB to file this patent application on your behalf.
Please sign (e-signatures are ok) and return to me at your convenience. Thanks

Best
-brett

Brett Adkins, JD, MS
Associate Legal Officer
Office of Technology Transfer

University of Texas Medical Branch
301 University Blvd., Galveston, TX 77555
P 409.772.0375
E btadkins@utmb.edu

utmb Health

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PTO/AIA/01 (06-12)
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U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

DECLARATION (37 CFR 1.63) FOR UTILITY OR DESIGN APPLICATION USING AN APPLICATION DATA SHEET (37 CFR 1.76)

Title of Invention	LIVE ATTENTUATED ZIKA VIRUS WITH 3'UTR DELETION, VACCINE CONTAINING AND USE THEREOF

As the below named inventor, I hereby declare that:

This declaration is directed to:

☐ The attached application, or

☒ United States application or PCT international application number 16/485,818 filed on August 14, 2019.

The above-identified application was made or authorized to be made by me.

I believe that I am the original inventor or an original joint inventor of a claimed invention in the application.

I hereby acknowledge that any willful false statement made in this declaration is punishable under 18 U.S.C. 1001 by fine or imprisonment of not more than five (5) years, or both.

WARNING:

Petitioner/applicant is cautioned to avoid submitting personal information in documents filed in a patent application that may contribute to identity theft. Personal information such as social security numbers, bank account numbers, or credit card numbers (other than a check or credit card authorization form PTO-2038 submitted for payment purposes) is never required by the USPTO to support a petition or an application. If this type of personal information is included in documents submitted to the USPTO, petitioners/applicants should consider redacting such personal information from the documents before submitting them to the USPTO. Petitioner/applicant is advised that the record of a patent application is available to the public after publication of the application (unless a non-publication request in compliance with 37 CFR 1.213(a) is made in the application) or issuance of a patent. Furthermore, the record from an abandoned application may also be available to the public if the application is referenced in a published application or an issued patent (see 37 CFR 1.14). Checks and credit card authorization forms PTO-2038 submitted for payment purposes are not retained in the application file and therefore are not publicly available.

LEGAL NAME OF INVENTOR

Inventor: Pei-Yong SHI Date (Optional) :_____

Signature: _____

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

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LEGAL NAME OF INVENTOR

Inventor: Xuping XIE Date (Optional) :_____

Signature: _____

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

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LEGAL NAME OF INVENTOR

Inventor: Chao SHAN Date (Optional) :_____

Signature: _____

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

552.107

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Inventor: Pei-Yong SHI Date (Optional) :_____

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Inventor: Chao SHAN Date (Optional) :_____

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US 20200197505A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2020/0197505 A1**

SHI et al. (43) **Pub. Date: Jun. 25, 2020**

(54) **LIVE ATTENUATED ZIKA VIRUS WITH 3'UTR DELETION, VACCINE CONTAINING AND USE THEREOF**

(71) Applicant: **THE BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM**, AUSTIN, TX (US)

(72) Inventors: **Pei-Yong SHI**, Galveston, TX (US); **Xuping XIE**, Galveston, TX (US); **Chao SHAN**, Galveston, TX (US)

(21) Appl. No.: **16/485,818**

(22) PCT Filed: **Feb. 14, 2018**

(86) PCT No.: **PCT/US18/18114**

§ 371 (c)(1),
(2) Date: **Aug. 14, 2019**

Related U.S. Application Data

(60) Provisional application No. 62/458,839, filed on Feb. 14, 2017.

Publication Classification

(51) **Int. Cl.**
A61K 39/12 (2006.01)
A61P 31/14 (2006.01)

(52) **U.S. Cl.**
CPC ***A61K 39/12*** (2013.01); *A61K 2039/53* (2013.01); ***A61P 31/14*** (2018.01)

(57) **ABSTRACT**

The present invention discloses a live attenuated strain of Zika virus (ZIKV) having a deletion in the 3' untranslated region (3'UTR) of the viral genome, which may affect viral RNA synthesis and sensitivity to type I interferon inhibition, but may not affect viral RNA translation. The present invention also discloses the use of these live attenuated ZIKV strains in the preparation of ZIKV vaccines and for providing immunoprotection against ZIKV infection and congenital ZIKV syndrome, particularly in pregnant females.

Specification includes a Sequence Listing.

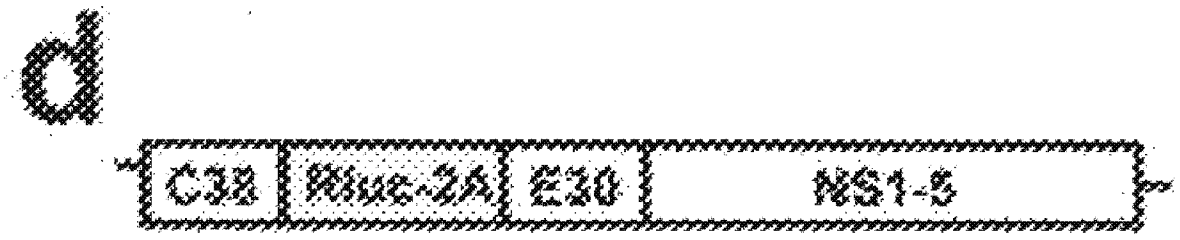


FIGURE 1A

FIGURE 1B

FIGURE 1D

FIGURE 1C

FIGURE 1E

FIGURE 1F

FIGURE 2A

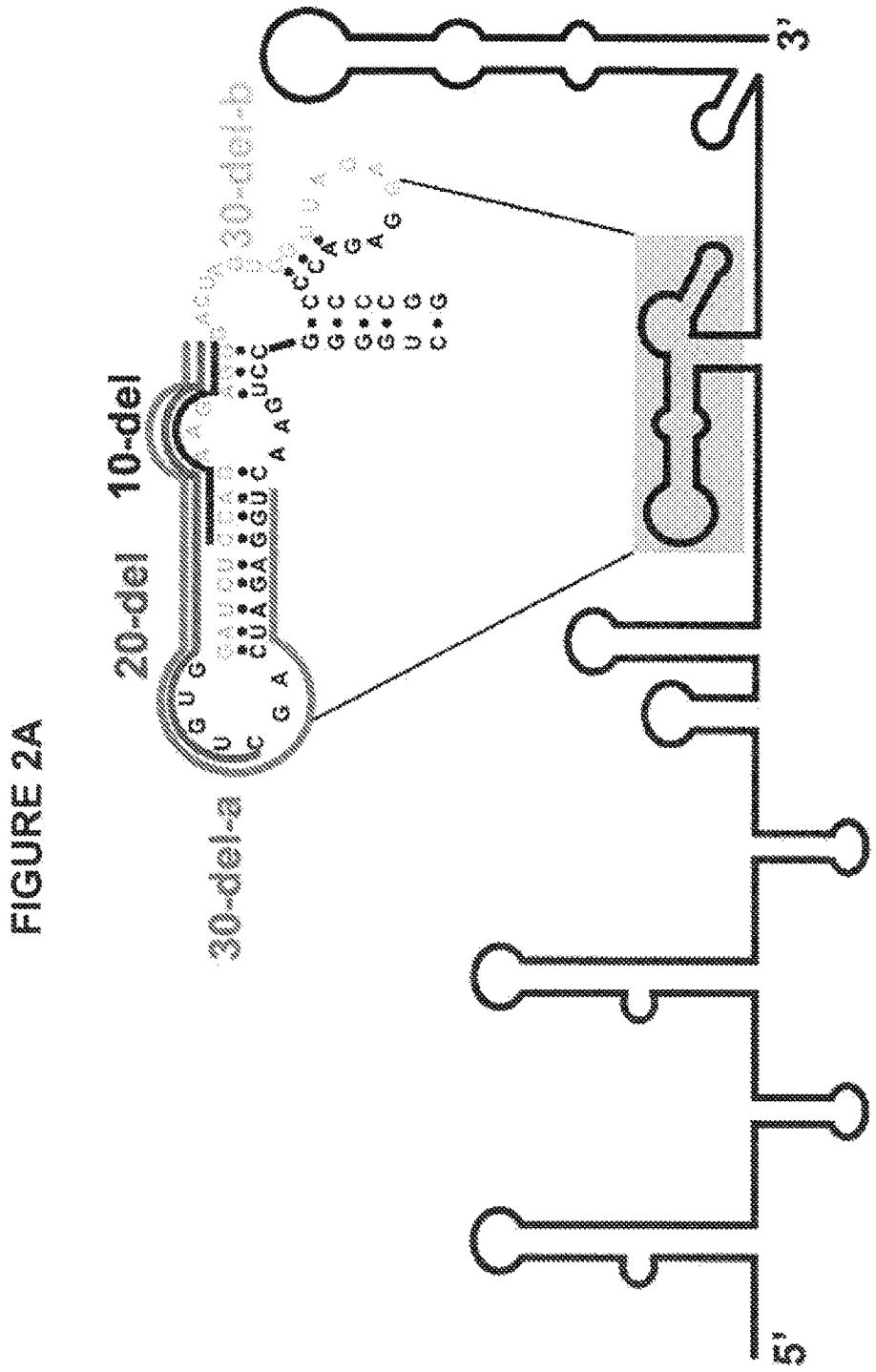


FIGURE 2B

10-del

	TGG AGA TCA GCT GTG GAT CTC CAG AAG AGG GAC TAG TGG TTA GAG
FSS13025/KU955593	* *
H/PF2013/KJ776791	* *
PRVABC 59/KU501215	* *
Natal RGN/KU527068	* *
ZKV2015/KU497555	* *
P6-740/KX377336	* G * * * * * * * C * *
MR 766/ AY632535	* * * * * * CT * * * * * * * * A * * * * * * C * * * * * * *
DAK-41525/KU955591	* * * * * * T * * * * * * * * A * * * * * G * C * * A * * *

FIGURE 3

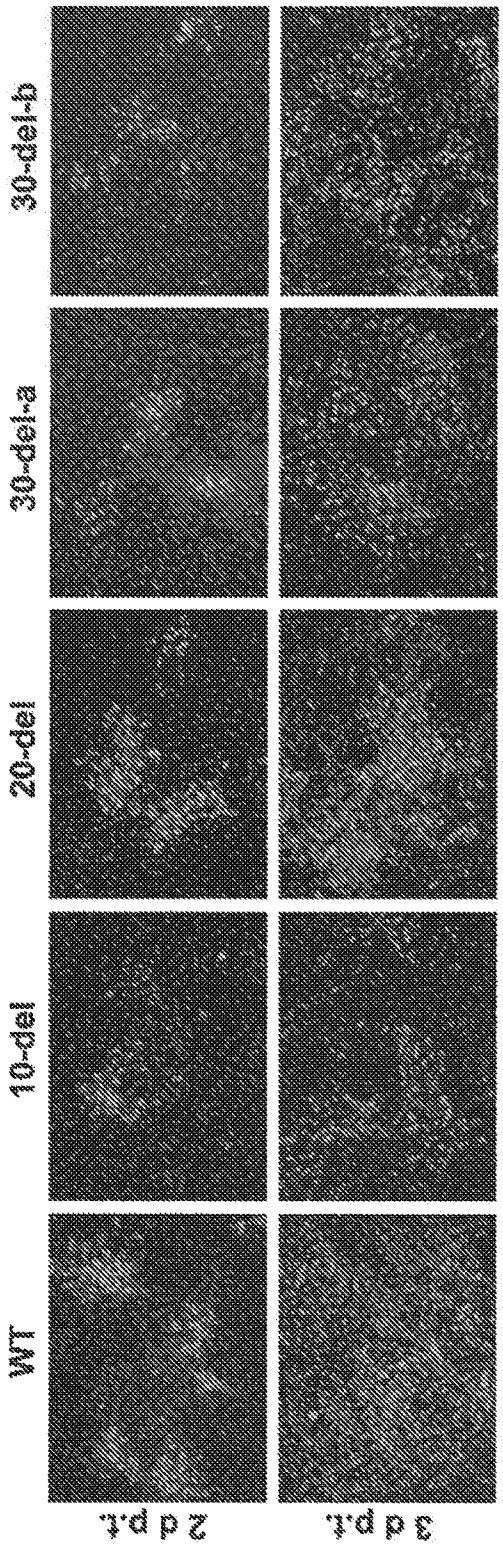


FIGURE 4A

FIGURE 4B

FIGURE 4C

C

	30-del-a	30-del-b	Day post-infection								
	10-del		20-del			30-del-a			30-del-b		
	I	II	III	I	II	III	I	II	III	I	II	III
E	R283W	H219L H219L R283W L441L K443N		T315I	K443N K443N		H401Y	H401Y H401Y	—	A501T	A501T A501T	A501T
NS1		R103K			W98L							

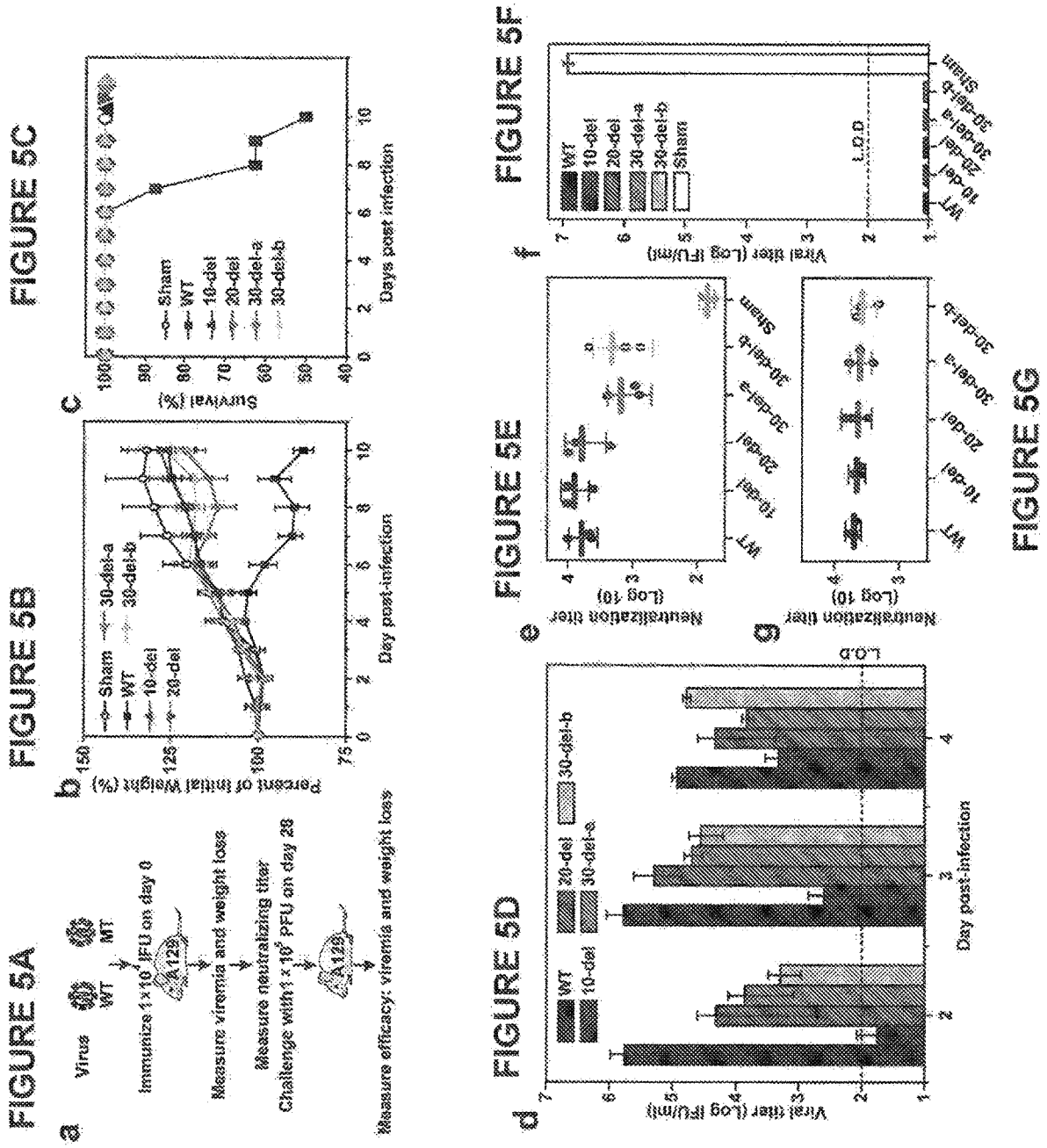


FIGURE 6A

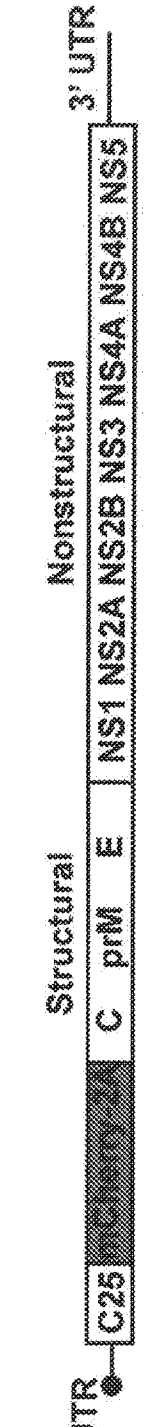
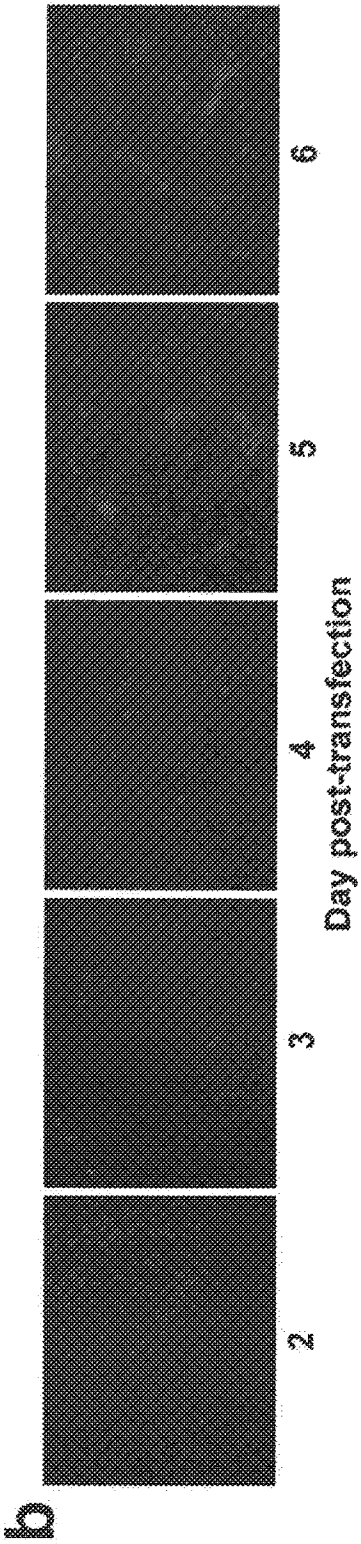


FIGURE 6B



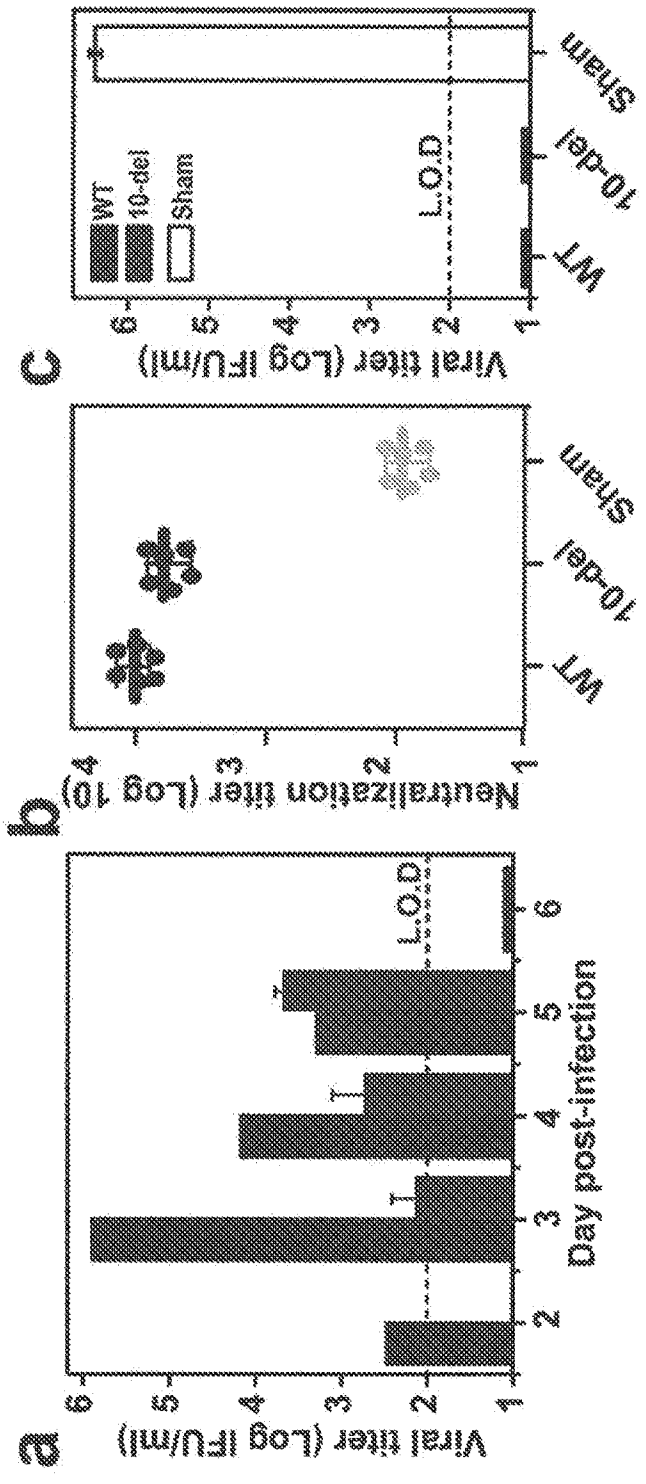


FIGURE 7A

FIGURE 7B

FIGURE 7C

FIGURE 8A

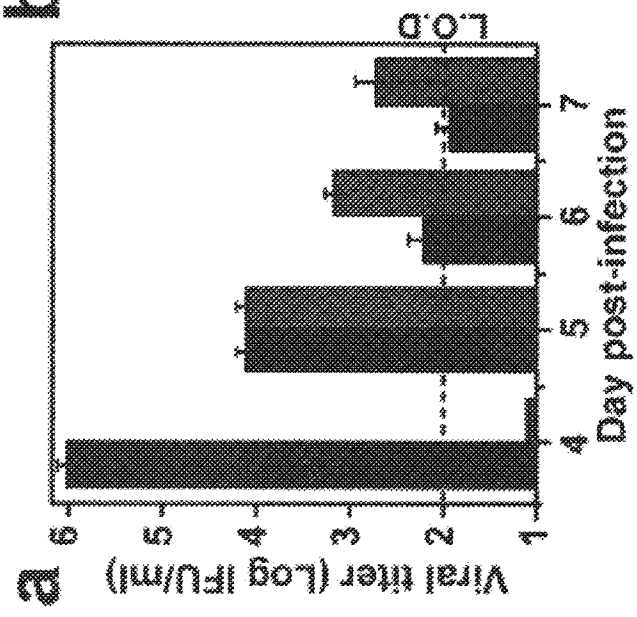


FIGURE 8B

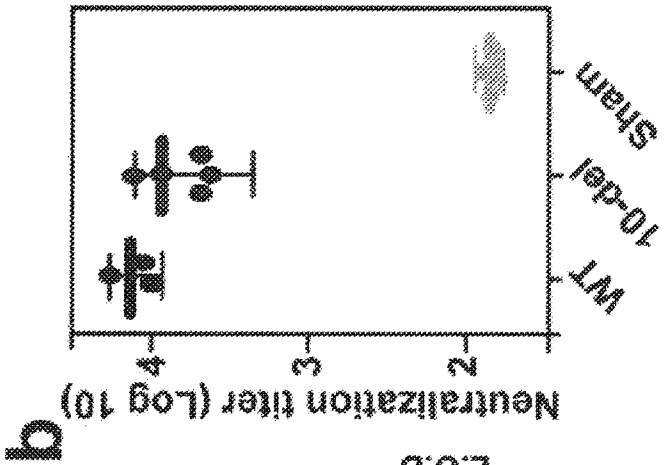


FIGURE 8C

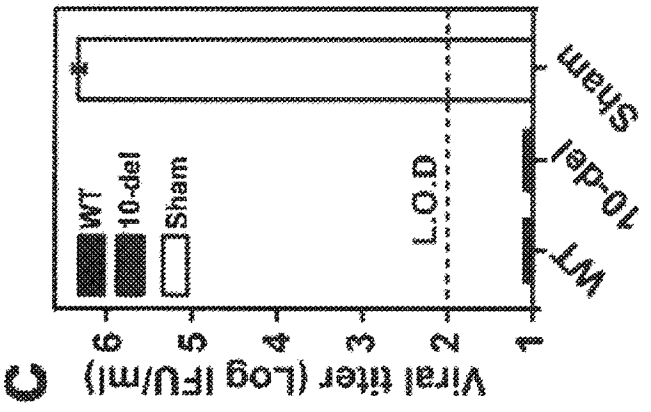


FIGURE 9A

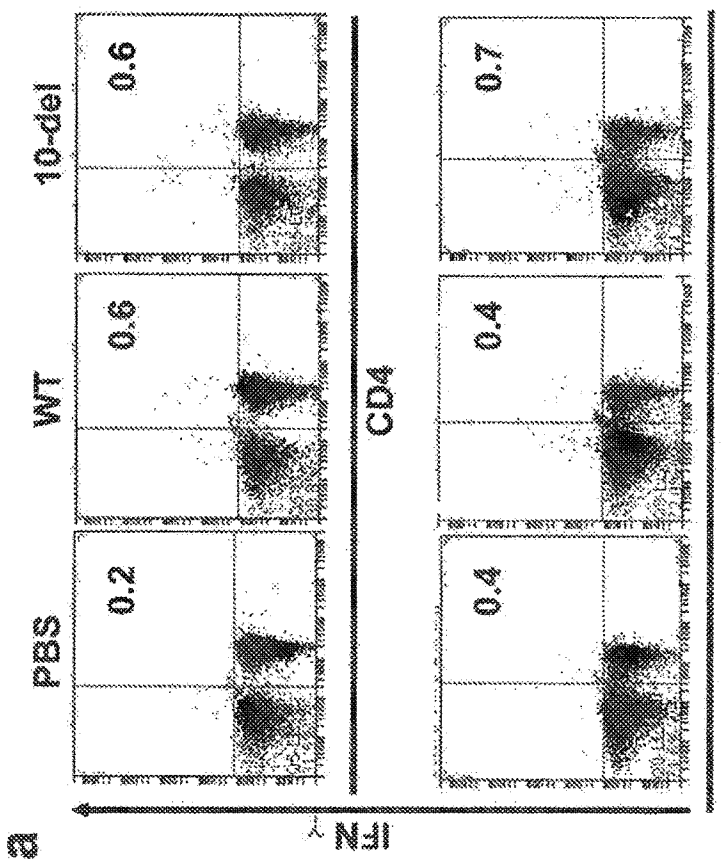


FIGURE 9B

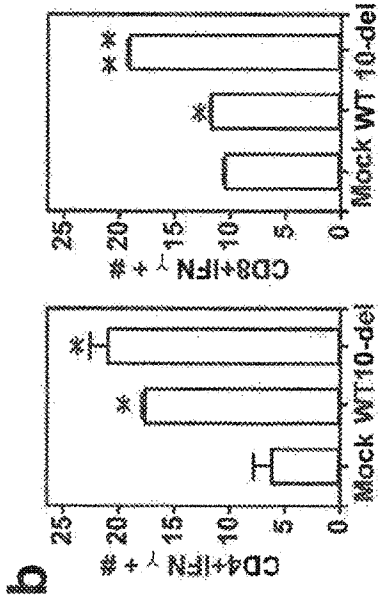


FIGURE 9C

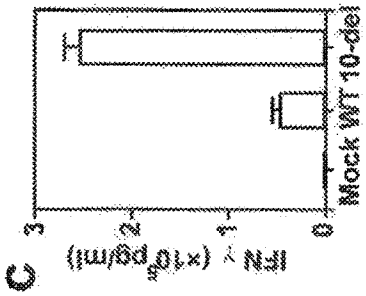
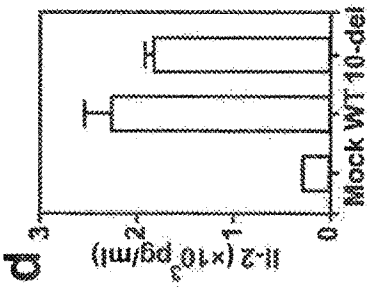


FIGURE 9D



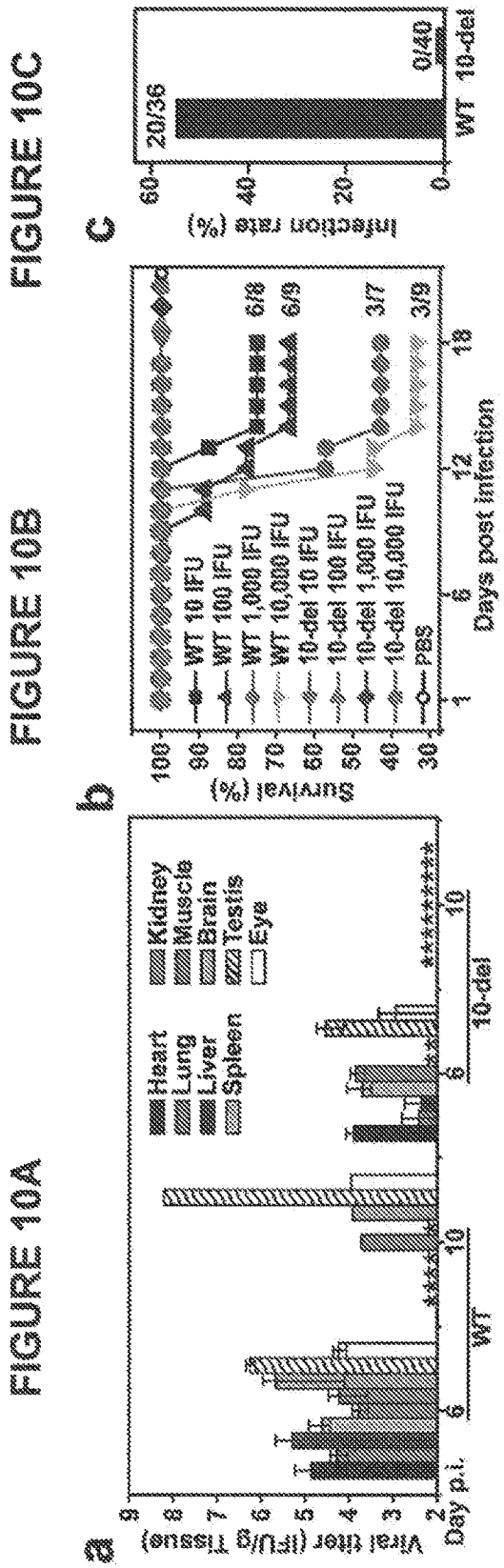


FIGURE 10A

FIGURE 10B

FIGURE 10C

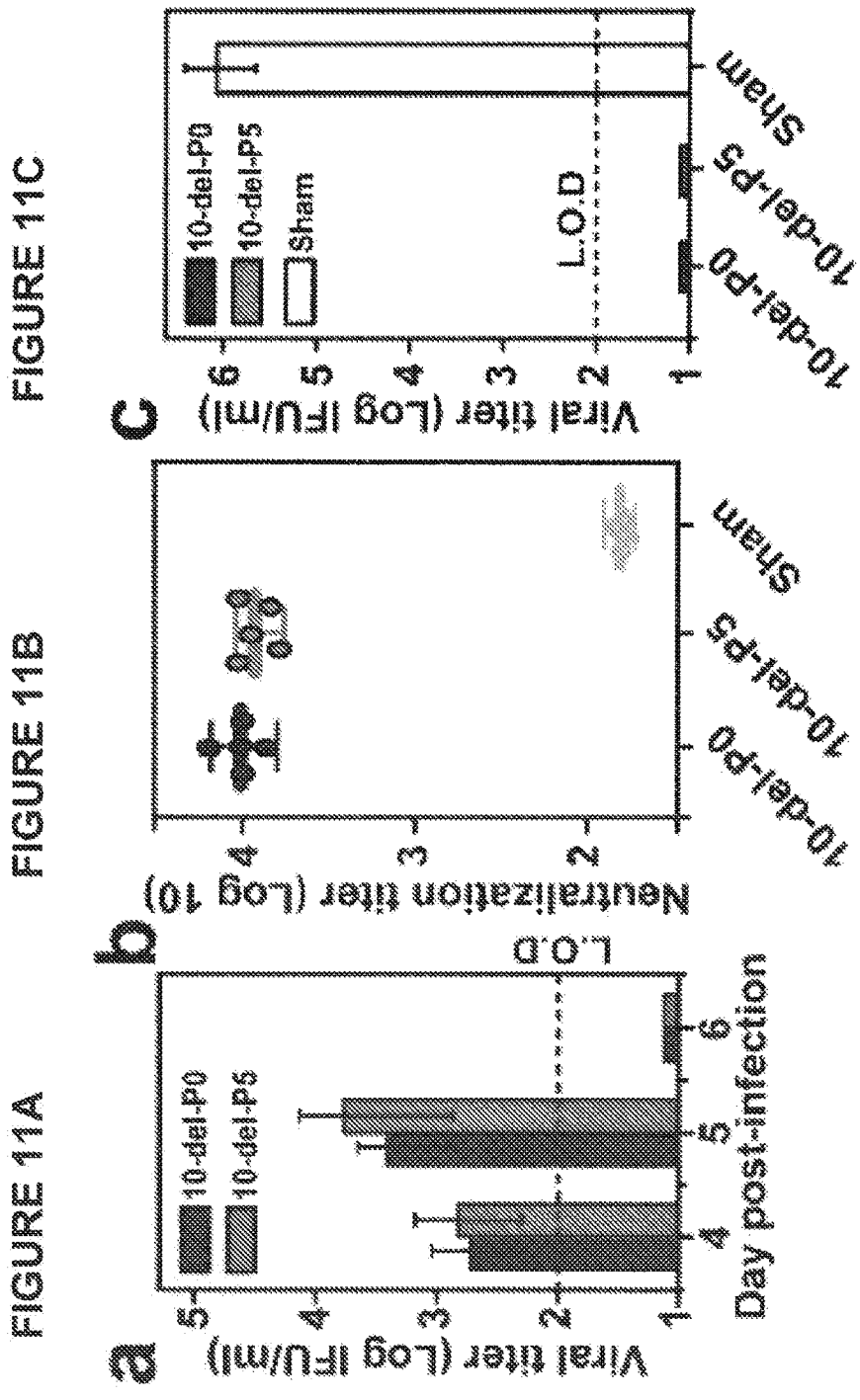


FIGURE 11A
FIGURE 11B
FIGURE 11C
a
Viral titer (Log IFU/ml)
10-del-P0
10-del-P5
L.O.D
Day post-infection
b
Neutralization titer (Log 10)
10-del-P0
10-del-P5
Sham
c
Viral titer (Log IFU/ml)
10-del-P0
10-del-P5
Sham
L.O.D

FIGURE 12A

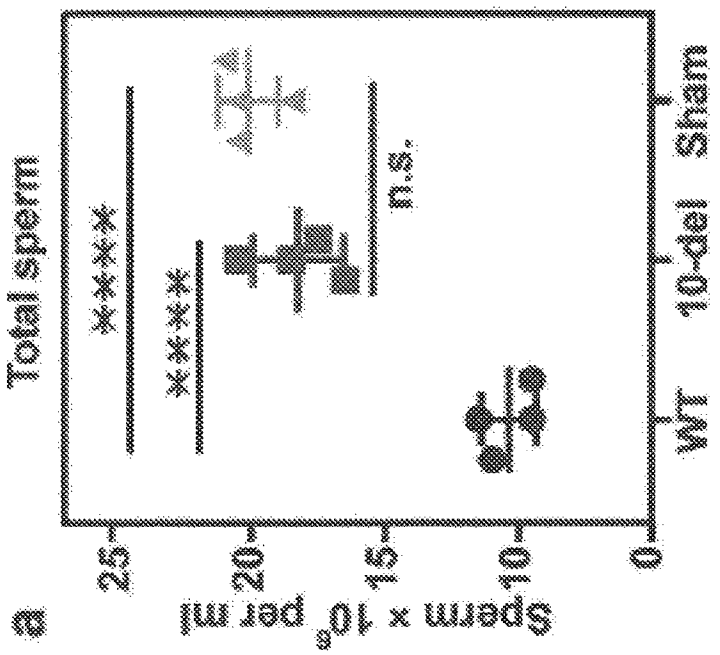


FIGURE 12B

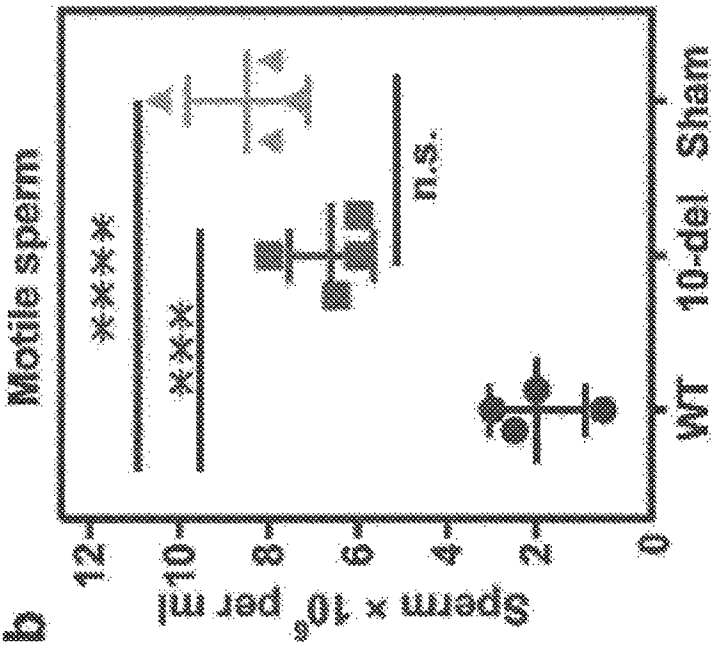


FIGURE 13A

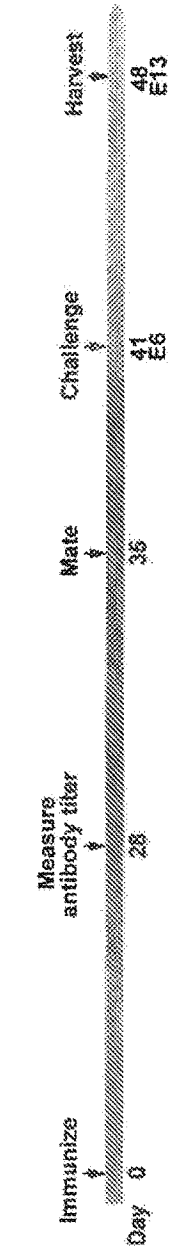


FIGURE 13B

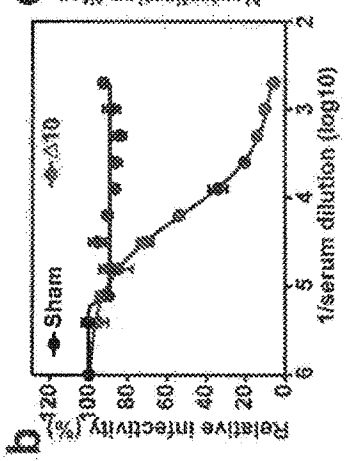


FIGURE 13C

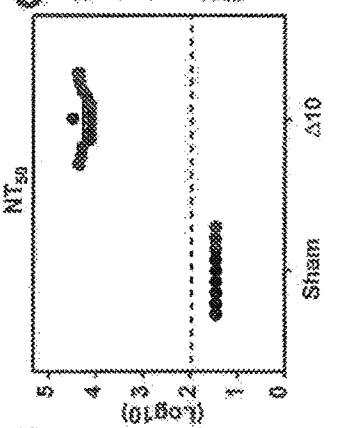


FIGURE 13D

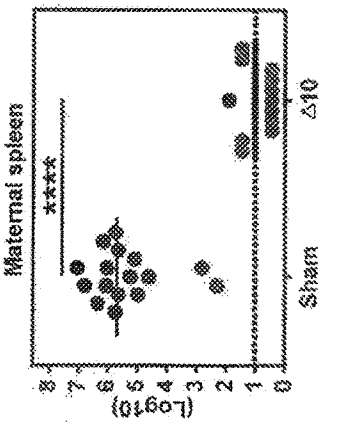


FIGURE 13E

FIGURE 13F

FIGURE 13G

FIGURE 14A

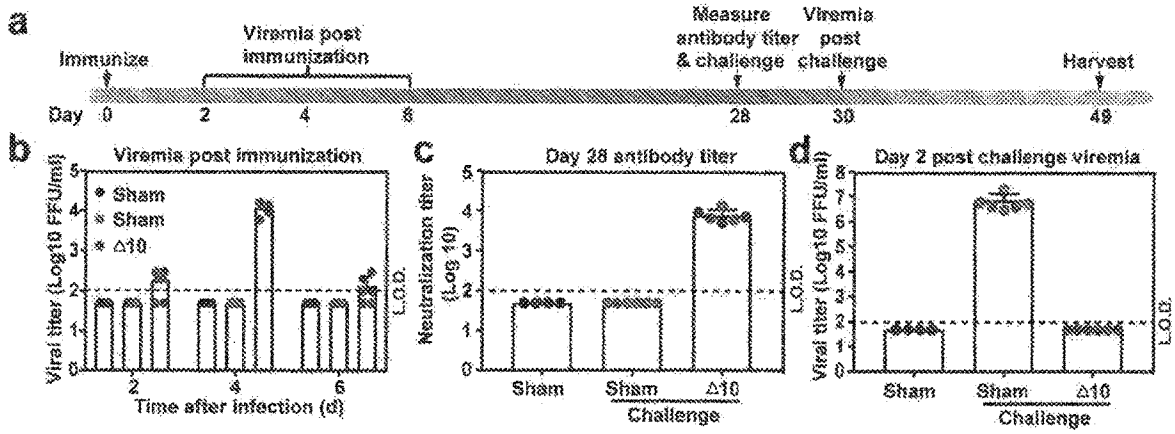


FIGURE 14B

FIGURE 14C

FIGURE 14D

FIGURE 14E

FIGURE 14F

FIGURE 14G

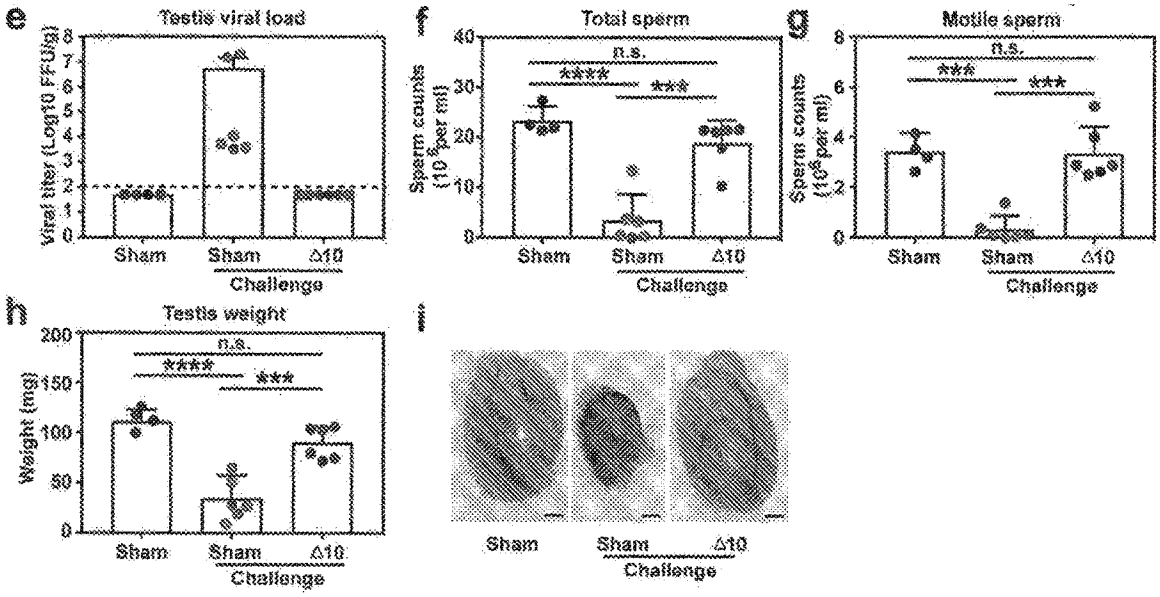


FIGURE 14H

FIGURE 14I

FIGURE 15A

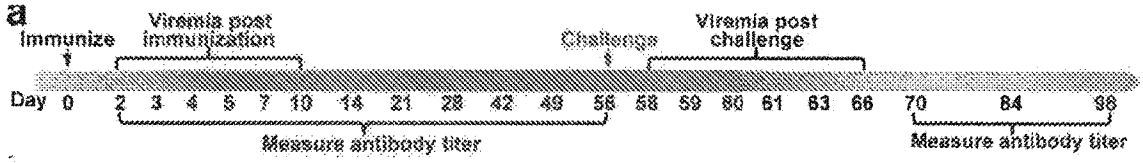
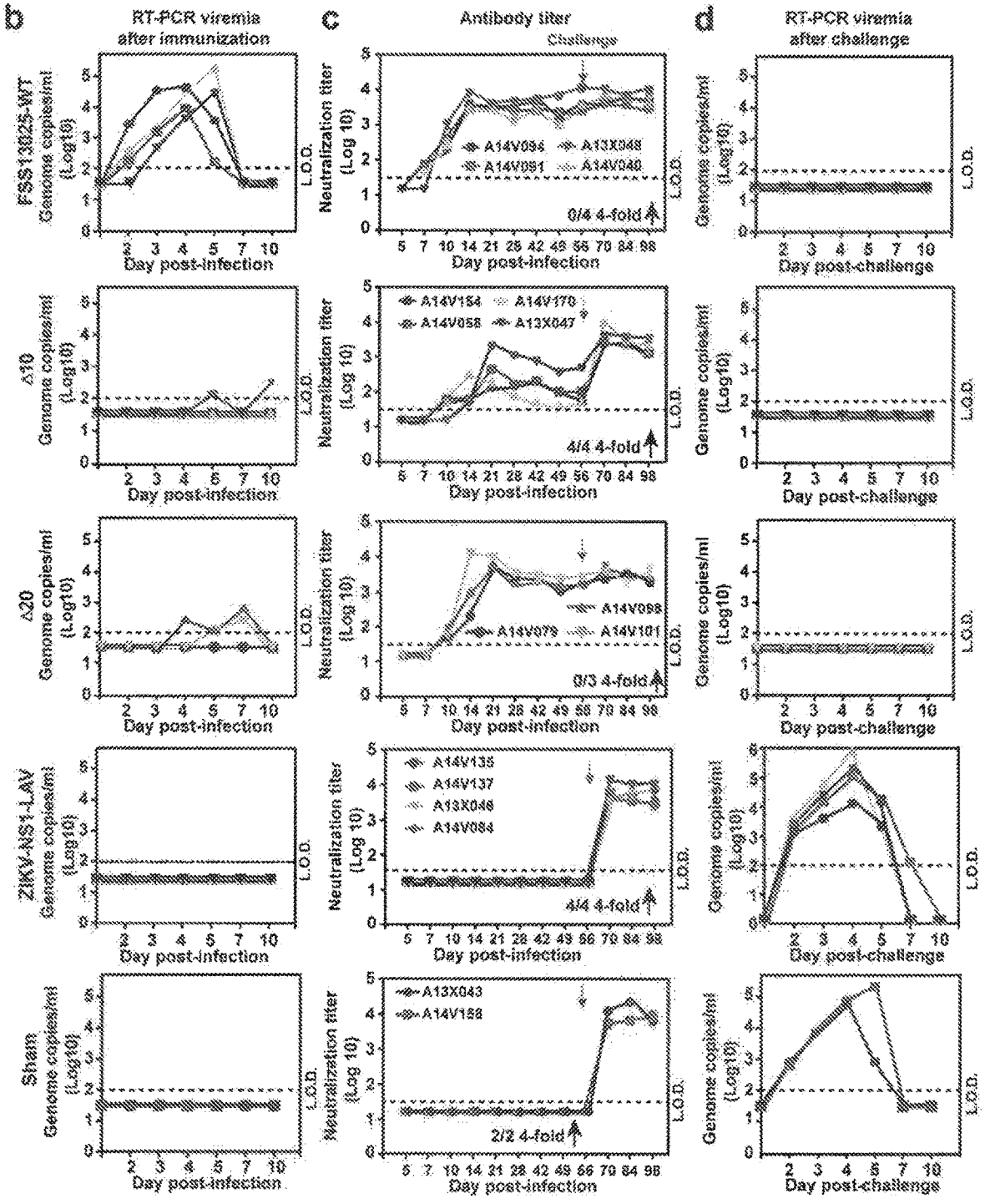
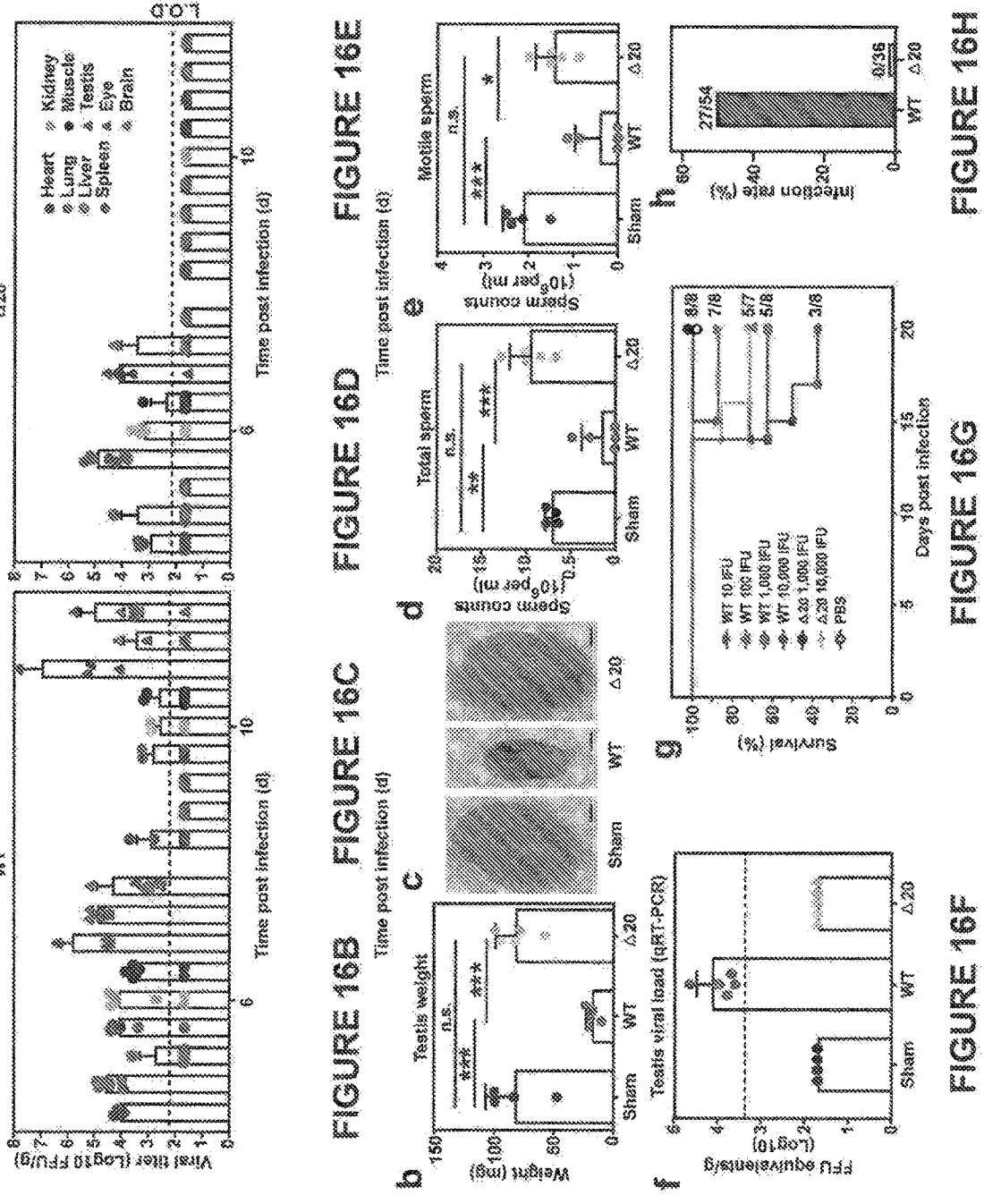


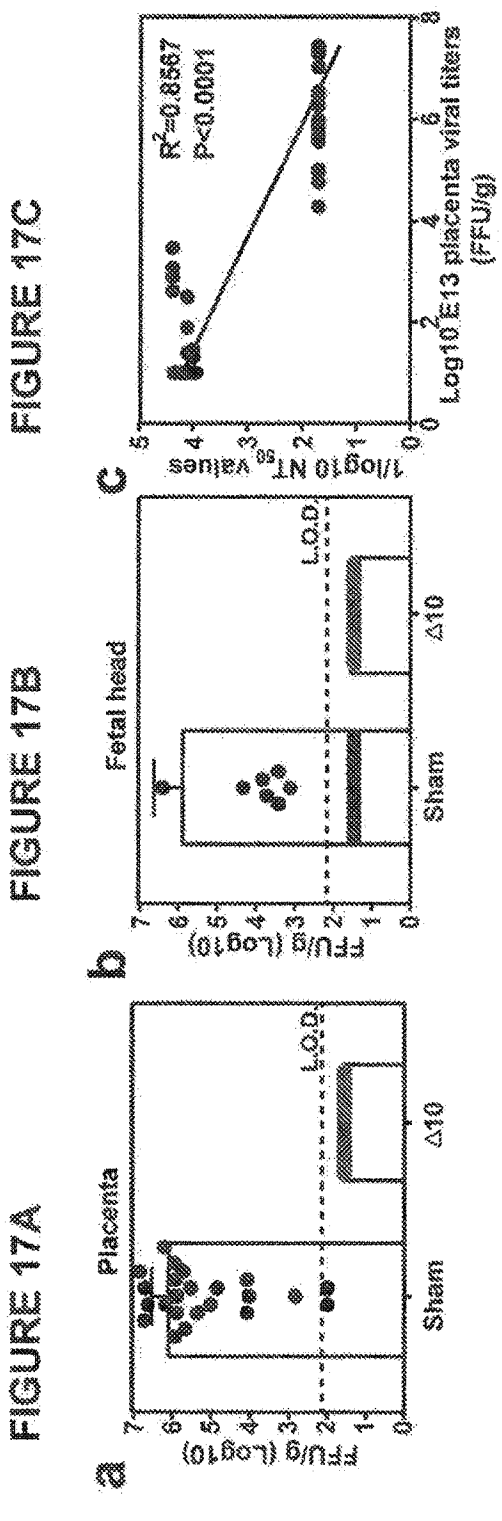
FIGURE 15B

FIGURE 15C

FIGURE 15D







Figures 17A-C. Infectious ZIKV burden in placentas and fetal heads from sham or ZIKV-3'UTR-Δ10-LAV-immunized dams. I

FIGURE 18A

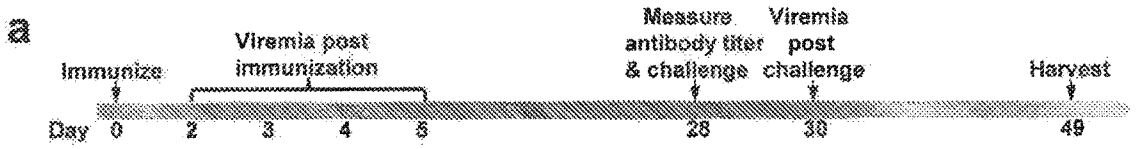


FIGURE 18B

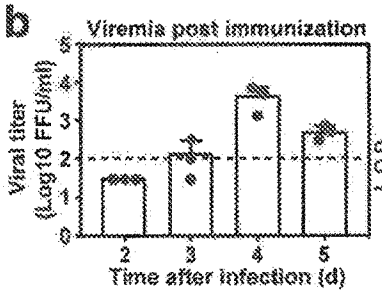


FIGURE 18C

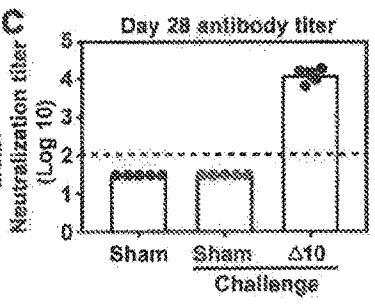


FIGURE 18D

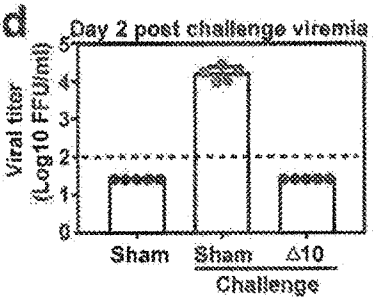


FIGURE 18E

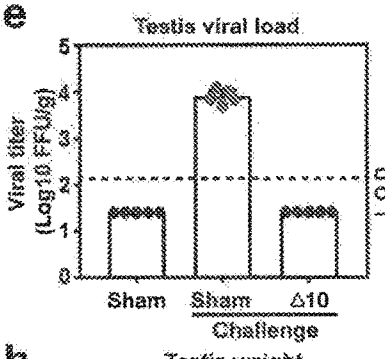


FIGURE 18F

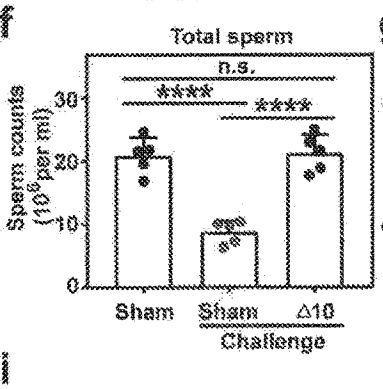
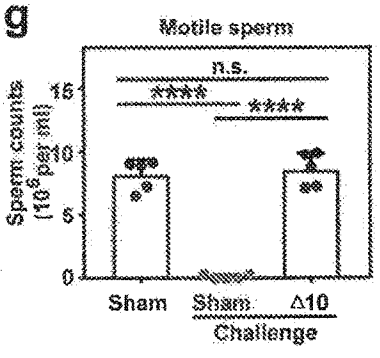


FIGURE 18G



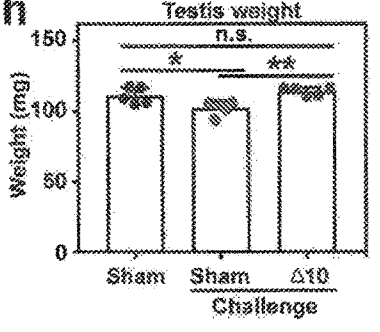


FIGURE 18H

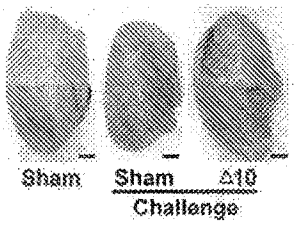
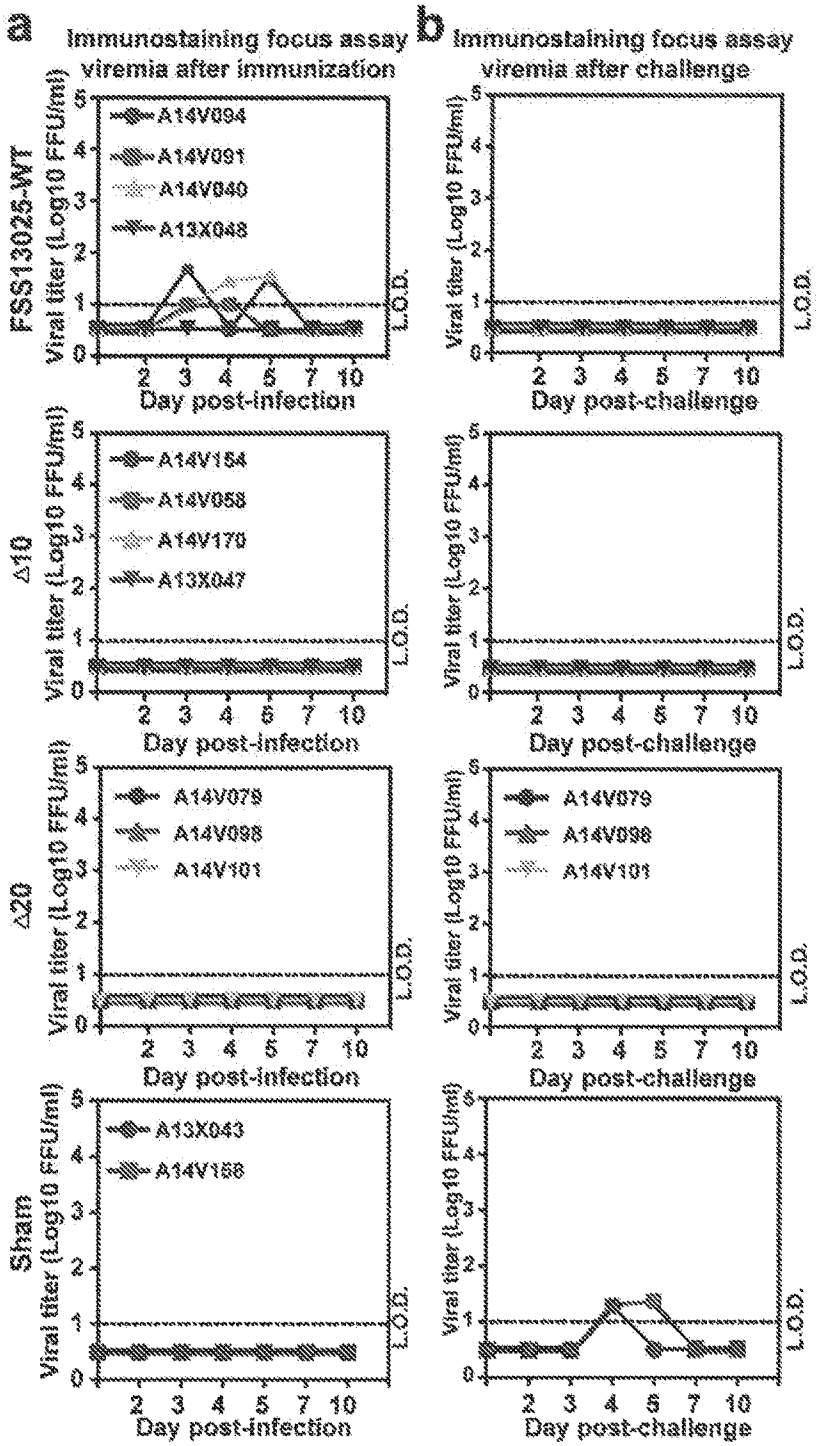


FIGURE 18I

Figures 18A-I. ZIKV-3'UTR-Δ10-LAV protects adult A129 male mice against testis infection and injury.

FIGURE 19A FIGURE 19B



Figures 19A-B. Infectious virus in serum of challenged rhesus macaque.

FIGURE 20A

FIGURE 20B

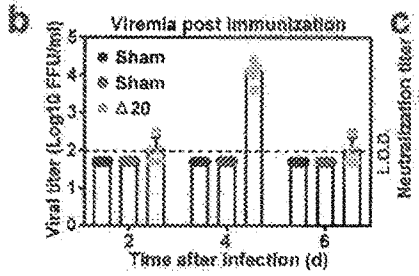


FIGURE 20C

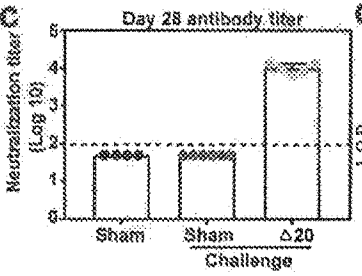


FIGURE 20D

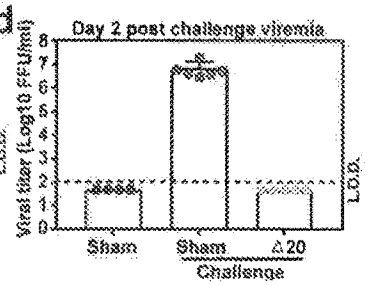


FIGURE 20E

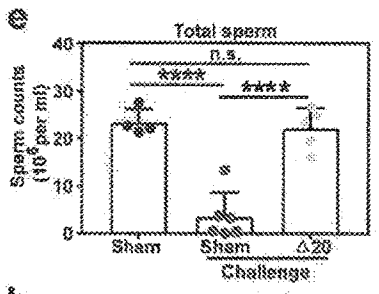


FIGURE 20F

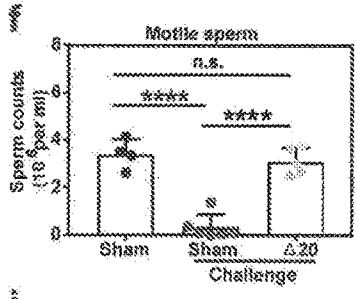
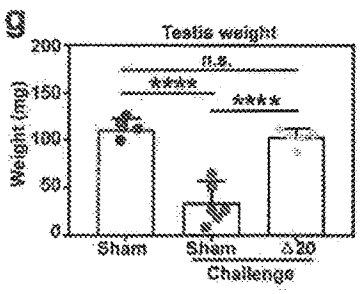


FIGURE 20G



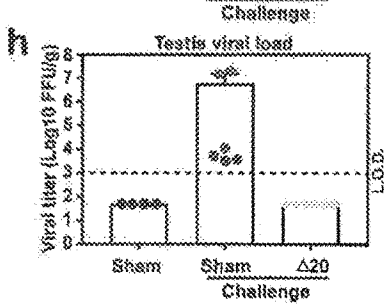


FIGURE 20H

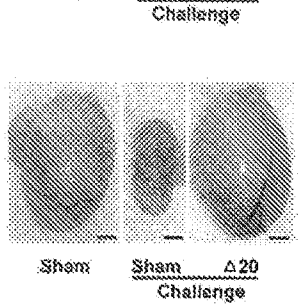


FIGURE 20 I

Figures 20A-I. ZIKV-3'-UTR-Δ20-LAV protects young A129 male mice against testis infection and injury.

FIGURE 21

Sequencing results for ZIKV-3'UTR-Δ20-LAV P5 viruses

	E	NS1
Selection I	T315I	-
Selection II	K443N	W98L
Selection III	K443N	-

Figure 21. Stability analysis of ZIKV-3'UTR-Δ20-LAV in cell culture.

FIGURE 22

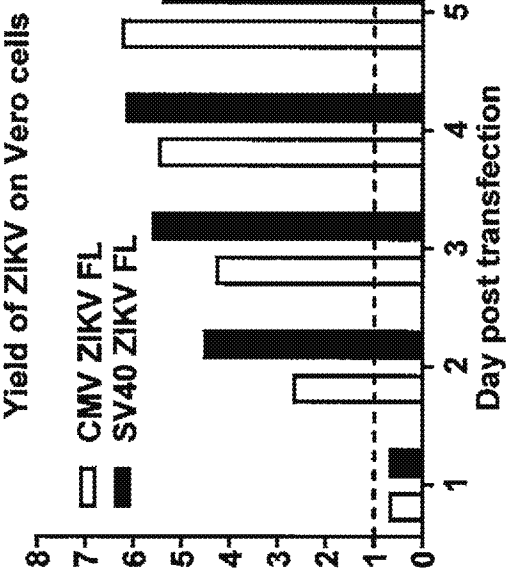


FIGURE 22: Yield of ZIKV on VERO cells.

FIGURE 23

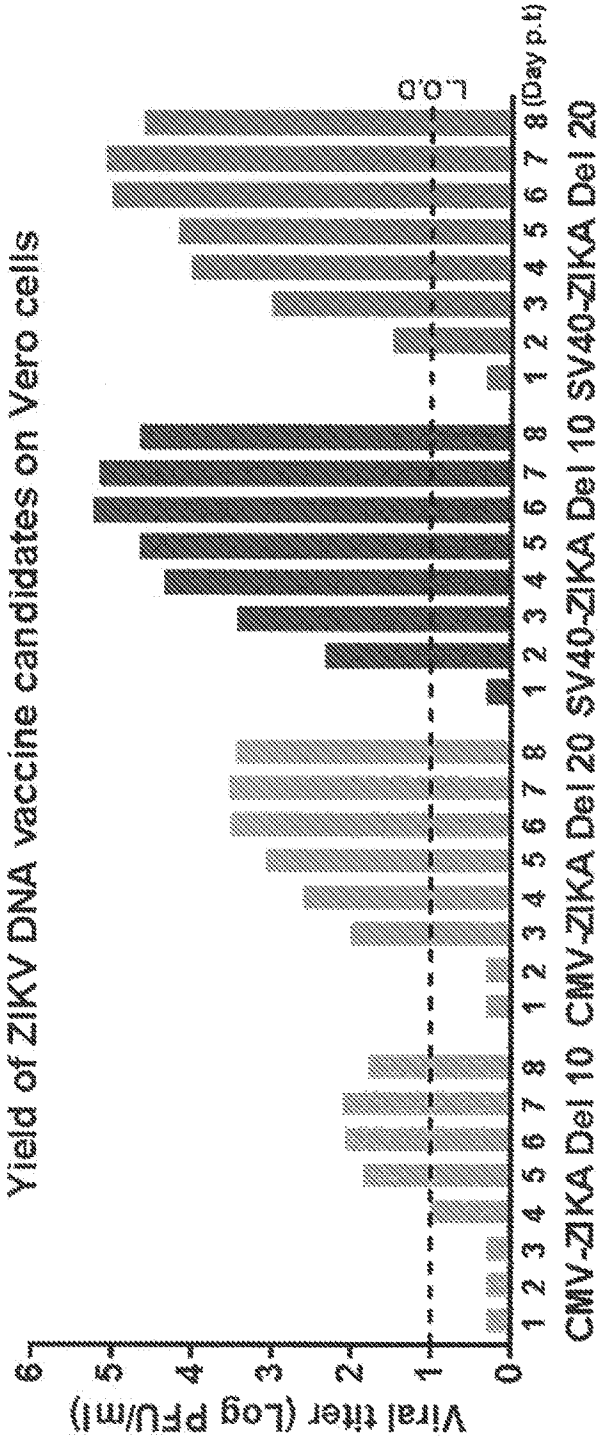


Figure 23. Yield of ZIKV DNA vaccine candidates on Vero cells.

LIVE ATTENUATED ZIKA VIRUS WITH 3'UTR DELETION, VACCINE CONTAINING AND USE THEREOF

RELATED APPLICATIONS

[0001] This PCT application claims priority to U.S. Provisional Application No. 62/458,839, filed on Feb. 14, 2017, the contents of which are incorporated by reference in their entirety herein.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] The invention was funded by NIH grant AI120942.

FIELD OF THE INVENTION

[0003] The invention generally relates to the development of a live attenuated strain of Zika virus (ZIKV) and vaccine compositions comprising this strain. The strain and vaccines comprising it may be used in humans and animals for treating or providing immunoprotection against ZIKV, which may cause congenital ZIKV syndrome and Guillan-Barré syndrome. The invention specifically discloses methods of protecting against congenital ZIKV syndrome, including microcephaly.

BACKGROUND OF THE INVENTION

[0004] The mosquito-borne ZIKV has recently caused a global threat to public health. The most devastating disease associated with Zika virus (ZIKV) infection is the wide range of congenital abnormalities (including microcephaly) now collectively known as congenital ZIKV syndrome (Reference 1). Prevention of congenital ZIKV syndrome is the most pressing task to reduce the burden of epidemics on family and society (Reference 2). In particular, pregnant women without ZIKV immunity in endemic countries are at risk for fetal infection and congenital defects. Since ZIKV could also be sexually transmitted, women living in non-endemic regions can also be at risk when exposed to men who have traveled to endemic countries.

[0005] ZIKV is spread to people primarily through the bite of an infected *Aedes* species mosquito. The most common symptoms of ZIKV are fever, rash, joint pain, and conjunctivitis. The illness is usually mild, with symptoms appearing 2 to 7 days after being bitten by an infected mosquito and lasting for several days to a week. However, there have been reports of congenital ZIKV syndrome, e.g., serious birth defects, especially microcephaly, and other poor pregnancy outcomes in babies of mothers who were infected with ZIKV while pregnant. There have also been cases of Guillain-Barré syndrome (GBS) reported in patients following suspected ZIKV infection. GBS is a rare disorder where a person's own immune system damages the nerve cells, causing muscle weakness and sometimes, paralysis. These symptoms can last anywhere from a few weeks to several months, although some people have permanent damage and, in rare cases, GBS may result in death.

[0006] ZIKV is a member of the *Flavivirus* genus (in the family Flaviviridae), which also includes other important human pathogens, e.g., yellow fever (YFV), West Nile (WNV), Japanese encephalitis (JEV), tick-borne encephalitis (TBEV), and Dengue viruses (DENV). Like other members of the *Flavivirus* genus, Zika contains a positive single-stranded genomic RNA, encoding a polyprotein that is processed into three structural proteins (capsid [C], premembrane [prM], and envelope [E] proteins) and seven nonstructural proteins (NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5). Structural proteins form virions, whereas nonstructural proteins participate in viral RNA synthesis, virion assembly, and evasion of immune response.

[0007] Both inactivated and live-attenuated vaccines have been developed for flaviviruses, including YFV, JEV, TBEV, and DENV (Reference 3). Rapid and promising progress has been made toward ZIKV vaccine development (References 4 and 5). Inactivated ZIKV and subunit vaccines (expressing viral prM/E proteins) have shown efficacy in mice and nonhuman primates (References 6-8). A successful vaccine requires a fine balance between immunogenicity and safety. Live-attenuated vaccines generally offer fast and durable immunity, but sometimes with the trade-off of reduced safety; whereas inactivated and subunit vaccines provide enhanced safety at the cost of reduced immunogenicity, and often require multiple doses and periodic boosters.

[0008] The present invention addresses the need for novel ZIKV vaccines that serve at-risk populations in order to treat and/or provide immunoprotection against infections elicited by ZIKV and to prevent congenital ZIKV syndrome, especially microcephaly.

BRIEF SUMMARY OF THE INVENTION

[0009] The invention in general relates to a live attenuated Zika virus (ZIKV) strain, comprising a deletion in the 3' untranslated region (3'UTR) of the ZIKV genome.

[0010] The invention more specifically relates to a live attenuated Zika virus (ZIKV) strain, wherein the 3'UTR deletion ranges from a 10-nucleotide deletion to a 50-nucleotide deletion (i.e., Δ10, Δ11, Δ12, Δ13, Δ14, Δ15, Δ16, Δ17, Δ18, Δ19, Δ20, Δ21, Δ22, Δ23, Δ24, Δ25, Δ26, Δ27, Δ28, Δ29, Δ30, Δ31, Δ32, Δ33, Δ34, Δ35, Δ36, Δ37, Δ38, Δ39, Δ40, Δ41, Δ42, Δ43, Δ44, Δ45, Δ46, Δ47, Δ48, Δ49 or Δ50 3'UTR deletion), in exemplary embodiments the 3'UTR deletion is a 10-nucleotide deletion, a 20-nucleotide deletion, or a 30-nucleotide deletion.

[0011] The invention more specifically relates to a live attenuated Zika virus (ZIKV) strain comprising a 3'UTR having at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identity to the nucleic acid sequence of SEQ ID NO: 2, 3, 4, or 5.

[0012] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which is incompetent in infecting mosquitoes.

[0013] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which exhibits decreased viral RNA synthesis compared to wildtype ZIKV strains.

[0014] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which exhibits increased sensitivity to type-I interferon inhibition compared to wildtype ZIKV strains.

[0015] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described wherein the deletion does not affect viral RNA translation.

[0016] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which is an mCherry ZIKV strain.

[0017] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which comprises or consists of a deletion variant of SEQ ID

NO:6 wherein the sequence "CCAGAAGAGG" (3'UTR 10-nucleotide deletion) (SEQ ID NO:8) is deleted therefrom.

[0018] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which comprises or consists of a deletion variant of SEQ ID NO:6 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (3'UTR 20-nucleotide deletion) (SEQ ID NO:9) is deleted therefrom.

[0019] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which comprises or consists of a deletion variant of SEQ ID NO:7 wherein the sequence "CCAGAAGAGG" (3'UTR 10-nucleotide deletion) (SEQ ID NO:8) is deleted therefrom.

[0020] The invention also specifically relates to a live attenuated Zika virus (ZIKV) strain as above-described which comprises or consists of a deletion variant of SEQ ID NO:7 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (3'UTR 20-nucleotide deletion) (SEQ ID NO:9) is deleted therefrom.

[0021] The invention also specifically relates to an immunogenic composition comprising a live attenuated ZIKV strain as above-described, which further comprises at least one pharmaceutically acceptable carrier or excipient.

[0022] The invention also specifically relates to an immunogenic composition comprising a live attenuated ZIKV strain as above-described, which is suitable for parenteral or enteral administration.

[0023] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described.

[0024] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, which induces a $CD8^+$ T cell response, an antibody response, and/or a cellular immune response against ZIKV.

[0025] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, which produces a neutralizing antibody titer equivalent to that of wildtype ZIKV infection.

[0026] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, wherein the subject is a pregnant female.

[0027] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, in order to prevent congenital ZIKV syndrome.

[0028] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, in order to prevent microcephaly.

[0029] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, wherein at least 1.0×10^1, 1.0×10^2, 1.0×10^3, 1.0×10^4, 1.0×10^5, or 1.0×10^6 IFUs of the live attenuated ZIKV strain is administered to the subject.

[0030] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, wherein the administration of said composition prevents viremia in said subject after subsequent challenge with a wildtype ZIKV strain.

[0031] The invention also specifically relates to a method of eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain or immunogenic composition as above-described, wherein the subject is a human.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0032] FIG. **1**A-**1**F contain characterizations of the 3'UTR deletion mutants in cell culture. FIG. **1**A provides sequences of the ZIKV 3'UTR deletions. FIG. **1**B shows an immunostaining focus assay of mutant viruses. Equal amounts of RNAs (10 μg) transcribed from their corresponding infectious cDNA clones were electroporated into Vero cells. On day 4 or 5 post-transfection, culture fluids from the transfected cells were harvested and quantified for infectious viruses (defined as P0 virus) using an immunostaining focus assay on Vero cells. FIG. **1**C demonstrates the replication kinetics of WT and mutant viruses. Vero cells in 24-well plates (2×10^5 cells per well) were infected with WT and mutant viruses at an MOI of 0.01. Culture fluids were quantified for infectious viruses on days 1 to 5 using the immunostaining focus assay. From left to right for each day, the bars correspond to: WT, 10-del, 20-del, 30-del-a, and 30-del-b. FIG. **1**D illustrates a Renilla luciferase reporter replicon construct. FIG. **1**E contains a replicon analysis of the 3'UTR deletions. A Renilla luciferase reporter replicon of ZIKV (FIG. **1**D) was engineered with various 3'UTR deletions. Equal amounts of replicon WT and mutant RNAs (10 μg) were electroporated into Vero cells. Luciferase signals were measured at the indicated time points. A non-replicative replicon containing an NS5 polymerase-inactive GDD mutation was included as a negative control. The averages of three replicates are presented. Error bars represent standard deviations. RLU, relative light units. The top curve corresponds to WT and the bottom curve corresponds to the GDD control. FIG. **1**F shows the interferon-β inhibition of WT and mutant ZIKVs. Vero cells were seeded in 96-well plate (1.5×10^4 cell per well) one day before interferon treatment and viral infection. The cells were infected at an MOI 0.05 in the presence of IFN-β (55, 167, 500, or 1,500 IU/ml). Viral infection and interferon treatment were initiated at the same time. At 48 h post-infection and interferon-β treatment, viral titers were quantified using

the immunostaining focus assay on Vero cells. Percentages of viral titer inhibition are presented in $\log_{10}$ scale. Viral titers without interferon-β treatment are set as 100%. Average results of three independent experiments are shown. Error bars represent standard deviations. Symbols ** and *** indicate P values <0.01 and <0.001, respectively. From left to right for each day, the bars correspond to: WT, 10-del, 20-del, 30-del-a, and 30-del-b.

[0033] FIG. **2**A-**2**B shows the sequence information of the 3'UTR and the deletion mutants. FIG. **2**A depicts the predicted RNA secondary structure of the ZIKV 3'UTR. The stem-loop structure of the 3'UTR of the ZIKV genome is presented as previously reported (References 33,34). The nucleotide sequence of the shaded stem-loop is shown. The deleted sequences for 10-del, 20-del, 30-del-a, and 30-del-b mutants are displayed in blue, magenta, green, and orange, respectively. FIG. **2**B shows a sequence alignment of the deleted region (nucleotide position 10,630-10,674) in the 3'UTR. The 10-del nucleotides are indicated. Within the 10-del region, sequence variations are observed for early isolates (P6-740, MR766, and DAK-41525 were isolated in 1966, 1947, and 1984, respectively), while an identical sequence is observed for the strains isolated after 2010 (FSS13025, H/PF2013, PRVABC 59, Natal RGN, and ZKV2015).

[0034] FIG. **3** shows an immunofluorescence assay (IFA) of viral protein expression in cells transfected with WT or 3'UTR deletion ZIKV RNA. Vero cells were electroporated with 10 μg of genomic WT or 3'UTR deletion RNA of ZIKV. On day 2 and 3 post-transfection, IFA was performed to examine viral E protein expression using a mouse mAb (4G2) and Alexa Fluor® 488 goat anti-mouse IgG as the primary and secondary antibodies, respectively. Green and blue represent E protein and nuclei (stained with DAPI), respectively. Viral E protein staining is visible for WT and all mutant groups on both days.

[0035] FIG. **4**A-**4**C contain a stability analysis of the 3'UTR deletion ZIKVs in cell culture. P0 viruses (derived from the culture fluids of RNA-transfected cells from FIG. **1**) were continuously cultured on Vero cells for five rounds (5 days for each round of culture), resulting in P5 viruses. The P5 viruses were then characterized. FIG. **4**A shows the results of an immunostaining focus assay. WT and P5 mutant viruses were analyzed using an immunostaining focus assay on Vero cells. For each mutant virus, three independent selections were performed on Vero cells. Representative images of infectious foci for each P5 mutant virus are presented. FIG. **4**B shows replication kinetics. Vero cells in 24-well plates (2×10^5 cells per well) were infected with WT and P5 mutant viruses at an MOI of 0.01. Culture fluids were quantified for infectious viruses on days 1 to 5 using the immunostaining focus assay on Vero cells. From left to right for each day, the bars correspond to: WT, 10-del, 20-del, 30-del-a, and 30-del-b. FIG. **4**C shows adaptive mutations in P5 mutant viruses. The complete genomes of P5 mutant viruses were sequenced for each of the three independent selections. The adaptive mutations are indicated by their amino acid positions of indicated genes based on ZIKV FSS13025 strain (GenBank number KU955593.1).

[0036] FIG. **5**A-**5**G show a characterization of 3'UTR mutants in the A129 mouse model. FIG. **5**A contains an experimental scheme. In two separate experiments, three-week old A129 mice (n=8) were immunized via the S.C. route with 1×10^4 IFU WT and mutant viruses. The immunized mice were monitored for weight loss, survival, and viremia. FIG. **5**B shows the results for weight loss. Weight loss is indicated by percentage using the weight on the day before immunization as 100%. The lowest curve corresponds to WT. FIG. **5**C shows the results for survival. The lowest curve corresponds to WT. FIG. **5**D shows the results for viremia. Viremias were quantified by an immunostaining focus assay from day 2 to 4 post-infection. From left to right for each day, the bars correspond to: WT, 10-del, 20-del, 30-del-a, and 30-del-b. FIG. **5**E shows the pre-challenge neutralization antibody titers. On day 28 post-immunization, mouse sera were measured for neutralizing titers using an mCherry ZIKV infection assay (FIG. **6**A-**6**B). FIG. **5**F shows the post-challenge viremia. On day 28 post-immunization, mice were challenged with 1×10^5 PFU parental virus (ZIKV strain FSS13025) via the I.P. route. Viremia on day 2 post-challenge was quantified using the immunostaining focus assay. FIG. **5**G shows the post-challenge neutralization antibody titer. On day 28 post-challenge, mouse sera were quantified for neutralizing titers using the mCherry ZIKV infection assay. L.O.D.: limit of detection.

[0037] FIG. **6**A-**6**B show the construction of mCherry ZIKV. FIG. **6**A shows a schematic genome of an mCherry ZIKV. A DNA fragment (encoding the first 25 amino acids of C gene, the mCherry gene, and the foot-and-mouth virus 2A protein) was in-frame fused with the open-reading-frame of ZIKV genome. FIG. **6**B shows the mCherry expression in Vero cells transfected with mCherry ZIKV RNA. The expression of mCherry in transfected Vero cells was analyzed by fluorescent microscopy at the indicated days post-transfection. The mCherry ZIKV was used to estimate antibody neutralization titers of mouse sera, as described in Methods.

[0038] FIG. **7**A-**7**C show the efficacy of immunization with 100 IFU 10-del virus. FIG. **7**A shows the viremia after immunization with 100 IFU of WT (left bar) or 10-del ZIKV (right bar). Three-week-old A129 mice (n=5) were immunized with 100 IFU WT or 10-del virus via the S.C. route. Viremia was quantified by immunostaining focus assay from day 2 to 6. L.O.D., limit of detection. FIG. **7**B shows the pre-challenge neutralization antibody titers. On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers. FIG. **7**C shows the viremia after challenge with ZIKV (Puerto Rico strain PRVABC59). On day 28 post-immunization, the mice were challenged with 1×10^6 IFU of ZIKV via the I.P. route. Viremias were quantified by immunostaining focus assay on day 2 post-challenge.

[0039] FIG. **8**A-**8**C show the efficacy of immunization with 10 IFU 10-del virus. FIG. **8**A shows the viremia after immunization with 10 IFU of WT or 10-del ZIKV. Three-week-old A129 mice (n=5) were immunized with 10 IFU WT or 10-del virus via the S.C. route. Viremia were quantified by immunostaining focus assay from day 4 to 7. L.O.D., limit of detection. FIG. **8**B shows the pre-challenge neutralization antibody titers. Three-week-old A129 mice (n=5) were immunized with 10 IFU 10-del ZIKV and PBS via the S.C. route. On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers. On the same day, the mice were challenged with 1×10^6 IFU of ZIKV (Puerto Rico strain PRVABC59) via the I.P. route. FIG. **8**B shows the viremia after challenge with epidemic ZIKV (Puerto Rico strain PRVABC59). On day 2 post-

challenge, viremias were quantified using an immunostaining focus assay. L.O.D.: limit of detection.

[0040] FIG. **9**A-**9**D show the T cell responses after primary infection with ZIKV WT or 10-del mutant. A129 mice were infected with 1×10^4 IFU WT and 10-del viruses. On day 28 post-infection, mouse spleens were harvested. Splenocytes were counted, cultured ex vivo with WT ZIKV for 24 h, and stained for markers (IFN-γ, CD3, and CD4 or CD8). The T cells were gated based on staining for these markers. FIG. **9**A shows percentages of $CD4^+IFN\text{-}\gamma^+$ cells and $CD8^+IFN\text{-}\gamma^+$ cells. FIG. **9**B shows the average total number of T cell subsets per spleen. Supernatants from the ex vivo culture were harvested on day 2 after WT ZIKV re-stimulation, and measured for IFN-γ and IL-2 production. FIG. **9**C shows IFN-γ production. FIG. **9**D shows IL-2 production. Data are presented as means±SEM, n=2-4 per group. *P<0.05 or **P<0.01 difference between the virus- and mock-infected mice.

[0041] FIG. **10**A-**10**C show the safety evaluation of 10-del virus. FIG. **10**A shows the viral loads in organs of infected A129 mice. Three-week-old A129 mice were immunized with 1×10^4 IFU of WT and 10-del viruses. Organs from infected mice were collected and homogenized on day 6 and 10 post-infection. The amounts of viruses were quantified on Vero cells using an immunostaining focus assay. The mean results from three animals are presented. Bars denote standard errors. "*" denotes no detectable virus. From left to right on each day, the bars correspond to: heart, lung, liver, spleen, kidney, muscle, brain, testis, and eye. FIG. **10**B shows a comparison of neurovirulence of WT and 10-del viruses in CD1 newborn mouse. Groups of one-day-old CD1 mice (n=7-10) were injected via the I.C. route with 10 to 1×10^4 IFU of WT or 10-del virus. All 10-del virus curves show 100% survival, while WT curves show less than 100% survival. FIG. **10**C shows the results of a mosquito infectivity assay. *Aedes aegypti* were fed with WT or 10-del virus on artificial blood-meals. On day 7 post-feeding, individual engorged, incubated mosquitoes were homogenized and infection was assayed by immunostaining of viral protein expression on inoculated Vero cells (see Methods for details). The number of infected mosquitos and total number of engorged mosquitoes are indicated.

[0042] FIG. **11**A-**11**C shows the comparison of viremia and efficacy of P0 and P5 10-del viruses. FIG. **11**A shows the viremia after immunization with 100 IFU of P0 or P5 10-del ZIKV. Three-week-old A129 mice (n=5) were immunized with 100 IFU P0 or P5 10-del virus via the S.C. route. Viremia was quantified by immunostaining focus assay from day 4 to 6. L.O.D., limit of detection. FIG. **11**B shows pre-challenge neutralization antibody titers. On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers. FIG. **11**C shows viremia after challenge with wild-type ZIKV. On day 28 post-immunization, the mice were challenged with 1×10^6 IFU of an epidemic strain of ZIKV (Puerto Rico strain PRVABC59) via the I.P. route. On day 2 post-challenge, viremias were quantified using an immunostaining focus assay.

[0043] FIG. **12**A-**12**B show a sperm count analysis of A129 mice infected with WT or 10-del mutant virus. Male A129 mice were infected with 1×10^4 IFU of WT and 10-del viruses (n=4 per group). On day 16 p.i., epididymis was harvested for sperm count analysis. FIG. **12**A shows total sperm counts. FIG. **12**B shows motile sperm counts. One-way ANOVA test was performed to indicate statistical significance among different infection groups. n.s., not significant; ***very significant (p value <0.001); ****extremely significant (p value <0.0001).

[0044] FIG. **13**A-G shows that ZIKV-3'UTR-Δ10-LAV protects pregnant C57BL/6 mice and their developing fetuses. FIG. **13**A shows the scheme of immunization of wild-type (WT) C57BL/6 female mice with 10^5 FFU of ZIKV-3'UTR-Δ10-LAV (Δ10; n=12) or PBS sham (n=16). FIG. **13**B shows experiments wherein serum was collected at day 28 post-immunization and analyzed for neutralizing activity using an mCherry infectious ZIKV. Representative neutralization curves are shown. Error bars denote the standard deviation (SD) of duplicate technical replicates. FIG. **13**C shows NT_{50} values of neutralizing antibodies were measured for individual animals. The dashed lines indicate the limit of detection (L.O.D.) of the assay. FIG. **13**D-G shows that at day 35 post-immunization, vaccinated female mice were mated with WT C57BL/6 males. A subset of the female mice developed vaginal plugs. Pregnant mice (n=8 pooled from two independent experiments) were administered 2 mg of anti-Ifnarl blocking antibody on E5, and one day later (E6), challenged with 10^5 FFU of a pathogenic, mouse adapted ZIKV Dakar 41519 strain. On E13, animals were euthanized; maternal spleen (FIG. **13**D), maternal brain (FIG. **13**E), placenta (FIG. **13**F), and fetal heads (FIG. **13**G) were harvested and quantified for viral RNA levels. Median viral RNA levels are indicated for each group. Asterisks indicate significant differences (Mann-Whitney test: ****, P value <0.0001). All negative samples are plotted at the half value of L.O.D. The results in the Figure are pooled from two independent experiments.

[0045] FIG. **14**A-I show that ZIKV-3'-UTR-Δ10-LAV protects young A129 male mice against testis infection and injury. FIG. **13**A contains the scheme of immunization of 3-week-old A129 male mice with 10^4 FFU of ZIKV-3'-UTR-Δ10-LAV (Δ10; n=6) or PBS sham (n=4 or 6). At day 28 post-immunization, mice were measured for neutralization antibody titers. On the same day, mice from one sham group and mice from Δ10-immunized group were challenged with 10^6 FFU of ZIKV-PRVABC59, and viremia was measured at day 2 post-challenge (day 30 post-immunization). At day 49 post-immunization, mice were analyzed for sperm counts and viral load in the testis. FIG. **14**A-B shows viremia after immunization with Δ0 vaccine candidate. FIG. **14**C contains NT50 values of antibody neutralization at day 28 post-immunization were measured for individual animals in each group. The dashed lines indicate the limit of detection (L.O.D.) of the assay. FIG. **14**D shows viremia at day 2 post-challenge (day 30 post-immunization) with ZIKV PRVABC59. FIG. **14**E shows viral load in the testis at day 21 post-challenge (day 49 post-immunization). FIG. **14**F-G show total (F) and motile (G) sperm counts at day 21 post-challenge. (H-I) Testis weight (H) and representative images of testis (i) from animals from sham, sham with challenge, and Δ10-immunized and challenged groups at day 21 post-challenge. Scale bar, 1 mm. Asterisks indicate significant differences (One-way ANOVA: ****, P value <0.0001; ***, P value <0.001). Non-significant (n.s.), P value >0.5. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0046] FIG. **15**A-D shows that ZIKV-3'UTR-Δ10-LAV and ZIKV-3'UTR-Δ20-LAV protect rhesus macaques (RM) from ZIKV infection. FIG. **15**A shows the scheme of immunization of RM with 10^3 FFU of WT ZIKV strain FSS13025

(n=4), ZIKV-3'UTR-Δ10-LAV (Δ10; n=4), ZIKV-3'UTR-Δ20-LAV (Δ20; n=3), or PBS sham (n=2) via the subcutaneous route. FIG. **15**B shows viremia measured at day 2, 3, 4, 5, 7, and 10 post-immunization by qRT-PCR. Each colored line represents data from different animals in each group. The dashed line indicates the limit of detection (L.O.D.) of the assay. FIG. **15**C shows pre- and post-challenge antibody neutralization titers. On various days post-immunization, sera were measured for neutralizing titers using an mCherry ZIKV infection assay. Red arrows indicate challenge with 10^3 FFU of epidemic ZIKV strain PRVABC59 via the subcutaneous route at day 56 post-immunization. The number of animals whose antibody neutralization titers increased by ≥4-fold after challenge is indicated by symbol "↑" for each experimental group. FIG. **15**D shows post-challenge viremia. Viremia was measured by qRT-PCR at day 2, 3, 4, 5, 7, and 10 post-challenge. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0047] FIG. **16**A-H shows a safety evaluation of ZIKV-3'-UTR-Δ20-LAV (Δ20) vaccine candidate. FIG. **16**A shows viral loads in organs of infected A129 mice. Three-week-old A129 mice (n=7) were subcutaneously immunized with 10^3 FFU of WT ZIKV FSS13025 (left panel) and its derivative Δ20 vaccine candidate (right panel). Organs from infected mice were collected and homogenized at day 6 and 10 post-infection. The amounts of viruses were quantified on Vero cells using a focus forming assay. The mean results from seven animals are presented. Bars denote standard errors. The dashed lines indicate the limit of detection (L.O.D.) of the assay. FIG. **16**D-F shows the effect of Δ20 vaccination on the testis. Three-week-old A129 mice (n=5) were subcutaneously infected with 1×10^3 FFU of WT ZIKV FSS13025 or Δ20 vaccine candidate. At day 28 post-infection, animals from each group were analyzed for testis weight (FIG. **16**B), testis size (FIG. **16**C), total sperm counts (FIG. **16**D), motile sperm counts (FIG. **16**E), and viral RNA load (FIG. **16**F). Scale bar, 1 mm. (FIG. **16**G) Comparison of neurovirulence of WT ZIKV FSS13025 and Δ20 vaccine candidate in outbred CD-1 mice. One-day-old CD-1 mice (n=7-8 per group) were injected intracranially with 10 to 10^4 FFU of WT ZIKV or 10^3 to 10^4 FFU of Δ20 vaccine candidate. Survival mice and total infected animals are indicated. (FIG. **16**H) Analysis of vector competency. *Aedes aegypti* were fed on artificial blood-meals spiked with 10^6 FFU/ml of WT ZIKV FSS13025 or Δ20 vaccine virus. At day 7 post-feeding, individual engorged mosquitoes were assayed for infection by immunostaining of viral protein expression on inoculated Vero cells. The number of infected mosquitos and total number of engorged mosquitoes are indicated. Asterisks indicate significant differences (One-way ANOVA: ***, P value <0.001; **, P value <0.01; *, P value <0.05). Non-significant (n.s.) with P value >0.5. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0048] FIG. **17**A-C shows the infectious ZIKV burden in placentas and fetal heads from sham or ZIKV-3'UTR-Δ10-LAV-immunized dams. In the pregnancy protection experiment (see details in FIG. **13**), at day 7 post-challenge (equivalent to E13), placenta (FIG. **17**A) and fetal heads (FIG. **17**B) were collected from PBS sham and ZIKV-3'UTR-Δ10-LAV-immunized dams, and quantified for infectious ZIKV using a focus forming assay. Dashed lines indicate limit of detection (L.O.D.) of the assays. Results are pooled from two independent biological experiments, and each symbol represents data from an individual placenta (n=23) or fetus (n=30). (FIG. **17**C) Correlation of E13 placenta viral burden with antibody neutralizing NT_{50} values of ZIKV-3'UTR-Δ10-LAV. P and R^2 values reflect Pearson correlation tests. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0049] FIG. **18** A-I contains experiments which show that ZIKV-3'UTR-Δ10-LAV protects adult A129 male mice against testis infection and injury. (A) Scheme of immunization of 15-week-old A129 male mice with 1×10^4 FFU of ZIKV-3'UTR-Δ10-LAV (Δ10; n=5) or PBS sham (n=5). At day 28 post-immunization, mice were measured for neutralizing antibody titers. On the same day, the mice were challenged with 10^6 FFU of ZIKV-PRVABC59. Peak viremia was measured at day 2 post-challenge (day 30 post-immunization). At day 49 post-immunization, mice were euthanized and measured for total and motile sperm counts and viral loads in the testis. FIG. **18**B shows viremia after ZIKV-3'UTR-Δ10-LAV immunization. FIG. **18**C shows NT_{50} values of antibody neutralization at day 28 post-immunization. Antibody neutralizing titers were measured for individual animals in each group by an mCherry ZIKV. The dashed lines indicate the limit of detection (L.O.D.) of the assay. FIG. **18**D shows day 2 post-challenge (day 30 post-immunization) viremia. At day 21 post-challenge, animals from each group were analyzed for testis viral load FIG. **18**E shows testis viral load, FIG. **18**F shows total sperm counts, FIG. **18**G shows motile sperm counts, FIG. **18**H shows testis weight, and FIG. **18**I shows testis size. Representative images of testis are presented in (i). Scale bar, 1 mm. Asterisks indicate significant differences (One-way ANOVA: *, P value <0.05; **, P value <0.01; ****, P value <0.0001). Non-significant (n.s.), P value >0.5. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0050] FIG. **19**A-B shows infectious virus in serum of challenged rhesus macaque. Infectious virus in RM serum (viremia) was collected at days 2, 3, 4, 5, 7, and 10 post-immunization (FIG. **19**A) or post-challenge (FIG. **19**B) was quantified by a focus forming assay. (See detailed experimental scheme in FIG. **15**A-D). Dashed lines indicate limit of detection (L.O.D.) of the assays. All negative samples are plotted at the half value of L.O.D.

[0051] FIG. **20**A-I shows that ZIKV-3'-UTR-Δ20-LAV protects young A129 male mice against testis infection and injury. FIG. **20**A shows the scheme of immunization of 3-week-old A129 male mice with 10^3 FFU of ZIKV-3'-UTR-Δ20-LAV (Δ20; n=6) or PBS sham (n=4 or 6). FIG. **20**B shows viremia post immunization. At day 28 post-immunization, immunized mice were measured for neutralization antibody titers. At the same day, mice from one sham group and mice from Δ20-immunized group were challenged with 10^6 FFU of ZIKV-PRVABC59. FIG. **20**D shows viremia measured at day 2 post-challenge (day 30 post-immunization). FIG. **20**E&F show that at day 49 post-immunization, mice were analyzed for sperm counts and viral loads in testis. FIG. **20**C shows NT_{50} values of antibody neutralization at day 28 post-immunization were measured for individual animals in each group. The dashed lines indicate the limit of detection (L.O.D.) of the assay. FIG. **20**D shows day 2 post-challenge (day 30 post-immunization) viremia. FIG. **20**E & F respectively show total (E) and motile (F) sperm

counts at day 21 post-challenge (equivalent to day 49 post-immunization). FIG. **20**G shows testis weight from animals from sham, sham with challenge, and Δ20-immunized and challenged groups at day 21 post-challenge. FIG. **20**H shows viral load in testis at day 21 post-challenge. FIG. **20**I contains representative images of testis harvested at day 21 post-challenge. Scale bar, 1 mm. Asterisks indicate significant differences (One-way ANOVA: ****, P value <0.0001). Non-significant (n.s.) with P value >0.5. All negative samples are plotted at the half value of L.O.D. Error bars represent standard deviations.

[0052] FIG. **21** contains a summary of experiments which evaluated the stability of ZIKV-3'UTR-Δ20-LAV in cell culture. P0 viruses (derived from the culture fluids of RNA-transfected cells) were continuously cultured on Vero cells for five rounds (5 days for each round of culture), resulting in P5 viruses. The complete genomes of P5 mutant viruses were sequenced. All P5 viruses retained the 20-nucleotide deletion in the 3'UTR. In addition, several adaptive mutations are recovered; these mutations are presented by their amino acid positions of indicated genes based on ZIKV FSS13025 strain (GenBank number KU955593.1). Results from three independent passages are presented.

[0053] FIG. **22** depicts the results of experiments wherein 5 micrograms of a Zika DNA plasmid according to the invention was transfected into Vero cells through electroporation. Culture fluids were collected from day 1 to 5. Infectious viral titers were measured by plaque assay on Vero cells.

[0054] FIG. **23** shows the yield of ZIKV DNA vaccine candidates on Vero cells. Five micrograms of indicated DNA plasmid was transfected into Vero cells through electroporation. Culture fluids were collected from day 1 to 5. Infectious viral titers were measured by plaque assay on Vero cells.

DETAILED DESCRIPTION OF THE INVENTION

[0055] The present invention in general relates to the construction and characterization of a novel live attenuated Zika virus (ZIKV) strain having one or more deletions in the 3' untranslated region (3'UTR). These ZIKV deletion mutants may have reduced RNA production and increased susceptibility to interferon-β inhibition, and thus can be utilized as effective live attenuated vaccines against ZIKV. Particularly we show herein that live-attenuated ZIKV vaccine candidates containing deletions in the 3' untranslated region of the ZIKV genome (ZIKV-3'UTR-LAV) prevent viral transmission during pregnancy and testis damage in mice, as well as inhibiting infection in non-human primates. We also demonstrate a desirable safety profile of the vaccine candidates. Our results suggest that ZIKV-3'UTR-LAV potentially may be used to vaccinate humans against Zika virus infection.

[0056] Moreover, as evidenced by the results disclosed herein mutated live attenuated Zika virus strains according to the invention and compositions containing same may be used in treating or providing immunoprotection against infections elicited by ZIKV, including congenital ZIKV syndrome, microcephaly, and Guillan-Barré syndrome (GBS).

[0057] The present invention provides a vaccine which may be used to prevent viremia in pregnant women and travelers to epidemic/endemic regions to avert congenital ZIKV syndrome and which may also be useful to suppress epidemic transmission. The ZIKV strain of the invention is a live-attenuated vaccine candidate that contains a deletion or "Δ" in the 3' untranslated region of ZIKV genome, preferably a 10-nucleotide deletion (10-del ZIKV) or a 20-nucleotide deletion (20-del ZIKV) and more preferably comprising or consisting of the Zika strains having the sequences in Appendix A modified as set forth in Appendix B. The 10-del ZIKV is highly attenuated, immunogenic, and protective in the A129 mouse model. A single dose of 10 IFU of 10-del ZIKV elicited a high level of neutralizing antibodies and completely prevented viremia after challenge. Besides the antibody response, the immunized mice also developed a robust T cell response. Intracranial inoculation of one-day-old CD1 mice with 1×10^4 IFU of 10-del ZIKV caused no detectable disease, whereas infections with 10 IFU of wild-type ZIKV were lethal. Mechanistically, the 10-del ZIKV attenuated its virulence through decreased viral RNA synthesis and increased sensitivity to type-I interferon inhibition. The attenuated 10-del ZIKV was incompetent in infecting mosquitoes, representing an additional safety feature for use in non-endemic regions. Collectively, the safety and efficacy results warrant further development of this promising live-attenuated ZIKV vaccine candidate.

[0058] The live attenuated ZIKV strains of the invention may further comprise additional mutations to the ZIKV genome. A mutation can be, but is not limited to, a deletion of non-coding or coding nucleotides, a deletion of one or more amino acids, an addition of one or more amino acids, a substitution (conserved or non-conserved) of one or more amino acids or a combination thereof ZIKV can be mutated, e.g., using deletions to the 3'UTR, such that the infectivity of ZIKV is reduced. In certain embodiments, the infectivity of ZIKV is reduced by a factor of at least 5, 10, 50, 100, 500, 10, 5×10^3, 10^4, 5×10^4, 10^5, 5×10^5, or at least 10^6.

[0059] Additionally, ZIKV can be mutated, e.g., having deletions to the 3'UTR and/or using point mutations, such that the rate of replication of the recombinant virus is reduced or increased. The rate of replication can be determined by any standard technique known to the skilled artisan. The rate of replication is represented by the growth rate of the virus and can be determined by plotting the viral titer over the time post infection. The viral titer can be measured by any technique known to the skilled artisan. In certain embodiments, a suspension containing the virus is incubated with cells that are susceptible to infection by the virus including, but not limited to, Vero cells, LLC-MK-2 cells, Hep-2 cells, LF 1043 (HEL) cells, MRC-5 cells, WI-38 cells, tMK cells, 293 T cells, QT 6 cells, QT 35 cells, or chicken embryo fibroblasts (CEF). Subsequent to the incubation of the virus with the cells, the number of infected cells is determined. In certain specific embodiments, the virus comprises a reporter gene. Thus, the number of cells expressing the reporter gene is representative of the number of infected cells. In a specific embodiment, the virus comprises a heterologous nucleotide sequence encoding mCherry, and the number of cells expressing mCherry, i.e., the number of cells infected with the virus, is determined using FACS.

[0060] The assays described herein may be used to assay viral titre over time to determine the growth characteristics of the virus. In a specific embodiment, the viral titre is determined by obtaining a sample from the infected cells or

the infected subject, preparing a serial dilution of the sample and infecting a monolayer of cells that are susceptible to infection with the virus at a dilution of the virus that allows for the emergence of single plaques. The plaques can then be counted and the viral titre express as plaque forming units per milliliter of sample. In a specific embodiment of the invention, the growth rate of a virus of the invention in a subject is estimated by the titer of antibodies against the virus in the subject. Without being bound by theory, the antibody titer in the subject reflects not only the viral titer in the subject but also the antigenicity. If the antigenicity of the virus is constant, the increase of the antibody titer in the subject can be used to determine the growth curve of the virus in the subject. In a preferred embodiment, the growth rate of the virus in animals or humans is best tested by sampling biological fluids of a host at multiple time points post-infection and measuring viral titer.

[0061] The expression of heterologous gene sequence in a cell culture system or in a subject can be determined by any technique known to the skilled artisan. In certain embodiments, the expression of the heterologous gene is measured by quantifying the level of the transcript. The level of the transcript can be measured by Northern blot analysis or by RT-PCR using probes or primers, respectively that are specific for the transcript. The transcript can be distinguished from the genome of the virus because the virus is in the antisense orientation whereas the transcript is in the sense orientation. In certain embodiments, the expression of the heterologous gene is measured by quantifying the level of the protein product of the heterologous gene. The level of the protein can be measured by Western blot analysis using antibodies that are specific to the protein.

[0062] The invention provides a live attenuated ZIKV strain comprising a deletion of one or more nucleotides in the 3'UTR of the ZIKV genome. In some embodiments, the ZIKV strain of the invention may comprise a 1-nucleotide deletion, a 2-nucleotide deletion, a 3-nucleotide deletion, a 4-nucleotide deletion, a 5-nucleotide deletion, a 6-nucleotide deletion, a 7-nucleotide deletion, an 8-nucleotide deletion, a 9-nucleotide deletion, a 10-nucleotide deletion, an 11-nucleotide deletion, a 12-nucleotide deletion, a 13-nucleotide deletion, a 14-nucleotide deletion, a 15-nucleotide deletion, a 16-nucleotide deletion, a 17-nucleotide deletion, an 18-nucleotide deletion, a 19-nucleotide deletion, a 20-nucleotide deletion, 21-nucleotide deletion, a 22-nucleotide deletion, a 23-nucleotide deletion, a 24-nucleotide deletion, a 25-nucleotide deletion, a 26-nucleotide deletion, a 27-nucleotide deletion, a 28-nucleotide deletion, a 29-nucleotide deletion, a 30-nucleotide deletion, 31-nucleotide deletion, a 32-nucleotide deletion, a 33-nucleotide deletion, a 34-nucleotide deletion, a 35-nucleotide deletion, a 36-nucleotide deletion, a 37-nucleotide deletion, a 38-nucleotide deletion, a 39-nucleotide deletion, a 40-nucleotide deletion, a 41-nucleotide deletion, a 42-nucleotide deletion, a 43-nucleotide deletion, a 44-nucleotide deletion, a 45-nucleotide deletion, a 46-nucleotide deletion, a 47-nucleotide deletion, a 48-nucleotide deletion, a 49-nucleotide deletion, or a 50-nucleotide deletion in the 3'UTR of the ZIKV genome.

[0063] The live attenuated ZIKV strains of the present invention, nucleotide sequences encoding the same, vectors encoding the same, and cells comprising nucleotide sequences encoding said strains may be further modified, engineered, optimized, or appended in order to provide or select for various features. In addition to deletions within the 3'UTR, the attenuated virus may also contain other mutations including, but not limited to, replacing a gene of the human virus with the analogous gene of a virus of a different species, of a different subgroup, or of a different variant.

[0064] In some embodiments, other mutations may be introduced into the virus (e.g., missense mutations) can be introduced into the C, prM, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B, or NS5 proteins of the recombinant virus. Also, the mutations may include additions, substitutions, deletions, or combinations thereof. For example a deletion mutation in any of the C, prM, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B, or NS5 proteins may be introduced. In other embodiments, a missense mutation may be introduced which results in a cold-sensitive mutation or a heat-sensitive mutation. In some embodiments, major phosphorylation sites of viral protein may be removed.

[0065] In other embodiments, deletions are introduced into the genome of the recombinant virus. In more specific embodiments, a deletion can be introduced into the C, prM, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B, or NS5 proteins of the recombinant virus.

[0066] In certain embodiments, the intergenic region of the recombinant virus is altered. In one embodiment, the length of the intergenic region is altered. In another embodiment, the intergenic regions may be shuffled from 5' to 3' end of the viral genome. In other embodiments, the genome position of a gene or genes of the recombinant virus can be changed.

[0067] In certain embodiments, attenuation of the virus is further enhanced by replacing a gene of the wild type virus with a gene of a virus of a different species, of a different subgroup, or of a different variant.

[0068] The attenuated phenotypes of a recombinant virus of the invention can be tested by any method known to the artisan. A candidate virus can, for example, be tested for its ability to infect a host or for the rate of replication in a cell culture system. In certain embodiments, growth curves at different temperatures are used to test the attenuated phenotype of the virus. For example, an attenuated virus is able to grow at 35° C., but not at 39° C. or 40° C. In certain embodiments, different cell lines can be used to evaluate the attenuated phenotype of the virus. For example, an attenuated virus may only be able to grow in monkey cell lines but not the human cell lines, or the achievable virus titers in different cell lines are different for the attenuated virus. In certain embodiments, viral replication in the respiratory tract of a small animal model, including but not limited to, hamsters, cotton rats, mice and guinea pigs, is used to evaluate the attenuated phenotypes of the virus. In other embodiments, the immune response induced by the virus, including but not limited to, the antibody titers (e.g., assayed by plaque reduction neutralization assay or ELISA) is used to evaluate the attenuated phenotypes of the virus. In certain embodiments, the ability of the recombinant virus to elicit pathological symptoms in an animal model can be tested. A reduced ability of the virus to elicit pathological symptoms in an animal model system is indicative of its attenuated phenotype. In a specific embodiment, the candidate viruses are tested in a monkey model for nasal infection, indicated by mucous production.

[0069] Various assays can be used to test the safety of a vaccine. For example, sucrose gradients and neutralization

assays can be used to test the safety. A sucrose gradient assay can be used to determine whether a heterologous protein is inserted in a virion. If the heterologous protein is inserted in the virion, the virion should be tested for its ability to cause symptoms even if the parental strain does not cause symptoms. Without being bound by theory, if the heterologous protein is incorporated in the virion, the virus may have acquired new, possibly pathological, properties.

[0070] Attenuated virus produced according to the invention will be used to confer prophylactic or therapeutic protection in susceptible hosts against ZIKV infection, e.g., to treat or prevent ZIKV infection and/or to prevent congenital ZIKV syndrome or GBS. The attenuated ZIKV strain may be formulated using known techniques for formulating attenuated viral vaccines or immunogenic compositions of viral vaccines.

[0071] In one embodiment, the 3'UTR of the ZIKV strain of the invention comprises the nucleic acid sequence of the 3'UTR of the 10-del mutant ZIKV strain, SEQ ID NO: 2.

[0072] In one embodiment, the 3'UTR of the ZIKV strain of the invention comprises the nucleic acid sequence of the 3'UTR of the 20-del mutant ZIKV strain, SEQ ID NO: 3.

[0073] In one embodiment, the 3'UTR of the ZIKV strain of the invention comprises the nucleic acid sequence of the 3'UTR of the 30-del-a mutant ZIKV strain, SEQ ID NO: 4.

[0074] In one embodiment, the 3'UTR of the ZIKV strain of the invention comprises the nucleic acid sequence of the 3'UTR of the 30-del-b mutant ZIKV strain, SEQ ID NO: 5.

[0075] In some exemplary embodiments the ZIKV strain of the invention comprises or consists of the sequences set forth in Appendix A modified as set forth in Appendix B.

[0076] In some exemplary embodiments immunogenic compositions are provided containing a therapeutically or prophylactically effective amount of a ZIKV strain which comprises or consists of the sequences set forth in Appendix A modified as set forth in Appendix B.

[0077] In some exemplary embodiments individuals in need thereof are administered therapeutically or prophylactically effective amount of a ZIKV strain which comprises or consists of the sequences set forth in Appendix A modified as set forth in Appendix B.

Administration

[0078] The immunogenic compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired. In exemplary embodiments administration may be topical, parenteral, or enteral.

[0079] The pharmaceutical compositions of the invention are typically suitable for parenteral administration. As used herein, "parenteral administration" of a pharmaceutical composition includes any route of administration characterized by physical breaching of a tissue of a subject and administration of the pharmaceutical composition through the breach in the tissue, thus generally resulting in the direct administration into the blood stream, into muscle, or into an internal organ. Parenteral administration thus includes, but is not limited to, administration of a pharmaceutical composition by injection of the composition, by application of the composition through a surgical incision, by application of the composition through a tissue-penetrating non-surgical wound, and the like. In particular, parenteral administration is contemplated to include, but is not limited to, subcutaneous, intraperitoneal, intramuscular, intrasternal, intravenous, intraarterial, intrathecal, intraventricular, intraurethral, intracranial, intrasynovial injection or infusions; and kidney dialytic infusion techniques.

[0080] Formulations of a pharmaceutical composition suitable for parenteral administration typically generally comprise the active ingredient combined with a pharmaceutically acceptable carrier, such as sterile water or sterile isotonic saline. Such formulations may be prepared, packaged, or sold in a form suitable for bolus administration or for continuous administration. Injectable formulations may be prepared, packaged, or sold in unit dosage form, such as in ampoules or in multi-dose containers containing a preservative. Formulations for parenteral administration include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and the like. Such formulations may further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents. In one embodiment of a formulation for parenteral administration, the active ingredient is provided in dry (i.e. powder or granular) form for reconstitution with a suitable vehicle (e.g. sterile pyrogen-free water) prior to parenteral administration of the reconstituted composition. Parenteral formulations also include aqueous solutions which may contain excipients such as salts, carbohydrates and buffering agents (preferably to a pH of from 3 to 9), but, for some applications, they may be more suitably formulated as a sterile non-aqueous solution or as a dried form to be used in conjunction with a suitable vehicle such as sterile, pyrogen-free water. Exemplary parenteral administration forms include solutions or suspensions in sterile aqueous solutions, for example, aqueous propylene glycol or dextrose solutions. Such dosage forms can be suitably buffered, if desired. Other parentally-administrable formulations which are useful include those which comprise the active ingredient in microcrystalline form, or in a liposomal preparation. Formulations for parenteral administration may be formulated to be immediate and/or modified release. Modified release formulations include delayed-, sustained-, pulsed-, controlled-, targeted and programmed release.

[0081] The terms "oral", "enteral", "enterally", "orally", "non-parenteral", "non-parenterally", and the like, refer to administration of a compound or composition to an individual by a route or mode along the alimentary canal. Examples of "oral" routes of administration of a vaccine composition include, without limitation, swallowing liquid or solid forms of a vaccine composition from the mouth, administration of a vaccine composition through a nasojejunal or gastrostomy tube, intraduodenal administration of a vaccine composition, and rectal administration, e.g., using suppositories for the lower intestinal tract of the alimentary canal.

[0082] Preferably, the formulated virus containing composition is suitable for intranasal, injection, topical or oral administration, for example as a dried stabilized powder for reconstitution in a suitable buffer prior to administration or in an aerosol composition. In a preferred embodiment, the composition is intranasally administered.

[0083] Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids, semi-solids, monophasic compositions, multiphasic compositions (e.g., oil-in-water, water-in-oil), foams microsponges, liposomes, nanoemulsions, aerosol

foams, polymers, fullerenes, and powders (see, e.g., Reference 35, Taglietti et al. (2008) Skin Ther. Lett. 13:6-8). Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable.

[0084] Compositions and formulations for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable.

[0085] Compositions and formulations for parenteral, intrathecal, or intraventricular administration may include sterile aqueous solutions that may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carder compounds and other pharmaceutically acceptable carriers or excipients.

[0086] Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids.

[0087] The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[0088] The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, liquid syrups, soft gels, suppositories, aerosols, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

[0089] In one embodiment of the present invention the pharmaceutical compositions may be formulated and used as foams. Pharmaceutical foams include formulations such as, but not limited to, emulsions, microemulsions, creams, jellies and liposomes. While basically similar in nature these formulations vary in the components and the consistency of the final product. Agents that enhance uptake of oligonucleotides at the cellular level may also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin, cationic glycerol derivatives, and polycationic molecules, such as polylysine, also enhance the cellular uptake of oligonucleotides.

[0090] The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions. Thus, for example, the compositions may contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present invention. The formulations can be sterilized and, if desired, mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

[0091] The compositions of the present invention may include excipients known in the art. Examples of excipients used for vaccine formulation such as adjuvants, stabilizers, preservatives, and trace products derived from vaccine manufacturing processes include but are not limited to: Aluminum Hydroxide, Amino Acids, Benzethonium Chloride, Formaldehyde or Formalin, Inorganic Salts and Sugars, Vitamins, Asparagine, Citric Acid, Lactose, Glycerin, Iron Ammonium Citrate, Magnesium Sulfate, Potassium Phosphate, Aluminum Phosphate, Ammonium Sulfate, Casamino Acid, Dimethyl-betacyclodextrin, 2-Phenoxyethanol, Bovine Extract, Polysorbate 80, Aluminum Potassium Sulfate, Gelatin, Sodium Phosphate, Thimerosal, Sucrose, Bovine Protein, Lactalbumin Hydrolysate, Formaldehyde or Formalin, Monkey Kidney Tissue, Neomycin, Polymyxin B, Yeast Protein, Aluminum Hydroxyphosphate Sulfate, Dextrose, Mineral Salts, Sodium Borate, Soy Peptone, MRC-5 Cellular Protein, Neomycin Sulfate, Phosphate Buffers, Polysorbate, Bovine Albumin or Serum, DNA, Potassium Aluminum Sulfate, Amorphous Aluminum Hydroxyphosphate Sulfate, Carbohydrates, L-histidine, Beta-Propiolactone, Calcium Chloride, Neomycin, Ovalbumin, Potassium Chloride, Potassium Phosphate, Sodium Phosphate, Sodium Taurodeoxychoalate, Egg Protein, Gentamicin, Hydrocortisone, Octoxynol-10,.α-Tocopheryl Hydrogen Succinate, Sodium Deoxycholate, Sodium Phosphate, Beta-Propiolactone, Polyoxyethylene 910, Nonyl Phenol (Triton N-101, Qctoxynol 9), Octoxinol-9 (Triton X-100), Chick Kidney Cells, Egg Protein, Gentamicin Sulfate, Monosodium Glutamate, Sucrose Phosphate Glutamate Buffer Calf Serum Protein, Streptomycin, Mouse Serum Protein, Chick Embryo Fibroblasts, Human Albumin, Sorbitol, Sodium Phosphate Dibasic, Sodium Bicarbonate, Sorbitol, Sucrose, Potassium Phosphate Monobasic, Potassium Chloride, Potassium Phosphate Dibasic, Phenol, Phenol Red (Phenolsulfonphthalein), Amphotericin B, Chicken Protein, Chlortetracycline, Ethylenediamine-Tetraacetic Acid Sodium (EDTA), Potassium Glutamate, Cell Culture Media, Sodium Citrate, Sodium Phosphate Monobasic Monohydrate, Sodium Hydroxide, Calcium Carbonate, D-glucose, Dextran, Ferric (III) Nitrate, L-cystine, L-tyrosine, Magnesium Sulfate, Sodium Hydrogenocarbonate, Sodium Pyruvate, Xanthan, Peptone, Disodium Phosphate, Monosodium Phosphate, Polydimethylsilozone, Hexadecyltrimethylammonium Bromide Ascorbic Acid, Casein, Galactose, Magnesium Stearate, Mannitol, Hydrolyzed Porcine Gelatin, Freund's emulsified oil adjuvants (complete and incomplete), Arlacel A, Mineral oil, Emulsified peanut oil adjuvant (adjuvant 65), Corynebacterium granulosum-derived P40 component, Lipopolysaccharide, Mycobacterium and its components, Cholera toxin, Liposomes, Immunostimulating complexes (ISCOMs), Squalene, and Sodium Chloride.

[0092] The vaccine or immunogenic composition may be used in the vaccination of a mammalian host, particularly a

human, nonhuman primate, ape, monkey, horse, cow, carabao, goat, duck, bat, or other suitable non-human host. A dosage may comprise at least 10 IFU, 10^1 IFU, 10^2 IFU, 10^3 IFU, 10^4 IFU, 5×10^4 IFU, 10^5 IFU, 5×10^5 IFU, 10^6 IFU, 5×10^6 IFU, 10^7 IFU, 5×10^7 IFU, 10^8 IFU, or 5×10^8 IFU of said live attenuated ZIKV strain. In some instances the subject may be immunocompromised or may have another condition, e.g., may be pregnant.

Definitions

[0093] The "3'UTR" or "3' untranslated region" or "three prime untranslated region" of the ZIKV genome corresponds to the section of RNA that immediately follows the translation termination codon of the genomic polyprotein.

[0094] An "adjuvant" refers to a substance that enhances an immune response, e.g., an antibody or cell-mediated immune response against a specific agent, e.g., an antigen, or an infectious agent.

[0095] An "attenuated" or "live attenuated" virus strain refers a mutated or modified or recombinant virus having reduced or no virulence or propensity to cause a disease or infection normally associated with the "wild-type" or "unmodified" (or in this case "non-mutated") virus.

[0096] An "attenuated" or "live attenuated" ZIKV strain, in particular, refers to a ZIKV strain that has been modified to have reduced or no virulence or propensity to cause a disease or infection which is normally associated with a "wild-type" or "unmodified" or "non-mutated" virus, in particular congenital ZIKV syndrome or GBS. More particularly, this includes "attenuated" ZIKV strains that are "modified" or "altered" or "mutated" to have one or more deletions in the 3'UTR of the ZIKV genome, e.g., a 10-nucleotide, 20-nucleotide, or 30-nucleotide deletion in the 3'UTR, preferably a 10-nucleotide deletion. The deletions may not disrupt RNA translation. The deletions may slow RNA production and increase interferon-β susceptibility. Such live attenuated ZIKV strain elicits immunoprotection against the virus, i.e., maintains an important immunogenic epitope.

[0097] "Heterologous" means derived from a genetically distinct entity from the rest of the entity to which it is being compared. For example, a polynucleotide may be placed by genetic engineering techniques into a plasmid or vector derived from a different source, and is a heterologous polynucleotide. A promoter removed from its native coding sequence and operatively linked to a coding sequence other than the native sequence is a heterologous promoter. The polynucleotides of the invention may comprise additional sequences, such as additional encoding sequences within the same transcription unit, controlling elements such as promoters, ribosome binding sites, 5'UTR, 3'UTR, transcription terminators, polyadenylation sites, additional transcription units under control of the same or a different promoter, sequences that permit cloning, expression, homologous recombination, and transformation of a host cell, and any such construct as may be desirable to provide embodiments of this invention.

[0098] An "immunogenic composition" herein refers to a composition containing a live attenuated ZIKV strain according to the invention which elicits an immune response in a susceptible host, e.g., an antibody, Th1 or cellular (e.g., T cell-mediated) immune response.

[0099] An "isolated" biological component (such as an isolated bacterium or nucleic acid) refers to a component that has been substantially separated or purified away from its environment or other biological components in the cell of the organism in which the component naturally occurs, for instance, other chromosomal and extra-chromosomal DNA and RNA, proteins, and organelles. Nucleic acids and proteins that have been "isolated" include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids and proteins prepared by recombinant technology as well as chemical synthesis.

[0100] The term "nucleic acid" and "polynucleotide" refer to RNA or DNA that is linear or branched, single or double stranded, or a hybrid thereof. The term also encompasses RNA/DNA hybrids. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars and linking groups such as fluororibose and thiolate, and nucleotide branches. The sequence of nucleotides may be further modified after polymerization, such as by conjugation, with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides or solid support. The polynucleotides can be obtained by chemical synthesis or derived from a microorganism. The term "gene" is used broadly to refer to any segment of polynucleotide associated with a biological function. Thus, genes include introns and exons as in genomic sequence, or just the coding sequences as in cDNAs and/or the regulatory sequences required for their expression. For example, gene also refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences.

[0101] A "pharmaceutically acceptable carrier" or "excipient" refers to compounds or materials conventionally used in immunogenic or vaccine compositions during formulation and/or to permit storage.

[0102] "Prophylactically effective amount" of a live attenuated ZIKV strain according to the invention refers to an amount sufficient to prevent or reduce the incidence of infection in a susceptible host.

[0103] The term "recombinant" means a polynucleotide with semisynthetic, or synthetic origin which either does not occur in nature or is linked to another polynucleotide in an arrangement not found in nature.

[0104] A "susceptible host" herein refers to a host or animal that may be infected by ZIKV. Such hosts include humans or animals, e.g., a human, nonhuman primate, ape, monkey, horse, cow, carabao, goat, duck, bat, or other suitable non-human host.

[0105] "Therapeutically effective amount" of a live attenuated ZIKV strain according to the invention refers to an amount sufficient to treat ZIKV infection or a disease associated therewith in a susceptible host.

[0106] A "vaccine" composition herein refers to a composition containing a live attenuated ZIKV strain according to the invention which elicits a therapeutic or prophylactic immune response against ZIKV.

[0107] "ZIKV infection" or "infection elicted by ZIKV" herein refers to the infection of a susceptible host with ZIKV and diseases associated therewith, including congenital ZIKV syndrome and Guillan-Barré syndrome (GBS).

[0108] The following examples are offered to illustrate, but not to limit, the claimed invention.

EXAMPLES

Example 1: Generating Live Attenuated ZIKV Strains with 3'UTR Deletions

[0109] Materials and Methods:

[0110] Viruses: The ZIKV Cambodian strain FSS13025 (GenBank number KU955593.1) was generated from an infectious cDNA clone pFLZIKV as described previously (Reference 10). All the cell lines are tested negative for mycoplasma.

[0111] Plasmid construction. Standard molecular biology procedures were performed for all plasmid constructions. Standard overlap PCR was performed to amplify the DNA fragment between unique restriction enzyme sites EcoRI and ClaI using corresponding primer pairs. The DNA fragment containing 3'UTR deletion mutations were individually introduced into the pFLZIKV and pZIKV Rep (replicon cDNA plasmid, Reference 11) through EcoRI and ClaI. All the constructs were verified by DNA sequencing. Primer sequences are available upon request. All restriction enzymes were purchased from New England BioLabs (Ipswitch, Mass.).

[0112] Results:

[0113] We chose to pursue a live-attenuated vaccine to capitalize on its advantages of single-dose immunization, a rapid and robust immune response, and long-lived protection. We attenuated wild-type (WT) ZIKV through deletion of a portion of the 3' untranslated region (3'UTR) of the viral genome, as has been successfully used to develop a DENY vaccine currently in a phase III clinical trial (Reference 9). Using an infectious cDNA clone of the ZIKV Cambodian strain FSS13025 (Reference 10) (which is closely related to strains now circulating in the Americas), we prepared a panel of recombinant viruses containing distinct 3'UTR deletions (FIG. **1**A). Mutants 10-del, 20-del, 30-del-a, and 30-del-b contained overlapping 10-to-30-nucleotide deletions, which were expected to change the local secondary structure of the viral 3'UTR (FIG. **2**).

Example 2: Replication and IFN-β Inhibition Analysis of ZIKV 3'UTR Deletion Mutants

[0114] Materials and Methods:

[0115] Cells and antibodies. Vero cells were purchased from the American Type Culture Collection (ATCC, Bethesda, Md.), and maintained in a high glucose Dulbecco modified Eagle medium (DMEM) (Invitrogen, Carlsbad, Calif.) supplemented with 10% fetal bovine serum (FBS) (HyClone Laboratories, Logan, Utah) and 1% penicillin/streptomycin (Invitrogen, Carlsbad, Calif.) at 37° C. with 5% CO_2. The following antibodies were used in this study: a mouse monoclonal antibody (mAb) 4G2 cross-reactive with flavivirus E protein (ATCC), ZIKV-specific HMAF (hyper-immune ascitic fluid), World Reference Center of Emerging Viruses and Arboviruses (WRCEVA) at the University of Texas Medical Branch], Anti-Mouse IgG (H+L) Antibody Horseradish Peroxidase-labeled (KPL, Gaithersburg, Md.), and goat anti-mouse IgG conjugated with Alexa Fluor 488 (Thermo Fisher Scientific).

[0116] RNA transcription and transfection. Full-genome ZIKV, mCherry ZIKV, and replicon RNAs were in vitro transcribed using a T7 mMessage mMachine kit (Ambion, Austin, Tex.) from cDNA plasmids pre-linearized by ClaI. The RNA was precipitated with lithium chloride, washed with 70% ethanol, re-suspended in RNase-free water, quantitated by spectrophotometry, and stored at −80° C. in aliquots. The RNA transcripts (10 μg) were electroporated into Vero cells following a protocol described previously (Reference 31).

[0117] Indirect immunofluorescence assays (IFA). Vero cells were electroporated with 10 μg of genomic WT or 3'UTR deletion RNA of ZIKV and grown in an 8-well Lab-Tek chamber slide (Thermo Fisher Scientific, Waltham, Mass.). On day 2 and 3 post-transfection, the cells were fixed in 100% methanol at −20° C. for 15 min. After 1 h incubation in a blocking buffer containing 1% FBS and 0.05% Tween-20 in PBS, the cells were treated with a mouse monoclonal antibody 4G2 for 1 h and washed three times with PBS (5 min for each wash). The cells were then incubated with Alexa Fluor® 488 goat anti-mouse IgG for 1 h in blocking buffer, after which the cells were washed three times with PBS. The cells were mounted in a mounting medium with DAPI (4',6-diamidino-2-phenylindole; Vector Laboratories, Inc.). Fluorescence images were observed under a fluorescence microscope equipped with a video documentation system (Olympus).

[0118] Immunostaining focus assay of mutant viruses. Equal amounts of RNAs (10 μg) transcribed from their corresponding infectious cDNA clones were electroporated into Vero cells. On day 4 or 5 post-transfection, culture fluids form the transfected cells were harvested and quantified for infectious viruses (defined as P0 virus) using an immunostaining focus assay on Vero cells.

[0119] Immunostaining focus assay and immunostaining. Viral samples were ten-fold serially diluted six times in DMEM. For each dilution, 100 μl sample was added to a 24-well plate containing Vero cells at about 90% confluency. The infected cells were incubated for 1 h and swirled every 15 min to ensure complete coverage of the monolayer for even infection. After 1 h incubation, 0.5 ml of methyl cellulose overlay containing 2% FBS 1% penicillin/streptomycin was added to each well. The plate was incubated at 37° C. for four days. Following the incubation, methyl cellulose overlay was removed and 0.5 ml methanol-acetone (1:1) solution was added into each well and incubated at room temperature for 15 min. Fixation solution was aspirated and plates were allowed to air dry, then washed three times with PBS and incubated in blocking buffer (PBS supplemented with 3% FBS), followed by 1 h incubation with ZIKV-specific HMAF. Plates were washed three times with PBS followed by an hour-long incubation with a secondary antibody conjugated to horseradish peroxidase (KPL, Gaithersburg, Md.). Detection proceeded with the addition of aminoethylcarbazole substrate (ENZO Life sciences, Farmingdale, Mass.) prepared according to the vendor's instructions.

[0120] Luciferase assay. The luciferase assay was performed as previously reported (Reference 11). Briefly, Vero cells transfected with WT or mutant ZIKV replicon RNAs (10 μg) were seeded in a 12-well plate. At various time points, the cells were washed once with phosphate-buffered

saline (PBS) and lysed using cell lysis buffer (Promega, Madison, Wis.). The cells were scraped from plates and stored at −80° C. The luciferase signals were measured by Cytation 5 (Biotek) according to the manufacturer's instructions.

[0121] Replication curves. Subconfluent Vero cells in 24-well plates (2×10^5 cells per well) were infected with WT or mutant P0 ZIKV at a multiplicity of infection (MOI) of 0.01 in triplicate wells. Virus stocks were diluted in DMEM containing 2% FBS and 1% penicillin/streptomycin. One hundred microliters of virus were added to each well of the 12-well plates. After 1 h attachment (5% CO_2 at 37° C.), the inocula were removed, monolayers were washed three times with PBS, and 1 ml DMEM medium containing 2% FBS and 1% penicillin/streptomycin was added to each well. Culture fluids were quantified for infectious viruses on days 1 to 5 using the immunostaining focus assay.

[0122] Replicon analysis of the 3'UTR deletions. A Renilla luciferase reporter replicon of ZIKV was engineered with various 3'UTR deletions. Equal amounts of replicon WT and mutant RNAs (10 μg) were electroporated into Vero cells. Luciferase signals were measured at several time points. A non-replicative replicon containing an NS5 polymerase-inactive GDD mutation was included as a negative control.

[0123] Interferon-β inhibition of WT and mutant ZIKVs. Vero cells were seeded in 96-well plate (1.5×10^4 cell per well) one day before interferon treatment and viral infection. The cells were infected at an MOI 0.05 in the presence of IFN-β (55, 167, 500, or 1,500 IU/ml). Viral infection and interferon treatment were initiated at the same time. At 48 h post-infection and interferon-β treatment, viral titers were quantified using the immunostaining focus assay on Vero cells.

[0124] Results:

[0125] Upon transfection into Vero cells, all mutant genomic RNAs generated viral E protein-expression cells (FIG. **3**) and infectious viruses (defined as P0 viruses). Compared with the WT, all mutants exhibited smaller infectious foci (FIG. **1**B), slower replication kinetics, and lower peak titers (FIG. **1**C). To examine the mutational effects on viral replication, we engineered the deletions into a luciferase ZIKV replicon (Reference 11). The replicon results showed that the 3'UTR deletions did not affect viral RNA translation (indicated by the luciferase signals at 2-6 h post-transfection), but decreased RNA synthesis (indicated by the luciferase activities at 24-48 h post-transfection; FIG. **1**D & **1**E); a similar observation was previously reported for West Nile virus, a closely related flavivirus (Reference 12). Since the 3'UTR of flavivirus may also modulate host innate immune response (References 13, 14), we compared the susceptibility of the WT and mutant viruses to interferon inhibition. All four mutant viruses were much more sensitive to interferon-β inhibition than the WT virus, among which mutant 10-del exhibited the greatest inhibition (FIG. **1**F). Collectively, these results indicate that 3'UTR deletions attenuate ZIKV replication through diminished viral RNA synthesis and increased vulnerability to type-I interferon inhibition.

Example 3: Stability of Mutant Viruses

[0126] Materials and Methods:

[0127] Stability of 3'UTR mutants, RNA extraction, and RT-PCR. To examine the stability of 3'UTR mutants, we passaged them on Vero cells for five rounds (5 days for each round of culture),. Briefly, 1.5×10^6 Vero cells were seeded into T-25 flask. The virus derived from RNA transfection, defined as P0 was used to infect the Vero cells. At 5 d p.i., culture fluid (100 μl) was transferred to a new T-25 flask containing Vero cells in 5 ml of culture medium. After five rounds of such passaging (P5), viral RNAs were extracted from the P5 culture fluids using QIAamp Viral RNA Kit (Qiagen). Viral RNAs were amplified by RT-PCR using SuperScript III one-step RT-PCR kits (Invitrogen). The P5 viruses were subjected to complete genome-length sequencing. Three independent passages were performed for each mutant virus.

[0128] Immunostaining focus assay. WT and P5 mutant viruses were analyzed using an immunostaining focus assay on Vero cells. For each mutant virus, three independent selections were performed on Vero cells.

[0129] Replication kinetics. Subconfluent Vero cells in 24-well plates (2×10^5 cells per well) were infected with WT and P5 mutant viruses at a multiplicity of infection (MOI) of 0.01 in triplicate wells. Virus stocks were diluted in DMEM containing 2% FBS and 1% penicillin/streptomycin. One hundred microliters of virus were added to each well of the 12-well plates. After 1 h attachment (5% CO_2 at 37° C.), the inocula were removed, monolayers were washed three times with PBS, and 1 ml DMEM medium containing 2% FBS and 1% penicillin/streptomycin was added to each well. Culture fluids were quantified for infectious viruses on days 1 to 5 using the immunostaining focus assay on Vero cells.

[0130] Results:

[0131] To test the stability of the mutant viruses, we passaged them five times on Vero cells (an approved cell line for vaccine production, see Reference 15). The passage 5 (P5) viruses developed larger infectious foci (FIG. **4**A) and faster replication kinetics than the corresponding P0 viruses on Vero cells (Compare FIG. **4**B with FIG. **1**C). Complete genome sequencing of P0 and P5 viruses showed that all mutants retained the original deletions, but the P5 viruses had accumulated additional mutations in the E and/or NS1 genes, which presumably were Vero cell-adaptive mutation (s) and/or compensatory mutation(s) to 3'UTR deletions (FIG. **4**C). In some embodiments, these mutations may be introduced into the infectious cDNA clone for vaccine production. Either way, the results indicated that the engineered deletions are stable when propagated on Vero cells, and further passaging of the mutant viruses on Vero cells to P20 did not change the engineered 3'UTR deletions.

Example 4: Characterization of 3'UTR Mutants in the A129 Mouse Model

[0132] Materials and Methods:

[0133] Vaccination and challenge of mice. Three-week old A129 mice (n=8) were immunized by the subcutaneous (S.C.) route with 1×10^4 IFU WT and mutant viruses. Mock-infected mice were given PBS by the same route. Mice were weighed and monitored daily for progression of disease. Mice were anesthetized and bled via the retro orbital sinus (R.O.) every two days. Viremias were quantified by an immunostaining focus assay from day 2 to 4 post-infection. On day 28 post-immunization, mice were anesthetized and bled to measure neutralization antibody titers using a mCherry ZIKV infection assay. The vaccinated mice were then challenged via the intraperitoneal (I.P.) route with 1×10^5 PFU parental virus (ZIKV strain FSS13025). On day 2 post-challenge, the mice were bled to measure viremia.

Blood was clarified post collection by centrifugation at 3,380×g for 5 min and immediately stored at −80° C. for storage. Viral titers of sera and inoculum were determined by an immunostaining focus assay on Vero cells, as described above. All animal testing was performed in accordance with UTMB policy as approved by the UTMB IACUC.

[0134] Construction of mCherry ZIKV. A DNA fragment encoding the first 25 amino acids of C gene, the mCherry gene, and the foot-and-mouth virus 2A protein was in-frame fused with the open-reading-frame of ZIKV genome. The expression of mCherry in transfected Vero cells was analyzed by a fluorescent microscopy at days 2-6 post-transfection. The mCherry ZIKV was used to estimate antibody neutralization titers of mouse sera.

[0135] Antibody neutralization assay. Neutralizing activity of mouse sera was assessed using a newly established mCherry ZIKV. The sera were 2-fold serially diluted starting at 1:100 in DMEM with 2% FBS and 1% penicillin/streptomycin. Serial dilution of mice sera was incubated with mCherry ZIKV at 37° C. for 2 h. Antibody-virus complexes were added to pre-seeded Vero cells in 96-well plates. After 48 h post-infection, cells were visualized by fluorescence microscopy using Cytation 5 Cell Imaging Multi-Mode Reader (Biotek) to quantify the mCherry fluorescence-positive cells. The percentage of fluorescence-positive cells in the non-treatment controls was set at 100%. The fluorescence-positive cells from serum-treated wells were normalized to those of non-treatment controls. A four-parameter sigmoidal (logistic) model in the software GraphPad Prism 7 was used to calculate the neutralization titers (NT_{50}).

[0136] Results:

[0137] We evaluated the immunogenicity and efficacy of the mutant viruses in an A129 (interferon α/β receptor-deficient) mouse model (Reference 16) (FIG. **5**A). After subcutaneous (S.C.) inoculation with 1×10^4 IFU of virus, mice infected with the WT virus had significantly more weight loss than those infected with mutant viruses; whereas the differences in mean weight loss among the four mutant virus-infected groups were not statistically significant (FIG. **5**B). About 50% of the mice succumbed to the WT virus infection, whereas no mortality was observed in the mutant virus-infected mice (FIG. **5**C). The WT virus produced significantly higher peak viremia than the mutant viruses, among which the 10-del virus had the lowest viremic profile (FIG. **5**D). The viremia for 10-del mutant dropped to 700 IFU, 350 IFU, and undetectable on days 5, 6, and 7 post-infection, respectively. Sequencing analysis confirmed that the engineered deletions were retained without other mutations in the mutant viruses recovered from the mouse sera. On day 28 post-infection, mouse sera were taken and quantified for pre-challenge neutralization titers using an mCherry ZIKV (FIG. **6**). Comparable pre-challenge neutralization titers of $(1.8\pm1.1)\times10^3$ to $(8.6\pm1.5)\times10^3$ were observed among the WT and mutant virus-infected mice (FIG. **5**E). After challenge with 1×10^5 IFU of WT ZIKV (Cambodian strain FSS13025) on day 28 post-immunization, the immunized mice had no detectable peripheral viremia, whereas the mock-immunized group produced a mean viremia of $(8.5\pm1.5)\times10^6$ IFU/ml on day 2 post-challenge (FIG. **5**F). On day 28 post-challenge, we measured the neutralization titers of the mouse sera again; remarkably, the post-challenge neutralization titers were equivalent to the pre-challenge neutralization titers (compare FIG. **5**E & **5**G), suggesting that a sterilizing antibody response had been achieved by a single vaccination. Altogether, the results demonstrate that the mutant viruses are highly attenuated, immunogenic, and protective in A129 mice.

Example 5: Further Characterization of 10-del Mutant ZIKV

[0138] Materials and Methods:

[0139] Viruses. The Puerto Rico strain PRVABC59 (GenBank number KU501215) was obtained from WRCEVA. All the cell lines are tested negative for mycoplasma.

[0140] Immunization with 100 IFU 10-del virus. Three-week-old A129 mice (n=5) were immunized with 100 IFU WT or 10-del virus via the S.C. route. Viremia was quantified by immunostaining focus assay from day 2 to 6. On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers. Also on day 28 post-immunization, the mice were challenged with 1×10^6 IFU of ZIKV (Puerto Rico strain PRVABC59) via the I.P. route. Viremias were quantified by immunostaining focus assay on day 2 post-challenge.

[0141] Immunization with 10 IFU 10-del virus. Three-week-old A129 mice (n=2 for each virus) were immunized with 10 IFU WT or 10-del ZIKV via the S.C. route. On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers. On the same day, the mice were challenged with 1×10^6 IFU of ZIKV (Puerto Rico strain PRVABC59) via the I.P. route. On day 2 post-challenge, viremias were quantified using an immunostaining focus assay.

[0142] Results:

[0143] Since the 10-del virus produced the lowest viremia in mice (FIG. **5**D), yet induced a neutralizing antibody response comparable to those of the WT and other mutants (FIG. **5**E-**5**G), we prioritized this mutant for further characterization. At a dose of 100 IFU, 10-del virus-infected mice showed a delayed peak viremia that was >100-fold lower than that of the WT virus (FIG. **7**A). Equivalent levels of pre-challenge neutralization titers were induced by the WT and 10-del viruses (FIG. **7**B), leading to complete protection from viremia after challenge with 1×10^6 IFU of Puerto Rico ZIKV strain PRVABC59 (FIG. **7**C). Furthermore, even when immunized at a dose of only 10 IFU, 10-del virus-infected mice generated a neutralization titer of $(9.7+6.8)\times10^3$, and were fully protected from viremia after challenge (FIG. **8**).

[0144] It is noteworthy that mice immunized with different doses of 10-del mutant (10, 10^2, and 10^4 IFU) induced similar neutralization antibody titers and completely prevented viremia upon challenge (compare FIG. **5** and FIGS. **7** & **8**).

[0145] Collectively, these results demonstrate that the 10-del virus is a potent vaccine candidate.

Example 6: Comparison of P0 and P5 10-del Viruses

[0146] Materials and Methods:

[0147] Immunization with P0 or P5 10-del virus: Three-week-old A129 mice (n=5) were immunized with 100 IFU P0 or P5 10-del virus via the S.C. route. Viremia were quantified by immunostaining focus assay from day 4 to 6.

[0148] Pre-challenge neutralization antibody titers: On day 28 post-immunization, mouse sera were quantified for ZIKV neutralizing antibody titers.

[0149] Viremia after challenge with wild-type ZIKV: On day 28 post-immunization, the mice were challenged with 1×10^6 IFU of an epidemic strain of ZIKV (Puerto Rico strain PRVABC59) via the I.P. route. On day 2 post-challenge, viremias were quantified using an immunostaining focus assay.

[0150] Results:

[0151] Since P5 virus accumulated Vero cell-adaptive mutations (FIG. **4**C), we compared the virulence and immunogenicity between the P0 and P5 10-del viruses in the A129 mice. After immunization with 100 IFU virus via the S.C. route, the P0 and P5 viruses generated comparable viremia and induced equivalent neutralization titers (FIG. **11**A & **11**B). After challenging with 1×10^6 IFU of Puerto Rico strain PRVABC59 ZIKV via the I.P. route, no viremia was detected in the P0 or P5 virus-vaccinated mice; in contrast, robust viremia were detected in the sham group (FIG. **11**C). These results indicate that the Vero cell-adaptive mutations recovered from the P5 virus do not significantly affect the virulence and immunogenicity of the 10-del virus.

Example 7: T Cell Responses in A129 Mice Immunized with 10-del ZIKV

[0152] Materials and Methods:

[0153] Measuring T cell responses in A129 mice. A129 mice were infected with 1×10^4 IFU WT and 10-del viruses. On day 28 post-infection, mouse spleens were harvested. Splenocytes were counted, cultured ex vivo with WT ZIKV for 24 h, and stained for markers (IFN-γ, CD3, and CD4 or CD8). The T cells were gated based on staining for these markers, percentages of $CD4^+IFN\text{-}\gamma^+$ cells and $CD8^+IFN\text{-}\gamma^+$ cells were counted, and average total number of T cell subsets per spleen was recorded. Supernatants from the ex vivo culture were harvested on day 2 after WT ZIKV re-stimulation, and measured for IFN-γ and IL-2 production.

[0154] Bio-Plex immuneassay. Approximately 3×10^5 splenocytes were plated in 96-well plates and stimulated with 1.25×10^4 IFU ZIKV strain FSS13025 for 48 h. Culture supernatants were harvested and cytokine production were measured using a Bio-Plex Pro Mouse Cytokine Assay (Bio-Rad, Hercules, Calif.).

[0155] Intracellular cytokine staining (ICS). Approximately 2.5×10^6 splenocytes were stimulated with 1×10^5 IFU live ZIKV (strain FSS13025) for 24 h. During the final 5 h of stimulation, BD GolgiPlug (BD Bioscience) was added to block protein transport. Cells were stained with antibodies for CD3, CD4, or CD8; fixed in 2% paraformaldehyde, and permeabilized with 0.5% saponin before addition of anti-IFN-γ, or control rat IgG1 (e-Biosciences). Samples were processed with a C6 Flow Cytometer instrument. Dead cells were excluded on the basis of forward and side light scatter. Data were analyzed with a CFlow Plus Flow Cytometer (BD Biosciences).

[0156] Results:

[0157] We analyzed the T cell responses in A129 mice immunized with 1×10^4 IFU of WT and 10-del viruses. On day 28 post-immunization, ZIKV-specific T cells were re-stimulated with live WT virus in vitro, and analyzed using an intracellular cytokine staining (ICS) assay and a Bio-Plex immunoassay. The results showed that both WT and mutant virus-immune $CD4^+$ and $CD8^+$ T cells had higher IFN-γ responses than the mock-immunized group (FIG. **9**A & **9**B). Furthermore, these immune T cells induced more IFN-γ (FIG. **9**C) and IL2 (FIG. **9**D) than the mock group; particularly, the 10-del mutant-immune T cells produced 4-fold higher IFN-γ than the WT virus-immune group. These results indicate that 10-del vaccine candidate induces a robust T cell response.

Example 8: Safety of 10-del Vaccine Candidate

[0158] Materials and Methods:

[0159] Organ virus titers. The heart, lung, liver, spleen, kidney, muscle, brain, testis, and eye were harvested on day 6 and 10 post-infection after 1×10^4 IFU of WT and 10-del virus vaccination via the S.C. route. Organ titrations were performed using a immunostaining focus assay as described above. In brief, 500 μl of DMEM with 2% FBS and penicillin/streptomycin along with a steel ball bearing were placed in a 2-ml Eppendorf tube. The organ (whole or part) was placed in the tube. Tubes were weighed, and organ weight was determined by subtracting the tube weight. Tissues were homogenized in a Qiagen TissueLyser II shaking at 26 p/second for 5 minutes. The homogenate was clarified by centrifugation for 5 min at 12,000 rpm and titrated on Vero monolayer using an immunostaining focus assay. The titer was then adjusted for volume and organ weight to report the organ loads as IFU/g (Reference 16).

[0160] Neurovirulence on newborn CD1 mice. Groups of 1-day-old outbred CD1 mice (n=7-10) were injected intracranially (I.C.) with WT or 10-del with serial tenfold dilutions from 10,000 IFU to 10 IFU. Mice were monitored daily for morbidity and mortality.

[0161] Experimental infection of mosquitoes with ZIKV. *Aedes aegypti* mosquitoes derived from a Galveston, Tex. colony were exposed for 45 min to blood-meals consisting of 1% (weight/volume) sucrose, 20% (vol/vol) FBS, 5 mM ATP, 33% (vol/vol) PBS-washed human blood cells (UTMB Blood Bank), and 33% (vol/vol) DMEM medium and combined with 1 ml virus offered in Hemotek 2-ml heated reservoirs (Discovery Workshops) covered with a mouse skin. Virus titers in the blood meals were 1×10^6 IFU/ml. Infectious blood meals were loaded on cartons containing *Ae. aegypti*. Fully engorged mosquitoes were incubated at 28° C., 80% relative humidity on a 12:12 h light:dark cycle with ad lib access to 10% sucrose solution for 7 days and harvested by freezing at -20° C. for 3 h. Whole mosquitoes were individually homogenized (Retsch MM300 homogenizer, Retsch Inc., Newton, Pa.) in DMEM with 20% FBS and 250 μg/ml amphotericin B and stored at −80° C. Samples were centrifuged for 10 min at 5,000 rpm, and 75 μl of each sample supernatant were inoculated into 96-well plates containing Vero cells at 37° C. and 5% CO_2 for 3 days, when they were fixed with a mixture of ice-cold acetone and methanol (1:1) solution and immunostained as described above. Infection was determined by detection of virus in the homogenized mosquito. The infection rate was recorded as the fraction of positive mosquitoes divided by the total number of engorged, incubated mosquitoes.

[0162] Testis and sperm count analyses: A129 mice were infected with 1×10^4 IFU of WT or 10-del mutant virus. A mock-infected group with PBS was included as a negative control. On day 16 p.i., the mice were euthanized and necropsied; epididymis and testes were harvested immediately as previously described (Reference 32). Briefly, the epididymis was placed into 1 ml of pre-warmed M2 media

at 37° C. To release the sperm, the epididymis was cut lengthwise six times and incubated for 10 min, agitating every 2 min at 37° C. Following the incubation, the media containing the sperm was immediately diluted 1:50 into pre-warmed M2 media and counted on a hemocytometer. Motile sperms were categorized into progressive and non-progressive. Progressively motile sperms are described as continuous displacement of the head by flagellar movement. Non-progressively motile sperms are described as little to no displacement of the head by flagellar movement. In the non-motile sperms, no flagellar movement was observed.

[0163] Results:

[0164] Three sets of experiments were performed to analyze the safety of the 10-del vaccine candidate. First, we measured the viral loads in different organs after S.C. inoculation of A129 mice with 1×10^4 IFU of WT or 10-del viruses (FIG. **10**A). On day 6 post-infection, the WT-infected mice had high viral loads in all organs tested, whereas the 10-del-infected mice had no virus in muscle or brain, and lower viral loads in heart, lung, liver, spleen, kidney, testes, and eye. On day 10 post-infection, WT virus-infected mice retained viral loads in kidney, brain, testis, and eye, among which testes had the highest mean titer; in contrast, no virus could be detected ($<10^2$ IFU/mL) in any organs from the 10-del-infected mice. Since ZIKV infection was reported to damage the testes in mice (References 17, 18), we examined the effect of immunization on the function of testes in the A129 mice. On day 16 post-immunization, similar weight and size of testes were recovered from the mock-, WT virus-, and 10-del mutant-infected mice. However, motile and total sperm counts were reduced in the WT virus-infected mice, whereas the 10-del virus-infected mice did not significantly compromise the sperm counts when compared with the mock group (FIG. **12**).

[0165] Second, we examined the neurovirulence of 10-del virus through intracranial (I.C.) injection of one-day-old CD1 mice (FIG. **10**B). The newborn mice succumbed to WT virus infection in a dose-responsive manner; even a dose of 10 IFU resulted in 25% mortality. Remarkably, mice infected with 10-del virus did not show any apparent disease or death, even at a dose of 1×10^4 IFU. Finally, we determined if 10-del virus could infect *Aedes aegypti* mosquitoes, the main transmission vector of ZIKV in the Americas (References 19, 20). After exposure to artificial blood-meals containing 1×10^6 IFU/ml of WT or 10-del virus and incubation for 7 days, 56% of the engorged mosquitoes were infected by the WT virus, whereas no mosquitoes were infected by the 10-del mutant. Furthermore, intrathorax injection of 10-del virus to mosquitoes did not yield any infectious virus on day 7 after injection. Collectively, our results demonstrated that the 10-del virus significantly reduced or eliminated viral loads in mouse organs, decreased neurovirulence by >1,000-fold, and attenuated its ability to infect the principal urban mosquito vector, all suggestive of an excellent safety profile.

[0166] Our data indicate that the 3'UTR 10-del ZIKV is a promising live-attenuated vaccine candidate with a good balance between immunogenicity and safety. A single immunization elicited robust antibody and T cell responses, and significantly, unlike the subunit and inactivated ZIKV vaccines published to date, likely induces sterilizing immunity and providing complete protection against parental and epidemic strains of ZIKV. Vaccine-induced sterilizing immunity is likely critical for a successful ZIKV vaccine to prevent viremia and congenital abnormalities. The safety profile of this vaccine candidate is highlighted by the low viremia, little and transient viral loads in organs, and limited weight loss in the severe A129 mouse model, as well as a complete lack of morbidity and mortality in one-day-old mice after receiving an intracranial (I.C.) injection. The latter safety result is impressive because I.C. inoculation with YFV 17D and JEV SA14-14-2 (two licensed live-attenuated flavivirus vaccines) results in lethal disease in one-day-old newborn mice (References 21, 22). Although potential homologous recombination between the WT and vaccine ZIKVs might pose a safety liability for the 10-del vaccine candidate, it should be noted that recombination events are rare and could not be detected in cell culture (References 23-27). Compared with the chimeric, live-attenuated ZIKV vaccine (e.g., YFV 17D expressing ZIKV prM-E or DENV expressing ZIKV prM-E (Reference 28)), our 3'UTR mutant vaccine has the advantage of retaining all ZIKV structural and nonstructural genes that may contribute to antiviral protection, as indicated from dengue vaccine studies (References 29, 30).

[0167] Compared with the chimeric, live-attenuated ZIKV vaccine (e.g., YFV 17D expressing ZIKV prM-E), our 3'UTR mutant vaccine has the advantage of retaining all ZIKV structural and nonstructural genes that may contribute to antiviral protection, as indicated from dengue vaccine studies (References 29, 30). Mechanistically, the 3'UTR mutant viruses appeared to be attenuated through decreased viral RNA replication and increased sensitivity to type-I interferon inhibition. The latter mechanism is in agreement with a recent report that genetic diversity at the 3'UTR of DENV contributes to epidemic potential (Reference 14). Taken together, our results indicate that the 3'UTR mutant ZIKV is an attractive vaccine candidate that should be advanced to non-human primates for further development.

Additional in Vivo Experiments to Characterize Safety and Efficacy of Live Attenuated ZIKV Strains with 3'UTR Deletions

[0168] Materials and Methods:

[0169] Additional in vivo systems using the Materials and Methods and the examples which follow were also employed to characterize the safety and efficacy of vaccine candidates, including C57BL/6J mouse pregnancy, A129 mouse testis protection, viral loading in A129 mouse organ, CD-1 mouse neurovirulence, and rhesus macaque efficacy (see details below). The protocols for each of these experimental systems have been previously established (e.g., inoculum dose, infection route, challenge dose, and end-point measurement), and were not altered when evaluating these vaccine candidates. Therefore, different inoculum doses, challenge doses, and end-point measurements (e.g., qRT-PCR to measure viral RNA and focus forming assay to measure infection virus) were used in different in vivo systems according to the established protocols. The detailed information is described below and indicated in the Examples which follow.

[0170] Mouse Studies: All in vivo experiments using mice were performed in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocols were approved by the Institutional Animal Care and Use Committee (IACUC) at the Washington University School of Medicine (Assurance Number A3381-01) and the IACUC at the University of Texas Medical Branch (UTMB; Protocol

Number 0209068B). Dissections and footpad injections were performed under anesthesia that was induced and maintained with ketamine hydrochloride and xylazine at the Washington University or isoflurane at UTMB. All efforts were made to minimize animal suffering. Rhesus macaque experiments were reviewed and approved by Vaccine Research Center Animal Care and Use Committee at the National Institute of Allergy and Infectious Diseases, the National Institutes of Health. The non-human primate experiments were performed in compliance with the pertinent regulations and policies from the National Institutes of Health.

[0171] Viruses and cells: The ZIKV Cambodian strain FSS13025 (GenBank number KU955593.1) was produced from an infectious cDNA clone (Reference 35). The ZIKV-3'UTR-Δ10-LAV and ZIKV-3'UTR-Δ20-LAV strains were generated as described. The Zika Puerto Rico strain PRVABC59 (GenBank number KU501215) and Dakar 41519 strain (GenBank number HQ234501.1) were obtained originally from Dr. Robert Tesh from the World Reference Center of Emerging Virus and Arboviruses (WRCEVA) at UTMB. The mouse-adapted ZIKV-Dakar 41519 strain was passaged twice in Rag1-/- mice (Jackson Laboratories) and described previously (Reference 29). Vero cells were purchased from the American Type Culture Collection (ATCC CCL-81; Bethesda, Md.), and maintained at 37° C. with 5% CO_2 in a high glucose Dulbecco modified Eagle medium (DMEM; Invitrogen, Carlsbad, Calif.) with 10% fetal bovine serum (FBS; HyClone Laboratories, Logan, Utah) and 1% penicillin/streptomycin (Invitrogen, Carlsbad, Calif.). All cell lines tested negative for mycoplasma.

[0172] Antibodies: The following antibodies were used in this study: anti-mouse IFN alpha/beta receptor 1 (Ifnar1) monoclonal antibody (clone MAR1-5A3; Leinco Technologies, Inc., St. Louis, Mo.); ZIKV-specific HMAF (hyperimmune ascites fluids; obtained from WRCEVA), anti-mouse IgG antibody labeled with horseradish peroxidase (KPL, Gaithersburg, Md.), and goat anti-mouse IgG conjugated with Alexa Fluor 488 (Thermo Fisher Scientific, Providence, R.I.).

[0173] A129 mouse experiments: A129 mice were bred in the animal facilities at UTMB. All mice were housed in pathogen-free mouse facilities. Three-week or 15-week old male A129 mice were infected with PBS (two sham groups), 10^4 FFU of ZIKV-3'UTR-Δ10-LAV (Δ10), or 10^3 FFU of ZIKV-3'UTR-Δ20-LAV (Δ20). Mice were anesthetized and bled via the retro orbital sinus (R.O.) for viremia testing. At day 28 post-immunization, mice were measured for neutralizing antibody titers using an mCherry ZIKV infection assay (Reference 36). On the same day, one sham group of PBS-immunized mice and Δ10- and Δ20-immunized mice were challenged with 10^6 FFU of ZIKV PRVABC59. Another sham group of mice was used as an unchallenged negative control. At day 49 post-immunization, mice were euthanized and necropsied. Epididymis and testes were harvested immediately as previously described (Reference 32). Motile and non-motile sperms were counted manually on an emocytometer by microscopy. Total sperm counts equal to the sum of motile and non-motile sperms. For quantification of viral loads, testes were homogenized and infectious viral levels were measured by a focus forming assay or quantitative reverse transcriptase PCR (qRT-PCR) (Reference 36).

[0174] The qRT-PCT primer/probe set includes forward primer (1193F: 5'-CCGCTGCCCAACACAAG-3'), reverse primer (1269R: 5'-CCACTAACGTTCTTTTGCAGACAT-3'), and probe (5'-FAM/AGCCTACCT/ZEN/TGACAAGCAATCAGACACTCAA/3IABkFQ-3'). The probe contains a 5'-FAM reporter dye, 3' IBFQ quencher, and an internal ZEN quencher.

[0175] Mouse pregnancy experiments: C57BL/6J mice were bred and housed in pathogen-free mouse facilities at Washington University School of Medicine. One day prior to immunization, the eight-week old female C57BL/6J mice were dosed with 0.5 mg of anti-Ifnar1 antibody via an intraperitoneal route. Subsequently, mice were subcutaneously inoculated in the footpad with 10^5 FFU of ZIKV-3'UTR-Δ10-LAV or PBS sham. Immunized wild-type (WT) C57BL/6 female mice were mated with naïve WT male mice. At embryonic day 5 (E5), pregnant dams were injected intraperitoneally with 2 mg of anti-Ifnar1 antibody. On E6, mice were inoculated subcutaneously with 10^5 FFU of mouse-adapted ZIKV Dakar 41519 via footpad injection. All animals were sacrificed on E13 and analyzed for viral loads in placentas, fetuses, and maternal tissues. Briefly, maternal blood, organs from dams (brain and spleen) and fetuses (placenta and fetal head) were collected. Serum was prepared after coagulation and centrifugation. Organs were weighed and homogenized using a bead-beater apparatus (MagNA Lyser, Roche). Viral RNA was extracted from serum and tissue samples using the RNeasy Mini kit (Qiagen). The viral RNA levels were determined by TaqMan one-step qRT-PCR on an ABI 7500 Fast Instrument using standard cycling conditions. Viral burden is expressed on a log10 scale as viral RNA equivalents per gram or per milliliter after comparison with a standard curve produced using serial 5-fold dilutions of ZIKV RNA from known quantities of infectious virus. The following primer/probe set was used for ZIKV qRT-PCR: forward primer (1183F: 5'-CCACCAATGTTCTCTTGCAGACATATTG-3'), reverse primer (1268R: 5'-TTCGGACAGCCGTTGTCCAACACAAG-3'), and probe (1213F: 5'-56-FAM/AGCCTACCTTGACAAGCAGTC/3IABkFQ-3'). Wherever indicated, viral burden for some samples was determined by focus forming assay on Vero cells (Reference 28).

[0176] Quantification of viral load in organs from A129 mice: A129 mice were infected and organs were quantified for viral load using a focus forming assay (Reference 28). Viral RNA in testis also was quantified by qRT-PCR. Briefly, testes were harvested and placed in DMEM with beads for homogenization. After homogenization, the supernatant was used to extract viral RNA using RNeasy Mini kit (Qiagen). Extracted RNA was eluted in 40 μl RNase-free water. qRT-PCR assays were performed on the LightCycler® 480 System (Roche) following the manufacturer's protocol by using a 50-μl reaction of the QuantiTect Probe RT-PCR Kit (QIAGEN) and 10 μl RNA template. The viral load was calculated based on a standard curve produced using serial 10-fold dilutions of ZIKV RNA from known quantities of infectious virus. The qRT-PCT primer/probe set includes forward primer (1193F: 5'-CCGCTGCCCAACACAAG-3'), reverse primer (1269R: 5'-CCACTAACGTTCTTTTGCAGACAT-3'), and probe (5'-FAM/AGCCTACCT/ZEN/TGACAAGCAATCAGACACTCAA/3IABkFQ-3'). The probe contains a 5'-FAM reporter dye, 3' IBFQ quencher, and an internal ZEN quencher.

[0177] Vaccination of non-human primates: Rhesus macaque (*Macaca mulatta*) experiments were performed at Bioqual, Inc. (Rockville, Md.). All animal experiments were reviewed and approved by the Animal Care and Use Committee of the Vaccine Research Center, the National Institute of Allergy and Infectious Diseases, the National Institutes of Health. Animals were housed and cared in accordance with local, state, federal, and institutional policies in an American Association for Accreditation of Laboratory Animal Care-accredited facility at the Bioqual Inc. Rhesus macaques (3-4/group) were randomized by body weight, gender, and age, and subcutaneously administered with 10^3 FFU of parental WT ZIKV strain FSS13025, ZIKV-3'UTR-Δ10-LAV, ZIKV-3'UTR-Δ20-LAV, or PBS sham at day 0. Blood was collected at day 2, 3, 4, 5, 7, and 10 for viremia testing and weekly for analysis of antibody responses by an mCherry ZIKV neutralization assay (References 36, 38). The immunized animals were subcutaneously challenged with 10^3 FFU of ZIKV strain PRVABC59 at week 8. Blood samples were collected for determination of viral load at day 2, 3, 4, 5, 7, and 10 and neutralization antibody at week 2, 4, and 6 post-challenge.

[0178] Viremia from rhesus macaques was quantified by a qRT-PCR assay and focus forming assay as described in the proceeding section. For qRT-PCR quantification, viral RNA was extracted from rhesus serum using QlAamp Viral RNA Kits (QIAGEN) following the manufacture instruction. Extracted RNA was eluted in 40 μl RNase-free water. qRT-PCR assay was performed as described above. In vitro transcribed full-length ZIKV RNA was used as a standard for qRT-PCR quantification. The primer/probe set is described in the proceeding section.

[0179] Neutralization assay and neurovirulence: All antibody neutralization titers were determined using an mCherry ZIKV as previously reported (Reference 36). The dilution folds that neutralized 50% of mCherry ZIKV infection (NT50) were presented. For measuring neurovirulence, 1-day-old outbred CD-1 mice (Charles River) were injected intracranially with indicated amounts of viruses. The infected mice were monitored for morbidity and mortality as reported previously (Reference 36).

[0180] Mosquito infection: For measuring mosquito infection, artificial blood-meal spiked with 10^6 FFU/ml of indicated viruses was used to feed *Aedes aegypti* mosquitoes (derived from a Galveston, Texas), and engorged mosquitoes were incubated at 28° C., 80% relative humidity on a 12:12 h light:dark cycle with ad libitum access to 10% sucrose. The infection rates were determined at day 7 post-feeding as reported previously (Reference 10).

[0181] Data analysis: All data from these experiments the results of which are described in the examples which follow and are contained in the figures referenced therein were analyzed with GraphPad Prism v7.02 software. Data are expressed as the mean±standard deviation (SD). Comparisons of groups were performed using Mann-Whitney test or one-way ANOVA with a multiple comparisons correction. A P value of <0.05 indicates statistically significant.

Example 9: Prevention of Vertical Transmission in Pregnant Mice

[0182] The live-attenuated vaccine candidate described herein which contains a 10-nucleotide deletion in the 3'UTR of ZIKV genome (ZIKV-3'UTR-Δ10-LAV) was tested for its ability to prevent in utero transmission. In these experiments we subcutaneously inoculated 10^5 focus-forming units (FFU) of ZIKV-3'UTR-Δ10-LAV or PBS-sham into 8-week-old wild-type C57BL/6 female mice (FIG. **13**A). Because mice are not a native host for ZIKV due in part to a species-dependent lack of antagonism of type I IFN signaling (References 39, 40), we administered 0.5 mg of anti-Ifnarl blocking antibody to female mice one day prior to vaccination to facilitate transient replication of ZIKV-3'UTR-Δ10-LAV and to attempt to produce disease (Reference 41). At day 28 post-vaccination, the animals were phlebotomized and serum was analyzed for neutralizing antibody (FIG. **13**B); all ZIKV-3'UTR-Δ10-LAV-immunized mice developed high neutralizing antibody titers of 18,900±5,900 (mean±standard deviation; n=13), whereas, as expected, the PBS-immunized animals did not develop detectable neutralizing antibodies (FIG. **13**C). At day 35 post-vaccination, the immunized females were mated with 12-week-old wild-type (WT) C57BL/6 male mice and monitored for vaginal plugs (FIG. **13**A). At embryo day 6 (E6), pregnant mice were challenged subcutaneously with 10^5 FFU of a mouse-adapted, pathogenic ZIKV African strain Dakar 41519 (Reference 42); to facilitate ZIKV-Dakar dissemination to the maternal decidua and fetal placenta, the pregnant mice were administered 2 mg of anti-Ifnarl antibody at E5, one day before the challenge. At E13, maternal and fetal organs were harvested and measured for viral load.

[0183] After a single immunization, ZIKV-3'UTR-Δ10-LAV reduced median viral loads in the maternal spleen and brain by ~49,000-fold and ~120-fold, respectively (FIG. **13**D-E). Placentas and fetal heads from the vaccinated dams showed 138,000-fold and 260-fold decreases in viral RNA loads, respectively, when compared with the PBS-immunized dams (FIG. **13**F-G). Notably, 21 of 30 (70%) placentas and 21 of 30 (70%) fetal heads from ZIKV-3'UTR-Δ10-LAV-immunized dams had viral RNA loads at or below the detection limit; no infectious virus was recovered by focus forming assay from the placentas or fetal heads from the vaccinated dams (FIG. **17**A-B). In addition, the immune correlate between the EC_{50} values and the levels of infectious viruses recovered in the placenta revealed an expected inverse relationship between neutralizing titers and levels of ZIKV particles in placenta (FIG. **17**C). Collectively, the data suggest that ZIKV-3'UTR-Δ10-LAV protects maternal organs from infection, partially prevents viral transmission to the fetus during an early stage of pregnancy, and limits fetal replication.

Example 10: Protection of ZIKV-Induced Damages to Testes

[0184] We examined the ability of ZIKV-3'UTR-Δ10-LAV to prevent testis infection and injury in $Ifnar1^{-/-}$ A129 mice (FIG. **14**A). Since male mice reach sexual maturity at 8-week-old, we tested the vaccine efficacy in two age groups of mice: 3-week-old young males and 15-week-old adult males. Three-week-old young A129 male mice were vaccinated with a single-dose of 10^4 FFU of ZIKV-3'UTR-Δ10-LAV or PBS sham. The ZIKV-3'UTR-Δ10-LAV generated a peak viremia of $1.2\pm0.34\times10^4$ FFU (n=6) at day 4 post-vaccination (FIG. **14**B). At day 28 post-vaccination, ZIKV-3'UTR-Δ10-LAV had induced robust neutralizing antibody titers of 7,700 ±2,600 (n=6) (FIG. **14**C). At the same day, the animals were challenged intraperitoneally with 10^6 FFU of an epidemic ZIKV strain from Puerto Rico (PRVABC59). No viremia was detected from the ZIKV-3'UTR-Δ10-LAV-

vaccinated mice after challenge, whereas the sham-vaccinated animals sustained a mean peak viremia of $7.1\pm5.9\times10^6$ FFU/ml (n=6) at day 2 post-challenge (FIG. **14**D). At day 21 post-challenge, viral burden in the testis of PBS-immunized mice reached $5.8\pm8.4\times10^6$ FFU/g (n=6), whereas no infectious virus was detected in the testes of ZIKV-3'UTR-Δ10-LAV-immunized mice (FIG. **14**E). Both total and motile sperm counts from the ZIKV-3'UTR-Δ10-LAV-immunized mice were equivalent to those from age-matched unvaccinated, unchallenged healthy male mice. In contrast, the PBS-immunized, ZIKV-challenged mice showed 85% and 90% reduction for total and motile sperm counts, respectively, at day 21 post-infection (FIG. **14**F&G). Consistent with these data, the testis weight and size from the PBS-immunized, ZIKV-challenged mice were reduced, whereas no such reduction was observed in the ZIKV-3'UTR-Δ10-LAV-immunized, ZIKV-challenged animals (FIG. **14**H&I).

[0185] In 15-week-old adult A129 male mice, vaccination with ZIKV-3'UTR-Δ10-LAV also protected against testis infection, injury, and oligospermia (FIG. **17**A-G). However, challenge of the PBS-vaccinated adult males with ZIKV PRVABC59 did not reduce the testis weight and size (FIG. **17**H&I) as much as that observed in the corresponding sham-vaccinated, young males (FIG. **17**H&I), suggesting an age-dependent testis pathology. Collectively, the results indicate that a single-dose immunization of ZIKV-3'UTR-Δ10-LAV protects the testis from infection and injury in male mice.

Example 11: Efficacy in Non-Human Primates

[0186] To determine whether the efficacy in mice extends to non-human primates (NHPs), we evaluated the viremia, immunogenicity, and potency of ZIKV-3'UTR-Δ10-LAV in rhesus macaques (RM; FIG. **15**A). First, we assessed the level of attenuation of ZIKV-3'UTR-Δ10-LAV in RM by comparing viremia to the parental WT virus. After subcutaneous inoculation with 10^3 FFU, WT ZIKV (2010 Cambodian strain FSS 13025) produced high levels of viremia in each of the four inoculated RM, with a mean peak viremia of 9.6 and 28.8×10^4 genome copies/ml at days 4 and 5 post-infection, respectively (FIG. **15**B, top panel). In contrast, only one of the four ZIKV-3'UTR-Δ10-LAV-inoculated RM exhibited viremia, and this level was just above the limit of detection of our qRT-PCR assay (FIG. **15**B, second panel); thus, ZIKV-3'UTR-Δ10-LAV is highly attenuated in RM.

[0187] We next evaluated the immunogenicity of ZIKV-3'UTR-Δ10-LAV by measuring neutralizing antibodies from serum at days 5-98 post-immunization. Neutralizing antibodies elicited by WT ZIKV were detectable at day 7-10, peaked at $1/1{,}000$ to $1/10{,}000$ at day 14, and plateaued thereafter (FIG. **15**C, top panel). Compared with the WT ZIKV infection, ZIKV-3'UTR-Δ10-LAV-inoculated animals showed slightly delayed production and lower levels of neutralizing antibody, with titers of ~$1/100$ at days 21-56 (FIG. **15**C, second panel). At day 56 post-immunization, all RM were challenged with 10^3 FFU of the epidemic ZIKV strain PRVABC59. Notably, no viremia was detected upon challenge in any of the RM that were pre-infected with WT ZIKV or vaccinated with the ZIKV-3'UTR-010-LAV (FIG. **15**D, top two panels). As controls, two PBS-inoculated RM were challenged in parallel and high levels of viremia were measured (FIG. **15**D bottom panel). In addition to analysis of viral RNA by qRT-PCR, we also performed focus forming assays to measure infectious virus; infectious ZIKV was detected only in naive RM challenged with WT ZIKV (FIG. **19**).

[0188] To examine whether the ZIKV challenge resulted in boosted immune responses, we measured neutralizing activity post-challenge. No increase in neutralizing activity was observed in the WT ZIKV-vaccinated RM after challenge (FIG. **15**C, top panel), indicating that the initial infection likely conferred sterilizing immunity. In contrast, the neutralizing antibody titers rose after challenge from approximately $1/100$ to $1/1{,}000$-$1/10{,}000$ in the ZIKV-3'UTR-Δ10-LAV-immunized animals (FIG. **15**C, second panel), demonstrating an anamnestic response and suggesting a low level of infection after challenge that was not detectable by qRT-PCR of serum. As expected, the PBS-inoculated control RM increased their neutralizing titers to ~$1/10{,}000$ after challenge (FIG. **15**C, bottom panel).

[0189] Since ZIKV-3'UTR-Δ10-LAV did not elicit sterilizing immunity in RM, we evaluated whether a second live-attenuated vaccine candidate ZIKV-3'UTR-Δ20-LAV (Reference 36), which contains a 20-nucleotide deletion in the 3'UTR, could induce a stronger immune response. ZIKV-3'UTR-Δ20-LAV was shown previously, and paradoxically, to be less attenuated than ZIKV-3'UTR-Δ10-LAV in A129 mice, most likely because it is less sensitive to type-I IFN inhibition compared to ZIKV-3'UTR-Δ10-LAV (Reference 36). After subcutaneous inoculation of 10^3 FFU of ZIKV-3'UTR-Δ20-LAV, two of the three RM had low, but detectable viremia (FIG. **15**B, third panel). The immunized animals rapidly produced neutralizing antibodies by day 10, with inhibitory titers plateauing at $1/1{,}000$ to $1/10{,}000$ by days 14-21 (FIG. **15**C, third panel). After challenge with 10^3 FFU of ZIKV PRVABC59 at day 56, viremia was not detected by qRT-PCR (FIG. **15**D, third panel) and no rise in neutralizing antibody titers was observed (FIG. **15**C, third panel) in the ZIKV-3'UTR-Δ20-LAV-immunized animals. Although low number of animals were used for each vaccine candidates, the results suggest that a single-dose vaccination of ZIKV-3'UTR-Δ20-LAV -induces sterilizing immunity in NHPs (i.e., no detectable viremia and no increase of neutralizing antibody titer after challenge).

[0190] We also evaluated another live-attenuated ZIKV vaccine candidate encoding an NS1 without glycosylation (ZIKV-NS1-LAV) in RM. ZIKV-NS1-LAV was recently shown to prevent in utero transmission in a mouse pregnancy model (Reference 43). After subcutaneous immunization of four RMs with 10^3 FFU of ZIKV-NS1-LAV, none of the animals showed any detectable viral RNA (FIG. **15**B, fourth panel). Back titering of the ZIKV-NS1-LAV inoculum using focus-forming assay confirmed the infectivity of viral stock with the expected infectious titer. Unexpectedly the immunization did not elicit any neutralizing activity (FIG. **15**C, fourth panel). After challenge with 10^3 FFU of ZIKV PRVABC59 at day 56, all four animals displayed robust viremia (FIG. **15**D, fourth panel) and generated neutralizing antibody titers (FIG. **15**C, fourth panel). These results indicate that ZIKV-NS1-LAV is incapable of replicating and triggering antibody responses in RM.

Example 12: Testis Protection and Safety Analysis of ZIKV-3'UTR-Δ20-LAV

[0191] Because of the highly desirable sterilizing immunity induced by ZIKV-3'UTR-Δ20-LAV in RM, we further tested its efficacy and safety. Similar to ZIKV-3'UTR-Δ10-

LAV, immunization of male A129 mice with 10^3 FFU of ZIKV-3'UTR-Δ20-LAV completely prevented viral infection and testis injury after challenge with ZIKV PRVABC59, as determined by a lack of detectable viremia post-challenge, the absence of oligospermia, and no decrease in testis weight and size (FIG. **20**). Next, five sets of experiments were performed to characterize the safety of ZIKV-3'UTR-Δ20-LAV.

[0192] First, we measured the organ viral loads after subcutaneous inoculation of A129 mice with 10^3 FFU of ZIKV-3'UTR-Δ20-LAV or parental WT ZIKV (FIG. **16**A). At day 6 post-infection, WT ZIKV-infected mice exhibited high viral loads in all tested organs, whereas no virus was detected ($\leq 10^2$ FFU/ml) in liver or brain from the ZIKV-3'UTR-Δ20-LAV-infected mice, with other organs (except spleen) exhibiting lower levels of the vaccine virus than those of the WT-infected animals. At day 10 post-infection, WT ZIKV-infected mice retained viral loads in the heart, spleen, kidney, testis, eye, and brain, whereas no organs from the ZIKV-3'UTR-Δ20-LAV-infected mice had any detectable virus.

[0193] Second, we examined the potential adverse effect of ZIKV-3'UTR-Δ20-LAV on the testis in 3-week-old A129 mice. As expected, at day 21 post-infection, WT ZIKV infection reduced testis weight and size (FIG. **16**A-C), lowered total and motile sperm counts (FIG. **16**D-E), and resulted in viral RNA in the shrunken testis (FIG. **16**F). In contrast, ZIKV-3'UTR-Δ20-LAV did not affect sperm counts or testis weight and size (FIG. **16**B-E), with no detectable viral RNA in the testes (FIG. **16**F).

[0194] Third, we evaluated the neurovirulence of ZIKV-3'UTR-Δ20-LAV through intracranial inoculation of 1-day-old CD-1 mice (FIG. **16**G). As reported previously (Reference 36), neonates succumbed to WT ZIKV infection; even a dose of only 10 FFU resulted in 13% mortality (FIG. **16**G). In contrast, no mortality was observed in mice that were inoculated with 10^3 FFU of ZIKV-3'UTR-Δ20-LAV; however, infection with 10^4 FFU of ZIKV-3'UTR-Δ20-LAV resulted in a mortality rate of 29%.

[0195] Fourth, we tested if the vaccine candidate could infect *Aedes aegypti* mosquitoes, the main vector of ZIKV (References 19, 20). After feeding on artificial blood-meals containing 10^6 FFU/ml of ZIKV-3'UTR-Δ20-LAV or WT ZIKV, 50% of the engorged mosquitoes were infected by WT ZIKV, whereas no mosquitoes were infected by ZIKV-3'UTR-Δ20-LAV (FIG. **16**H).

[0196] Finally, we tested the stability of ZIKV-3'UTR-Δ20-LAV in cell culture. After continuous culture of ZIKV-3'UTR-Δ20-LAV on Vero cells (an approved cell line for vaccine production (Reference 44) for five rounds, all recovered P5 viruses (derived from three independent experiments) retained the 20-nucleotide deletion. However, the P5 viruses accumulated additional mutations in the E- and NS1-encoding genes (FIG. **21**), which may represent Vero-cell-adaptive mutation(s) or compensatory mutation(s) to 3'UTR deletion. Further passaging of the viruses to P10 did not change the 20-nucleotide deletion, indicating that the deletion is stable in cell culture. Moreover, we passaged ZIKV-3'UTR-Δ20-LAV in A129 mice for three rounds (3 days per round); all recovered viruses retained the 20-nucleotide deletion, further suggesting the stability of the mutant virus. Taken together, these results demonstrate an excellent safety profile of ZIKV-3'UTR-Δ20-LAV, including limited, transient viral loads in mouse organs, no adverse effect on testicular function, decreased neurovirulence, incompetency to infect mosquitoes, and good stability.

CONCLUSIONS

[0197] Herein we demonstrate that live-attenuated ZIKV vaccine candidates containing deletions in the 3' untranslated region of the ZIKV genome (ZIKV-3'UTR-LAV), i.e., 10 and 20 nucleotide deletions, prevent viral transmission during pregnancy and testis damage in mice, as well as infection of non-human primates. After a single-dose vaccination, pregnant mice challenged with ZIKV at embryonic day 6 (E6) and evaluated at E13 show markedly diminished levels of viral RNA in maternal, placental, and fetal tissues. Vaccinated male mice challenged with ZIKV are protected against testis infection, injury, and oligospermia. A single immunization of rhesus macaques elicited a rapid and robust antibody response, conferring complete protection upon challenge. Furthermore, the ZIKV-3'UTR-LAV vaccine candidates have a desirable safety profile. These results suggest that further development of ZIKV-3'UTR-LAV is warranted for humans.

[0198] Particularly our results showed that a single immunization of ZIKV-3'UTR-Δ10-LAV prevented maternal-to-fetal transmission early during pregnancy in C57BL/6 mice. Although no infectious challenge virus was detected, very low levels of viral RNA were recovered from ~30% of placenta and fetal heads from the vaccinated dams after challenge; these breakthrough viral RNAs might derive from stable antibody-virus complexes, which can last for several days in vivo (Reference 47).

[0199] Based on these results the clinical implications of such breakthrough non-infectious viral RNA will be determined in other species and in particular will be evaluated in non-human primates (NHPs) and if successful in humans. In male A129 mice, a single-dose immunization of either ZIKV-3'UTR-Δ10-LAV or ZIKV-3'UTR-Δ20-LAV prevented testis infection and injury after challenge, indicating an additional benefit of vaccination to protect the male reproductive system. Notably, unprotected young A129 mice (3- or 7-week-old) infected with ZIKV developed smaller testes, whereas adult mice (19-week-old when infected) did not, suggesting that ZIKV infection might cause more severe reproductive damage in younger males. As noted above the clinical relevance of this observation will be confirmed in NHPs and humans.

[0200] In NHPs, a single-dose vaccination with ZIKV-3'UTR-Δ10-LAV or ZIKV-3'UTR-Δ20-LAV induced sufficient immune responses to prevent viremia, with the ZIKV-3'UTR-Δ10-LAV eliciting greater immunogenicity, as reflected by its ability to induce sterilizing immunity against challenge. One limitation of the current non-human primate results is the low number of animals used for each vaccine candidates (n=3-4). ZIKV vaccine-induced sterilizing immunity might be critical for protection of congenital abnormalities in humans.

[0201] Live-attenuated vaccines generally have the advantage of single dose, rapid induction of durable immunity. Since ZIKV is endemic primarily in low income countries, a vaccine with single-dose efficacy is of practical importance, particularly when controlling an explosive outbreak or immunizing population in remote areas where multiple doses and periodic boosting will be challenging (Reference 45). Thus, live-attenuated vaccines may be useful for immunizing populations living in and traveling to ZIKV-endemic

areas. Besides our ZIKV-3'UTR-LAV, a single-dose immunization with nucleoside-modified mRNA expressing ZIKV prM-E (50 μg) (Reference 46) or a recombinant rhesus adenovirus serotype 52 vector expressing ZIKV prM-E (10^{11} viral particles) (Reference 8) was also shown to rapidly elicit antibody response and prevent viremia in NHPs; whether these two vaccines achieved sterilizing immunity was not determined. All other vaccine platforms, including inactivated vaccine and prM-E DNA vaccine, need two shots to elicit robust antibody response for viremia protection in NHPs (References 7, 8).

[0202] It is conceivable that in immunocompromised individuals and pregnant women, vaccination with live-attenuated virus may be contraindicated to avoid potential adverse risks. However, these individuals could be protected using inactivated, subunit, or gene-based replication-defective vaccines. Therefore, it is desirable that multiple vaccine platforms be developed in parallel with those described herein in order to provide complementary options for preventing and controlling ZIKV infection and disease.

Example 13: DNA Plasmid-Launched Wild-Type Zika Virus and Vaccines

[0203] In order to facilitate the development of vaccines for preventing and controlling ZIKV infection and disease the inventors have developed a DNA plasmid that can be directly transfected into cells to generate Zika virus (ZIKV). The new DNA-launched ZIKV full-length (FL) clone is assembled in the backbone of the pCC1 vector. Besides the pCC1 vector sequence, it contains an eukaryotic promoter CMV or SV40, the full genome of ZIKV strain FSS13025, HDVr sequence, and poly-A tail. The clones are named as CMV ZIKV FL and SV40 ZIKV FL depending on the types of promoters used to transcribe the viral RNA. DNA-launched ZIKV full-length clones used to construct live attenuated ZIKV vaccine candidates are listed in Appendix A.

[0204] As shown in FIG. **22**, both pCC1-CMV ZIKV FL and pCC1-SV40 ZIKV FL can efficiently launch wild-type ZIKV by transfection of DNA plasmid into Vero cells. In the experiments 5 micrograms of indicated DNA plasmid was transfected into Vero cells through electroporation. Culture fluids were collected from day 1 to 5. Infectious viral titers were measured by plaque assay on Vero cells.

[0205] Using the DNA-launched ZIKV FL clones (SEQ ID NO:6 and 7), we made DNA-launched live attenuated ZIKV vaccine candidates. Specifically, we engineered the 3'UTR 10-del or 20-del mutations (References 19, 48) into the DNA-launched ZIKV FL clones, resulting in ZIKV Del 10 and ZIKV Del 20, respectively. Depending on the promoter types, these DNA vaccine candidates are named as CMV ZIKV Del 10, CMV ZIKV Del 20, SV40 ZIKV Del 10, and SV40 ZIKV Del 20. Detailed description of the sequences of these particular DNA vaccine candidates is summarized in Appendix B. As shown in FIG. **23**, the four DNA-launched live-attenuated ZIKV vaccine plasmids can also produce robust levels of vaccines after transfecting the DNA into Vero cells.

Appendix A: ZIKV Full-Length Clones used to Construct Live Attenuated ZIKV Vaccine Candidates

[0206] 1. CMV ZIKV Full Length (FL) sequence: SEQ ID NO: 6 in Sequence Listing

[0207] 2. SV40 ZIKV Full Length (FL) sequence: SEQ ID NO:7 in Sequence Listing

Appendix B: Detailed Description of Sequences of Exemplary Live Attenuated ZIKV Vaccine Candidates

[0208] CMV ZIKV Del 10: Consists of a deletion variant of SEQ ID NO: 6 wherein the sequence "CCAGAAGAGG" (SEQ ID NO: 8 in Sequence Listing) is deleted.

[0209] CMV ZIKV Del 20: Consists of a deletion variant of SEQ ID NO: 6 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (SEQ ID NO: 9 in Sequence Listing) is deleted.

[0210] SV40 ZIKV Del 10: Consists of a deletion variant of SEQ ID NO: 7 wherein the sequence "CCAGAAGAGG" (SEQ ID NO: 8 in Sequence Listing) is deleted.

[0211] SV40 ZIKV Del 10: Consists of a deletion variant of SEQ ID NO: 7 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (SEQ ID NO: 9 in Sequence Listing) is deleted.

[0212] One skilled in the art will readily appreciate that the present invention is adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The prior examples along with the methods, procedures, treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are examples, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

SEQUENCES

3'UTR-WT

SEQ ID NO: 1

GCACCAATCTTAGTGTTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTG

TGCAGCCTGTGACCCCCCCAGGAGAAGCTGGGAAACCAAGCCCATAGTCAGGCC

GAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACA

CTGAGTCAAAAAACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGG

CGACCTTCCCCACCCTTTAATCTGGGGCCTGAACTGGAGATCAGCTGTGGATCTC

CAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCCGGAAAACGCAAAACAGCAT

ATTGACGCTGGGAAAGACCAGAGACTCCATGAGTTTCCACCACGCTGGCCGCCA

GGCACAGATCGCCGAATAGCGGCGGCCGGTGTGGGGAAATCCATGGTTTCT

-continued

3'UTR-10-del

SEQ ID NO: 2

GCACCAATCTTAGTGTTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTG

TGCAGCCTGTGACCCCCCCAGGAGAAGCTGGGAAACCAAGCCCATAGTCAGGCC

GAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACA

CTGAGTCAAAAAACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGG

CGACCTTCCCCACCCTTTAATCTGGGGCCTGAACTGGAGATCAGCTGTGGATCTG

ACTAGTGGTTAGAGGAGACCCCCCGGAAAACGCAAAACAGCATATTGACGCTGG

GAAAGACCAGAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCG

CCGAATAGCGGCGGCCGGTGTGGGGAAATCCATGGTTTCT

3'UTR-20-del

SEQ ID NO: 3

GCACCAATCTTAGTGTTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTG

TGCAGCCTGTGACCCCCCCAGGAGAAGCTGGGAAACCAAGCCCATAGTCAGGCC

GAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACA

CTGAGTCAAAAAACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGG

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AGAGGAGACCCCCCGGAAAACGCAAAACAGCATATTGACGCTGGGAAAGACCA

GAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGC

GGCGGCCGGTGTGGGGAAATCCATGGTTTCT

3'UTR-30-del-a

SEQ ID NO: 4

GCACCAATCTTAGTGTTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTG

TGCAGCCTGTGACCCCCCCAGGAGAAGCTGGGAAACCAAGCCCATAGTCAGGCC

GAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACA

CTGAGTCAAAAAACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGG

CGACCTTCCCCACCCTTTAATCTGGGGCCTGAACGACTAGTGGTTAGAGGAGACC

CCCCGGAAAACGCAAAACAGCATATTGACGCTGGGAAAGACCAGAGACTCCATG

AGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGGCGGCCGGTG

TGGGGAAATCCATGGTTTCT

3'UTR-30-del-b

SEQ ID NO: 5

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TGCAGCCTGTGACCCCCCCAGGAGAAGCTGGGAAACCAAGCCCATAGTCAGGCC

GAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACA

CTGAGTCAAAAAACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGG

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AGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGGCGGCCGGTG

TGGGGAAATCCATGGTTTCT

CMV ZIKV FL sequence:

SEQ ID NO: 6

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3' UTR Zika 20 Nucleotide Deletion

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[0213] The contents of the following references and all other references which are cited in this application are incorporated by reference in their entirety.

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tggagattag ctgtgaatct ccggcagaag gactagtggt tagag 45

1. A live attenuated Zika virus (ZIKV) strain, comprising a deletion in the 3' untranslated region (3'UTR) of the ZIKV genome.

2-26. (canceled)

27. The live attenuated ZIKV strain of claim **1**, wherein

(i) the 3'UTR deletion ranges from a 10-nucleotide deletion to a 50-nucleotide deletion (i.e., Δ10, Δ11, Δ12, Δ13, Δ14, Δ15, Δ16, Δ17, Δ18, Δ19, Δ20, Δ21, Δ22, Δ23, Δ24, Δ25, Δ26, Δ27, Δ28, Δ29, Δ30, Δ31, Δ32, Δ33, Δ34, Δ35, Δ36, Δ37, Δ38, Δ39, Δ40, Δ41, Δ42, Δ43, Δ44, Δ45, Δ46, Δ47, Δ48, Δ49 or Δ50 3'UTR deletion);

(ii) the 3'UTR deletion is a 10-nucleotide deletion, a 20-nucleotide deletion, or a 30-nucleotide deletion;

(iii) the 3'UTR deletion is a 10-nucleotide deletion; or

(iv) the 3'UTR deletion is a 20-nucleotide deletion.

28. The live attenuated ZIKV strain of claim **1**, comprising a 3'UTR having at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identity to the nucleic acid sequence of SEQ ID NO: 2, 3, 4, or 5.

29. The live attenuated ZIKV strain of claim **27**, comprising a 3'UTR having at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identity to the nucleic acid sequence of SEQ ID NO: 2, 3, 4, or 5.

30. The live attenuated ZIKV strain of claim **1**, which comprises at least one of the following:

(i) is incompetent in infecting mosquitoes;

(ii) exhibits decreased viral RNA synthesis compared to wildtype ZIKV strains;

(iii) exhibits increased sensitivity to type-1 interferon inhibition compared to wildtype ZIKV strains;

(iv) the deletion does not affect viral RNA translation; or

(v) it comprises an mCherry ZIKV strain.

31. The live attenuated ZIKV strain of claim **1**, which comprises at least one of the following:

(i) comprises or consists of a deletion variant of SEQ ID NO:6 wherein the sequence "CCAGAAGAGG" (3'UTR 10-nucleotide deletion) (SEQ ID NO:8) is deleted therefrom;

(ii) comprises or consists of a deletion variant of SEQ ID NO:6 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (3'UTR 20-nucleotide deletion) (SEQ ID NO:9) is deleted therefrom;

(iii) comprises or consists of a deletion variant of SEQ ID NO:7 wherein the sequence "CCAGAAGAGG" (3'UTR 10-nucleotide deletion) (SEQ ID NO:8) is deleted therefrom; or

(iv) comprises or consists of a deletion variant of SEQ ID NO:7 wherein the sequence "CTGTGGATCTCCAGAAGAGG" (3'UTR 20-nucleotide deletion) (SEQ ID NO:9) is deleted therefrom.

32. An immunogenic composition comprising a live attenuated ZIKV strain according to claim **1**, which further comprises at least one pharmaceutically acceptable carrier or excipient

33. The immunogenic composition of claim **32**, which is suitable for parenteral or enteral administration.

34. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **1** in a subject in need thereof.

35. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **27**, in a subject in need thereof.

36. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **28**, in a subject in need thereof.

37. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **29**, in a subject in need thereof.

38. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **30**, in a subject in need thereof.

39. A method for eliciting an immune response in a subject in need thereof comprising administering a prophylactically or therapeutically effective amount of a live attenuated ZIKV strain according to claim **31**, in a subject in need thereof.

40. The method of claim **34**, wherein the immune response comprises a $CD8^+$ T cell response, an antibody response, and/or a cellular immune response against ZIKV and/or the immune response comprises a neutralizing antibody titer equivalent to that of wildtype ZIKV infection.

41. The method of claim **34**, wherein the subject is a pregnant female.

42. The method of claim **34**, which (i) prevents congenital ZIKV syndrome, and/or (ii) prevents microcephaly.

43. The method of claim **34**, wherein the prophylactically or therapeutically effective amount of the live attenuated ZIKV strain comprises at least 1.0×10^1, 1.0×10^2, 1.0×10^3, 1.0×10^4, 1.0×10^5, or 1.0×10^6 IFUs.

44. The method of claim **34**, which prevents viremia in said subject after subsequent challenge with a wildtype ZIKV strain.

45. The method of claim **34**, wherein the subject treated is a human.

* * * * *

PTO/AIA/01 (06-12)
Approved for use through 11/30/2020. OMB 0651-0032
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

DECLARATION (37 CFR 1.63) FOR UTILITY OR DESIGN APPLICATION USING AN APPLICATION DATA SHEET (37 CFR 1.76)

Title of Invention	LIVE ATTENTUATED ZIKA VIRUS WITH 3'UTR DELETION, VACCINE CONTAINING AND USE THEREOF

As the below named inventor, I hereby declare that:

This declaration is directed to:

☐ The attached application, or

☒ United States application or PCT international application number 16/485,818 filed on August 14, 2019.

The above-identified application was made or authorized to be made by me.

I believe that I am the original inventor or an original joint inventor of a claimed invention in the application.

I hereby acknowledge that any willful false statement made in this declaration is punishable under 18 U.S.C. 1001 by fine or imprisonment of not more than five (5) years, or both.

WARNING:

Petitioner/applicant is cautioned to avoid submitting personal information in documents filed in a patent application that may contribute to identity theft. Personal information such as social security numbers, bank account numbers, or credit card numbers (other than a check or credit card authorization form PTO-2038 submitted for payment purposes) is never required by the USPTO to support a petition or an application. If this type of personal information is included in documents submitted to the USPTO, petitioners/applicants should consider redacting such personal information from the documents before submitting them to the USPTO. Petitioner/applicant is advised that the record of a patent application is available to the public after publication of the application (unless a non-publication request in compliance with 37 CFR 1.213(a) is made in the application) or issuance of a patent. Furthermore, the record from an abandoned application may also be available to the public if the application is referenced in a published application or an issued patent (see 37 CFR 1.14). Checks and credit card authorization forms PTO-2038 submitted for payment purposes are not retained in the application file and therefore are not publicly available.

LEGAL NAME OF INVENTOR

Inventor: Pei-Yong SHI Date (Optional) :_____

Signature: _____

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

PTO/AIA/01 (06-12)
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LEGAL NAME OF INVENTOR

Inventor: Xuping XIE Date (Optional) :_____

Signature: _____

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

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This declaration is directed to:

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LEGAL NAME OF INVENTOR

Inventor: Chao SHAN Date (Optional): Oct 19, 2020

Signature: /Chao Shan/

Note: An application data sheet (PTO/SB/14 or equivalent), including naming the entire inventive entity, must accompany this form or must have been previously filed. Use an additional PTO/AIA/01 form for each additional inventor.

To: Liu, Shan-Lu[liu.6244@osu.edu]; zhengzhiming4@gmail.com[zhengzhiming4@gmail.com]; haitguo@iupui.edu[haitguo@iupui.edu]; tzhou@mail.nih.gov[tzhou@mail.nih.gov]; GCheng@mednet.ucla.edu[GCheng@mednet.ucla.edu]; liangy@umn.edu[liangy@umn.edu]; rli@vcu.edu[rli@vcu.edu]; wjma@ksu.edu[wjma@ksu.edu]; xjmeng@vt.edu[xjmeng@vt.edu]; Zhijian.Chen@UTSouthwestern.edu[Zhijian.Chen@UTSouthwestern.edu]; mluo@gsu.edu[mluo@gsu.edu]; zhangyj@umd.edu[zhangyj@umd.edu]; xzhu1@umd.edu[xzhu1@umd.edu]; jqiu@kumc.edu[jqiu@kumc.edu]; lijun@uic.edu[lijun@uic.edu]; fengwei.bai@usm.edu[fengwei.bai@usm.edu]; andyu@iupui.edu[andyu@iupui.edu]; reachxw@vt.edu[reachxw@vt.edu]; gluo@uab.edu[gluo@uab.edu]; ldu@nybc.org[ldu@nybc.org]; hxu@tulane.edu[hxu@tulane.edu]; liu_fy@berkeley.edu[liu_fy@berkeley.edu]; shitao.li@okstate.edu[shitao.li@okstate.edu]; Shan.lu@umassmed.edu[Shan.lu@umassmed.edu]; Hu, Haitao[haihu@UTMB.EDU]; wenzheho@temple.edu[wenzheho@temple.edu]; Qfeng4@central.uh.edu[Qfeng4@central.uh.edu]; tang@bio.fsu.edu[tang@bio.fsu.edu]; feng.li@sdstate.edu[feng.li@sdstate.edu]; ruilu@lsu.edu[ruilu@lsu.edu]; sxiang2@unl.edu[sxiang2@unl.edu]; dingsw@ucr.edu[dingsw@ucr.edu]; guohua@missouri.edu[guohua@missouri.edu]; bling@tulane.edu[bling@tulane.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; lifang@umn.edu[lifang@umn.edu]; wang518@umd.edu[wang518@umd.edu]; gaos8@upmc.edu[gaos8@upmc.edu]; Wang,Penghua[pewang@uchc.edu]; xiangy@uthscsa.edu[xiangy@uthscsa.edu]; fzhu@bio.fsu.edu[fzhu@bio.fsu.edu]; chen.liang@mcgill.ca[chen.liang@mcgill.ca]; lyuan@vt.edu[lyuan@vt.edu]; fgao@duke.edu[fgao@duke.edu]; wangjw28@163.com[wangjw28@163.com]; xfyu1@zju.edu.cn[xfyu1@zju.edu.cn]; bzhao@partners.org[bzhao@partners.org]; jianw@musc.edu[jianw@musc.edu]; zyang@ksu.edu[zyang@ksu.edu]; yu.cong@nih.gov[yu.cong@nih.gov]; weiming.yuan@usc.edu[weiming.yuan@usc.edu]; Zongdi.feng@nationwidechildrens.org[Zongdi.feng@nationwidechildrens.org]; juh13@psu.edu[juh13@psu.edu]; hengx@missouri.edu[hengx@missouri.edu]; lsu@med.unc.edu[lsu@med.unc.edu]; ywu8@gmu.edu[ywu8@gmu.edu]; jwu@whu.edu.cn[jwu@whu.edu.cn]; tshuo@uic.edu[tshuo@uic.edu]; Shibojiang@fudan.edu.cn[Shibojiang@fudan.edu.cn]; sjiang@nybc.org[sjiang@nybc.org]; pinwang@usc.edu[pinwang@usc.edu]; rzhao@som.umaryland.edu[rzhao@som.umaryland.edu]; shuylong@mail.sysu.edu.cn[shuylong@mail.sysu.edu.cn]; xuefeng.liu@georgetown.edu[xuefeng.liu@georgetown.edu]; yuxingli@som.umaryland.edu[yuxingli@som.umaryland.edu]; shixia.wang@umassmed.edu[shixia.wang@umassmed.edu]; yhe@ipbcams.ac.cn[yhe@ipbcams.ac.cn]; Pinghui.feng@usc.edu[Pinghui.feng@usc.edu]; ju-tao.guo@bblumberg.org[ju-tao.guo@bblumberg.org]; lin.liu@okstate.edu[lin.liu@okstate.edu]; hua.zhu@rutgers.edu[hua.zhu@rutgers.edu]; Jinhong.chang@bblumberg.org[Jinhong.chang@bblumberg.org]; jianzhu1012@gmail.com[jianzhu1012@gmail.com]; ronghai@ucr.edu[ronghai@ucr.edu]; jun.zhu@nih.gov[jun.zhu@nih.gov]; jliu4@uams.edu[jliu4@uams.edu]; xiangpeng.kong@med.nyu.edu[xiangpeng.kong@med.nyu.edu]; haoquanwu@outlook.com[haoquanwu@outlook.com]; Wenjun.liu@defence.gov.au[Wenjun.liu@defence.gov.au]; Liang.shan@wustl.edu[Liang.shan@wustl.edu]; hliao@duke.edu[hliao@duke.edu]; yuan2@upenn.edu[yuan2@upenn.edu]; zxing@umn.edu[zxing@umn.edu]; hongmin.li@health.ny.gov[hongmin.li@health.ny.gov]; pzheng@ihv.umaryland.edu[pzheng@ihv.umaryland.edu]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; jxw103@case.edu[jxw103@case.edu]; xiangguo.qiu@canada.ca[xiangguo.qiu@canada.ca]; Feng Shao[shaofeng@nibs.ac.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; klan@whu.edu.cn[klan@whu.edu.cn]; zengmsh@mail.sysu.edu.cn[zengmsh@mail.sysu.edu.cn]; Nan Yan[Nan.Yan@UTSouthwestern.edu]; Zhang, Rong[rongzhang@wustl.edu]; liliwang@upenn.edu[liliwang@upenn.edu]; Linheng Li[LIL@stowers.org]; kli1@uthsc.edu[kli1@uthsc.edu]; tsx@case.edu[tsx@case.edu]; ssun@mdanderson.org[ssun@mdanderson.org]; ysang@tnstate.edu[ysang@tnstate.edu]; wu@crystal.harvard.edu[wu@crystal.harvard.edu]; Sun.Jie@mayo.edu[Sun.Jie@mayo.edu]; peijun@strubi.ox.ac.uk[peijun@strubi.ox.ac.uk]; jiayu@coh.org[jiayu@coh.org]; bchen@crystal.harvard.edu[bchen@crystal.harvard.edu]; Wen, Haitao[Haitao.Wen@osumc.edu]; Qu, Feng[qu.28@osu.edu]; Hezhao.Ji@umanitoba.ca[Hezhao.Ji@umanitoba.ca]; Li, Zihai[zihai@musc.edu]; zhengyo@msu.edu[zhengyo@msu.edu]; zhanglinqi@tsinghua.edu.cn[zhanglinqi@tsinghua.edu.cn]; wxiao@temple.edu[wxiao@temple.edu]; Whu@temple.edu[Whu@temple.edu]; RSun@mednet.ucla.edu[RSun@mednet.ucla.edu]; Guangping.Gao@umassmed.edu[Guangping.Gao@umassmed.edu]; pzheng@ihv.umaryland.edu[pzheng@ihv.umaryland.edu]; GMSWANG@nus.edu.sg[GMSWANG@nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; ziying-yan@uiowa.edu[ziying-yan@uiowa.edu]; lqiao@luc.edu[lqiao@luc.edu]; yong.xiong@yale.edu[yong.xiong@yale.edu]; Wang, Qiuhong[wang.655@osu.edu]; shuping_tong_md@brown.edu[shuping_tong_md@brown.edu]; pinghuif@usc.edu[pinghuif@usc.edu]; gaof@im.ac.cn[gaof@im.ac.cn]
From: Tang, Qiyi[qiyi.tang@Howard.edu]
Sent: Tue 7/7/2020 10:47:05 PM (UTC-05:00)
Subject: Re: Happy Thanksgiving and meeting next year, June 12-13, 2020

Hi professors,

I apologize if you are bothered by this email. I am helping my friend, Ed Seto to advertise his recruiting post-doc:

Postdoctoral Position

Applications are invited for a postdoctoral fellowship to study the structures, functions, and mechanisms of histone deacetylases. Candidates with experiences in biochemical, molecular, and

cell biological approaches are preferred.

Recent selected articles from our lab:
PMID: 32540961
PMID: 32457045
PMID: 31162605
PMID: 30517871
PMID: 30456376
PMID: 29958910

Please send a CV and names of three references to:

Ed Seto, Ph.D.
Email: seto@gwu.edu

To: zhengzhiming4@gmail.com[zhengzhiming4@gmail.com]; tzhou@mail.nih.gov[tzhou@mail.nih.gov]; GCheng@mednet.ucla.edu[GCheng@mednet.ucla.edu]; liangy@umn.edu[liangy@umn.edu]; rli@vcu.edu[rli@vcu.edu]; xjmeng@vt.edu[xjmeng@vt.edu]; Zhijian.Chen@UTSouthwestern.edu[Zhijian.Chen@UTSouthwestern.edu]; mluo@gsu.edu[mluo@gsu.edu]; zhangyj@umd.edu[zhangyj@umd.edu]; xzhu1@umd.edu[xzhu1@umd.edu]; jqiu@kumc.edu[jqiu@kumc.edu]; lijun@uic.edu[lijun@uic.edu]; fengwei.bai@usm.edu[fengwei.bai@usm.edu]; andyu@iupui.edu[andyu@iupui.edu]; reachxw@vt.edu[reachxw@vt.edu]; gluo@uab.edu[gluo@uab.edu]; ldu@nybc.org[ldu@nybc.org]; hxu@tulane.edu[hxu@tulane.edu]; liu_fy@berkeley.edu[liu_fy@berkeley.edu]; Shan.lu@umassmed.edu[Shan.lu@umassmed.edu]; Hu, Haitao[haihu@UTMB.EDU]; wenzheho@temple.edu[wenzheho@temple.edu]; Qfeng4@central.uh.edu[Qfeng4@central.uh.edu]; tang@bio.fsu.edu[tang@bio.fsu.edu]; feng.li@sdstate.edu[feng.li@sdstate.edu]; ruilu@lsu.edu[ruilu@lsu.edu]; sxiang2@unl.edu[sxiang2@unl.edu]; qiyi.tang@howard.edu[qiyi.tang@howard.edu]; dingsw@ucr.edu[dingsw@ucr.edu]; guohua@missouri.edu[guohua@missouri.edu]; bling@tulane.edu[bling@tulane.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; lifang@umn.edu[lifang@umn.edu]; wang518@umd.edu[wang518@umd.edu]; gaos8@upmc.edu[gaos8@upmc.edu]; Wang,Penghua[pewang@uchc.edu]; xiangy@uthscsa.edu[xiangy@uthscsa.edu]; fzhu@bio.fsu.edu[fzhu@bio.fsu.edu]; chen.liang@mcgill.ca[chen.liang@mcgill.ca]; lyuan@vt.edu[lyuan@vt.edu]; fgao@duke.edu[fgao@duke.edu]; wangjw28@163.com[wangjw28@163.com]; xfyu1@zju.edu.cn[xfyu1@zju.edu.cn]; bzhao@partners.org[bzhao@partners.org]; jianw@musc.edu[jianw@musc.edu]; zyang@ksu.edu[zyang@ksu.edu]; yu.cong@nih.gov[yu.cong@nih.gov]; weiming.yuan@usc.edu[weiming.yuan@usc.edu]; Zongdi.feng@nationwidechildrens.org[Zongdi.feng@nationwidechildrens.org]; juh13@psu.edu[juh13@psu.edu]; hengx@missouri.edu[hengx@missouri.edu]; lsu@med.unc.edu[lsu@med.unc.edu]; ywu8@gmu.edu[ywu8@gmu.edu]; jwu@whu.edu.cn[jwu@whu.edu.cn]; tshuo@uic.edu[tshuo@uic.edu]; Shibojiang@fudan.edu.cn[Shibojiang@fudan.edu.cn]; sjiang@nybc.org[sjiang@nybc.org]; pinwang@usc.edu[pinwang@usc.edu]; rzhao@som.umaryland.edu[rzhao@som.umaryland.edu]; shuylong@mail.sysu.edu.cn[shuylong@mail.sysu.edu.cn]; xuefeng.liu@georgetown.edu[xuefeng.liu@georgetown.edu]; yuxingli@som.umaryland.edu[yuxingli@som.umaryland.edu]; shixia.wang@umassmed.edu[shixia.wang@umassmed.edu]; yhe@ipbcams.ac.cn[yhe@ipbcams.ac.cn]; Pinghui.feng@usc.edu[Pinghui.feng@usc.edu]; ju-tao.guo@bblumberg.org[ju-tao.guo@bblumberg.org]; lin.liu@okstate.edu[lin.liu@okstate.edu]; hua.zhu@rutgers.edu[hua.zhu@rutgers.edu]; Jinhong.chang@bblumberg.org[Jinhong.chang@bblumberg.org]; jianzhu1012@gmail.com[jianzhu1012@gmail.com]; ronghai@ucr.edu[ronghai@ucr.edu]; jliu4@uams.edu[jliu4@uams.edu]; xiangpeng.kong@med.nyu.edu[xiangpeng.kong@med.nyu.edu]; haoquanwu@outlook.com[haoquanwu@outlook.com]; Wenjun.liu@defence.gov.au[Wenjun.liu@defence.gov.au]; Liang.shan@wustl.edu[Liang.shan@wustl.edu]; hliao@duke.edu[hliao@duke.edu]; yuan2@upenn.edu[yuan2@upenn.edu]; zxing@umn.edu[zxing@umn.edu]; hongmin.li@health.ny.gov[hongmin.li@health.ny.gov]; pzheng@ihv.umaryland.edu[pzheng@ihv.umaryland.edu]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; jxw103@case.edu[jxw103@case.edu]; Feng Shao[shaofeng@nibs.ac.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; klan@whu.edu.cn[klan@whu.edu.cn]; zengmsh@mail.sysu.edu.cn[zengmsh@mail.sysu.edu.cn]; Nan Yan[Nan.Yan@UTSouthwestern.edu]; liliwang@upenn.edu[liliwang@upenn.edu]; Linheng Li[LIL@stowers.org]; kli1@uthsc.edu[kli1@uthsc.edu]; tsx@case.edu[tsx@case.edu]; ssun@mdanderson.org[ssun@mdanderson.org]; ysang@tnstate.edu[ysang@tnstate.edu]; Liu, Shan-Lu[liu.6244@osu.edu]; wu@crystal.harvard.edu[wu@crystal.harvard.edu]; Sun.Jie@mayo.edu[Sun.Jie@mayo.edu]; peijun@strubi.ox.ac.uk[peijun@strubi.ox.ac.uk]; jiayu@coh.org[jiayu@coh.org]; bchen@crystal.harvard.edu[bchen@crystal.harvard.edu]; Wen, Haitao[Haitao.Wen@osumc.edu]; Qu, Feng[qu.28@osu.edu]; Hezhao.Ji@umanitoba.ca[Hezhao.Ji@umanitoba.ca]; zhengyo@msu.edu[zhengyo@msu.edu]; zhanglinqi@tsinghua.edu.cn[zhanglinqi@tsinghua.edu.cn]; Whu@temple.edu[Whu@temple.edu]; RSun@mednet.ucla.edu[RSun@mednet.ucla.edu]; Guangping.Gao@umassmed.edu[Guangping.Gao@umassmed.edu]; PZheng@ihv.umaryland.edu[PZheng@ihv.umaryland.edu]; GMSWANG@nus.edu.sg[GMSWANG@nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; ziying-yan@uiowa.edu[ziying-yan@uiowa.edu]; lqiao@luc.edu[lqiao@luc.edu]; yong.xiong@yale.edu[yong.xiong@yale.edu]; Wang, Qiuhong[wang.655@osu.edu]; shuping_tong_md@brown.edu[shuping_tong_md@brown.edu]; Pinghui Feng[pinghuif@usc.edu]; gaof@im.ac.cn[gaof@im.ac.cn]; zihai@musc.edu[zihai@musc.edu]; zqin@uams.edu[zqin@uams.edu]; guoh4@upmc.edu[guoh4@upmc.edu]; wma@missouri.edu[wma@missouri.edu]; Feng.Li@uky.edu[Feng.Li@uky.edu]; xiaow@iu.edu[xiaow@iu.edu]; sli38@tulane.edu[sli38@tulane.edu]; guodeyin@mail.sysu.edu.cn[guodeyin@mail.sysu.edu.cn]; hli1@pharmacy.arizona.edu[hli1@pharmacy.arizona.edu]; xiaow@iu.edu[xiaow@iu.edu]; ashuang@caltech.edu[ashuang@caltech.edu]; jamesou@usc.edu[jamesou@usc.edu]; cwood1@unl.edu[cwood1@unl.edu]; dongfang.liu@rutgers.edu[dongfang.liu@rutgers.edu]
From: Liu, Shan-Lu[liu.6244@osu.edu]
Sent: Fri 4/9/2021 9:12:11 AM (UTC-05:00)
Subject: FW: Tell the NIH to Stop the Racial Profiling of Asian Scientists and Researchers (Due Fri 4/9 at 5pm ET)

From: Chinese Biological Investigators Society <cbisociety@gmail.com>
Date: Thursday, April 8, 2021 at 9:59 AM
To: Chinese Biological Investigators Society <cbisociety@gmail.com>
Subject: Tell the NIH to Stop the Racial Profiling of Asian Scientists and Researchers (Due Fri 4/9 at 5pm ET)

Hi all,

Asian Americans Advancing Justice | AAJC is submitting a comment to the National Institutes of Health (NIH) to raise our concern on the mass racial profiling and discriminatory investigations and prosecutions of Asian American and immigrant scientists, researchers, and scholars and NIH's role in these efforts.

Asian American communities have been grossly impacted by the profiling and unjust prosecutions for espionage of students, scientists, and researchers of Asian descent under the pretext of securing American research particularly under the Justice Department's "China Initiative." NIH intervention and investigations have led to the dismissal, resignation, and termination of Asian scientists, as well as a growing fear among Asian Americans and Asian immigrants of being targeted and scapegoated based on their race, ethnicity, and national origin.

NIH has launched an effort to end structural racism in biomedical research through its new UNITE initiative. Individuals and organizations are invited to submit suggestions through its Request for Information (RFI) platform on ways NIH can stand against structural racism and achieve racial equity in biomedical research.

Join us by signing on to Asian Americans Advancing Justice | AAJC's comment or submitting your own comment to NIH on the harms resulting from the racial discrimination and profiling of Asian Americans and Asian immigrants in the scientific research environment. The comment also includes a set of recommendations on appropriate measures to address racial profiling and promote racial equity within the agency.

Full text of Advancing Justice | AAJC's comment is available here.

You can take action now by:

- **Signing on to our comment to NIH** on the racial profiling and targeting of Asian American and Asian immigrant scientists, researchers, and scholars. **The deadline to sign on is April 9 at 5pm ET.**

**Please note we accept both individual and organizational signatories. We encourage impacted persons to consult with their attorneys first before signing on to the comment to reduce risk. If you are concerned about signing publicly, you may also submit comments anonymously.*

- **Submitting your own comment to NIH** We encourage you to add new recommendations, modify existing recommendations to align with your priorities, and include additional evidence, data and references. Comments may be submitted anonymously. **The submission deadline is April 9 at 11:59PM ET.**

  - Letter template for individuals
  - Letter template for organizations
  - Note: If you are submitting a letter using this template, please send a copy to Vivin Qiang at vqiang@advancingjustice-aajc.org. This assists our organization in further combating the racial profiling of Asian Americans and Asian immigrants.

If you have any questions, please reach out to Gisela Kusakawa at gkusakawa@advancingjustice-aajc.org.

If you believe you are being targeted by the government and you are looking for attorney referrals, please contact 202-935-6014 using the Signal app and a staff member from Advancing Justice | AAJC will reach out to you directly (Available in English & Mandarin/普通话). Please contact Vivin Qiang to learn more.

We hope you consider signing on or submitting your own comment to NIH. Thank you for your time and consideration of this request!

If you would no longer like to receive updates and action alerts from Advancing Justice | AAJC, please contact Vivin Qiang.

Best,

Vivin

Vivin Qiang | 强雪儿 | she/hers
Program Coordinator, Anti-Racial Profiling Project
1620 L Street NW, Suite 1050 Washington, DC 20036
vqiang@advancingjustice-aajc.org
Asian Americans Advancing Justice | AAJC
Join our email list
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To: zhengzhiming4@gmail.com[zhengzhiming4@gmail.com]; tzhou@mail.nih.gov[tzhou@mail.nih.gov]; GCheng@mednet.ucla.edu[GCheng@mednet.ucla.edu]; liangy@umn.edu[liangy@umn.edu]; rli@vcu.edu[rli@vcu.edu]; xjmeng@vt.edu[xjmeng@vt.edu]; Zhijian.Chen@UTSouthwestern.edu[Zhijian.Chen@UTSouthwestern.edu]; mluo@gsu.edu[mluo@gsu.edu]; zhangyj@umd.edu[zhangyj@umd.edu]; xzhu1@umd.edu[xzhu1@umd.edu]; jqiu@kumc.edu[jqiu@kumc.edu]; lijun@uic.edu[lijun@uic.edu]; fengwei.bai@usm.edu[fengwei.bai@usm.edu]; andyu@iupui.edu[andyu@iupui.edu]; reachxw@vt.edu[reachxw@vt.edu]; gluo@uab.edu[gluo@uab.edu]; ldu@nybc.org[ldu@nybc.org]; hxu@tulane.edu[hxu@tulane.edu]; liu_fy@berkeley.edu[liu_fy@berkeley.edu]; Shan.lu@umassmed.edu[Shan.lu@umassmed.edu]; Hu, Haitao[haihu@UTMB.EDU]; wenzheho@temple.edu[wenzheho@temple.edu]; Qfeng4@central.uh.edu[Qfeng4@central.uh.edu]; tang@bio.fsu.edu[tang@bio.fsu.edu]; feng.li@sdstate.edu[feng.li@sdstate.edu]; ruilu@lsu.edu[ruilu@lsu.edu]; sxiang2@unl.edu[sxiang2@unl.edu]; qiyi.tang@howard.edu[qiyi.tang@howard.edu]; dingsw@ucr.edu[dingsw@ucr.edu]; guohua@missouri.edu[guohua@missouri.edu]; bling@tulane.edu[bling@tulane.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; lifang@umn.edu[lifang@umn.edu]; wang518@umd.edu[wang518@umd.edu]; gaos8@upmc.edu[gaos8@upmc.edu]; Wang,Penghua[pewang@uchc.edu]; xiangy@uthscsa.edu[xiangy@uthscsa.edu]; fzhu@bio.fsu.edu[fzhu@bio.fsu.edu]; chen.liang@mcgill.ca[chen.liang@mcgill.ca]; lyuan@vt.edu[lyuan@vt.edu]; fgao@duke.edu[fgao@duke.edu]; wangjw28@163.com[wangjw28@163.com]; xfyu1@zju.edu.cn[xfyu1@zju.edu.cn]; bzhao@partners.org[bzhao@partners.org]; jianw@musc.edu[jianw@musc.edu]; zyang@ksu.edu[zyang@ksu.edu]; yu.cong@nih.gov[yu.cong@nih.gov]; weiming.yuan@usc.edu[weiming.yuan@usc.edu]; Zongdi.feng@nationwidechildrens.org[Zongdi.feng@nationwidechildrens.org]; juh13@psu.edu[juh13@psu.edu]; hengx@missouri.edu[hengx@missouri.edu]; lsu@med.unc.edu[lsu@med.unc.edu]; ywu8@gmu.edu[ywu8@gmu.edu]; jwu@whu.edu.cn[jwu@whu.edu.cn]; tshuo@uic.edu[tshuo@uic.edu]; Shibojiang@fudan.edu.cn[Shibojiang@fudan.edu.cn]; sjiang@nybc.org[sjiang@nybc.org]; pinwang@usc.edu[pinwang@usc.edu]; rzhao@som.umaryland.edu[rzhao@som.umaryland.edu]; shuylong@mail.sysu.edu.cn[shuylong@mail.sysu.edu.cn]; xuefeng.liu@georgetown.edu[xuefeng.liu@georgetown.edu]; yuxingli@som.umaryland.edu[yuxingli@som.umaryland.edu]; shixia.wang@umassmed.edu[shixia.wang@umassmed.edu]; yhe@ipbcams.ac.cn[yhe@ipbcams.ac.cn]; Pinghui.feng@usc.edu[Pinghui.feng@usc.edu]; ju-tao.guo@bblumberg.org[ju-tao.guo@bblumberg.org]; lin.liu@okstate.edu[lin.liu@okstate.edu]; hua.zhu@rutgers.edu[hua.zhu@rutgers.edu]; Jinhong.chang@bblumberg.org[Jinhong.chang@bblumberg.org]; jianzhu1012@gmail.com[jianzhu1012@gmail.com]; ronghai@ucr.edu[ronghai@ucr.edu]; jliu4@uams.edu[jliu4@uams.edu]; xiangpeng.kong@med.nyu.edu[xiangpeng.kong@med.nyu.edu]; haoquanwu@outlook.com[haoquanwu@outlook.com]; Wenjun.liu@defence.gov.au[Wenjun.liu@defence.gov.au]; Liang.shan@wustl.edu[Liang.shan@wustl.edu]; hliao@duke.edu[hliao@duke.edu]; yuan2@upenn.edu[yuan2@upenn.edu]; zxing@umn.edu[zxing@umn.edu]; hongmin.li@health.ny.gov[hongmin.li@health.ny.gov]; pzheng@ihv.umaryland.edu[pzheng@ihv.umaryland.edu]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; jxw103@case.edu[jxw103@case.edu]; Feng Shao[shaofeng@nibs.ac.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; klan@whu.edu.cn[klan@whu.edu.cn]; zengmsh@mail.sysu.edu.cn[zengmsh@mail.sysu.edu.cn]; Nan Yan[Nan.Yan@UTSouthwestern.edu]; liliwang@upenn.edu[liliwang@upenn.edu]; Linheng Li[LIL@stowers.org]; kli1@uthsc.edu[kli1@uthsc.edu]; tsx@case.edu[tsx@case.edu]; ssun@mdanderson.org[ssun@mdanderson.org]; ysang@tnstate.edu[ysang@tnstate.edu]; Liu, Shan-Lu[liu.6244@osu.edu]; wu@crystal.harvard.edu[wu@crystal.harvard.edu]; Sun.Jie@mayo.edu[Sun.Jie@mayo.edu]; peijun@strubi.ox.ac.uk[peijun@strubi.ox.ac.uk]; jiayu@coh.org[jiayu@coh.org]; bchen@crystal.harvard.edu[bchen@crystal.harvard.edu]; Wen, Haitao[Haitao.Wen@osumc.edu]; Qu, Feng[qu.28@osu.edu]; Hezhao.Ji@umanitoba.ca[Hezhao.Ji@umanitoba.ca]; zhengyo@msu.edu[zhengyo@msu.edu]; zhanglinqi@tsinghua.edu.cn[zhanglinqi@tsinghua.edu.cn]; Whu@temple.edu[Whu@temple.edu]; RSun@mednet.ucla.edu[RSun@mednet.ucla.edu]; Guangping.Gao@umassmed.edu[Guangping.Gao@umassmed.edu]; PZheng@ihv.umaryland.edu[PZheng@ihv.umaryland.edu]; GMSWANG@nus.edu.sg[GMSWANG@nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; yaliu@ihv.umaryland.edu[yaliu@ihv.umaryland.edu]; ziying-yan@uiowa.edu[ziying-yan@uiowa.edu]; lqiao@luc.edu[lqiao@luc.edu]; yong.xiong@yale.edu[yong.xiong@yale.edu]; Wang, Qiuhong[wang.655@osu.edu]; shuping_tong_md@brown.edu[shuping_tong_md@brown.edu]; Pinghui Feng[pinghuif@usc.edu]; gaof@im.ac.cn[gaof@im.ac.cn]; zihai@musc.edu[zihai@musc.edu]; zqin@uams.edu[zqin@uams.edu]; guoh4@upmc.edu[guoh4@upmc.edu]; wma@missouri.edu[wma@missouri.edu]; Feng.Li@uky.edu[Feng.Li@uky.edu]; xiaow@iu.edu[xiaow@iu.edu]; sli38@tulane.edu[sli38@tulane.edu]; guodeyin@mail.sysu.edu.cn[guodeyin@mail.sysu.edu.cn]; hli1@pharmacy.arizona.edu[hli1@pharmacy.arizona.edu]; xiaow@iu.edu[xiaow@iu.edu]; ashuang@caltech.edu[ashuang@caltech.edu]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; jamesou@usc.edu[jamesou@usc.edu]; cwood1@unl.edu[cwood1@unl.edu]
From: Liu, Shan-Lu[liu.6244@osu.edu]
Sent: Fri 1/1/2021 9:03:49 AM (UTC-06:00)
Subject: Thank you and happy new year!

Dear colleagues:

Greetings and happy new year!

I hope that you all have enjoyed our annual meeting last two days, which I consider as a success. There were more than 300 registrations, and in each session, there were at least 100 attendees at various times. Once again, I wish to thank all the speakers, cochairs, panelists and all of you for your participation and discussion. I especially want to thank the organizing committee

members, Genhong Cheng, Haitao Guo, Renfeng Li, Yuying Liang, Wenjun Ma, Tongqing Zhou, and hi-Ming Zheng for their help that made this symposium possible. I would hope that our annual meeting next year will happen in person.

As I finish my term as the Founding President of this association, which is effective today, I would like to offer my most sincere appreciation and thanks for your care, trust, understanding, patience, and support. It is all because of you last few years that this association and the WeChat group is so strong, entertaining, and full of fun!

In the meantime, I would like to introduce the new leadership team of SCBA-Virology Division as follows:

President: Haitao Guo, Ph.D, University of Pittsburgh School of Medicine
Secretary: Tongqing Zhou, Ph.D, Vaccine Research Center, NIAID, NIH
Treasurers: Yuying Liang , Ph.D, University of Minnesota, and Wenjun Ma, Ph.D, University of Missouri

I wish you all a happy, healthy, and prosperous 2021!

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
The Ohio State University
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

CENTER TO STOP COVID

To: shanchao@wh.iov.cn[shanchao@wh.iov.cn]; jling56@hotmail.com[jling56@hotmail.com]; Dunn, Tiffany J.[jtdunn@utmb.edu]; Xie, Xuping[xuxie@UTMB.EDU]; Zou, Jing[jizou@UTMB.EDU]; Thames, Beatriz H.[bhthames@UTMB.EDU]; Sajja, Amulya[amsajja@UTMB.EDU]; Yu, Yongjia[yoyu@UTMB.EDU]; Vasilakis, Nikolaos[nivasila@utmb.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Wu, Ping[piwu@UTMB.EDU]
From: Xu, Pei[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=3E811492647F44F385A217F50A9F15DF-XU, PEI]
Sent: Wed 8/19/2020 9:17:10 PM (UTC-05:00)
Subject: Zika stem cell manuscript
Manu in vitro 8-19-2020 Pei.docx

Hi All,

Please see the attached manuscript. Could you help me review it and provide feedback? Do you have any suggestions for journals to submit to?

Beatriz and Amulya, please add your department information.

Thank you very much for your help.

Best,

Pei

To: Xu, Pei[pexu@UTMB.EDU]; shanchao@wh.iov.cn[shanchao@wh.iov.cn]; jling56@hotmail.com[jling56@hotmail.com]; Dunn, Tiffany J.[jtdunn@utmb.edu]; Xie, Xuping[xuxie@UTMB.EDU]; Zou, Jing[jizou@UTMB.EDU]; Thames, Beatriz H.[bhthames@UTMB.EDU]; Sajja, Amulya[amsajja@UTMB.EDU]; Yu, Yongjia[yoyu@UTMB.EDU]; Vasilakis, Nikolaos[nivasila@utmb.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Wu, Ping[piwu@UTMB.EDU]
From: Weaver, Scott[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=780D6A531FDE43B997BAFA26AD1150BD-WEAVER, SCO]
Sent: Tue 9/1/2020 9:08:58 AM (UTC-05:00)
Subject: Re: Zika stem cell manuscript
Manu in vitro 8-19-2020 Pei_SW.docx

Hi Pei,

The paper reads very well, I just have a few minor suggestions.

Best,

Scott

From: Pei Xu <pexu@UTMB.EDU>
Date: Wednesday, August 19, 2020 at 9:18 PM
To: "shanchao@wh.iov.cn" <shanchao@wh.iov.cn>, "jling56@hotmail.com" <jling56@hotmail.com>, "Dunn, Tiffany J." <jtdunn@utmb.edu>, "Xie, Xuping" <xuxie@UTMB.EDU>, "Zou, Jing" <jizou@UTMB.EDU>, "Thames, Beatriz H." <bhthames@UTMB.EDU>, "Sajja, Amulya" <amsajja@UTMB.EDU>, "Yu, Yongjia" <yoyu@UTMB.EDU>, Nikos Vasilakis <nivasila@utmb.edu>, Pei-yong Shi <peshi@UTMB.EDU>, Scott Weaver <sweaver@UTMB.EDU>, Ping Wu <piwu@UTMB.EDU>
Subject: Zika stem cell manuscript

Hi All,

Please see the attached manuscript. Could you help me review it and provide feedback? Do you have any suggestions for journals to submit to?

Beatriz and Amulya, please add your department information.

Thank you very much for your help.

Best,

Pei

To: Shi, Pei yong[peshi@UTMB.EDU]; Zhang, Wenbo[we2zhang@UTMB.EDU]; Wang, Tian[ti1wang@UTMB.EDU]; 单超[shanchao@wh.iov.cn]; Zou, Jing[jizou@UTMB.EDU]; Ha, Yonju[yoha@UTMB.EDU]; Shi, Shuizhen[shushi@UTMB.EDU]; Xia, Fan[faxia@UTMB.EDU]; Liu, Hua[hualiu@UTMB.EDU]; Zhang, Ming[MZHANG@augusta.edu]; ophthal.ly@gmail.com[ophthal.ly@gmail.com]
From: Adam, Awad[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=1E029A853FC74556A11300A60161D480-ADAM, AWADA]
Sent: Fri 5/7/2021 11:50:25 AM (UTC-05:00)
Subject: Re: Decision has been reached on your submission to Acta Neuropathologica Communications - ANEC-D-21-00206R1 - [EMID:c7dc225b8e660493]

Hi Wenbo and Yi,

Congratulation! Very good news.

Thanks,
Awad

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Friday, May 7, 2021 11:53 AM
To: Zhang, Wenbo <we2zhang@UTMB.EDU>; Wang, Tian <ti1wang@UTMB.EDU>; 单超 <shanchao@wh.iov.cn>; Zou, Jing <jizou@UTMB.EDU>; Adam, Awad <awadam@UTMB.EDU>; Ha, Yonju <yoha@UTMB.EDU>; Shi, Shuizhen <shushi@UTMB.EDU>; Xia, Fan <faxia@UTMB.EDU>; Liu, Hua <hualiu@UTMB.EDU>; Zhang, Ming <MZHANG@augusta.edu>; ophthal.ly@gmail.com <ophthal.ly@gmail.com>
Subject: Re: Decision has been reached on your submission to Acta Neuropathologica Communications - ANEC-D-21-00206R1 - [EMID:c7dc225b8e660493]

Dear Wenbo and Yi,
Thanks for the great news. Congratulations to the team for the amazing work!
Best, Pei-Yong

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From: Zhang, Wenbo <we2zhang@UTMB.EDU>
Sent: Friday, May 7, 2021 8:42:38 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; Wang, Tian <ti1wang@UTMB.EDU>; 单超 <shanchao@wh.iov.cn>; Zou, Jing <jizou@UTMB.EDU>; Adam, Awad <awadam@UTMB.EDU>; Ha, Yonju <yoha@UTMB.EDU>; Shi, Shuizhen <shushi@UTMB.EDU>; Xia, Fan <faxia@UTMB.EDU>; Liu, Hua <hualiu@UTMB.EDU>; Zhang, Ming <MZHANG@augusta.edu>; ophthal.ly@gmail.com <ophthal.ly@gmail.com>
Subject: FW: Decision has been reached on your submission to Acta Neuropathologica Communications - ANEC-D-21-00206R1 - [EMID:c7dc225b8e660493]

Dear All,

Good morning. I am so excited that our work is accepted by Acta Neuropathologica Communications which is an excellent journal in the field of neurodegenerative diseases. Both reviewers liked this manuscript very much in particular the novel finding about retinal vascular degeneration after zika virus infection. Thank you very much for your critical contributions to this work. Moreover, as you know, Yi has left my lab in March. So this publication is a fruit of her work in the past three years. We appreciated all of her contributions and wish the best for her next journey!

Cheers,
Wenbo

-----Original Message-----
From: em.anec.0.7322b0.046bfd3b@editorialmanager.com [mailto:em.anec.0.7322b0.046bfd3b@editorialmanager.com] On Behalf Of Acta Neuropathologica Communications Editorial office
Sent: Friday, May 07, 2021 7:10 AM
To: Zhang, Wenbo <we2zhang@UTMB.EDU>
Subject: Decision has been reached on your submission to Acta Neuropathologica Communications - ANEC-D-21-00206R1 -

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CC: anc@biomedcentral.com

ANEC-D-21-00206R1
Zika virus induces neuronal and vascular degeneration in developing mouse retina Yi Li; Shuizhen Shi; Fan Xia; Chao Shan; Yonju Ha; Jing Zou; Awadalkareem Adam; Ming Zhang; Tian Wang; Hua Liu; Pei-Yong Shi; Wenbo Zhang Acta Neuropathologica Communications

Dear Professor Zhang,

I am pleased to inform you that your manuscript "Zika virus induces neuronal and vascular degeneration in developing mouse retina" (ANEC-D-21-00206R1) has been accepted for publication in Acta Neuropathologica Communications.

Before publication, our production team will check the format of your manuscript to ensure that it conforms to the standards of the journal. They will be in touch shortly to request any necessary changes, or to confirm that none are needed.

Articles in this journal may be held for a short period of time prior to publication. If you have any concerns please contact the journal.

Please quote your manuscript number, ANEC-D-21-00206R1, when inquiring about this submission.

We look forward to publishing your manuscript and I do hope you will consider Acta Neuropathologica Communications again in the future.

Best wishes,

Jeroen J.M. Hoozemans
Acta Neuropathologica Communications
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Our flexible approach during the COVID-19 pandemic

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To: ophthal.ly@gmail.com[ophthal.ly@gmail.com]; Shi, Shuizhen[shushi@UTMB.EDU]; Xia, Fan[faxia@UTMB.EDU]; shanchao@wh.iov.cn[shanchao@wh.iov.cn]; Ha, Yonju[yoha@UTMB.EDU]; Zou, Jing[jizou@UTMB.EDU]; Adam, Awad[awadam@UTMB.EDU]; Zhang, Ming[MZHANG@augusta.edu]; Wang, Tian[ti1wang@UTMB.EDU]; Liu, Hua[hualiu@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]
From: Zhang, Wenbo[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=20857D4378DE49909C112784C71353F2-ZHANG, WENB]
Sent: Wed 5/26/2021 8:01:54 AM (UTC-05:00)
Subject: Our published paper-ZIKV in the retina
ZIKV-retina.pdf

Dear All,

Good morning. Our paper is just published online. Please see the attached file for your reference. Thank you again for your critical contributions that made this final product possible. We look forward to our continuous and successful collaborations in the future.

Best regards,
Wenbo

Acta Neuropathologica Communications

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Zika virus induces neuronal and vascular degeneration in developing mouse retina

Yi Li[1], Shuizhen Shi[1], Fan Xia[1], Chao Shan[2], Yonju Ha[1], Jing Zou[2], Awadalkareem Adam[3], Ming Zhang[4], Tian Wang[3], Hua Liu[1,5*], Pei-Yong Shi[2,6*] and Wenbo Zhang[1,6,7*]

Abstract

Zika virus (ZIKV), a mosquito-borne flavivirus, can cause severe eye disease and even blindness in newborns. However, ZIKV-induced retinal lesions have not been studied in a comprehensive way, mechanisms of ZIKV-induced retinal abnormalities are unknown, and no therapeutic intervention is available to treat or minimize the degree of vision loss in patients. Here, we developed a novel mouse model of ZIKV infection to evaluate its impact on retinal structure. ZIKV (20 plaque-forming units) was inoculated into neonatal wild type C57BL/6J mice at postnatal day (P) 0 subcutaneously. Retinas of infected mice and age-matched controls were collected at various ages, and retinal structural alterations were analyzed. We found that ZIKV induced progressive neuronal and vascular damage and retinal inflammation starting from P8. ZIKV-infected retina exhibited dramatically decreased thickness with loss of neurons, initial neovascular tufts followed by vessel dilation and degeneration, increased microglia and leukocyte recruitment and activation, degeneration of astrocyte network and gliosis. The above changes may involve inflammation and endoplasmic reticulum stress-mediated cell apoptosis and necroptosis. Moreover, we evaluated the efficacy of preclinical drugs and the safety of ZIKV vaccine candidate in this mouse model. We found that ZIKV-induced retinal abnormalities could be blocked by a selective flavivirus inhibitor NITD008 and a live-attenuated ZIKV vaccine candidate could potentially induce retinal abnormalities. Overall, we established a novel mouse model and provide a direct causative link between ZIKV and retinal lesion in vivo, which warrants further investigation of the underlying mechanisms of ZIKV-induced retinopathy and the development of effective therapeutics.

Keywords: Zika virus, Retina, Neuronal degeneration, Vascular degeneration, Inflammation, Endoplasmic reticulum stress, Drug efficacy, Vaccine safety

Introduction

Zika virus (ZIKV) is an enveloped and spherical flavivirus which is transmitted by *Aedes* mosquitoes [15]. The virus was initially isolated from a rhesus monkey in the Zika Forest of Uganda in 1947 [8], and has caused outbreaks in Asia, the Pacific island and more recently in South and Central America [3, 4, 24], followed by a rapid spread to other countries during 2015–2016 including autochthonous transmissions in Florida and Texas in the United States [11]. Although symptomatic infection in humans results in mostly a mild and self-limiting febrile disease, it has also been linked to a neurological autoimmune disorder Guillain-Barré syndrome in adults and microcephaly in fetuses and infants born to infected mothers during pregnancy [3, 15, 34]. In addition to neuronal damage in the brain, infants with congenital ZIKV infection are associated with a high rate of ocular abnormalities in which the most common lesions are retinal lesions, chorioretinal atrophy and optic nerve abnormalities.

*Correspondence: hualiu@utmb.edu; peshi@utmb.edu; we2zhang@utmb.edu
[1] Department of Ophthalmology and Visual Sciences, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX 77555-0144, USA
[2] Department of Biochemistry and Molecular Biology, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX 77555-0144, USA
Full list of author information is available at the end of the article

Occasionally calcification in the retina and lens are also noted [5]. Mechanisms of ZIKV-induced retinal abnormalities are unknown and no therapeutic intervention is available to treat or minimize the degree of vision loss in patients.

Studies of pathology related to ZIKV infection in human subjects have been limited since most of the infected individuals are asymptomatic or mildly symptomatic; and only 4–8% fetuses or infants from pregnant women with confirmed ZIKV infection exhibit ZIKV-associated birth defects [28, 38]. Therefore animal models are critical for investigation of ZIKV-induced pathology. Mouse models have been widely used in biomedical research due to low-cost maintenance, a short reproductive cycle and easy genetic modification. Because ZIKV does not replicate efficiently in adult wild type (WT) mice, blocking type I interferon receptor (IFNAR1) by gene deletion or blocking antibody is necessary to overcome infection barrier [1]. However, no apparent retinal pathology or abnormality was observed in ZIKV-infected adult mice with IFNAR blockade or in IFNAR heterozygous fetuses from ZIKV-infected IFNAR deficient ($IFNAR1^{-/-}$) dam despite the presence of viremia [16] and moderate loss of retinal ganglion cells (RGCs) and cones at 60–70 days after infecting 3-week-old A129 $IFNAR1^{-/-}$ mice [36]. Moreover, blockade of IFN pathway causes immune deficiency which may compromise the understanding of pathological changes upon ZIKV infection. Chorioretinitis and retinal cell death were found in adult WT mice receiving injections of a substantial amount of ZIKV into vitreous or aqueous humor [30, 31]. Nevertheless, intravitreal injection or intra-aqueous injection is not a disease-relevant route for ZIKV transmission to the retina. Two studies show intra-amniotic injection of ZIKV into C57BL/6 WT mice at embryonic day 13.5 (E13.5) or E15 allow infected mice to grow into puberty and recapitulate several symptoms of clinical congenital Zika syndrome including severe retinal neuronal degeneration [6, 29]. The limitation of intra-amniotic injection is that this procedure requires surgery and special skills and the maternal immune response and placental insufficiency may affect neural development, making it complicated to interpret the data.

Mouse retinal development is initiated at approximately E12. It continues during the first 3 weeks after birth in a process very similar to human retinal development during the third trimester of pregnancy [9]. At birth (postnatal day (P) 0), mouse retina consists of a multitude of neuroblasts (progenitors) and some differentiated RGCs, amacrine cells and horizontal cells. From P0 to P8, retinal development continues, including the formation of bipolar cells, photoreceptors (rods and cones) and a single glial cell type (Müller cells) by neuroblasts in a temporally ordered sequence [18], the formation of each retinal layers, and the maturation of neuronal synapses [9]. Coincident with the final stages of neuronal differentiation, the eyes are open and the vision process is initiated at P14. Mouse retinal vascularization begins at P0 and completes by P21 [9]. Taking these advantages, we established a novel mouse model using postnatally developing mouse retina to study retinal abnormalities associated with ZIKV, provided a causative link between ZIKV and retinal lesion in vivo, and demonstrated its use to test the efficacy and safety of therapeutic interventions.

Materials and methods

Mice

C57BL/6J mouse colony was purchased from Jackson Laboratory (Bar Harbor, ME) and maintained in the animal facility at the University of Texas Medical Branch. Mice were housed under standard conditions of 12:12 light/dark cycle with food and water available ad libitum. Animal protocols were approved by the Institutional Animal Care and Use Committee. All experimental procedures and use of animals were performed in accordance with the Association for Research in Vision and Ophthalmology Statement for the Use of Animals in Ophthalmic and Vision Research.

ZIKV infection and inhibitor treatment

ZIKV Cambodian strain FSS13025 that is phylogenetically closely related to those circulating in the Americas was produced using an infectious complementary DNA (cDNA) clone as described previously [26]. A live-attenuated ZIKV vaccine candidate that contains a 10-nucleotide deletion in the 3' untranslated region of the ZIKV genome (10-del ZIKV) was developed and produced using the FSS13025 infectious clone [25]. ZIKV (20 PFU in 10 μl PBS) or 10-del ZIKV (20 or 200 or 2000 PFU in 10 μl PBS) was injected into neonatal mice at Postnatal day (P) 0 subcutaneously. Sofosbuvir (SOF) (80 mg/kg) was injected right after ZIKV injection once every day until day 13 (P0–P7: subcutaneously; P8-P13: intraperitoneally). NITD008 (5 mg/kg) was injected right after ZIKV injection and once every other day until day 12 (P0–P6: subcutaneously; P8–P12: intraperitoneally). Vehicle (PBS with 1% DMSO) was injected into control mice. All infected mice were observed every day. The eyeballs were harvested at P5, P8, P11, P14 and P21.

Immunofluorescence staining of retinal sections

Eyeballs were fixed in 4% paraformaldehyde (PFA) for 60 min, equilibrated in 30% sucrose overnight, and embedded in OCT compound. Cryosections (10 μm) were cut through the optic nerve, post-fixed with 4% PFA for 10 min, rinsed with PBS, permeabilized with

PBS containing 0.1% Triton X-100 for 15 min at room temperature, and blocked with PowerBlock (BiogenX, San Ramon, CA) for 1 h at room temperature. Next, sections were probed with primary antibodies against calbindin (1:1000, ab82812, Abcam, Cambridge, MA), CD31 (1:1000. 553369, BD Biosciences, San Jose, CA), cleaved-caspase3 (1:400, 9661, Cell signaling, Danvers, MA), cone-arrestin (1:5000, AB15282, MilliporeSigma, Burlington, MA), Dab1 (1:3000, 18936, Rockland, Pottstown, PA), GFAP (1:500, Z033401-2, Agilent Technologies, Santa Clara, CA), glutamine synthetase (1:1000, MAB302, MilliporeSigma), PKCα (1:500, P5704, MilliporeSigma), pRIP3 (1:1000, 205421, Abcam), rhodopsin (1:2000, sc-57432, Santa Cruz Biotechnology, Santa Cruz, CA) and ZIKV antibody (1:500, NBP2-52666, Novus Biologicals, Littleton, CO) overnight at 4 °C. After washing with PBS, sections were incubated with appropriate secondary antibodies for 1 h and mounted with medium containing DAPI (Abcam) or nuclei were counterstained with propidium iodide (PI; ThermoFisher Scientific, Waltham, MA). Images were taken with confocal microscopy (LSM 800, Carl Zeiss, Inc., Thornwood, NY).

Immunostaining of retinal whole-mounts

Eyes were enucleated and fixed in 4% PFA at 4 °C overnight. Next day, retinas were dissected, washed with PBS, blocked and permeabilized with PBS containing 5% normal goat serum and 0.3% Triton X-100 for 3 h at room temperature. Retinas were then incubated with isolectin B4 (ThermoFisher Scientific) or primary antibodies against Iba1 (1:200, 019–19741, FUJIFILM Wako Chemicals, Richmond, VA), Tuj1 (1:400, 801202, BioLegend, San Diego, CA), RBPMs (1:200, ABN1376 (guinea pig) or ABN1362 (rabbit), MilliporeSigma), CD31 (1:200), CD45 (1:400, 550539, BD Biosciences) and GFAP (1:500) overnight at 4 °C. Subsequently, retinas were washed with PBS and then incubated with appropriate secondary antibodies at 4 °C for 4 h. Finally, retinas were mounted with aqua-mount medium (ThermoFisher Scientific), and images were captured with confocal microscopy.

Hematoxylin and Eosin (H&E) staining

After fixation, retinal frozen sections were immersed into hematoxylin for 5 min followed by washing in double distilled water (ddH_2O). Slides were then dipped in 0.5% Eosin for 45 s, washed in ddH_2O, dehydrated in graded ethanol and vitrified by xylene. Slides were mounted with Permount mounting medium (ThermoFisher Scientific). Images were captured by a digital camera in a bright field microscope (Leica Camera Inc., Allendale, NJ) for retinal structure.

Real-time quantitative PCR

Retinas were collected at P5 or P8 from control and ZIKV-infected mice. Total retinal mRNA was isolated using miRNeasy Mini Kit (Qiagen, Germantown, MD), quantified using NanoDrop (ThermoFisher Scientific), and converted to cDNA using High-Capacity cDNA Reverse Transcription Kit (ThermoFisher Scientific). Quantitative PCR was performed with SYBR Green Master Mix (Applied Biosystems, Waltham, MA) using a PCR system (StepOnePlus; Applied Biosystems). Primer sequences for mouse transcripts were as follows: Hprt For-5′-GAA AGA CTT GCT CGA GAT GTC ATG-3′; Hprt Rev-5′-CAC ACA GAG GGC CAC AAT GT-3′; ZIKV prM gene For-5′-GAG AGC GAG GAA CAT CCA GAC T-3′; ZIKV prM gene Rev-5′-CCT GAA GTT CCT GCT GGG TAG T-3′. Inflammatory genes: CXCL10 For-5′-GGA CGG TCC GCT GCA A-3′; CXCL10 Rev-5′-CCC TAT GGC CCT CAT TCT CA-3′; MCP1 For-5′-GGC TCA GCC AGA TGC AGT TAA-3′; MCP1 Rev-5′-CCT ACT CAT TGG GAT CAT CTT GCT-3; ICAM-1 For-5′-CAG TCC GCT GTG CTT TGA GA-3′; ICAM-1Rev-5′-CGG AAA CGA ATA CAC GGT GAT-3′; IL-1β For-5′-AGT TGA CGG ACC CCA AAA GA-3′; Il-1β Rev-5′-GGA CAG CCC AGG TCA AAG G-3′; IL-6 For-5′-CCA CGG CCT TCC CTA CTT C-3′; IL-6 Rev-5′-TTG GGA GTG GTA TCC TCT GTG A-3′; iNos For-5′-GGC AGC CTG TGA GAC CTT TG-3′; iNos Rev-5′-TGC ATT GGA AGT GAA GCG TTT-3′; TNFα For-5′-GGT CCC CAA AGG GAT GAG AA-3′; TNFα Rev-5′-TGA GGG TCT GGG CCA TAG AA-3′; VCAM-1 For-5′-ACA AGT CTA CAT CTC TCC CAG GAA TAC-3′; VCAM-1 Rev-5′-CAC AGC ACC ACC CTC TTG AA-3′. ER stress genes: GRP78 For-5′-ACT TGG GGA CCA CCT ATT CCT-3′; GRP78 Rev-5′-ATC GCC AAT CAG ACG CTC C-3′; XBP1s For-5′-TGC TGA GTC CGC AGC AGG TG-3′; XBP1s Rev-5′-GCT GGC AGG CTC TGG GGA AG-3′; ATF4 For-5′-TCC TGA ACA GCG AAG TGT TG-3′; ATF4 Rev-5′-ACC CAT GAG GTT TCA AGT GC-3′; CHOP For-5′-CTG GAA GCC TGG TAT GAG GAT-3′; CHOP Rev-5′-CAG GGT CAA GAG TAG TGA AGG T-3′; ATF6 For-5′-TGC CTT GGG AGT CAG ACC TAT-3′; ATF6 Rev-5′-GCT GAG TTG AAG AAC ACG AGT C-3′. Data were normalized to internal control Hprt and the fold difference in different transcripts was calculated by the ΔΔCT method.

Fluorescence in situ hybridization (FISH) using RNAscope technology

Eyeballs were fixed in 4% PFA for 60 min, equilibrated in 30% sucrose overnight, and embedded in OCT compound. Cryosections (10 μm) were cut through the

optic nerve. Then retinal sections were boiled in the target retrieval reagent (Cat #322000, Advanced Cell Diagnostics, Hayward, CA); and protease digestion was performed using protease 3 (Cat #322337, Advanced Cell Diagnostics). Next, the tissue slides were immediately rinsed with water and incubated with Zika probe (Cat #467771, Advanced Cell Diagnostics) targeting JN860885.1, and then hybridized with the signal amplification reagents of RNAscope Fluorescent Multiplex detection kit (Advanced Cell Diagnostics) following the manufacturer's instructions. At the last step, sections were counterstained with DAPI to label nuclei, and images were taken by confocal microscopy.

Statistical analysis

Statistical analysis was conducted using GraphPad Prism program (GraphPad Software, Version 8.0, La Jolla, CA). Results were presented as mean ± standard error of mean (SEM) and analyzed by Student's t-test. A P value < 0.05 was considered statistically significant.

Results

ZIKV infection induces retinal neuronal loss and glial disruption and activation

To develop a simple and reproducible animal model of ZIKV, we inoculated ZIKV (20 plaque-forming units (PFU)) into neonatal C57BL/6J mice at P0 subcutaneously (Fig. 1a) and observed mouse behavior afterwards until P21. We found that ZIKV-infected mice exhibited less movement, tremors and bilateral hind limb paralysis. They had significantly reduced body weight, body length and head length compared to age-matched uninfected mice (Fig. 1b).

To test whether retinal pathology occurs in mice infected with ZIKV, we stained retinal sections from ZIKV-infected and control mice at P21 by H&E and examined their structures (Fig. 1c). In control group, all retinal layers were intact and noted with dense ganglion cell layer (GCL), inner nuclear layer (INL) and outer nuclear layer (ONL), which were separated by two plexiform layers (inner plexiform layer (IPL) and outer plexiform layer (OPL). However, the retinas of ZIKV-infected mice exhibited greatly reduced total retinal thickness with few GCL cells, attenuated INL and almost disappeared IPL and OPL (Fig. 1c).

To further define the morphological alterations in the retinas of ZIKV-infected mice (Fig. 2a), we performed immunohistochemical staining with antibodies against retinal cell specific markers. In the outer retinas of ZIKV-infected mice, the expression of rhodopsin, the marker for rod photoreceptor cells, showed an apparent decline in immunointensity compared with control retinas (Fig. 2b, g). Moreover, cone photoreceptor cells, evaluated by the staining with antibody against cone arrestin, distributed evenly throughout the retina in control group. In comparison, cone arrestin staining was aberrant, and the number and length of cone photoreceptor cells were significantly decreased in ZIKV-infected retinas (Fig. 2c, h).

We also evaluated alternations of horizontal cells, amacrine cells and rod bipolar cells, which are intermediate neurons connecting photoreceptors and retinal ganglion cells (RGCs), with antibodies against calbindin, Dab1 and PKCα, respectively. We observed that the horizontal cell bodies were located in the INL of control retinas, but they were largely decreased in ZIKV-infected retinas (Fig. 2d, i). Similarly, Dab1, the marker for amacrine cells that contribute to vertical communication within the retina, was expressed in the retinal INL in control mice, whereas it was barely found in ZIKV-infected mice (Fig. 2e, j). Rod bipolar cells are responsible for transmitting signals from photoreceptors to RGCs. In control retina, PKCα was expressed in rod bipolar cell bodies and axon terminals which reach the border between the IPL and GCL. But less rod bipolar cell bodies and axon terminals, and shorter axons were found in ZIKV-infected retinas (Fig. 2f, k).

RGCs are the only output neurons of the retina which collect visual information and send it to the brain through their axons. To further investigate whether RGCs were affected by ZIKV infection, we used Tuj1 antibody, a marker for RGCs in the retina to stain retinal flatmounts from two groups of mice at P21. We found that the number of RGCs and the diameter of axons in the peripheral, middle and central area of the retina were dramatically decreased in ZIKV-infected mice compared to control mice (Fig. 2l). These results indicate all retinal neurons undergo significant loss during ZIKV infection.

Retinal glial cells, which include both Müller cells and astrocytes, are crucial for maintaining normal function of the retina. To assess their changes in the retina after ZIKV infection, we stained retinal flatmounts or sections with antibody against-GFAP, a marker for astrocytes and gliosis, or antibody against-glutamine synthetase (GS), which is expressed in Müller cells and their processes. We observed that the astrocyte network, which serves as a template for angiogenesis and maintains vascular integrity [21], was disorganized and astrocyte gliosis was dramatically increased (Fig. 3a, b). Moreover, GFAP level was dramatically increased in Müller cells (Fig. 3b), which were GS-positive and became shorter with abnormal morphology in ZIKV-infected retinas (Fig. 3c).

These results indicate that ZIKV infection at P0 leads to thinning and aberrant retinal structure and marked loss of retinal neurons, associated with the disruption of astrocyte network and gliosis.

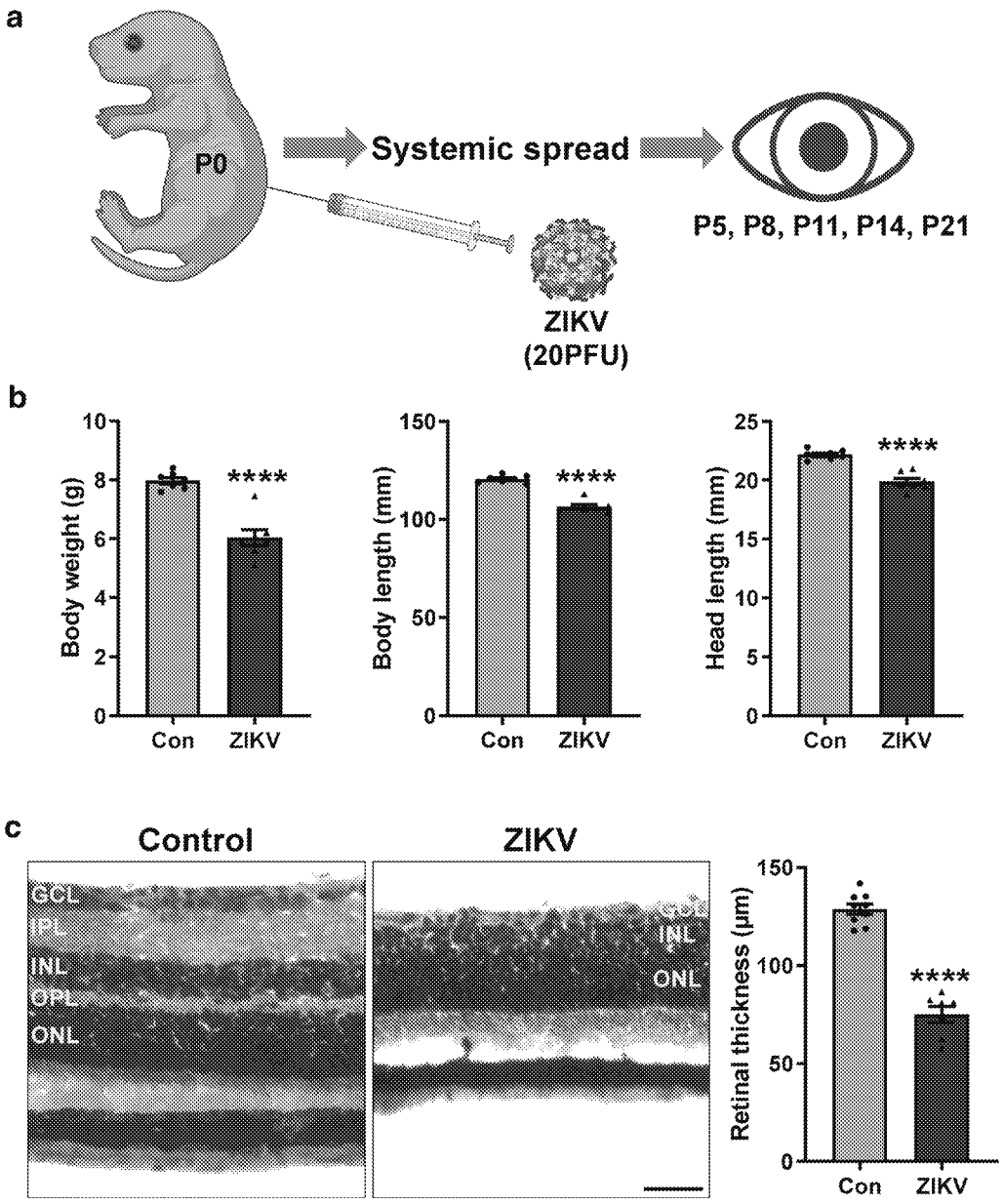


Fig. 1 The effects of ZIKV infection on mouse development. **a** Schematic presentation of our model (generated using BioRender). Neonatal C57BL/6 mice were injected with 20 PFU ZIKV at postnatal day (P) 0 subcutaneously. Eyeballs were collected at P5, P8, P11, P14 and P21. **b** Graphs represent body weight, body length including tail and head length of control and ZIKV-infected mice at P21. **c** Representative images of H&E-stained retinal sections from control and ZIKV-infected mice at P21. Graph represents retinal thickness from GCL to ONL. GCL: ganglion cell layer; IPL: inner plexiform layer; INL: inner nuclear layer; OPL: outer plexiform layer; ONL: outer nuclear layer. Scale bar = 50 μm. Data are presented as mean ± S.E.M. n = 7–9 per group. ****$p < 0.0001$ compared to control mice

ZIKV infection elicits loss of retinal vasculature and increase in inflammation

To further characterize the influence of ZIKV on retinal vasculature, we stained ZIKV-infected and control retinas with antibody for endothelial cell marker CD31 at P21. In control mice, the inner retinal vasculature had developed into three layers: the superficial, intermediate and deep layers at P21. In contrast, only the superficial layer of vasculature was observed in retinal section of ZIKV-infected mice (Fig. 3d, upper panel). Moreover, vessel density was greatly decreased while large avascular area was observed in the superficial layer of

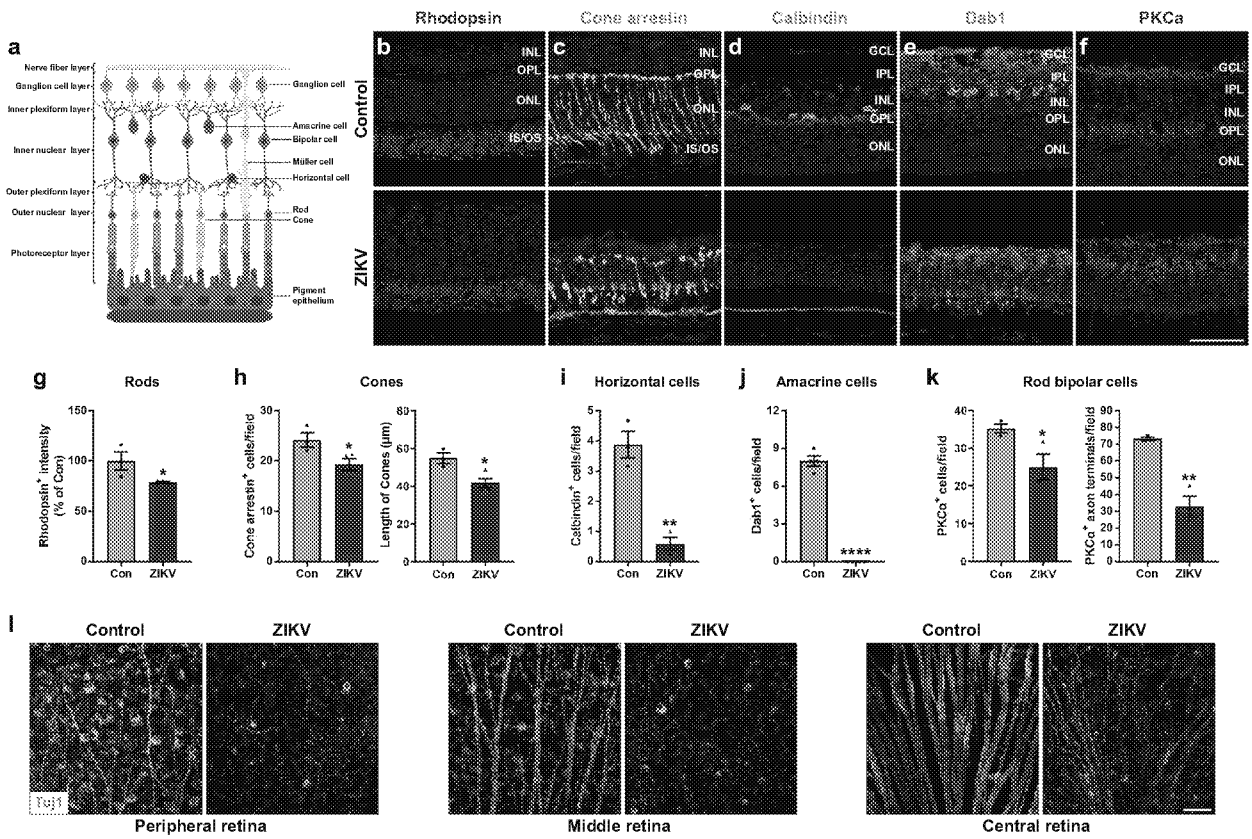


Fig. 2 ZIKV infection impairs retinal neurons. **a** Schematic illustration of retinal structure (generated using BioRender). **b**–**f** Immunohistochemical staining on retinal sections from control and ZIKV-infected mice with retinal specific markers, including rhodopsin for rods, cone arrestin for cones, calbindin for horizontal cells, Dab1 for amacrine cells, PKCα for rod bipolar cells at P21. Blue: DAPI staining for nuclei. **g**–**k** Graphs represent the quantification of these cells. **l** Representative images of Tuj1-stained RGCs and their axons in the peripheral, middle and central area of retinal flatmounts at P21. Scale bar = 50 μm. Data are presented as mean ± S.E.M. n = 3–4 per group. $^{*}p < 0.05$, $^{**}p < 0.01$, $^{****}p < 0.0001$ compared to control mice

ZIKV-infected retinas (Fig. 3d, middle and lower panels), suggesting ZIKV infection either inhibits vessel development or induces vessel degeneration.

Immune response and inflammatory cascade play an important role in retinal pathology. Therefore, we further investigated whether ZIKV could cause inflammatory immune response in mice retina. Whole-mount retinas were stained with antibody against CD45, which was expressed on leukocytes. In control group, there were few leukocytes. However, CD45-positive cells were abundant in ZIKV-infected retinas, suggesting ZIKV infection increases leukocyte infiltration in the retina (Fig. 3e). In addition to leukocytes from circulation, microglia play an important role in retinal inflammation by functioning as resident innate immune cells. We subsequently investigated changes of microglia in retinal flatmounts by labeling them with anti-Iba1 antibody. While microglia were sparsely distributed and exhibited a highly ramified morphology (resting state) in control retinas, ZIKV-infected retinas showed massive amount of microglia with retracted processes and amoeboid soma (activated state) [23] (Fig. 3f).

Overall, these data indicate that ZIKV infection can cause a severe vascular phenotype with prominently reduced vascular coverage and vessel density, accompanied with increased inflammation in the retina.

ZIKV induces progressive retinal degeneration and inflammation

To determine the onset of ZIKV-induced retinopathy in our mouse model, we collected samples from ZIKV-infected and control mice at P5, P8, P11 and P14, respectively. ZIKV RNA was detected in 50% of P5 retinas and all P8 retinas, and its average level in P8 retinas was more than 1000-fold higher than that in P5 retinas (Fig. 4a), suggesting P5 was a very early stage when ZIKV entered retinas. Analysis of ZIKV RNA by RNAscope and protein by a pan flavivirus antibody (4G2) revealed

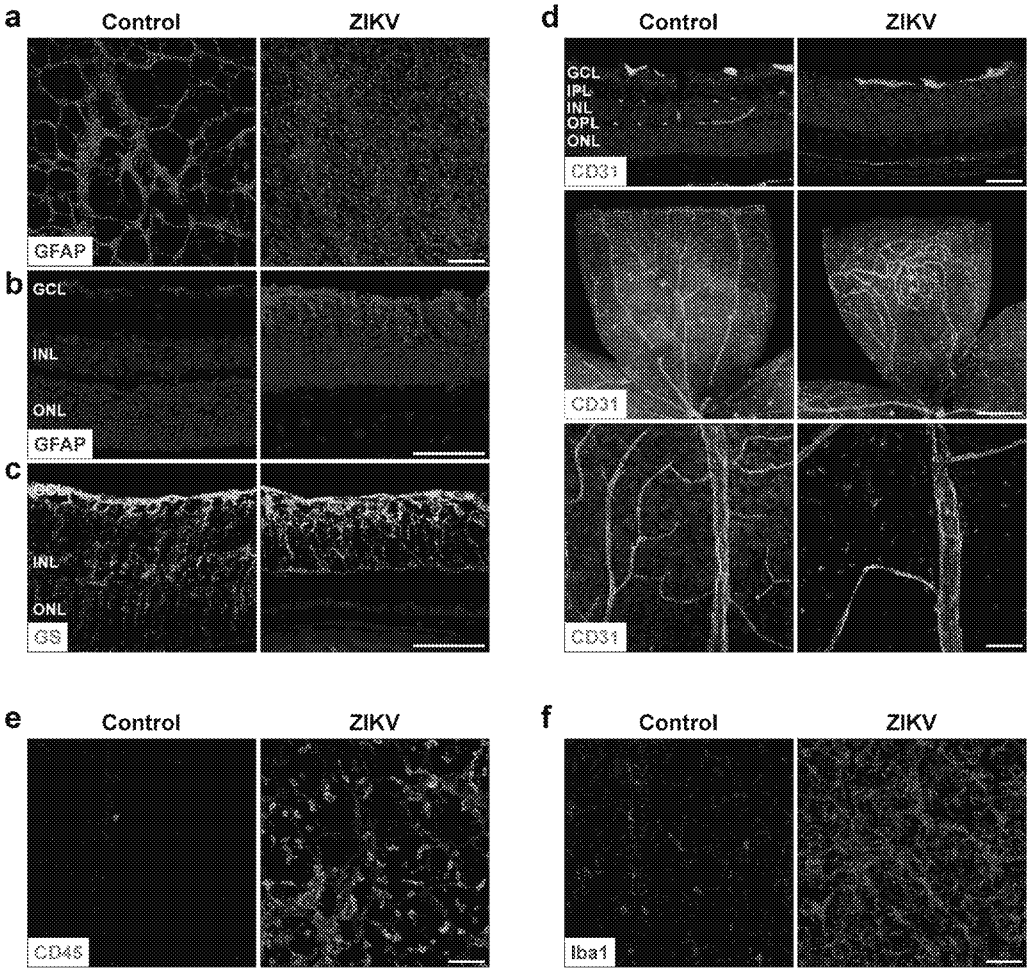


Fig. 3 ZIKV infection induces retinal gliosis, vessel impairment and inflammation. ZIKV was injected into neonatal mice at P0 and retinas were collected at P21. **a**, **b** Representative images of GFAP staining in retinal flatmounts and sections. **c** Representative images of glutamine synthetase (GS) staining in retinal sections. **d** CD31 staining for vasculature in retinal sections (upper panel) and flatmounts (middle and lower panels). **e** CD45 staining for leukocytes. **f** Iba1 staining for microglia. Blue: DAPI staining for nuclei. Scale bar = 50 μm except the middle panel in d where scale bar = 500 μm. n = 3–6 per group

that ZIKV-infected cells were mainly present in the GCL and INL at P8 (Fig. 4b, c). Morphologically, at P5, there was no evident difference in retinal thickness (Additional file 1: Fig. S1a), vascular area and vessel density (Additional file 1: Fig. S1b), the number and morphology of RGCs and their axons (Additional file 1: Fig. S1c, S1d and S1g), astrocyte network (Additional file 1: Fig. S1e), and the number of leucocytes (Additional file 1: Fig. S1f and S1h) between ZIKV-infected and control mice. At P8, retinal thickness (Fig. 5a), vascular area and vessel density (Fig. 5b) and astrocyte network (Fig. 5e) were indistinguishable in control and ZIKV-infected retinas. However, a close examination revealed that abnormal neovascular tufts (Fig. 5b, lower panel), increased microglia with activated morphology (Fig. 5f and i) and many leukocytes ($CD45^+$ cells) (Fig. 5g and j) were present in ZIKV-infected retinas. Moreover, although no significant difference was observed in the number and morphology of RGCs and their axons (Fig. 5c, d and h), there was a slight trend toward reduced RGCs.

At P11, vessel density was significantly decreased accompanied with microvessel enlargement (Additional file 1: Fig. S2a), and prominent loss of RGC and their axons were observed in ZIKV-infected retinas (Additional file 1: Fig. S2b). As time went on, ZIKV-infected mice turned to be weaker with unsteady gait and mild ataxia at P14. At this time point, retinal morphological changes were much similar to what occurred at P21 (Fig. 6). The thickness of total retina, IPL and INL was all significantly decreased (Fig. 6a).

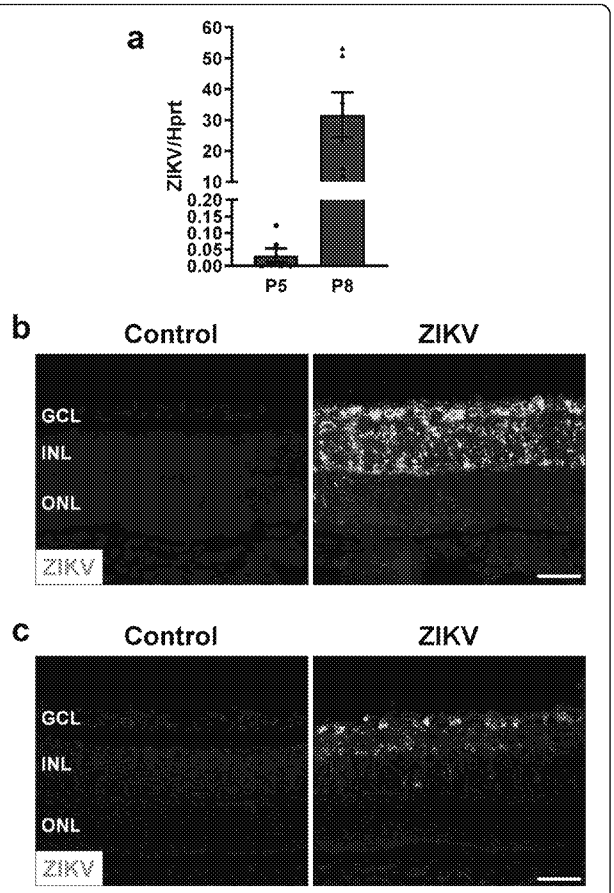


Fig. 4 ZIKV expression in the retina. ZIKV was injected into neonatal mice at P0 and retinas were collected at P5 and P8. **a** Viral RNA in the retinas was detected by qPCR. n = 6 per group. **b** Zika viral RNA in retinal sections was assessed by FISH at P8. **c** ZIKV protein expression was examined by immunostaining with a pan flavivirus antibody (4G2) at P8. n = 3 per group

Vascular density was further decreased (Fig. 6b), RGCs and their axons were largely diminished (Fig. 6c) and astrocyte network was disrupted (Fig. 6d), associated with exacerbated microglial recruitment and activation (Fig. 6e) and leukocyte infiltration (Fig. 6f). These results indicate that ZIKV induces progressive retinal degeneration and inflammation from P8 although it does not affect initial vascular development and formation of retinal layers.

Potential mechanisms of ZIKV-induced retinal degeneration

Excessive or uncontrolled inflammation and endoplasmic reticulum (ER) stress are key mediators for cell death [13]. To determine the potential mechanisms of ZIKV-induced retinal degeneration, we analyzed retinal inflammation and ER stress in P8 retinas (Fig. 7a and b). We found that levels of several key inflammatory molecules including chemokines (CCL2 and CXCL10), pro-inflammatory cytokines (TNFα, IL-1β and IL-6), adhesion molecules (ICAM-1 and VCAM-1) and iNOS were all increased 1.6–1300 folds in ZIKV-infected retinas. Similarly, key molecules involved in ER stress, including XBP1s, GRP78 and CHOP, were significantly increased. Associated with increases in inflammation and ER stress, analysis of cleaved caspase 3, a marker for apoptosis, and phosphorylated receptor-interacting protein 3 (pRIP3), a marker for necroptosis, revealed that both cleaved caspase 3 and pRIP3 were significantly increased in ZIKV-infected retinas in which cleaved caspase 3-positive cells were mainly localized in the INL whereas pRIP3-positive cells were mainly located in the GCL and IPL (Fig. 7c). These results suggest that ZIKV-induced retinal degeneration may involve inflammation and ER stress-mediated cell apoptosis and necroptosis.

Evaluation of the drug efficacy in the model of ZIKV-induced retinopathy

Having established and characterized this mouse model of ZIKV-induced retinopathy, we assessed whether it could be used for drug discovery. Recent studies have showed that antiviral agent sofosbuvir (SOF; a clinically approved drug for hepatitis C virus) could reduce ZIKV viral load [2, 10], therefore we tested if SOF can inhibit ZIKV-induced retinal degeneration. P0 pups were infected with ZIKV, followed by administration of SOF (80 mg/kg) or vehicle control every day until P13. At P14 when ZIKV-induced retinal degeneration was evident, we examined ZIKV-induced retinal alternations. We found that there was significant variation in SOF-treated pups in which SOF only successfully blocked ZIKV-induced retinal degeneration in 44% pups (Table 1 and Additional file 1: Fig. S3), suggesting SOF is not a sufficient inhibitor for ZIKV infection. NITD008 is a selective flavivirus inhibitor that shows potent efficacy against ZIKV infection [7, 35]. We administered NITD008 (an adenosine analog, 5 mg/kg) or vehicle control right after ZIKV injection and once every other day until day 12, and found that all NITD008-treated ZIKV-infected mice exhibited normal retinal structure which was comparable with non-infected mice (Table 1 and Fig. 8a). Moreover, NITD008 treatment blocked ZIKV-induced degeneration of retinal vasculature (Fig. 8b) and RGCs (Fig. 8c), and gliosis and inflammation (Fig. 8d–f). Collectively, these results indicate that our model can be used to evaluate drug efficacy and NITD008 is an effective candidate to treat ZIKV-induced retinopathy.

Evaluation of the safety of ZIKV vaccine candidate

There is currently no licensed human vaccine for ZIKV, but several vaccine candidates have been developed

and evaluated in preclinical and clinical studies [27]. We tested whether our mouse model can be used to evaluate the safely of ZIKV vaccine candidates. We chose to evaluate a live-attenuated ZIKV vaccine with a 3'UTR deletion (10-del ZIKV) [25] in the current model. After subcutaneously inoculating the live-attenuated ZIKV vaccine (20, 200, or 2000 PFU) into neonatal C57BL/6 mice at P0 and collecting retinas at P21, we found the low dose had no effect on retinal structure, but medium and high doses of vaccine candidate caused retinal pathology at rates of 50% and 87.5% respectively (Table 2). The retinas with abnormality exhibited decreased retinal thickness (Fig. 9a), reduced vasculature (Fig. 9b), loss of RGCs (Fig. 9c), and/or increased gliosis (Fig. 9d) and microglial activation and leukocyte infiltration (Fig. 9e and f) as seen in ZIKV-infected WT retinas. These data suggest that this live-attenuated ZIKV vaccine may potentially induce retinal degeneration if non-optimal dose was provided during pregnancy.

Discussion

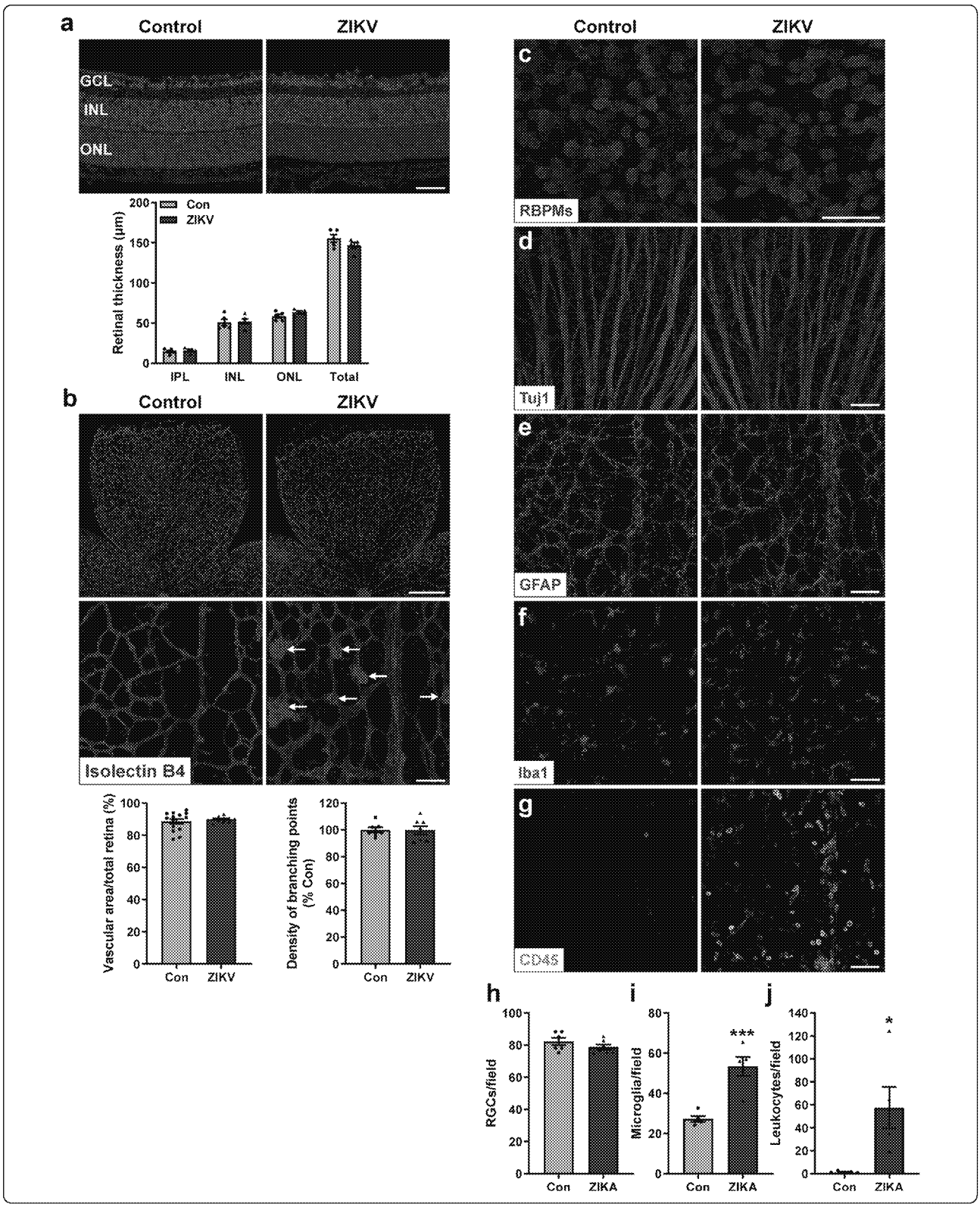
Mouse models have been widely used in biomedical research due to low-cost maintenance, a short reproductive cycle and easy genetic modification. In this study, we developed a novel and reproducible model of ZIKV-induced retinopathy using immunocompetent C57BL/6 mice. We demonstrated that P0 pups inoculated with ZIKV developed significant loss of RGCs and their axons, and retinal thinning during growing-up, which recapitulates a series of clinical features reflecting retinal neuronal and axonal degeneration when using non-invasive imaging to examine infants with Congenital Zika Syndrome, including neurosensory retinal thinning, discontinuation of the photoreceptor inner and outer segment junction, and optic nerve hypoplasia [33]. Moreover, retinal pathologic changes and the severity of retinal neuronal degeneration in our model are comparable to those when mice are infected at E13.5 and E15 via intra-amniotic injection with ZIKV [6, 29] though it is much easier to infect neonatal mice by subcutaneous injection of ZIKV, which brings virus to the retina via blood circulation, similar to what occurs following intra-amniotic injection. Clinically, among completed pregnancies with positive nucleic acid tests confirming ZIKV infection identified in the first, second, and third trimesters, CDC's analysis demonstrated the percentage of fetuses or infants with possible Zika-associated birth defects was 8%, 5%, and 4%, respectively [28]; another study of pregnancy outcomes after ZIKV infection in French Territories in the Americas also found that neurologic and ocular defects were 12.7%, 3.6% and 5.3%, respectively [14]. Therefore, our model is disease-relevant since pups are infected with ZIKV at a time point equivalent to human retinal development in the third trimester when ZIKV infection could still cause birth defects.

In addition to neurodegeneration, we found dramatic decreases of retinal vascular coverage and density in ZIKV-infected retinas. While ZIKV-induced neuronal damage is well appreciated in the brain and retina, the impact of ZIKV on vessels is largely unknown although a few in vitro studies demonstrate ZIKV could infect and replicate in endothelial cells, break down endothelial barriers and impair endothelial cell lipid homeostasis [17, 20, 22, 37], and Garcez et al. reported reduction in the vasculature density and vessel branching in the brain from IFN-deficient mouse with congenital ZIKV infection and reduced retinal vascular network was displayed in one image of this article [12]. Our study represents the first one to investigate ZIKV-induced retinal vasculature changes in detail. Unlike Garcez et al.'s study suggesting that the reduction of vasculature is caused by perturbation of vascular development by ZIKV [12], we found that initial retinal vascular development at P5 and P8 after ZIKV inoculation was not retarded although vascular tufts were noticed at P8. From P11 to P21, progressive reduction of vascular network was observed and large avascular area in the retina was found at P21, associated with extensive alterations in astrocyte morphology and disruption of its network that is usually in line with vasculature and supports vessels. These data suggest that ZIKV indeed induces significant retinal vascular degeneration in addition to possible perturbation of vascular development.

Of note, significant changes in vasculature are also found in infants with congenital Zika syndrome. In one study using OCT to examine retinal abnormalities, vessels appear very sparse and thin in some fundus

(See figure on next page.)

Fig. 5 ZIKV induces subtle retinal pathology at P8. ZIKV was injected into neonatal mice at P0 and retinas were collected at P8. **a** Representative images of PI-stained retinal sections at P8. Graph represents the thickness of individual retinal layers and total retina from GCL to ONL. n = 5 per group. **b** Representative images of retinal flatmounts labeled with isolectin B4 for vasculature. Arrows indicate neovascular tufts. Graphs represent vascular area (n = 11–14 per group) and the density of vessel branching points (n = 7–8 per group). **c**–**g** Representative images of retinal flatmounts labeled with anti-RBPMs and Tuj1 for RGCs and their axons, anti-GFAP for astrocytes, anti-Iba1 for microglia, and anti-CD45 for leukocytes. **h**–**j** Graphs represent the quantification of numbers of RGCs (n = 6–7 per group), microglia and leukocytes (n = 5 per group). Scale bar = 50 μm except the upper panel in b where scale bar = 500 μm. $^{*}p < 0.05$, $^{***}p < 0.001$ compared to control mice



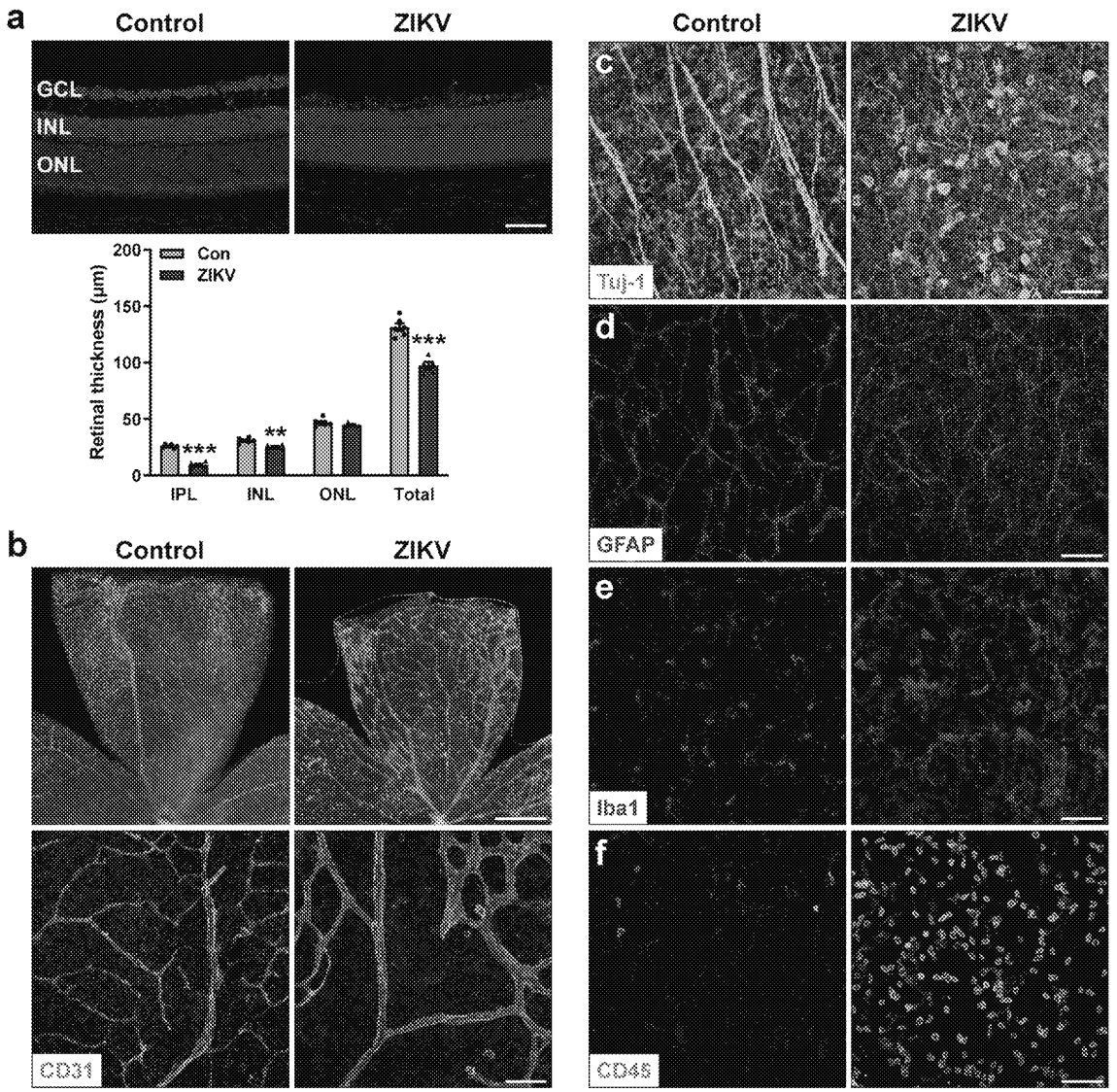


Fig. 6 ZIKV further exacerbates retinal degeneration at P14. ZIKV was injected into neonatal mice at P0 and retinas were collected at P14. **a** Representative images of PI-stained retinal sections at P14. Graph represents the thickness of individual retinal layers and total retina from GCL to ONL. **b** Representative images of retinal flatmounts labeled with CD31 for vasculature. **c**–**f** Representative images of retinal flatmounts labeled with anti-Tuj1 for RGCs and their axons, anti-GFAP for astrocytes, anti-Iba1 for microglia, and anti-CD45 for leukocytes. Scale bar = 50 μm except the upper panel in b where scale bar = 500 μm. Data are presented as mean ± S.E.M. n = 5–6 per group. $^{**}p < 0.01$, $^{***}p < 0.001$ compared to control mice

photography images [33]. In another study using fluorescein angiography to evaluate retinal vasculature changes, diffuse avascularity of the peripheral retina, retinal vessels rectification, abnormal arteriovenous shunts, and vascular attenuation, leakage and tuft are observed [32]. These observations further support that our model is clinically relevant.

Using this model, we performed studies with drug and vaccine discovery. We evaluated the therapeutic effects of two potential ZIKV antiviral compounds. While the administration of sofosbuvir at 20–33 mg/kg/day was shown to increase survival rate and prevent body weight loss in Swiss mice infected with ZIKV (i.p., 2×10^7 PFU) at P3 [10] and in anti-IFNAR1 antibody-treated C57BL/6J mice infected with ZIKV (s.c., 10^5 PFU) at 5 weeks of age [2], sofosbuvir at 80 mg/kg/day in our model only exhibited protection in a portion of mice. In contrast, adenosine analog NITD008 which exhibits potential antiviral activity against several Flaviviruses including ZIKV [7] potently prevented ZIKV-induced retinal neuronal and

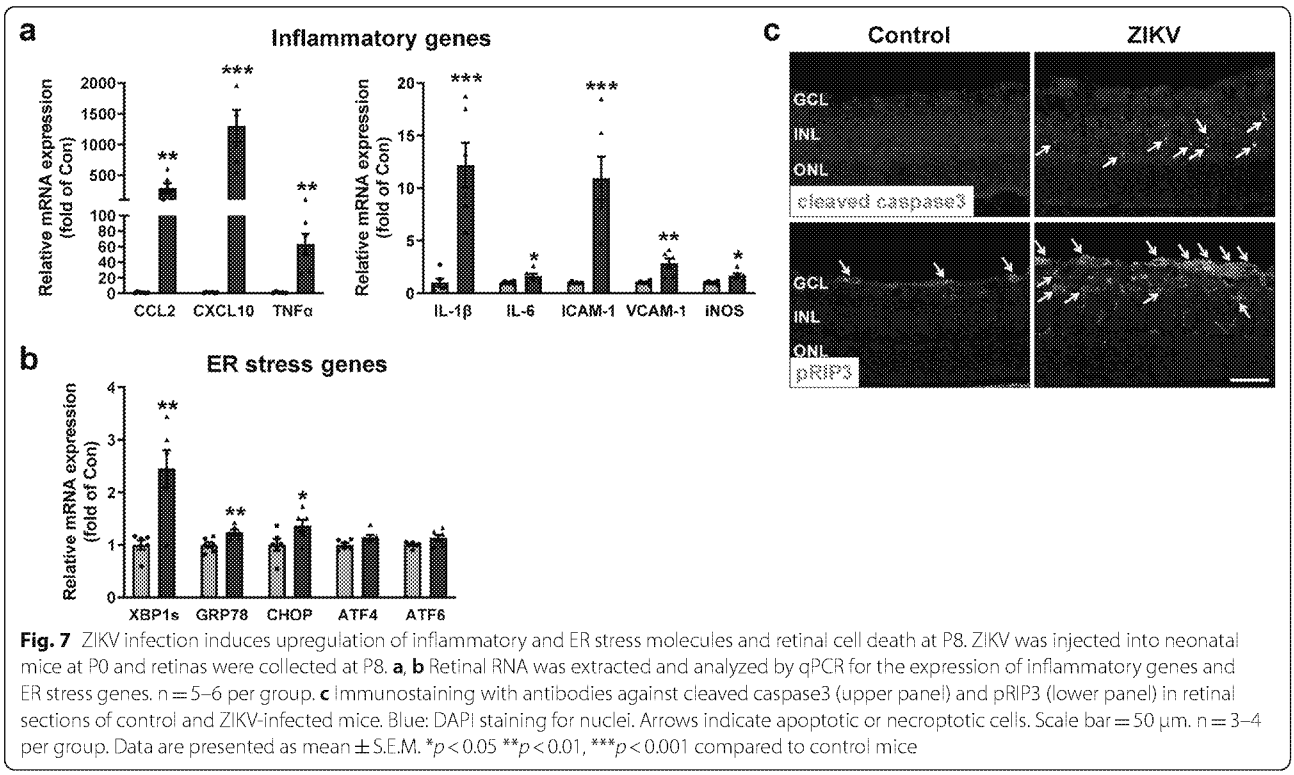


Fig. 7 ZIKV infection induces upregulation of inflammatory and ER stress molecules and retinal cell death at P8. ZIKV was injected into neonatal mice at P0 and retinas were collected at P8. **a**, **b** Retinal RNA was extracted and analyzed by qPCR for the expression of inflammatory genes and ER stress genes. n = 5–6 per group. **c** Immunostaining with antibodies against cleaved caspase3 (upper panel) and pRIP3 (lower panel) in retinal sections of control and ZIKV-infected mice. Blue: DAPI staining for nuclei. Arrows indicate apoptotic or necroptotic cells. Scale bar = 50 μm. n = 3–4 per group. Data are presented as mean ± S.E.M. *$p < 0.05$ **$p < 0.01$, ***$p < 0.001$ compared to control mice

Table 1 Comparison of the efficacy of SOF and NITD008 against ZIKV-induced retinal pathology

Inhibitor	ZIKV-infected mice with inhibitor	Mice with normal retinas	Inhibition rate (%)
SOF	9	4	44
NITD008	12	12	100

ZIKV was injected into neonatal mice at P0, followed by SOF or NITD008 treatment, and retinas were collected at P14 and compared for abnormalities

vascular degeneration and inflammation at 5 mg/kg once every other day. The different effects between NITD008 and sofosbuvir are consistent with their in vitro efficacies in which NITD008 inhibits ZIKV in Vero cells with an IC50 of less than 1 μM whereas sofosbuvir inhibits ZIKV in Huh7 cells with an IC50 around 4 μM but has no effects in Vero and A549 cells even at 50 μM [19]. Therefore NITD008 is a more effective candidate than sofosbuvir against ZIKV-induced retinal pathology and warrants to further investigate the efficacy of this compound against ZIKV in pre-clinical and clinical studies. In addition, we investigated the safety of a live-attenuated ZIKV vaccine candidate (10-del ZIKV) [25]. While 10-del ZIKV does not cause mortality when it is intracranially inoculated into P1 CD-1 mice at 1000 times of lethal infectious focus units of wild-type ZIKV [25], it induced retinal abnormality in this model though at much attenuated effects compared to wild-type ZIKV. Therefore, precautions and further optimization of the candidate vaccine are needed to achieve better safety when it is given to pregnant women. Altogether, these studies indicate this model is a sensitive one for drug and vaccine discovery. It has clinically relevant features and can provide additional information which other models may have overlooked.

At present, the mechanisms underlying ZIKV-induced retinal degeneration remains to be elucidated. By analyzing retinal changes at different time points after ZIKV infection, we found retinal neural and vascular development appeared normal at P5 and P8 but expressions of genes involved in inflammation and ER stress were significantly upregulated in P8 retinas of ZIKV-infected pups. Considering inflammation and ER stress play key roles in cell death, it is possible that they are partially involved in ZIKV-induced increases in retinal cell apoptosis and necroptosis at P8 and subsequent progress of retinal degeneration from P11 to P21. Further studies to modulate these two pathways and determine their effects on ZIKV-induced retinopathy are needed to test this possibility. Moreover, an integrated approach with single-cell and omics technologies would often provide better insights on this process. One advantage of our model is that it is easier to study molecular mechanisms with genetically modified mice than the model with intra-amniotic injection since transgenic mice often have lower

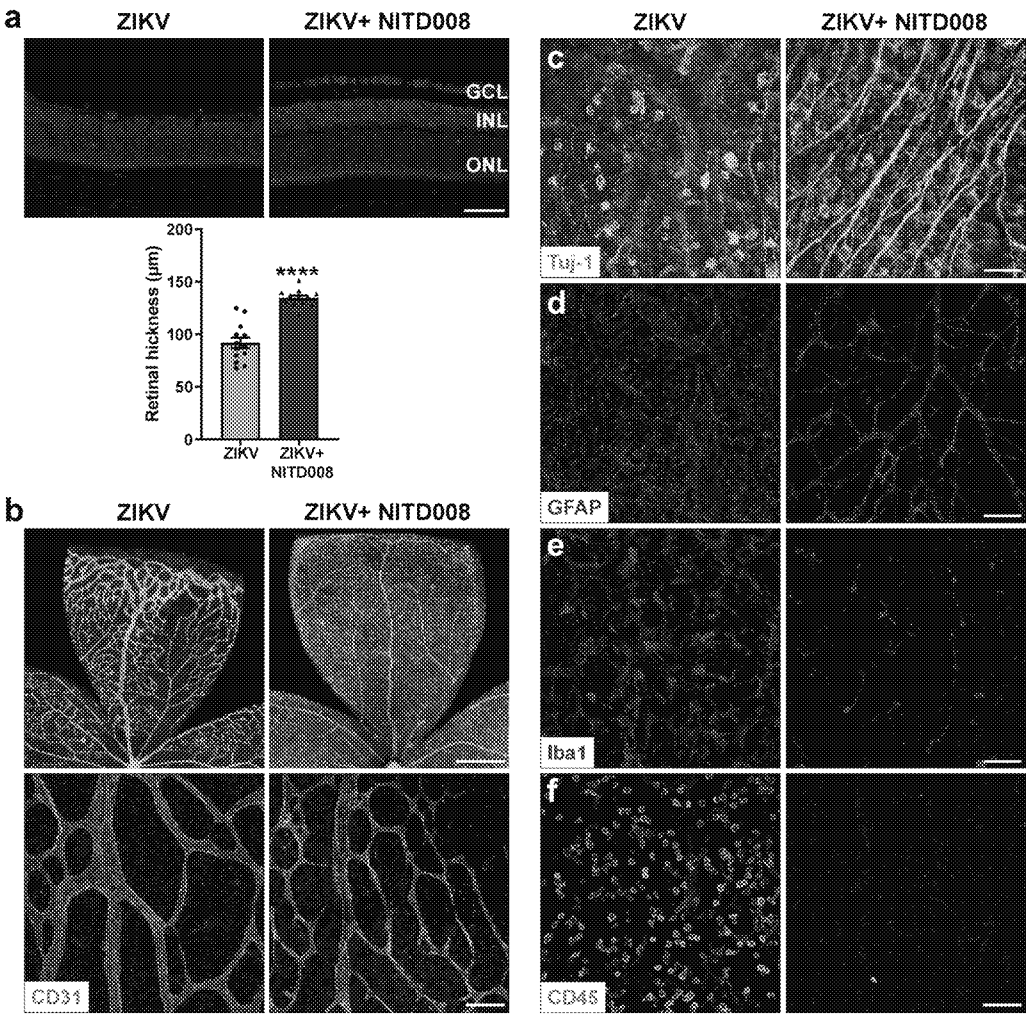


Fig. 8 NITD008 treatment blocks ZIKV-induced retinal abnormalities. ZIKV was injected into neonatal mice at P0, followed by NITD008 treatment right after ZIKV infection and every other day until day 12, and retinas were collected at P14. **a** Representative images of PI-stained retinal sections at P14. Graph represents the thickness of total retina from GCL to ONL. n = 12–13 per group. **b** Representative images of retinal flatmounts labeled with CD31 (green) for vasculature. **c**–**f** Representative images of retinal flatmounts labeled with anti-Tuj1 for RGCs, anti-GFAP for astrocytes, anti-Iba1 for microglia, and anti-CD45 for leukocytes. n = 4–8 per group. Scale bar = 50 μm except the upper panel in b where scale bar = 500 μm. Data are presented as mean ± S.E.M. ****$p < 0.0001$ compared to control mice

Table 2 The abnormal rate of the retinas after injection with ZIKV vaccine candidate

ZIKV-vaccine dose (PFU)	Total vaccinated mice	Mice with abnormal retina	Abnormal rate (%)
20	5	0	0
200	8	4	50
2000	8	7	87.5

Various dose of a live-attenuated ZIKV vaccine candidate was injected into neonatal mice at P0, and retinas were collected at P21 and compared for abnormalities

birth rates than WT mice and ZIKV infection during pregnancy could further reduce it [6, 29].

Conclusions

In summary, we developed an easily inducible, reproducible and clinic-relevant mouse model of ZIKV-induced retinopathy. Using this model, we provided the first evidence that retinal vessels similar to neurons underwent progressive degeneration after ZIKV infection, and inflammation, ER stress, apoptosis and necroptosis may be potentially involved in this process. Moreover, we demonstrated the feasibility of using this model in drug discovery and vaccine safety evaluation and found that

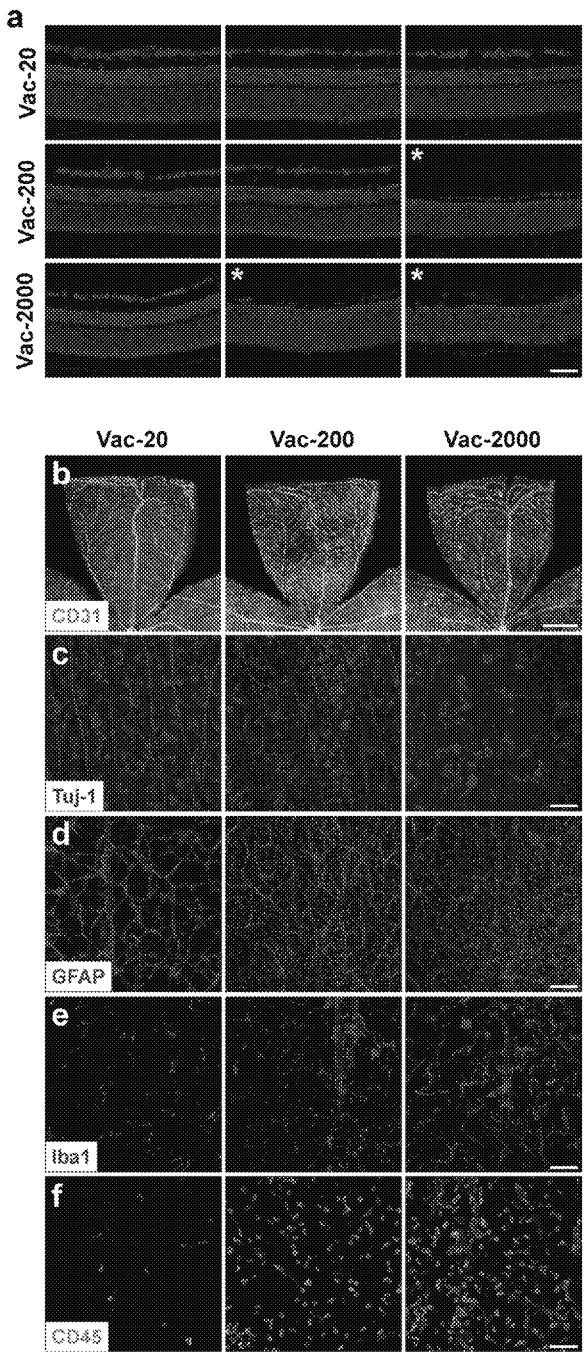


Fig. 9 The effects of live attenuated ZIKV vaccine candidate on retina. Various dose of a live-attenuated ZIKV vaccine candidate (Vac-20 or 200 or 2000 PFU) was subcutaneously injected into neonatal mice at P0 and retinas were collected at P21. **a** Representative images of PI-stained retinal sections. Stars indicate retinal samples with decreased thickness. **b**–**f** Representative images of retinal flatmounts labeled with anti-CD31 for vessels, anti-Tuj1 for RGCs and their axons, anti-GFAP for astrocytes, anti-Iba1 for microglia, and anti-CD45 for leukocytes. Scale bar = 50 μm except b where scale bar = 500 μm. n = 5 for Vac-20; n = 8 for Vac-200 and Vac-2000

NITD008 is a better drug candidate than sofosbuvir in treating ZIKV-induced retinopathy.

Abbreviations

cDNA: Complementary DNA; ddH_2O: Double distilled water; E: Embryonic day; ER: Endoplasmic reticulum; FISH: Fluorescence in situ hybridization; GCL: Ganglion cell layer; GS: Glutamine synthetase; H&E: Hematoxylin and Eosin; IFNAR1: Type I interferon receptor; INL: Inner nuclear layer; IPL: Inner plexiform layer; ONL: Outer nuclear layer; OPL: Outer plexiform layer; P: Postnatal day; PFA: Paraformaldehyde; PFU: Plaque-forming units; pRIP3: Phosphorylated receptor-interacting protein 3; RGCs: Retinal ganglion cells; SOF: Sofosbuvir; WT: Wild type; ZIKV: Zika virus.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s40478-021-01195-6.

Additional file 1: Supplementary Figures.

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Author's contributions

YL, SS, FX, CS, YH, JZ, and AA performed experiments and data analysis. YL, SS, FX, TW, HL, P-YS., and WZ designed the experiments and interpreted the results. YL, SS, YH, MZ, TW, HL, P-YS, and WZ wrote the manuscript. All authors read and approved the final manuscript.

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Availability of data and materials

All data generated or analyzed during this study are included in this published article and its supplementary information files.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

[1]Department of Ophthalmology and Visual Sciences, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX 77555-0144, USA. [2]Department of Biochemistry and Molecular Biology, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX 77555-0144, USA. [3]Department of Microbiology and Immunology, University of Texas Medical Branch, Galveston, TX, USA. [4]Department of Cellular Biology and Anatomy, Augusta University, Augusta, GA, USA. [5]Sealy Center for Vector-Borne and Zoonotic Diseases, University of Texas Medical Branch, Galveston, TX 77555, USA.

[6]Institute for Human Infections and Immunity, University of Texas Medical Branch, Galveston, TX 77555, USA. [7]Departments of Neuroscience, Cell Biology and Anatomy, University of Texas Medical Branch, Galveston, TX, USA.

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To: shanchao@wh.iov.cn[shanchao@wh.iov.cn]; Weaver, Scott[sweaver@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]
From: onmedic[info@onmedic.com]
Sent: Thur 10/8/2020 1:23:32 AM (UTC-05:00)
Subject: Hoping to help

Dear Chao,
We've just read your article published in Proceedings of the National Academy of Sciences of the United States of America (http://www.ncbi.nlm.nih.gov/pubmed/32747564), and, first of all, congrats, it's very interesting. We are writing to the email we found in affiliation.
We are contacting to present you our services. We are known by our ehealth products like websites, big data, machine learning, Gsuite (e.g. automate pdf report creation from google sheets), etc, but today we want to offer you a service to help you in the social media field for researchers, especially twitter. Every time more scientists ask us about managing his/her online profile, marketing is also coming to our field... We are data scientist.
We can help to improve your social presence. I hope you think we can help you, it would be a pleasure. Just answer and we can discuss by email o teleconference.
Kind regards,
onmedic team
onmedic.com

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; fjc37@cam.ac.uk; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; alex@lji.org; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ZHOU, Tiequn;

lschwartz36; Kristina Peachman; Important; Racine, Trina; Liz Miller; Liz Miller

Sent: Mon 11/16/2020 7:44:47 AM (UTC-06:00)

Subject: [COVID-19] 38th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting.

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To: Shi, Pei yong[peshi@UTMB.EDU]
From: 单超[shanchao@wh.iov.cn]
Sent: Wed 12/9/2020 11:42:09 PM (UTC-06:00)
Subject: Re: FW: Proofs

Hi Pei-Yong,

The name and affiliation are correct.

Thanks，

Chao

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-12-10 00:14:09 (星期四)
收件人: "单超" <shanchao@wh.iov.cn>
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主题: FW: Proofs

Shi, Pei yong has shared a OneDrive for Business file with you. To view it, click the link below.

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FYI

From: Diamond, Michael <mdiamond@wustl.edu>
Sent: Wednesday, December 9, 2020 7:34 AM
To: Nair, Sharmila <sharmila.nair@wustl.edu>
Cc: Mazzoccoli, Luciano <lmazzoccoli@wustl.edu>; Jash, Arijita (aj9du) <aj9du@virginia.edu>; Sujan <sujan@lji.org>; Shi, Pei yong <peshi@UTMB.EDU>; Jeremy Rich <drjeremyrich@gmail.com>; Chheda, Milan <mchheda@wustl.edu>
Subject: Proofs

All - proofs are in - we have 36 hours

PIs - - check names, affiliations, and COIs

SN, LM, and AJ - read over very carefully - mark changes on document

Milan - you and I will read over separatel

Mike

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; william.lee; ASiyer@mgh.harvard.edu; MAFUNGA, Neddy

Location: https://who-e.zoom.us/j/8348590949

Importance: Normal

Subject: WHO working group on COVID-19 assays

Dear All,

Please find below the agenda for our group call on Wednesday December 2, 2020 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Jilian Sacks, FIND – Assessment of serologic assays
2. Paul Bieniasz, Rockefeller – Coronavirus neutralizing antibodies before and after SARS-CoV-2 infection

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Meeting ID: 834 859 0949
Passcode: **552.136**
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Join by SIP
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162.255.37.11 (US West)
162.255.36.11 (US East)
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115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 834 859 0949
Passcode: **552.136**

Join by Skype for Business
https://who-e.zoom.us/skype/8348590949

To: Shi, Pei yong[peshi@UTMB.EDU]; Steve Daniels[steve.daniels@sheridan.com]; 'shanchao@wh.iov.cn'[shanchao@wh.iov.cn]
Cc: SJS_PNAS_Specialist[PNAS_Specialist.djs@sheridan.com]
From: Daniela Blaise[Daniela.Blaise@sheridan.com]
Sent: Thur 7/30/2020 9:39:22 AM (UTC-05:00)
Subject: RE: PNAS MS# 2020-05722R Publication Update

You're welcome, Pei-Yong!

Stay safe,

Dani

From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Thursday, July 30, 2020 10:23 AM
To: Daniela Blaise; Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Dear Daniela and Steve,

Thanks so much for your help!

Best regards,
Pei-Yong

From: Daniela Blaise <Daniela.Blaise@sheridan.com>
Sent: Thursday, July 30, 2020 9:01 AM
To: Steve Daniels <steve.daniels@sheridan.com>; Shi, Pei yong <peshi@UTMB.EDU>; 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Dear Dr. Shi and Dr. Shan,

Based on the reasoning provided, Steve obtained approval to proceed with these changes. We will update your article as requested and approve the revised proof for publication on your behalf.

Thank you,

Dani

Daniela Blaise
Senior Production Editor

Sheridan
A CJK Group Company

Sheridan Journal Services
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
www.sheridan.com
www.cjkgroup.com

From: Steve Daniels

Sent: Wednesday, July 29, 2020 2:26 PM
To: 'Shi, Pei yong'; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Thanks for confirming, Pei-Yong.

To consider this change, we need you to provide the reason this change is required. In other words: What is the impact of this change?

Steve Daniels
Production Editor

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5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 2:10 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Yes. You are right. I have included an image for the correction.

Thank you so much!

Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 1:06 PM
To: Shi, Pei yong <peshi@UTMB.EDU>; 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Pei-Yong,

Please confirm that the new change swaps the positions and letters for affiliations a and b, but no author affiliations are changed (only letters).

I will check with the editorial office to see if an exception can be made, but I want to be sure that I understand the details.

Thank you.

Steve Daniels
Production Editor

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From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 1:59 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

We really have to correct this by all possible means.

I greatly appreciate your help!

Best regards,
Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 12:45 PM
To: 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: Shi, Pei yong <peshi@UTMB.EDU>; SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Chao,

Unfortunately, we're unable to make this change because this paper has already been approved for publication.

Let me know if you have any questions.

Thank you.

Steve Daniels
Production Editor

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Waterbury, VT 05676
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From: shanchao@wh.iov.cn [mailto:shanchao@wh.iov.cn]
Sent: Wednesday, July 29, 2020 8:32 AM
To: Steve Daniels
Cc: peshi; SJS_PNAS_Specialist
Subject: Fw: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Could you help to make a change for the paper "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R?

We would like to switch the affiliation order between a and b (see attachment). Could you help on this?

Many thanks for your help.

Best,
Chao

---

shanchao@wh.iov.cn

From: journalstaff
Date: 2020-07-28 02:51
To: peshi
CC: shanchao; hoxia; shhaller; srazar; yaliu2; jianyliu; aemuruat; rubing.chen; slrossi; mawakami; nivasila; rongjuan_pei; crfontes; sksingh; xuxie; sweaver
Subject: PNAS MS# 2020-05722R Publication Update

Dear Dr. Shi,

PNAS has scheduled publication of your article, "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R, in Latest Articles the week of August 3, 2020. Your article may publish in Latest Articles any day during that week. The Latest Articles publication date is the official date of record.

PNAS will not publish your article until the production vendor, Sheridan Journal Services, has incorporated the changes you made on the proofs. If you have requested a second set of proofs, your article will not publish until you have reviewed the edits. If you have questions about proofs, please contact (PNAS_Specialist.djs@sheridan.com).

The press embargo on your article will lift on August 3, 2020 at 3:00 PM U.S. Eastern time. The embargo date is the earliest possible date that your article can publish. Embargoed copies of your accepted article will be available to journalists starting Wednesday, July 29, 2020, on a secure reporters-only web site. Should you or your institution's public relations office have any press- or embargo-related questions, please contact the PNAS News Office at pnasnews@nas.edu or 202-334-1310.

Public Information Officers (PIOs) and authors may post an embargoed press release to EurekAlert! as early as 2:00 PM US ET the Wednesday afternoon before the embargo lifts. Embargo information must be noted in ALL CAPS at the top of the press release. Authors and press officers are responsible for ensuring that embargoed press releases are not published, broadcast, or posted online in any form in the public domain, including any open access site, prior to the embargo date and time. Failure to comply with the PNAS embargo policy may result in author sanctions.

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If you must delay publication for a special reason, please notify the PNAS News Office immediately, no later than noon US ET on Tuesday, July 28, 2020.

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Best regards,
PNAS News Office
Phone: 202-334-1310
E-mail: PNASNews@nas.edu

To: Shi, Pei yong[peshi@UTMB.EDU]
From: 陈新文[chenxw@wh.iov.cn]
Sent: Sat 1/23/2021 4:27:25 AM (UTC-06:00)
Subject: Fw: Nature 2020-12-22159 out to review; possible response required

Pei-Yong,

Here is the replay from Nature. Sound good.

My regards,

Xinwen

-----原始邮件-----
发件人:c.thomas@nature.com
发送时间:2021-01-22 22:11:48 (星期五)
收件人: chenxw@wh.iov.cn
抄送:
主题: Nature 2020-12-22159 out to review; possible response required

Dear Professor Chen,

Thank you for submitting your manuscript entitled "Glucagon-like peptide-2 receptor is a receptor for tick-borne encephalitis virus to infect nerve cells" to Nature. I am pleased to tell you that we are sending your paper out for review. (I apologise for the delay in letting you know. The holidays and the increased submissions due to the new SARS-CoV-2 variants caused some delay.)

We are continually improving the quality of methods and statistics reporting in our papers. To that end, we now ask that two items are completed for all life sciences papers: an editorial policy checklist that verifies compliance with all required editorial policies, and a reporting summary that collates information on experimental design and reagents. Links to these checklists are found here:

Reporting summary: https://www.nature.com/authors/policies/ReportingSummary.pdf
Editorial policy checklist: https://www.nature.com/authors/policies/Policy.pdf

Please return the completed forms within 48 hours. These forms are dynamic 'smart pdfs' and must therefore be downloaded and completed in Adobe Reader (i.e. they cannot be opened in a web browser). For guidance, see http://www.nature.com/authors/policies/availability.html.

Papers containing structural data (X-ray, NMR, or cryoEM) must contain a completed standard table for such data at submission (https://www.nature.com/nature/for-authors/forms-and-declarations). In addition, both crystallographic and NMR structures (but not cryoEM structures) must now be submitted to the PDB, and a validation report provided, before the paper can be sent to referees.

The reporting summary (and validation report if appropriate) will be made available to the referees to aid in their evaluation of your work; if you have selected double-blind peer review, you should ensure that they do not contain any information that could potentially identify you.

Please note that Nature implements transparent peer review of original research manuscripts, in which we publish the

reviewer comments to the authors and author rebuttal letters as a supplementary peer review file, if the author agrees at the point of acceptance. This will apply to new manuscripts submitted on or after 1st February 2020. Upon author request, confidential information and data can be removed from the reviewer reports and rebuttal letters prior to publication. For more information, please refer to our FAQ page.

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https://www.springernature.com/gp/researchers/orcid/orcid-for-nature-research

For more information please visit http://www.springernature.com/orcid

If you experience problems in linking your ORCID, please contact the Platform Support Helpdesk.

Finally, we would like to inform you that on a case by case basis we coordinate a brief consultation between referees and editors after all referee reports have been received. This is to improve the peer review process and the feedback provided to authors. Referees are given the opportunity to make comments on their peers' concerns and update their reports to comment on issues raised by the other reviewers. If we feel it would be helpful, we will engage reviewers in this additional consultation with the goal of providing you with the most valuable feedback possible.

We will be in touch again as soon as we have received comments from our referees. In the meantime - the status of your manuscript can be followed in the manuscript tracking system.

Yours sincerely,

Clare Thomas
Senior Editor
Nature

* Nature Research's author and referees' website (www.nature.com/authors) contains information about and links to policies and resources.

Our flexible approach during the COVID-19 pandemic
If you need more time at any stage of the peer-review process, please do let us know. While our systems will continue to remind you of the original timelines, we aim to be as flexible as possible during the current pandemic. We are committed to processing manuscripts related to COVID-19 with our highest priority, and endeavour to expedite the peer-review process for COVID-19 submissions as much as is possible. Thank you for your understanding.

To: Shi, Pei yong[peshi@UTMB.EDU]
From: 单超[shanchao@wh.iov.cn]
Sent: Fri 11/27/2020 2:43:49 AM (UTC-06:00)
Subject: Re: Fwd: Happy Thanksgiving!

Thanks， Pei-Yong. We can achieve more in the future.

Best,

Chao

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2020-11-27 08:32:55 (星期五)
收件人: "'shanchao@wh.iov.cn'" <shanchao@wh.iov.cn>
抄送:
主题: Fwd: Happy Thanksgiving!

Happy Thanksgiving！I should have copied you

Get Outlook for Android

From: Shi, Pei yong
Sent: Thursday, November 26, 2020 6:15:17 PM
To: Xie, Xuping <xuxie@UTMB.EDU>; Zou, Jing <jizou@UTMB.EDU>; Xia, Hongjie <hoxia@UTMB.EDU>; Fontes-Garfias, Camila R. <crfontes@UTMB.EDU>; Muruato, Antonio E. <aemuruat@UTMB.EDU>; Baker, Coleman K. <ckbaker@UTMB.EDU>; Liu, Yang <yaliu2@UTMB.EDU>; Liu, Jianying <jianyliu@UTMB.EDU>; Zhang, Xianwen <zhxianwe@UTMB.EDU>; Cao, Zengguo <zecao@UTMB.EDU>; John Yun-Chung Chen <johchen@UTMB.EDU>
Subject: Happy Thanksgiving!

Dear all,

Happy Thanksgiving to you and your family!

It is unfortunate we could not be together to celebrate this special day. As my postdoc mentor, Alan Weiner, wrote to me today, "It may be a crazy year, but it's also a well-deserved year for you. Now everybody around the world understands what you do, how well you do it, and above all why."

Congratulations to everyone for your accomplishments! Our work has changed the world. I'm so proud of you and thankful for your dedication to our noble mission.

All the best, Pei-Yong

To: 单超[shanchao@wh.iov.cn]; 朱毅斌[zhuyibin1989@126.com]; Wang,Penghua[pewang@uchc.edu]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: 程功 老师[gongcheng@mail.tsinghua.edu.cn]
From: 余茜[nikkiyu223@163.com]
Sent: Thur 12/3/2020 10:27:07 AM (UTC-06:00)
Subject: Manuscript for coauthors
Manuscript for coauthors 2020-12-03.docx

Dear all,

Thanks for your great contributions in the study entitled "A mutation-mediated evolutionary adaptation of Zika virus in mosquito and mammal host".
As you are reviewing the manuscript, please keep in mind the following:

1. Please confirm that your author information is correct.
2. Please feedback if there are any errors.

I would greatly appreciate it if you could give me feedback before 9 am on December 5th.

Looking forward to hearing from you.

Best regards,

Xi Yu

--
余 茜 Xi YU
School of Life Sciences, Tsinghua University, Beijing

Tel：+86 185-1087-1723
Email：nikkiyu223@163.com

To: weisssr@pennmedicine.upenn.edu[weisssr@pennmedicine.upenn.edu]; xjmeng@vt.edu[xjmeng@vt.edu]; dyjin@hku.hk[dyjin@hku.hk]; shibojiang@fudan.edu.cn[shibojiang@fudan.edu.cn]; Shi, Pei yong[peshi@UTMB.EDU]; peijun@strubi.ox.ac.uk[peijun@strubi.ox.ac.uk]; GMSWANG@nus.edu.sg[GMSWANG@nus.edu.sg]; lzhang2@unl.edu[lzhang2@unl.edu]; Wang,Penghua[pewang@uchc.edu]; Liang.shan@wustl.edu[Liang.shan@wustl.edu]; DengL@MSKCC.ORG[DengL@MSKCC.ORG]; rli@vcu.edu[rli@vcu.edu]; Sun.Jie@mayo.edu[Sun.Jie@mayo.edu]; jianw@musc.edu[jianw@musc.edu]; dongfang.liu@rutgers.edu[dongfang.liu@rutgers.edu]; junwang@pharmacy.arizona.edu[junwang@pharmacy.arizona.edu]; Zongdi.feng@nationwidechildrens.org[Zongdi.feng@nationwidechildrens.org]; zyang@ksu.edu[zyang@ksu.edu]; zhengzhiming4@gmail.com[zhengzhiming4@gmail.com]; hengx@missouri.edu[hengx@missouri.edu]; wux4@ccf.org[wux4@ccf.org]; GCheng@mednet.ucla.edu[GCheng@mednet.ucla.edu]; liangy@umn.edu[liangy@umn.edu]; wma@missouri.edu[wma@missouri.edu]; tzhou@mail.nih.gov[tzhou@mail.nih.gov]; guoh4@upmc.edu[guoh4@upmc.edu]; Liu, Shan-Lu[liu.6244@osu.edu]; Feng Gao[fgao@duke.edu]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Shan.lu@umassmed.edu[Shan.lu@umassmed.edu]; chen.liang@mcgill.ca[chen.liang@mcgill.ca]; uefeng.liu@georgetown.edu[uefeng.liu@georgetown.edu]; xiangy@uthscsa.edu[xiangy@uthscsa.edu]; cxiao@utep.edu[cxiao@utep.edu]; ywu8@gmu.edu[ywu8@gmu.edu]; dingsw@ucr.edu[dingsw@ucr.edu]; lsu@med.unc.edu[lsu@med.unc.edu]; Feng.Li@uky.edu[Feng.Li@uky.edu]; zqin@lsuhsc.edu[zqin@lsuhsc.edu]; Zihai.Li@osumc.edu[Zihai.Li@osumc.edu]; lijun@uic.edu[lijun@uic.edu]; wangx472@umn.edu[wangx472@umn.edu]; wenzheho@temple.edu[wenzheho@temple.edu]; gaos8@upmc.edu[gaos8@upmc.edu]; lyuan@vt.edu[lyuan@vt.edu]; juh13@psu.edu[juh13@psu.edu]; yuan2@upenn.edu[yuan2@upenn.edu]; jling@txbiomed.org[jling@txbiomed.org]; reachxw@vt.edu[reachxw@vt.edu]; andyu@iupui.edu[andyu@iupui.edu]; fzhu@bio.fsu.edu[fzhu@bio.fsu.edu]; qiyi.tang@howard.edu[qiyi.tang@howard.edu]; Wang, Qiuhong[wang.655@osu.edu]; gluo@uab.edu[gluo@uab.edu]
From: Liu, Shan-Lu[liu.6244@osu.edu]
Sent: Tue 12/22/2020 7:28:10 AM (UTC-06:00)
Subject: Pre-registration confirmation

Dear colleagues and friends:

Happy holidays!

I wish to thank you all for your help in planning our symposium Dec 30-31. By now, you should have received an email for confirmation of pre-registration, with a valid link. If you have not received email, please reply to this email and I will look into it. You may add the Zoom link to your calenda directly – there should be such an option in your email.

For direct login, please use the following information. You may save it somewhere just in case.

Webinar ID: 889 1229 6155
Password: **552.136**

Thanks again, all the best.

Shan-Lu

THE OHIO STATE UNIVERSITY

Shan-Lu Liu, M.D., Ph.D.
Professor
Co-Director, Viruses and Emerging Pathogens Program
Infectious Diseases Institute
Center for Retrovirus Research
Veterinary Biosciences, Microbial Infection and Immunity, and Microbiology
The Ohio State University
1900 Coffey Rd, Room 480 VMAB
Columbus, Ohio 43210
Phone: (614) 292-8690
Fax: (614) 292-6473
Email: liu.6244@osu.edu; shan-lu.liu@osumc.edu

CENTER TO STOP COVID

To: Shi, Pei yong[peshi@UTMB.EDU]
From: 陈新文[chenxw@wh.iov.cn]
Sent: Wed 12/9/2020 5:33:30 AM (UTC-06:00)
Subject: 1 Crispr screen data
1 Crispr screen data.xlsx
2 GOTERM_BP_DIRECT.xlsx
3 GOTERM_MF_DIRECT.xlsx
4 GOTERM_CC_DIRECT.xlsx
BHK-21 RNASeq Gene Expression data.xlsx
mice brain RNASeq Gene Expression data.xlsx
T98G RNASeq Gene Expression data.xlsx
Vero-E6 RNASeq Gene Expression data.xlsx

Here is the raw data.regards, Xinwen

To: 杨琪[yangqi@wh.iov.cn]; 陈继征[chenjz@wh.iov.cn]; 'rongjuan_pei'[rongjuan_pei@wh.iov.cn]; Shi, Peiyong[peshi@UTMB.EDU]
From: 陈新文[chenxw@wh.iov.cn]
Sent: Mon 3/1/2021 6:31:53 PM (UTC-06:00)
Subject: Fw: Decision on Nature manuscript 2020-12-22159

大家好！

应该是不错的结果， 请大家先研究一下， 然后讨论一次。

祝好！

新文

-----原始邮件-----
发件人:c.thomas@nature.com
发送时间:2021-03-01 18:52:05 (星期一)
收件人: chenxw@wh.iov.cn
抄送:
主题: Decision on Nature manuscript 2020-12-22159

* Please ensure you delete the link to your home page in this e-mail if you wish to forward it to your co-authors.

Dear Professor Chen

Your manuscript entitled "Glucagon-like peptide-2 receptor is a receptor for tick-borne encephalitis virus to infect nerve cells" has now been seen by 3 referees, whose comments are attached below. While they find your work of potential interest, as do we, they have raised important concerns that in our view need to be addressed before we can consider publication in Nature.

Should further experimental data allow you to address these criticisms, we would be happy to consider a revised manuscript (unless something similar has been accepted at Nature or appeared elsewhere in the meantime). To make a good case for reconsideration we feel that it would be essential, in particular, to improve the experiments pertaining to binding of TBEV to GLP2R, provide more mechanistic insight into the proposed receptor function of GLP2R and to perform the in vivo experiments using a more natural route of infection.

We are committed to providing a fair and constructive peer-review process. Please do not hesitate to contact us if there are specific requests from the reviewers that you believe are technically impossible or unlikely to yield a meaningful outcome.

Any revised manuscript should conform to our format instructions and publication (see https://www.nature.com/nature/for-authors). We would appreciate your careful attention to the following:

STATISTICS: When revising your manuscript, you should ensure that any statistical analysis used is sound and that it conforms to Nature's guidelines (https://www.nature.com/nature/for-authors/formatting-guide). A collection of articles explaining the basics of statistical analysis and advice on how to best present it can be found at https://www.nature.com/collections/qghhqm.

REPRODUCIBILITY: We ask authors to provide a Reporting Summary and Editorial Policy Checklist to improve the

quality and transparency of methods and statistical reporting (see https://www.nature.com/news/announcement-reducing-our-irreproducibility-1.12852). These should be updated to reflect the revisions made and submitted with the revised manuscript.

DATA AND CODE AVAILABILITY STATEMENTS: We strongly support public availability of data and custom code. All Nature papers must include a Data Availability Statement (DAS) and (if applicable) a Code Availability Statement (CAS) after the main text statements and before the Extended Data legends. A detailed document outlining the data availability policy, containing various DAS examples you may use or modify, can be found at https://www.nature.com/documents/nr-data-availability-statements-data-citations.pdf. For some data types, deposition in a public repository is mandatory (see https://www.nature.com/nature-research/editorial-policies/reporting-standards#availability-of-data).

EXTENDED DATA: Extended Data do not appear in the print version of the paper but are included online within the full-text HTML and at the end of the online PDF. Extended Data are an integral part of the paper, and only data that directly contribute to the main message should be included. All Extended Data must be referred to in the main text, and their legends should be listed sequentially at the end of the main text, not in the Extended Data files. The Extended Data should be assembled into a maximum of 10 A4 size, multi-panelled display items, submitted as individual files in .jpg, .tif or .eps format only. They should be of the same quality as print figures, but there are important differences in their formatting. More specific instructions are provided here: http://s3-service-broker-live-19ea8b98-4d41-4cb4-be4c-d68f4963b7dd.s3.amazonaws.com/uploads/ckeditor/attachments/7823/3h_Extended_data.pdf. We encourage authors who are describing complex processes to include a schematic
of the main finding as part of the Extended Data to aid readers unfamiliar with the immediate discipline.

SUPPLEMENTARY INFORMATION: Supplementary Information (SI) is online-only, peer-reviewed material that is essential background to the study (e.g., large data sets, more complex methods, and calculations), but which is too large or impractical, or of interest only to a few specialists, to justify inclusion in the print version of the paper (see https://www.nature.com/nature/for-authors/supp-info for further details). While SI should not typically contain data figures (any figures additional to those appearing in the main text should be formatted as Extended Data), we require that the raw, uncropped data for gels be presented as an SI figure (see below). Tables may be included in SI, but only if they are unsuitable for formatting as Extended Data (e.g., tables containing large data sets or raw data tables that are best suited to Excel files). If a manuscript has SI, each discrete item of the SI (e.g., videos, tables) must be referred to at an appropriate point in the main manuscript.

SOURCE DATA (GRAPHS): To increase transparency, we strongly encourage you to provide, in spreadsheet form, the data underlying the graphical representations used in figures. In the case of all experiments presenting data from animal models, this is a requirement and is not optional. This is in addition to our well-established data-deposition policy for specific types of experiments and large datasets. Online readers of the manuscript will be able to access the graphical source data directly from the figure legend. Spreadsheets must be submitted in .xls, .xlsx or .csv formats. One file per figure is permitted. If there is a multi-panelled figure, the source data for each panel should be clearly labeled in the file; alternatively the source data for a figure can be included in multiple, clearly labeled sheets within an Excel file. File sizes of up to 30 MB are permitted, but it is expected that the vast majority of graphical source data files will be considerably smaller than this.
When submitting these files with your manuscript, you should select the "Source Data" file type and use the title field in the file description tab to indicate the figure(s) to which the source data pertain.

RAW DATA (GELS): You must provide the original source images for all data obtained by electrophoretic separation (e.g., EMSA, northern/Southern/western blots, etc). The raw images should be assembled into a single .pdf or .tif file (multiple gels on a single page is encouraged). The file should be uploaded as Supplementary Figure 1. The full scanned images must be in uncropped form and contain labeled size/molecular weight markers and loading controls. There should be an accurate indication of how the gels were cropped for the final figure. The figure legends and raw data files should indicate whether controls (such as beta-actin) were run on the same gel as loading controls, or on separate gels as sample processing controls (see https://www.nature.com/authors/policies/image.html). While the data can be displayed in a relatively informal style, there must be a correspondence between each source data image and a specific main text or Extended Data figure. The main text or Extended
Data figure legends should refer to the uncropped scans explicitly (e.g., “For gel source data, see Supplementary Figure

1."). For examples, see
https://images.nature.com/full/nature-assets/nature/journal/v520/n7547/extref/nature14363-s1.pdf or
https://images.nature.com/full/nature-assets/nature/journal/v521/n7550/extref/nature14415-s1.pdf.

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https://www.springernature.com/gp/researchers/orcid/orcid-for-nature-research. If you do not yet have an ORCID you will be able to create one in minutes.

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To support ORCID's aims, we only allow a single ORCID identifier to be attached to one account. If you have any issues attaching an ORCID identifier to your MTS account, please contact the Platform Support Helpdesk.

The revised paper should be submitted using the link below:

https://mts-nature.nature.com/cgi-bin/main.plex?el=A6K4DbF4A4EPNg2J3A9ftdu9qZwBTzfQBA5p7nH4GxbgZ

NOTE: This url links to your confidential home page and therefore to manuscripts you may have submitted or be reviewing for us. If you wish to forward this email to co-authors, please delete the link to your home page first.

In the meantime, we hope that you will find our referees' comments helpful. Please do not hesitate to contact me if there is anything you would like to discuss.

Yours sincerely

Clare Thomas
Senior Editor
Nature

Referees' comments:

Referee #1 (Remarks to the Author):

This manuscript identified a cellular receptor required for TBEV entry, GPCR glucagon-like peptide-2 receptor (GLP2R), by performing a genome-wide CRISPR-Cas9 screening in human glioma T98G cells. Briefly, GLP2R deficiency specifically disrupted TBEV infection, but does not affect other neurotropic viruses. They found that the extracellular loop 1 (ECL1) of GLP2R was mainly responsible for TBEV binding through its envelope (E) protein, and this interaction was inhibited with a synthetic peptide Y41L demonstrating the importance of ECL1 in viral E protein binding. In vivo, glp2r-/- mice showed significant reduction of virus titers and 100% survival, together with little or no infectious virus detected in blood or tissues, suggesting that glp2r is important for TBEV pathogenesis. Overall, the strengths of the paper include using unbiased CRISPR-Cas9 screen to identify a novel TBEV entry receptor which is crucial for developing pathogenesis in vivo and identifying a specific
GLP2R's ECL1 domain that could provide potential antiviral insights. However, it is concerning that why are non-neuronal cells still susceptible to infection even with no GLP2R gene expression. Despite claiming that GLP2R is mainly expressed in the CNS and enteric neurons, the manuscript failed to show the specificity of GLP2R expression in different cell types and organs. Overall, several points are raised below to strengthen this manuscript.

Major

1. The authors should indicate how many of the genes targeted by the screen are considered as "top candidate". Is GLP2R the best gene in the screening list? The author should include other top candidate genes and verify their function to further validate their screening results.

2. In Figure 1c and 1d, the authors should clarify and include the detailed method of GLP2R trans-complement and shows the efficiency of GLP2R trans-complement.

3. In Figure 1c, even though glp2r gene was knocked out, there are still virus infection occurring and titer still increases over time. In extended data figure 6 (e), there is still virus infection in BHK-21 cells and Vero E6 cells with or without GLP2R. Hence, GLP2R could be involved in facilitating the virus entry as a co-receptor but not a “true” receptor of TBEV.

4. Extended data Fig 6a, surface protein expression of GLP2R in cell lines and primary astrocytes should be performed instead of mRNA gene expression to correlate with viral entry.

5. For the specificity of receptor, the authors should compare other glucagon receptors for TBEV binding and infection. Moreover, all interaction experiments utilized GFP- or HA-tagged GLP2R. Authors should show the interaction between endogenous GLP2R and TBEV.

6. In Figure 2, the authors should clarify the exact binding site of H33D as a functional ligand of GLP2R to inhibit TBEV infection. Does H33D bind to the region in GLP2R similar to TBEV?

7. In Figure 3, TBEV envelope domain III binds to the extracellular domain loop1 of GLP2R to modulate TBEV attachment and internalization. But what is the function of cytosolic domain of GLP2R in TBEV infection? Is it be involved in endocytosis or internalization of the virus?

8. For the therapeutic approach, the ECL1 peptide such as Y41L has to be determined in vivo pathogenesis of TBEV.

9. If GLP2R is also specific to enteric neurons, neuronal cells should be used instead of primary brain astrocytes. Did the authors identify if TBEV infect enteric neurons as well?

10. In Figure 4, the authors claimed that “GLP2R is specifically required for TBEV infection of human nerve cells and mainly expressed in the central nervous system and enteric neurons”. This is not supported by the data shown, where TBEV-infected wild type mice showed lesions in the spleen and small intestine, yet there are no infection and lesions in the spleen and small intestine of glp2r-/- mice. Hence, the author should clarify if GLP2R is potentially a TBEV receptor specific to certain cell types in different organs.

11. Please explain the reason that HE staining showed lesions to the brain, spleen, and small intestine in the TBEV-infected wild type mice but showed no such pathology in glp2r-/- mice since glp2r is not the only receptor and there exists additional receptor which means TBEV can also infect glp2r-/- mice as well in other organs except for brain.

12. In H&E staining, the detection of viral RNA by using in-situ hybridization has to be shown to prove the existence of virus infection in tissues. In addition, is it not clear what cell types are expressing GLP2R, Hence, the authors should include IHC staining or in-situ hybridization data of viral and GLP2R in WT and knockout tissues.

Minor

1. In Figure 4, the display of both WT and Glp2r -/- needs to be identical to other figures.

2. There is no specific experiment on HSPG. Is HSPG still required for the function of GLP2R as a receptor? If HSPG is deficient in cells, Does TBEV still utilize GLP2R in this condition?

Referee #2 (Remarks to the Author):

Yang et al report on studies with the goal of identifying the entry receptor for tick-borne encephalitis virus (TBEV). The authors performed a genome-wide CRISPR-Cas9 knockout screen using human glioma T98G cells exposed to TBEV-FE, strain WH2012 and identified G-protein-coupled receptor glucagon-like peptide-2 receptor (GLP2R) as a putative receptor for TBEV to infect nerve cells. In vitro knockdown or knockout of GLP2R reduced TBEV infection of a variety of tumor, neuronal and other human cell lines, and trans supply of GLP2R restored viral replication levels. Importantly, they demonstrate specificity for TBEV via direct comparisons with other flaviviruses, which do not show any impairment in viral replication in glp2r-/- cell lines.
The authors also convincingly demonstrate that GLP2R directly binds to viral envelope domain III through its extracellular loop 1 (ECL1), using immunoprecipitation and site directed mutagenesis approaches. Binding studies using ECL1 peptide, and GLP2R antibodies were less convincing and less direct in assessing protein-protein interactions. GLP2R-deficient mice, generated by the authors, survived TBEV infection with minimal detection of viral RNA and without detectable infectious virus in multiple organs, including the brain. The route of administration in these studies was not via a natural route, and the results suggest that GLP2R is not necessarily neural cell specific, as the title of the manuscript states.

Specific Comments:
1. The article needs to begin with an introduction to TBEV as a cause of viral encephalitis including epidemiology and countries where it is endemic, and all target cell types. It also lacks a more thorough discussion of GLP2R expression and function in neural cell types. This is important information with regard to what is known about cellular targets and course of disease.

The approaches are well designed and use of appropriate controls demonstrates their success in identifying GLPR2 via CRISPR-Cas9 knockout screen, knocking down and knocking out this gene in glioma tumor and neuronal cell lines, and demonstrating that GLPR2 deficiency dose-dependently decreases TBEV replication rates in cell lines. They also demonstrate that increased expression of GLPR2 in a number of human cell lines increased TBEV replication. It is also important that the authors examined both viral RNA levels and infectious virions using appropriate assays.

The authors found that BHK and Vero cells, however, do not require GLPR2 for TBEV replication, supporting the notion that only human cells utilize GLPR2 during TMEV infection.

The binding experiments in Fig 2 do not directly assess interaction with GLPR2. Quantitative competitive binding assays with controls are needed. Detection of viral RNA does not assess binding and the Ab-based assays are not convincing. Also, as use of ligand for GLPR2 only modestly prevents TBEV replication without dose-dependency, studies are needed to assess whether binding sites differ between ligand and viral envelope. The analyses determining the effect of TBEV replicon indirectly supports the notion that TBEV binds GLPR2.

Fig 3 more convincingly demonstrates direct interactions between TBEV envelope and GLPR2 via immunoprecipitation and site-specific mutagenesis.

Fig 4 shows that loss of GLPR2 results in diminished detection of virus within the blood, spleen, intestine, and brain. As GLPR2 is expressed in brain and intestine, it is unclear why the blood and spleen exhibit much lower viral titers, and does not completely support the conclusion that GLPR2 is a neural cell specific receptor for TBEV. The authors also inoculated virus intraperitoneally, which apparently allows limited infection via a different entry mechanisms. The authors should repeat the murine infection studies using a subcutaneous inoculation route and assess the skin, draining lymph nodes, blood, intestine, spleen and brain for viral RNA and infectious virions.

Referee #3 (Remarks to the Author):

In this study, Yang et al. have conducted a CRISPR-cas9 screen in a human glioma cell line to identify host factors essential for the infectious life cycle of Tick-Borne Encephalitis Virus (TBEV), a member of the flavivirus genus that

causes severe encephalitis disease. The authors identified the G-protein coupled receptor glucagon-like peptide-2 (GLP2R) as a receptor for TBEV. The authors showed that GLP2R expression blockage by RNA interference or deletion of the glp2R gene by CRISPR inhibits infection of some cell lines by different TBEV strains. GLP2R interacts, through its extracellular ECL1 region, with the domain III of the TBEV envelope glycoprotein. Importantly, mice lacking the glp2r gene survive TBEV infection and present no detectable infectious particles in the brain.
Altogether, the data presented in this paper are potentially interesting but remain very weak to conclude that GLP2R is a key host factor for TBEV entry. A major weakness of this study is that the authors have never proved that GLP2R fullfills the criteria of a viral entry receptor. For instance, there is no data showing a clear relationship between TBEV infection and GLP2R cell surface expression. If GLP2R is an authentic receptor, ectopic expression of this protein in cells poorly susceptible or refractory to TBEV should render them permissive to infection. Furthermore, the authors claim that GLP2R modulates TBEV internalization. Unfortunalely, the data supporting this conclusion (Fig 2) are not convincing since the authors did not perform specific entry experiments to prove that GLP2R triggers TBEV particle uptake (for instance: live imaging, TIRFF microscopy, receptor-virus co-internalization assay etc…). The data with the H33D peptide are also not in favor of a major role
of GLP2R in TBEV entry. It is unclear whether the moderate inhibitory effect observed is due to the ability of this product to compete with TBEV binding, to block virus entry by promoting GLP2R endocytosis or to activate intracellular signaling that might impact indirectly with the early stages of virus infection.

In conclusion, the data presented in this paper indicated that GLP2R is a proviral factor for TBEV. However, this study suffers from a lack of important mechanistic insights about the precise function of this G-protein coupled receptor during TBEV entry. In my opinion, in its current form, this manuscript doesn't meet the high-quality standards for publication in this prestigious journal.

To: 单超[shanchao@wh.iov.cn]; Shi, Pei yong[peshi@UTMB.EDU]
From: Zhang, Wenbo[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=20857D4378DE49909C112784C71353F2-ZHANG, WENB]
Sent: Fri 3/5/2021 7:02:27 AM (UTC-06:00)
Subject: RE: RE: our manuscript

Dear Chao,

Thank you for helping and collaborating with us in this project. Keep in touch.

Best regards,
Wenbo

From: 单超 [mailto:shanchao@wh.iov.cn]
Sent: Thursday, March 04, 2021 6:38 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Zhang, Wenbo <we2zhang@UTMB.EDU>
Subject: Re: RE: our manuscript

Thanks Dr. Zhang and Pei-Yong. Good luck with submission.

Best,

Chao

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2021-03-05 06:21:49 (星期五)
收件人: "Zhang, Wenbo" <we2zhang@UTMB.EDU>
抄送: "shanchao@wh.iov.cn" <shanchao@wh.iov.cn>
主题: RE: our manuscript

Thanks, Wenbo

Chao's email: shanchao@wh.iov.cn

Grant acknowledgement:
"P.-Y.S. was supported by NIH grants AI134907 and UL1TR001439, and awards from the Sealy & Smith Foundation, Kleberg Foundation, the John S. Dunn Foundation, the Amon G. Carter Foundation, the Gilson Longenbaugh Foundation, and the Summerfield Robert Foundation."

Best, Pei-Yong

From: Zhang, Wenbo <we2zhang@UTMB.EDU>
Sent: Thursday, March 4, 2021 4:12 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: our manuscript

Dear Dr. Shi,

Thank you very much. Do you want to include any of your grant support in the acknowledgement? Also, could you please give me Chao's current email address so that I can use during manuscript

submission?

Best regards,
Wenbo

From: Shi, Pei yong
Sent: Thursday, March 04, 2021 3:41 PM
To: Zhang, Wenbo <we2zhang@UTMB.EDU>
Subject: RE: our manuscript

Dear Wenbo,

Thank you for this well executed and written study. Please see my edits.

Four potential reviewers:
- Margo Ann Brinton <mbrinton@gsu.edu>, Georgia State University
- Kristen Barnard: kristen.bernard@wisc.edu, https://www.vetmed.wisc.edu/people/kbernard/
- Saguna Verma <saguna@hawaii.edu>, https://manoa.hawaii.edu/tropicalmedicine/?page_id=674
- Chengfeng Qin: <chengfeng_qin@126.com>

Cheng-Feng (Chengfeng) Qin, Ph.D.
Professor & Chair, Dept. of Virology,
State Key Laboratory of Pathogen and Biosecurity,
Beijing Institute of Microbiology and Epidemiology,
Academy of Military Medical Sciences,
No.20 Dongda Street, Fengtai District,
Beijing 100071, China

Best, Pei-Yong

From: Zhang, Wenbo <we2zhang@UTMB.EDU>
Sent: Wednesday, March 3, 2021 2:13 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: our manuscript

Dear Dr. Shi,

Thank you very much for collaborating with us in this project. Please revise it freely and let us know which title is good or what title you would suggest. Moreover, as we discussed, please suggest 4-5 potential reviewers. We expect to get the manuscript submitted Monday or Tuesday to Nature Communication or other journals you suggested. In addition, please share it with Chao and Jin because all authors need to approve it before submission.

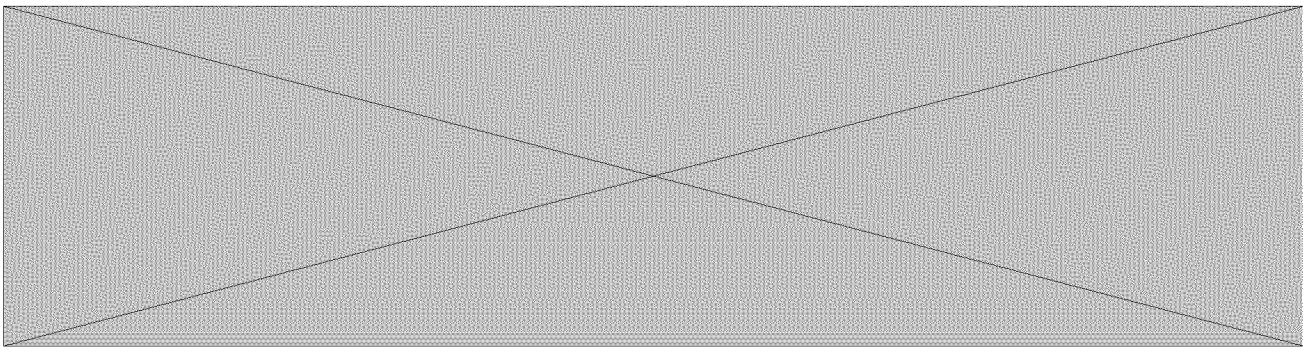
Cheers,
Wenbo

To: zengli Shi[zlshi@wh.iov.cn]; Yuan Zhiming[yzm@wh.iov.cn]; Shi, Pei yong[peshi@UTMB.EDU]
From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: Fri 7/24/2020 8:22:40 PM (UTC-05:00)
Subject: Fwd: Weekly Roundup of AJTMH COVID-19 Articles, 7/24

You May find the first two papers of special interest.
Best wishes. Jim
Sent from my iPhone

Begin forwarded message:

From: ASTMH <info@astmh.org>
Date: July 24, 2020 at 4:04:55 PM CDT
To: "LeDuc, James W." <jwleduc@UTMB.EDU>
Subject: Weekly Roundup of AJTMH COVID-19 Articles, 7/24
Reply-To: info@astmh.org



Weekly Roundup of COVID-19 Articles

Journal Editor-in-Chief Philip Rosenthal, Managing Editor Cathi Siegel, and Editorial Assistant Alison Jaeb are giving high priority to all COVID-19 manuscripts. Accepted manuscripts are posted to the Journal website almost immediately and are open to all. To keep you apprised of the latest research, we are sending a weekly roundup of the newly published articles on Friday.

We extend our deep thanks to the *Journal*'s Editors and staff who are working together to review and publish all accepted articles as quickly as possible.

► **Keep Politics out of Funding Decisions for Medical Research and Public Health**

Philip J. Rosenthal, Daniel G. Bausch, Karen A. Goraleski, David R. Hill, Julie A. Jacobson, Chandy C. John and Joel G. Breman

► **The Origin of COVID-19 and Why It Matters**

David M. Morens, Joel G. Breman, Charles H. Calisher, Peter C. Doherty, Beatrice H. Hahn, Gerald T. Keusch, Laura D. Kramer, James W. LeDuc, Thomas P. Monath and Jeffery K. Taubenberger

► **More Studies are Needed on the Link between Metformin and Decreased Mortality in Diabetic COVID-19 Patients**

Marinos Fysekidis, Régis Cohen and Abdallah Al-Salameh

► **Artemisia Spp. Derivatives for COVID-19 Treatment: Anecdotal Use, Political Hype, Treatment Potential, Challenges, and Road Map to Randomized Clinical Trials**

Paulin M. Kapepula, Jimmy K. Kabengele, Micheline Kingombe, Françoise Van Bambeke, Paul M. Tulkens, Antoine Sadiki Kishabongo, Eric Decloedt, Adam Zumla, Simon Tiberi, Fatima Suleman, Léon Tshilolo, Jean-Jacques Muyembe-TamFum, Alimuddin Zumla and Jean B. Nachega

► **Case Report: Pneumothorax and Pneumomediastinum as Uncommon Complications of COVID-19 Pneumonia—Literature Review**

Alvaro Quincho-Lopez, Dania L. Quincho-Lopez and Fernando D. Hurtado-Medina

► **Predicting the Impact of COVID-19 and the Potential Impact of the Public Health Response on Disease Burden in Uganda**

David Bell, Kristian Schultz Hansen, Agnes N. Kiragga, Andrew Kambugu, John Kissa and Anthony K. Mbonye

► **Incident SARS-CoV-2 Infection and a Shared Latrine**

Oscar H. Del Brutto, Aldo F. Costa and Héctor H. García

► **A University-Wide Preparedness Effort in the Alert Phase of COVID-19 Incorporating Community Mental Health and Task-Shifting Strategies: Experience from a Bornean Institute of Higher Learning**

Mohamad Hafiz Mukhsam, Mohammad Saffree Jeffree, Nicholas Tze Ping Pang, Syed Sharizman Syed Abdul Rahim, Azizan Omar, Muhammad Syafiq Abdullah, Khamisah Awang Lukman, Nelbon Giloi, Loganathan Salvaraji, Mohd Rahimie Abd Karim, Sahipudin Saupin, Yeap Boon Tat, Mohd Firdaus Mohd Hayati, Mohd Yusof Ibrahim, Assikin Muhamad and Syaza Putri Zainudin

All COVID-19 articles are being made freely available on the *Journal* website. Click here for the most up-to-date list of what's been published.

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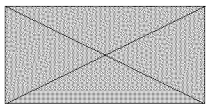

Every donation helps us continue to work towards our mission of reducing the worldwide burden of tropical infectious diseases and improving global health.

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241 18th Street South, Suite 501 • Arlington, VA 22202 USA

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To: Shi, Pei yong[peshi@UTMB.EDU]; 'shanchao@wh.iov.cn'[shanchao@wh.iov.cn]
Cc: SJS_PNAS_Specialist[PNAS_Specialist.djs@sheridan.com]
From: Steve Daniels[steve.daniels@sheridan.com]
Sent: Wed 7/29/2020 1:25:45 PM (UTC-05:00)
Subject: RE: PNAS MS# 2020-05722R Publication Update

Thanks for confirming, Pei-Yong.

To consider this change, we need you to provide the reason this change is required. In other words: What is the impact of this change?

Steve Daniels
Production Editor

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Waterbury, VT 05676
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From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 2:10 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Yes. You are right. I have included an image for the correction.

Thank you so much!

Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 1:06 PM
To: Shi, Pei yong <peshi@UTMB.EDU>; 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Pei-Yong,

Please confirm that the new change swaps the positions and letters for affiliations a and b, but no author affiliations are changed (only letters).

I will check with the editorial office to see if an exception can be made, but I want to be sure that I understand the details.

Thank you.

Steve Daniels
Production Editor

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Waterbury, VT 05676
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From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 1:59 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

We really have to correct this by all possible means.

I greatly appreciate your help!

Best regards,
Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 12:45 PM
To: 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: Shi, Pei yong <peshi@UTMB.EDU>; SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Chao,

Unfortunately, we're unable to make this change because this paper has already been approved for publication.

Let me know if you have any questions.

Thank you.

Steve Daniels
Production Editor
Sheridan
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Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: shanchao@wh.iov.cn [mailto:shanchao@wh.iov.cn]
Sent: Wednesday, July 29, 2020 8:32 AM
To: Steve Daniels
Cc: peshi; SJS_PNAS_Specialist
Subject: Fw: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Could you help to make a change for the paper "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R?

We would like to switch the affiliation order between a and b (see attachment). Could you help on this?

Many thanks for your help.
Best,
Chao

---

shanchao@wh.iov.cn

From: journalstaff
Date: 2020-07-28 02:51
To: peshi
CC: shanchao; hoxia; shhaller; srazar; yaliu2; jianyliu; aemuruat; rubing.chen; slrossi; mawakami; nivasila; rongjuan_pei; crfontes; sksingh; xuxie; sweaver
Subject: PNAS MS# 2020-05722R Publication Update

Dear Dr. Shi,

PNAS has scheduled publication of your article, "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R, in Latest Articles the week of August 3, 2020. Your article may publish in Latest Articles any day during that week. The Latest Articles publication date is the official date of record.

PNAS will not publish your article until the production vendor, Sheridan Journal Services, has incorporated the changes you made on the proofs. If you have requested a second set of proofs, your article will not publish until you have reviewed the edits. If you have questions about proofs, please contact (PNAS_Specialist.djs@sheridan.com).

The press embargo on your article will lift on August 3, 2020 at 3:00 PM U.S. Eastern time. The embargo date is the earliest possible date that your article can publish. Embargoed copies of your accepted article will be available to journalists starting Wednesday, July 29, 2020, on a secure reporters-only web site. Should you or your institution's public relations office have any press- or embargo-related questions, please contact the PNAS News Office at pnasnews@nas.edu or 202-334-1310.

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Best regards,
PNAS News Office
Phone: 202-334-1310
E-mail: PNASNews@nas.edu

To: Daniela Blaise[Daniela.Blaise@sheridan.com]; Shi, Pei yong[peshi@UTMB.EDU]; 'shanchao@wh.iov.cn'[shanchao@wh.iov.cn]
Cc: SJS_PNAS_Specialist[PNAS_Specialist.djs@sheridan.com]
From: Steve Daniels[steve.daniels@sheridan.com]
Sent: Thur 7/30/2020 11:07:44 AM (UTC-05:00)
Subject: RE: PNAS MS# 2020-05722R Publication Update

Thanks for your patience as we worked to resolve this request, Pei-Yong.

Steve Daniels
Production Editor
Sheridan
A CJK Group Company
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: Daniela Blaise
Sent: Thursday, July 30, 2020 10:39 AM
To: 'Shi, Pei yong'; Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

You're welcome, Pei-Yong!

Stay safe,

Dani

From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Thursday, July 30, 2020 10:23 AM
To: Daniela Blaise; Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Dear Daniela and Steve,

Thanks so much for your help!

Best regards,
Pei-Yong

From: Daniela Blaise <Daniela.Blaise@sheridan.com>
Sent: Thursday, July 30, 2020 9:01 AM
To: Steve Daniels <steve.daniels@sheridan.com>; Shi, Pei yong <peshi@UTMB.EDU>; 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Dear Dr. Shi and Dr. Shan,

Based on the reasoning provided, Steve obtained approval to proceed with these changes. We will update your article as requested

and approve the revised proof for publication on your behalf.

Thank you,

Dani

Daniela Blaise
Senior Production Editor
Sheridan
A CJK Group Company
Sheridan Journal Services
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
www.sheridan.com
www.cjkgroup.com

From: Steve Daniels
Sent: Wednesday, July 29, 2020 2:26 PM
To: 'Shi, Pei yong'; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Thanks for confirming, Pei-Yong.

To consider this change, we need you to provide the reason this change is required. In other words: What is the impact of this change?

Steve Daniels
Production Editor
Sheridan
A CJK Group Company
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 2:10 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Yes. You are right. I have included an image for the correction.

Thank you so much!

Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 1:06 PM
To: Shi, Pei yong <peshi@UTMB.EDU>; 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Pei-Yong,

Please confirm that the new change swaps the positions and letters for affiliations a and b, but no author affiliations are changed (only letters).

I will check with the editorial office to see if an exception can be made, but I want to be sure that I understand the details.

Thank you.

Steve Daniels
Production Editor

Sheridan
A CJK Group Company
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: Shi, Pei yong [mailto:peshi@UTMB.EDU]
Sent: Wednesday, July 29, 2020 1:59 PM
To: Steve Daniels; 'shanchao@wh.iov.cn'
Cc: SJS_PNAS_Specialist
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Steve,

We really have to correct this by all possible means.

I greatly appreciate your help!

Best regards,
Pei-Yong

From: Steve Daniels <steve.daniels@sheridan.com>
Sent: Wednesday, July 29, 2020 12:45 PM
To: 'shanchao@wh.iov.cn' <shanchao@wh.iov.cn>
Cc: Shi, Pei yong <peshi@UTMB.EDU>; SJS_PNAS_Specialist <PNAS_Specialist.djs@sheridan.com>
Subject: RE: PNAS MS# 2020-05722R Publication Update

Hi Chao,

Unfortunately, we're unable to make this change because this paper has already been approved for publication.

Let me know if you have any questions.

Thank you.

Steve Daniels
Production Editor

Sheridan
A CJK Group Company
5 Pilgrim Park Road, Suite 5
Waterbury, VT 05676
802-882-1608 | www.sheridan.com

From: shanchao@wh.iov.cn [mailto:shanchao@wh.iov.cn]
Sent: Wednesday, July 29, 2020 8:32 AM
To: Steve Daniels
Cc: peshi; SJS_PNAS_Specialist
Subject: Fw: PNAS MS# 2020-05722R Publication Update

Hi Steve,

Could you help to make a change for the paper "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R?

We would like to switch the affiliation order between a and b (see attachment). Could you help on this?

Many thanks for your help.
Best,
Chao

---

shanchao@wh.iov.cn

From: journalstaff
Date: 2020-07-28 02:51
To: peshi
CC: shanchao; hoxia; shhaller; srazar; yaliu2; jianyliu; aemuruat; rubing.chen; slrossi; mawakami; nivasila; rongjuan_pei; crfontes; sksingh; xuxie; sweaver
Subject: PNAS MS# 2020-05722R Publication Update

Dear Dr. Shi,

PNAS has scheduled publication of your article, "**A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission**," 2020-05722R, in Latest Articles the week of August 3, 2020. Your article may publish in Latest Articles any day during that week. The Latest Articles publication date is the official date of record.

PNAS will not publish your article until the production vendor, Sheridan Journal Services, has incorporated the changes you made on the proofs. If you have requested a second set of proofs, your article will not publish until you have reviewed the edits. If you have questions about proofs, please contact (PNAS_Specialist.djs@sheridan.com).

The press embargo on your article will lift on August 3, 2020 at 3:00 PM U.S. Eastern time. The embargo date is the earliest possible date that your article can publish. Embargoed copies of your accepted article will be available to journalists starting Wednesday, July 29, 2020, on a secure reporters-only web site. Should you or your institution's public relations office have any press- or embargo-related questions, please contact the PNAS News Office at pnasnews@nas.edu or 202-334-1310.

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Best regards,
PNAS News Office
Phone: 202-334-1310
E-mail: PNASNews@nas.edu

To: shanchao[shanchao@wh.iov.cn]; Weaver, Scott[sweaver@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]
From: 李鑫[lixin@bioart.com.cn]
Sent: Sat 8/8/2020 12:21:23 AM (UTC-05:00)
Subject: BioArt-We would like to report your study on PNAS

Dear Professors,

This is Xin from BioArt, which is one of the best online scientific media in China.

I'm writing this email to see whether you would like to provide a short report introducing your study on ***PNAS*** and entitled **"A Zika virus envelope mutation preceding the 2015 epidemic enhances virulence and fitness for transmission"**. If this is inconvenient to you, would you please forward this email to the first author to see if he is willing to write? It is a solid and decent research, we would like to introduce it to more scholars.

BioArt is an online media based on WeChat platform in China. We have almost 300 thousands followers, in which most are PhD researchers in life science and medicine fields. BioArt enjoys a high reputation in Chinese biological and medical community for our professional contents and it has been continuously voted Top 1 academic WeChat official account for three years.

Thank you for your attention. If you have any question, please don't hesitate to let me know. And we are looking forward to your reply.

Best,

Xin

Xin Li, Ph. D.
Deputy Editor-in-Chief，BioArt
Cell Phone：（+86-17600871720）
WeChat（微信号）：17600871720
E-mail：lixin@bioart.com.cn

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: editorial@virosin.org[editorial@virosin.org]; vs@wh.iov.cn[vs@wh.iov.cn]
From: Virologica Sinica[onbehalfof@manuscriptcentral.com]
Sent: Sun 2/21/2021 9:10:31 PM (UTC-06:00)
Subject: Manuscript ID VS-2021-5507 "Two inhibitors against the 3C-like proteases of feline coronavirus and swine coronavirus" removed from your Editor Center

22-Feb-2021

Dear Prof. Shi:

How are you!
We heard that the extreme cold snap bring historic snow strom and power problem in Texas. Hope you are fine and everything is going well.

We thought it is not suitable for you to organize the reviewing process at this time, thus we removed the manuscript from your Editor Center. And hope to have the chance to invite you again when future manuscripts come in that fall under your area of expertise.

Wish you and your family a healthy, smooth and auspicious year of 2021!

Best regards,

Editorial Office, Virologica Sinica

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Zhang, Wenbo[we2zhang@UTMB.EDU]
From: 单超[shanchao@wh.iov.cn]
Sent: Thur 3/4/2021 6:38:00 PM (UTC-06:00)
Subject: Re: RE: our manuscript

Thanks Dr. Zhang and Pei-Yong. Good luck with submission.

Best,

Chao

-----原始邮件-----
发件人:"Shi, Pei yong" <peshi@UTMB.EDU>
发送时间:2021-03-05 06:21:49 (星期五)
收件人: "Zhang, Wenbo" <we2zhang@UTMB.EDU>
抄送: "shanchao@wh.iov.cn" <shanchao@wh.iov.cn>
主题: RE: our manuscript

Thanks, Wenbo

Chao's email: shanchao@wh.iov.cn

Grant acknowledgement:

"P.-Y.S. was supported by NIH grants AI134907 and UL1TR001439, and awards from the Sealy & Smith Foundation, Kleberg Foundation, the John S. Dunn Foundation, the Amon G. Carter Foundation, the Gilson Longenbaugh Foundation, and the Summerfield Robert Foundation."

Best, Pei-Yong

From: Zhang, Wenbo <we2zhang@UTMB.EDU>
Sent: Thursday, March 4, 2021 4:12 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: our manuscript

Dear Dr. Shi,

Thank you very much. Do you want to include any of your grant support in the acknowledgement? Also, could you please give me Chao's current email address so that I can use during manuscript submission?

Best regards,

Wenbo

From: Shi, Pei yong
Sent: Thursday, March 04, 2021 3:41 PM
To: Zhang, Wenbo <we2zhang@UTMB.EDU>
Subject: RE: our manuscript

Dear Wenbo,

Thank you for this well executed and written study. Please see my edits.

Four potential reviewers:

- Margo Ann Brinton <mbrinton@gsu.edu>, Georgia State University
- Kristen Barnard: kristen.bernard@wisc.edu, https://www.vetmed.wisc.edu/people/kbernard/
- Saguna Verma <saguna@hawaii.edu>, https://manoa.hawaii.edu/tropicalmedicine/?page_id=674
- Chengfeng Qin: <chengfeng_qin@126.com>

Cheng-Feng (Chengfeng) Qin, Ph.D.

Professor & Chair, Dept. of Virology,

State Key Laboratory of Pathogen and Biosecurity,

Beijing Institute of Microbiology and Epidemiology,

Academy of Military Medical Sciences,

No.20 Dongda Street, Fengtai District,

Beijing 100071, China

Best, Pei-Yong

From: Zhang, Wenbo <we2zhang@UTMB.EDU>
Sent: Wednesday, March 3, 2021 2:13 PM
To: Shi, Pei yong <peshi@UTMB.EDU>
Subject: our manuscript

Dear Dr. Shi,

Thank you very much for collaborating with us in this project. Please revise it freely and let us know which title is good or what title you would suggest. Moreover, as we discussed, please suggest 4-5 potential reviewers. We expect to get the manuscript submitted Monday or Tuesday to Nature Communication or other journals you suggested. In addition, please share it with Chao and Jin because all authors need to approve it before submission.

Cheers,

Wenbo

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Virologica Sinica[virosin@wh.iov.cn]
Sent: Tue 3/30/2021 8:37:30 AM (UTC-05:00)
Subject: To Dr.Shi - Virologica Sinica online first article collection in Jan-Mar 2021

Dear Dr. Shi,

We are pleased to share with you the latest online first articles published in *Virologica Sinica*.

1. Human Endogenous Retrovirus Type W Envelope from Multiple Sclerosis Demyelinating Lesions Shows Unique Solubility and Antigenic Characteristics.
   Benjamin Charvet, Justine Pierquin, Joanna Brunel, Rianne Gorter, Christophe Quétard, Branka Horvat, Sandra Amor, Jacques Portoukalian, Hervé Perron
   Virol Sin. 2021 Mar 26. doi: 10.1007/s12250-021-00372-0. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00372-0

2. Role of Intracellular Distribution of Feline and Bovine SAMHD1 Proteins in Lentiviral Restriction.
   Chu Wang, Lina Meng, Jialin Wang, Kaikai Zhang, Sizhu Duan, Pengyu Ren, Yingzhe Wei, Xinyu Fu, Bin Yu, Jiaxin Wu, Xianghui Yu
   Virol Sin. 2021 Mar 22. doi: 10.1007/s12250-021-00351-5. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00351-5

3. Significant Inhibition of Porcine Epidemic Diarrhea Virus In Vitro by Remdesivir, Its Parent Nucleoside and β-D-N^4-hydroxycytidine.
   Yuanchao Xie, Xiaozhen Guo, Tianwen Hu, Daibao Wei, Xiuli Ma, Jiaqiang Wu, Bing Huang , Jingshan Shen
   Virol Sin. 2021 Mar 22:1–9. doi: 10.1007/s12250-021-00362-2. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00362-2

4. Surveillance of Class I Newcastle Disease Virus at Live Bird Markets and Commercial Poultry Farms in Eastern China Reveals the Epidemic Characteristics.
   Xiaolong Lu, Xiaoquan Wang, Tiansong Zhan, Yifan Sun, Xin Wang, Naiqing Xu, Tianxing Liao, Yu Chen, Min Gu, Shunlin Hu, Xiaowen Liu, Xiufan Liu
   Virol Sin. 2021 Mar 15. doi: 10.1007/s12250-021-00357-z. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00357-z

5. Porcine Coronaviruses: Overview of the State of the Art.
   Hanna Turlewicz-Podbielska, Małgorzata Pomorska-Mól
   Virol Sin. 2021 Mar 15:1–19. doi:10.1007/s12250-021-00364-0. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00364-0

6. The CREB Regulated Transcription Coactivator 2 Suppresses HIV-1 Transcription by Preventing RNA Pol II from Binding to HIV-1 LTR.
   Ling Ma, Shumin Chen, Zhen Wang, Saisai Guo, Jianyuan Zhao, Dongrong Yi, Quanjie Li, Zhenlong Liu, Fei Guo, Xiaoyu Li, Pingping Jia, Jiwei Ding, Chen Liang, Shan Cen
   Virol Sin. 2021 Mar 15. doi: 10.1007/s12250-021-00363-1. Epub ahead of print.
   https://link.springer.com/article/10.1007/s12250-021-00363-1

7. Exploration of a Sequential Gp140-Gp145 Immunization Regimen with Heterologous Envs to Induce a Protective Cross-Reactive HIV Neutralizing Antibody Response In Non-human Primates.
   Xiangqing Ding, Kangli Cao, Jing Wang, Yanmin Wan, Qinyun Chen, Yanqin Ren, Yongtang Zheng, Mingzhao Zhu, Renrong

Tian, Wenjun Wang, Chen Zhao, Xiaoyan Zhang, Jianqing Xu
Virol Sin. 2021 Mar 15:1–12. doi: 10.1007/s12250-021-00361-3. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00361-3

8. Porcine Picornavirus 3C Protease Degrades PRDX6 to Impair PRDX6-mediated Antiviral Function.
Congcong Wang, Huanhuan Feng, Xiangle Zhang, Kangli Li, Fan Yang, Weijun Cao, Huisheng Liu, Lili Gao, Zhaoning Xue, Xiangtao Liu, Zixiang Zhu, Haixue Zheng
Virol Sin. 2021 Mar 15:1–10. doi:10.1007/s12250-021-00352-4. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00352-4

9. Autographa Californica Multiple Nucleopolyhedrovirus orf13 Is Required for Efficient Nuclear Egress of Nucleocapsids.
Xingang Chen, Xiaoqin Yang, Chengfeng Lei, Fujun Qin, Xiulian Sun, Jia Hu
Virol Sin. 2021 Mar 15. doi: 10.1007/s12250-021-00353-3. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00353-3

10. Establishment of a Reverse Genetic System of Severe Fever with Thrombocytopenia Syndrome Virus Based on a C4 Strain.
Mingyue Xu, Bo Wang, Fei Deng, Hualin Wang, Manli Wang, Zhihong Hu, Jia Liu
Virol Sin. 2021 Mar 15. doi: 10.1007/s12250-021-00359-x. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00359-x

11. Effects of N-Linked Glycan on Lassa Virus Envelope Glycoprotein Cleavage, Infectivity, and Immune Response.
Xueqin Zhu, Yang Liu, Jiao Guo, Junyuan Cao, Zonglin Wang, Gengfu Xiao, Wei Wang
Virol Sin. 2021 Mar 10:1–10. doi: 10.1007/s12250-021-00358-y. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00358-y

12. African Swine Fever Virus MGF-110-9L-deficient Mutant Has Attenuated Virulence in Pigs.
Dan Li, Yinguang Liu, Xiaolan Qi, Yuan Wen, Pan Li, Zhao Ma, Yongjie Liu, Haixue Zheng, Zhijie Liu
Virol Sin. 2021 Mar 10. doi: 10.1007/s12250-021-00350-6. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00350-6

13. Systematic Analysis of 42 Autographa Californica Multiple Nucleopolyhedrovirus Genes Identifies An Additional Six Genes Involved in the Production of Infectious Budded Virus.
Tong Chen, Xiaoyan Duan, Hengrui Hu, Yu Shang, Yangbo Hu, Fei Deng, Hualin Wang, Manli Wang, Zhihong Hu
Virol Sin. 2021 Mar 8. doi: 10.1007/s12250-021-00355-1. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00355-1

14. Effects of Overwintering on the Survival and Vector Competence of Aedes albopictus in the Urban Life Cycle of Dengue Virus in Guangzhou, China.
Yue Chen, Ronghua Chen, Jianrong Gao, Chunyuan Li, Jun Liu, Zhijian Zhou, Ruiwen Ren
Virol Sin. 2021 Mar 5. doi:10.1007/s12250-021-00356-0. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00356-0

15. Sustainability of SARS-CoV-2 Induced Humoral Immune Responses in COVID-19 Patients from Hospitalization to Convalescence Over Six Months.
Yang Zheng, Qing Zhang, Ashaq Ali, Ke Li, Nan Shao, Xiaoli Zhou, Zhiqin Ye, Xiaomin Chen, Shanshan Cao, Jing Cui, Juan Zhou, Dianbing Wang, Baidong Hou, Min Li, Mengmeng Cui, Lihua Deng, Xinyi Sun, Qian Zhang, Qinfang Yang, Yong li, Hui Wang, Yake Lei, Bo Yu, Yegang Cheng, Xiaolin Tong, Dong Men, Xian-En Zhang
Virol Sin. 2021 Mar 4:1–10. doi:10.1007/s12250-021-00360-4. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00360-4

16.

Artesunate and Dihydroartemisinin Inhibit Rabies Virus Replication.

Jun Luo, Yue Zhang, Yang Wang, Qing Liu, Jiesen Li, Hongling He, Yongwen Luo, Shile Huang, Xiaofeng Guo
Virol Sin. 2021 Mar 4:1–9. doi: 10.1007/s12250-021-00349-z. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00349-z

17. A Novel 2-dimensional Multiplex qPCR Assay for Single-Tube Detection of Nine Human Herpesviruses.
Yingxue Li, Zhenzhou Wan, Lulu Zuo, Shenwei Li, Honglian Liu, Yingying Ma, Lianqun Zhou, Xia Jin, Yuye Li, Chiyu Zhang
Virol Sin. 2021 Feb 26. doi: 10.1007/s12250-021-00354-2. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00354-2

18. Development of A MERS-CoV Replicon Cell Line for Antiviral Screening.
Jing Chen, Bing-Jie Hu, Kai Zhao, Yun Luo, Hao-Feng Lin, Zheng-Li Shi
Virol Sin. 2021 Feb 22:1–6. doi:10.1007/s12250-020-00341-z. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-020-00341-z

19. Current Status and Challenge of Pseudorabies Virus Infection in China.
Lei Tan, Jun Yao, Yadi Yang, Wei Luo, Xiaomin Yuan, Lingchen Yang, Aibing Wang
Virol Sin. 2021 Feb 22:1–20. doi: 10.1007/s12250-020-00340-0. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-020-00340-0

20. HRV16 Infection Induces Changes in the Expression of Multiple piRNAs.
Jie Li, Xinling Wang, Yanhai Wang, Juan Song, Qinqin Song, Yanbin Wang, Jun Han
Virol Sin. 2021 Feb 22. doi:10.1007/s12250-021-00344-4. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00344-4

21. Alterations in Phenotypes and Responses of T Cells Within 6 Months of Recovery from COVID-19: A Cohort Study.
Bali Zhao, Maohua Zhong, Qingyu Yang, Ke Hong, Jianbo Xia, Xia Li, Ying Liu, Yao-Qing Chen, Jingyi Yang, Chaolin Huang, Huimin Yan
Virol Sin. 2021 Feb 9:1–10. doi:10.1007/s12250-021-00348-0. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00348-0

22. Evaluation of the Safety and Immune Efficacy of Recombinant Human Respiratory Syncytial Virus Strain Long Live Attenuated Vaccine Candidates.
Li-Nan Wang, Xiang-Lei Peng, Min Xu, Yuan-Bo Zheng, Yue-Ying Jiao, Jie-Mei Yu, Yuan-Hui Fu, Yan-Peng Zheng, Wu-Yang Zhu, Zhong-Jun Dong, Jin-Sheng He
Virol Sin. 2021 Feb 9. doi: 10.1007/s12250-021-00345-3. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00345-3

23. Human PRV Infection in China: An Alarm to Accelerate Eradication of PRV in Domestic Pigs.
Zhenhua Guo, Xin-Xin Chen, Gaiping Zhang
Virol Sin. 2021 Feb 4. doi:10.1007/s12250-021-00347-1. Epub ahead of print.
https://link.springer.com/article/10.1007/s12250-021-00347-1

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To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: vs@wh.iov.cn[vs@wh.iov.cn]; editorial@virosin.org[editorial@virosin.org]
From: Lijun Rong[onbehalfof@manuscriptcentral.com]
Sent: Thur 5/13/2021 2:35:15 PM (UTC-05:00)
Subject: Manuscript review for Virologica Sinica Manuscript ID VS-2021-5603 - "Inhibition of Chikungunya virus Replication by Lycorine".

14-May-2021

Dear Prof. Shi:

Thank you for replying to my invitation to review for Virologica Sinica entitled "Inhibition of Chikungunya virus Replication by Lycorine"

It is unfortunate that you are unable to review this manuscript this time. I will keep you in mind when future manuscripts come in that fall under your area of expertise.

Sincerely,
Lijun Rong
Editor, Virologica Sinica
lijun@uic.edu

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Cc: editorial@virosin.org[editorial@virosin.org]; vs@wh.iov.cn[vs@wh.iov.cn]
From: Lijun Rong[onbehalfof@manuscriptcentral.com]
Sent: Thur 5/13/2021 2:12:21 PM (UTC-05:00)
Subject: Invitation for Manuscript Review, Virologica Sinica VS-2021-5603

VS-2021-5603 - “Inhibition of Chikungunya virus Replication by Lycorine”.

14-May-2021

Dear Prof. Shi,

Manuscript ID VS-2021-5603 entitled "Inhibition of Chikungunya virus Replication by Lycorine" with Dr. Bo Zhang as corresponding author has been submitted to Virologica Sinica.

I invite you to review this manuscript. The author list and abstract are appended below, plus more detailed information about Virologica Sinica and its editorial criteria.

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Once you accept my invitation to review this manuscript, an e-mail will be sent to you (within 10min) about how to access Manuscript Central, our online review system. You will then have access to the manuscript and reviewer instructions in your Reviewer Center.

If you are unable to review at this time, I would appreciate you recommending another expert reviewer.

Thank you for your participation. If you have any questions or concerns, please do not hesitate to contact me, or the VS editorial office at editorial@virosin.org.

Sincerely,

Lijun Rong
Editor, Virologica Sinica
lijun@uic.edu

MANUSCRIPT DETAILS

TITLE: Inhibition of Chikungunya virus Replication by Lycorine

AUTHORS: Li, Na; Wang, Zhen; Wang, Rui; Zhang, Zherui; Zhang, Ya-Nan; Deng, Cheng-Lin; Zhang, Bo; Shang, Lu-Qing; Ye, Hanqing

ABSTRACT: Chikungunya virus (CHIKV) is a mosquito-borne alphavirus. As an emerging virus, CHIKV imposes a threat to public health. Currently, there are no vaccine or antiviral available for prevention of CHIKV infection. In this study, we found that lycorine could inhibit CHIKV in cell culture without apparent cytotoxicity. In addition, it exhibited broad-spectrum anti-alphavirus activity, including Sindbis virus (SINV), Semliki Forest virus (SFV), and Venezuelan equine encephalomyelitis virus (VEEV). The time of addition studies indicated that lycorine functions at an early post-entry stage of CHIKV life cycle. The results based on two different CHIKV replicons provided further evidence that lycorine exerts its antiviral activity mainly by inhibiting CHIKV translation.

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lorenzo.zammarchi@unifi.it[lorenzo.zammarchi@unifi.it]; giulia.stella441@gmail.com[giulia.stella441@gmail.com]; antoniamantella@libero.it[antoniamantella@libero.it]; bartolozzid@aou-careggi.toscana.it[bartolozzid@aou-careggi.toscana.it]; guenther@bnitm.de[guenther@bnitm.de]; oestereich@bnitm.de[oestereich@bnitm.de]; cadar@bnitm.de[cadar@bnitm.de]; cesar.munoz-fontela@hpi.uni-hamburg.de[cesar.munoz-fontela@hpi.uni-hamburg.de]; alessandro.bartoloni@unifi.it[alessandro.bartoloni@unifi.it]; jonassi@gmx.de[jonassi@gmx.de]; masrimaha@yahoo.com[masrimaha@yahoo.com]; croche@ilm.pf[croche@ilm.pf]; tnhan@ilm.pf[tnhan@ilm.pf]; e.grange@cht.nc[e.grange@cht.nc]; ateissier@ilm.pf[ateissier@ilm.pf]; mlormeau@ilm.pf[mlormeau@ilm.pf]; laura.hermann@afrims.org[laura.hermann@afrims.org]; arodriguez@jidc.org[arodriguez@jidc.org]; maubry@ilm.pf[maubry@ilm.pf]; ctdiagne@pasteur.sn[ctdiagne@pasteur.sn]; ddiallo@pasteur.sn[ddiallo@pasteur.sn]; ba@pasteur.sn[ba@pasteur.sn]; agaye@pasteur.sn[agaye@pasteur.sn]; 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leo.travassos@biof.ufrj.br[leo.travassos@biof.ufrj.br]; K.Bourtzis@iaea.org[K.Bourtzis@iaea.org]; R.S.Lees@iaea.org[R.S.Lees@iaea.org]; J.Hendrichs@iaea.org[J.Hendrichs@iaea.org]; M.Vreysen@iaea.org[M.Vreysen@iaea.org]; jason@jasontetro.com[jason@jasontetro.com]; drousset@pasteur-cayenne.fr[drousset@pasteur-cayenne.fr]; khank@smh.ca[khank@smh.ca]; philippe.gautret@club-internet.fr[philippe.gautret@club-internet.fr]; sonare.since1192@gmail.com[sonare.since1192@gmail.com]; lavinia.faccini@ufrgs.br[lavinia.faccini@ufrgs.br]; asow@pasteur.sn[asow@pasteur.sn]; cloucoubar@pasteur.sn[cloucoubar@pasteur.sn]; diawod@yahoo.fr[diawod@yahoo.fr]; oumarfaye@pasteur.sn[oumarfaye@pasteur.sn]; youndiaye@hotmail.com[youndiaye@hotmail.com]; doczenghos@yahoo.fr[doczenghos@yahoo.fr]; adia@ised.sn[adia@ised.sn]; ofaye@pasteur.sn[ofaye@pasteur.sn]; diallo@pasteur.sn[diallo@pasteur.sn]; denis.malvy@chu-bordeaux.fr[denis.malvy@chu-bordeaux.fr]; asall@pasteur.sn[asall@pasteur.sn]; diego.ruizmoreno.phd@gmail.com[diego.ruizmoreno.phd@gmail.com]; afaccini@gmail.com[afaccini@gmail.com]; shlomit@geo.haifa.ac.il[shlomit@geo.haifa.ac.il]; tans@cpqam.fiocruz.br[tans@cpqam.fiocruz.br]; akampango@gmail.com[akampango@gmail.com]; anabilio1408@gmail.com[anabilio1408@gmail.com]; derek.macfadden@mail.utoronto.ca[derek.macfadden@mail.utoronto.ca]; orattatjana.avsic@mf.uni-lj.si[orattatjana.avsic@mf.uni-lj.si]; zmemish@yahoo.com[zmemish@yahoo.com]; a.goorhuis@amc.uva.nl[a.goorhuis@amc.uva.nl]; david.heymann@phe.gov.uk[david.heymann@phe.gov.uk]; andreas.neumayr@unibas.ch[andreas.neumayr@unibas.ch]; mewilson@hsph.harvard.edu[mewilson@hsph.harvard.edu]; thomas.weitzel@gmail.com[thomas.weitzel@gmail.com]; m.roa@womenslinkworldwide.org[m.roa@womenslinkworldwide.org]; bpinsky@stanford.edu[bpinsky@stanford.edu]; RBrasilMartines@cdc.gov[RBrasilMartines@cdc.gov]; gretchen_birbeck@urmc.rochester.edu[gretchen_birbeck@urmc.rochester.edu]; abispo@ioc.fiocruz.br[abispo@ioc.fiocruz.br]; david.baud@chuv.ch[david.baud@chuv.ch]; Daniel.Pastula@ucdenver.edu[Daniel.Pastula@ucdenver.edu]; rcarri1@lsu.edu[rcarri1@lsu.edu]; zgr1965@sina.com[zgr1965@sina.com]; k.shakib@nhs.net[k.shakib@nhs.net]; jcurrie@princeton.edu[jcurrie@princeton.edu]; valter.ecologia@gmail.com[valter.ecologia@gmail.com]; amartine@cinvestav.mx[amartine@cinvestav.mx]; petrusv@nicd.ac.za[petrusv@nicd.ac.za]; citrome@cnsconsultant.com[citrome@cnsconsultant.com]; richardastein@gmail.com[richardastein@gmail.com]; duncan_r_smith@hotmail.com[duncan_r_smith@hotmail.com]; davisf@micro.ufrj.br[davisf@micro.ufrj.br]; iancropley@nhs.net[iancropley@nhs.net]; Andrew.Ustianowski@pat.nhs.uk[Andrew.Ustianowski@pat.nhs.uk]; peter.byass@umu.se[peter.byass@umu.se]; mauricio.barreto@bahia.fiocruz.br[mauricio.barreto@bahia.fiocruz.br]; nishiurah@gmail.com[nishiurah@gmail.com]; tsolomon@liv.ac.uk[tsolomon@liv.ac.uk]; megershwin@ucdavis.edu[megershwin@ucdavis.edu]; heukelbach@web.de[heukelbach@web.de]; molly.killion@ucsf.edu[molly.killion@ucsf.edu]; akelvinphd@jidc.org[akelvinphd@jidc.org]; isabel.kantor@gmail.com[isabel.kantor@gmail.com]; baldfons@fmrp.usp.br[baldfons@fmrp.usp.br]; iburd@jhmi.edu[iburd@jhmi.edu]; ajrodriguezmmd@gmail.com[ajrodriguezmmd@gmail.com]; antoniobandeira@gmail.com[antoniobandeira@gmail.com]; cparedes@ppmh.org[cparedes@ppmh.org]; kyyuen@hku.hk[kyyuen@hku.hk]; ZikaMCH@cdc.gov[ZikaMCH@cdc.gov]; knielsen@mednet.ucla.edu[knielsen@mednet.ucla.edu]; mdupont@pasteur.nc[mdupont@pasteur.nc]; peshi@utmb.gov[peshi@utmb.gov]; sippenbauch@gmail.com[sippenbauch@gmail.com]; sroura.mn.ics@gencat.cat[sroura.mn.ics@gencat.cat]; atrilla@clinic.cat[atrilla@clinic.cat]; annie.lannuzel@chu-guadeloupe.fr[annie.lannuzel@chu-guadeloupe.fr]; fontanet@pasteur.fr[fontanet@pasteur.fr]; dattaway@esri.com[dattaway@esri.com]; david.smith@health.wa.gov.au[david.smith@health.wa.gov.au];

jsegars2@jhmi.edu[jsegars2@jhmi.edu]; mansuy.jm@chu-toulouse.fr[mansuy.jm@chu-toulouse.fr];
david.cabrerag@imss.gob.mx[david.cabrerag@imss.gob.mx]; dcpreventiva@gmail.com[dcpreventiva@gmail.com];
antonio.barrera@imss.gob.mx[antonio.barrera@imss.gob.mx]; adibij@pitt.edu[adibij@pitt.edu];
guillaume.carteaux@yahoo.fr[guillaume.carteaux@yahoo.fr]; a.i.zumla@gmail.com[a.i.zumla@gmail.com];
ig299@cam.ac.uk[ig299@cam.ac.uk]; kasolof@who.int[kasolof@who.int]; fntoumi@fcrm-congo.com[fntoumi@fcrm-congo.com];
philippe.x.buchy@gsk.com[philippe.x.buchy@gsk.com]; matthew.bates@ucl.ac.uk[matthew.bates@ucl.ac.uk];
eazhar@kau.edu.sa[eazhar@kau.edu.sa]; mc13@sanger.ac.uk[mc13@sanger.ac.uk]; eskildp@dadlnet.dk[eskildp@dadlnet.dk];
helen.lazear@med.unc.edu[helen.lazear@med.unc.edu]; pascal.imperato@downstate.edu[pascal.imperato@downstate.edu];
skashima@hemocentro.fmrp.usp.br[skashima@hemocentro.fmrp.usp.br]; a-tridane@uaeu.ac.ae[a-tridane@uaeu.ac.ae];
nastaran.rafiei@uqconnect.edu.au[nastaran.rafiei@uqconnect.edu.au]; simon.cauchemez@pasteur.fr[simon.cauchemez@pasteur.fr];
caowc@bmi.ac.cn[caowc@bmi.ac.cn]; laura.rodrigues@lshtm.ac.uk[laura.rodrigues@lshtm.ac.uk];
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pbachiller@gmail.com[pbachiller@gmail.com]; Waqas1184@hotmail.com[Waqas1184@hotmail.com];
l.gardner@unsw.edu.au[l.gardner@unsw.edu.au]; Weaver, Scott[sweaver@UTMB.EDU];
arrfreitas2010@gmail.com[arrfreitas2010@gmail.com]; rodrigo.angerami@gmail.com[rodrigo.angerami@gmail.com];
andreabrunovonzuben@gmail.com[andreabrunovonzuben@gmail.com]; rita.donalisio@gmail.com[rita.donalisio@gmail.com];
eriloyola@hotmail.com[eriloyola@hotmail.com]; r.shakir@imperial.ac.uk[r.shakir@imperial.ac.uk];
anayajm@gmail.com[anayajm@gmail.com]; RWSteele@aol.com[RWSteele@aol.com]; skr9@cdc.gov[skr9@cdc.gov];
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pedrovasconcelos@iec.pa.gov.br[pedrovasconcelos@iec.pa.gov.br]; dorothee.misse@ird.fr[dorothee.misse@ird.fr];
jorge.kalil@butantan.gov.br[jorge.kalil@butantan.gov.br];
kathryn.taylor1@hnehealth.nsw.gov.au[kathryn.taylor1@hnehealth.nsw.gov.au];
jyoung@silverfallsderm.net[jyoung@silverfallsderm.net]; Rossi, Shannan L.[slrossi@UTMB.EDU];
mbesnard@nohao.net[mbesnard@nohao.net]; Hugh.Willison@glasgow.ac.uk[Hugh.Willison@glasgow.ac.uk];
ssmattos@cardiol.br[ssmattos@cardiol.br]; amaeda@worldbank.org[amaeda@worldbank.org]; nzr5@cdc.gov[nzr5@cdc.gov];
DRL23@georgetown.edu[DRL23@georgetown.edu]; adam@adamcraig.com.au[adam@adamcraig.com.au];
fauziahmi@usm.my[fauziahmi@usm.my]; fgodlee@bmj.com[fgodlee@bmj.com]; clinbelf@uol.com.br[clinbelf@uol.com.br];
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a.alcantara.montero@hotmail.com[a.alcantara.montero@hotmail.com];
sampathkumar.priya@mayo.edu[sampathkumar.priya@mayo.edu]; aporett1@jhmi.edu[aporett1@jhmi.edu];
nunes@pucrs.br[nunes@pucrs.br]; d.focosi@ao-pisa.toscana.it[d.focosi@ao-pisa.toscana.it];
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michael.rajnik@usuhs.edu[michael.rajnik@usuhs.edu]; jean-marie.jouannic@aphp.fr[jean-marie.jouannic@aphp.fr];
francois.bricaire@psl.aphp.fr[francois.bricaire@psl.aphp.fr]; cristinabocanegra@gmail.com[cristinabocanegra@gmail.com];
yazdan.yazdanpanah@aphp.fr[yazdan.yazdanpanah@aphp.fr]; edmarchiori@gmail.com[edmarchiori@gmail.com];
ysadovsky@mwri.magee.edu[ysadovsky@mwri.magee.edu]; Coyne, Carolyn[coynec2@pitt.edu];
tang@bio.fsu.edu[tang@bio.fsu.edu]; giovanetti.marta@gmail.com[giovanetti.marta@gmail.com];
fatima.vascoaragao@gmail.com[fatima.vascoaragao@gmail.com]; drgovindzoo@yahoo.com[drgovindzoo@yahoo.com];
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mysorekari@wudosis.wustl.edu[mysorekari@wudosis.wustl.edu]; diamond@borcim.wustl.edu[diamond@borcim.wustl.edu]; mmtex@icb.ufmg.br[mmtex@icb.ufmg.br]; er@blonz.com[er@blonz.com]; giuseppina.liuzzi@inmi.it[giuseppina.liuzzi@inmi.it]; emanuele.nicastri@inmi.it[emanuele.nicastri@inmi.it]; Vincenzo.Puro@inmi.it[Vincenzo.Puro@inmi.it]; a.zumla@ucl.ac.uk[a.zumla@ucl.ac.uk]; giuseppe.ippolito@inmi.it[giuseppe.ippolito@inmi.it]; anneliesws@gmail.com[anneliesws@gmail.com]; neurona23@hotmail.com[neurona23@hotmail.com]; bouyer@cirad.fr[bouyer@cirad.fr]; cboete@gmail.com[cboete@gmail.com]; laith.yakob@lshtm.ac.uk[laith.yakob@lshtm.ac.uk]; Shi, Pei yong[peshi@UTMB.EDU]; silveirafd@upmc.edu[silveirafd@upmc.edu]; m.p.grobusch@amc.uva.nl[m.p.grobusch@amc.uva.nl]; fqin1@foxmail.com[fqin1@foxmail.com]; vorou@keelpno.gr[vorou@keelpno.gr]; shiwf@ioz.ac.cn[shiwf@ioz.ac.cn]; zhpchen@cdc.zj.cn[zhpchen@cdc.zj.cn]; janneke.duijster@rivm.nl[janneke.duijster@rivm.nl]; oladapoo@who.int[oladapoo@who.int]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; broniatowski@gwu.edu[broniatowski@gwu.edu]; crbrites@gmail.com[crbrites@gmail.com]; guanzhu@email.arizona.edu[guanzhu@email.arizona.edu]; wviroj@yahoo.com[wviroj@yahoo.com]; rrochat@emory.edu[rrochat@emory.edu]; robertsonnp@cardiff.ac.uk[robertsonnp@cardiff.ac.uk]; ruzekd@paru.cas.cz[ruzekd@paru.cas.cz]; gorben.pijlman@wur.nl[gorben.pijlman@wur.nl]; dariusm@stanford.edu[dariusm@stanford.edu]; kanpharm2002@gmail.com[kanpharm2002@gmail.com]; arodriguezm@utp.edu.co[arodriguezm@utp.edu.co]; miae@ewha.ac.kr[miae@ewha.ac.kr]; beuyjoob@hotmail.com[beuyjoob@hotmail.com]; pavel.calda@vfn.cz[pavel.calda@vfn.cz]; pauloivf@aol.com[pauloivf@aol.com]; harachand@gmail.com[harachand@gmail.com]; pavel.calda@lf1.cuni.cz[pavel.calda@lf1.cuni.cz]; wildriss.viranaicken@univ-reunion.fr[wildriss.viranaicken@univ-reunion.fr]; philippe.despres@univ-reunion.fr[philippe.despres@univ-reunion.fr]; vanda.bostikova@pmfhk.cz[vanda.bostikova@pmfhk.cz]; g.benelli@sssup.it[g.benelli@sssup.it]; oacostal@unal.edu.co[oacostal@unal.edu.co]; dmusso@ilm.pf[dmusso@ilm.pf]; duane.gubler@duke-nus.edu.sg[duane.gubler@duke-nus.edu.sg]; atulgogia@yahoo.com[atulgogia@yahoo.com]; rpardot@unal.edu.co[rpardot@unal.edu.co]; pvial@udd.cl[pvial@udd.cl]

From: Orient Star Group English[orientstar.english@gmail.com]
Sent: Fri 4/16/2021 4:47:17 AM (UTC-05:00)
Subject: Inquiry for a business partnership from Uzbekistan & Central Asia

Dear Colleagues

It is important to mention that from 2020, Uzbekistan introduced a visa free regime for 85 countries up to 30days regardless of their visit.

The local incoming travel agency **"ORIENT STAR GROUP"** was established by a team of professionals. **(Licence number: T-0017-18).** Our office is located in the capital of **Uzbekistan,** in **Tashkent** city, one of the important and tourist cities of **Uzbekistan and Central Asia**. We organize tours throughout Uzbekistan as well as combined tours in Central Asia along the legendary **"Great Silk Road".** The agency is still young, founded in 2016 and the professional team we speak in different languages. We started to work with the following language markets such as Spanish, French, German, Italian, English, Russian, Turkish, Arabic, Japanese, Chinese. In the bellow**, some tour packages with rates for 2021.** With these different tour packages, tourists will have the opportunity to get to know not only the history and architecture of Uzbekistan, but also the country and **its people, customs, traditions, daily life of the current local people.**

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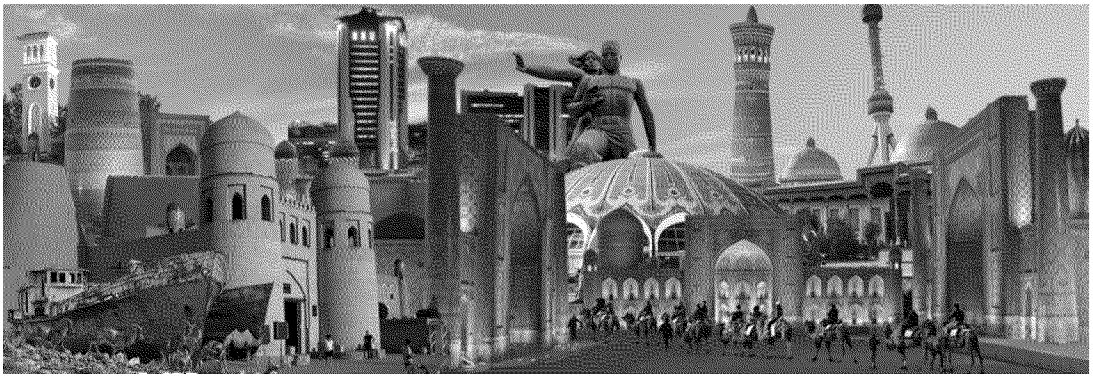

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Albrecht, Randy; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Alyson Kelvin; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); JOHN JAMES BACZENAS; BAMFORD, Pearl; rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); sinabavari@comcast.net; Martin.Beer (Martin.Beer@fli.de); Neil Berry (Neil.Berry@nibsc.org); terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); dbolton@hivresearch.org; mopargal (mopargal@rams.colostate.edu); SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion (rcarrion@TxBiomed.org); Miles.Carroll (Miles.Carroll@phe.gov.uk); Cartner, Samuel Corbin; Cassels, Fred; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); lisa.chakrabarti@pasteur.fr; jfwchan (jfwchan@hku.hk); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); hlchen (hlchen@hku.hk); Carolyn Clark (carolyn.clark@cepi.net); yu.cong@nih.gov; scordo (scordo@qb.fcen.uba.ar); lisette.cornelissen; Crozier, Ian (NIH) [C]; kai.dallmeier (kai.dallmeier@kuleuven.be); Damron, Fredrick; que.dang@nih.gov; sodas; sharon.daye2.mil@mail.mil; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); De wit, Emmie (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mdiamond (mdiamond@wustl.edu); dgdiel@cornell.edu; CDillen@som.umaryland.edu; Dohm, Erik Daniel; Donis, Ruben (OS/ASPR/BARDA); William Dowling (william.dowling@cepi.net); mariette.ducatez@envt.fr; Duprex, Paul; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson (Karl.Erlandson@hhs.gov); marlene.espinozamoraga; mesteban (mesteban@cnb.csic.es); Falzarano, Darryl; feldmannh@niaid.nih.gov; Florence, Clint (NIH/NIAID) [E]; Flynn, Joanne L; thomasf@primate.wisc.edu; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Juan García Arriaza (jfgarcia@cnb.csic.es); Garcia-Sastre, Adolfo; Olinger, Gene; anna (anna@thsti.res.in); Volker.gerdts (Volker.gerdts@usask.ca); Gerhards, Nora; Christiane Gerke (christiane.gerke@pasteur.fr); Golding, Hana; Graham, Barney (NIH/VRC) [E]; lgralins@email.unc.edu; GREY Finn (fgrey@exseed.ed.ac.uk); Griffiths, Anthony; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); B.L. Haagmans (b.haagmans@erasmusmc.nl); rhakami@gmu.edu; Yper.Hall (Yper.Hall@phe.gov.uk); kevinharrod (kevinharrod@uabmc.edu); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; S. Herfst; seos@cnu.ac.kr; Hild, Sheri (NIH/OD) [E]; Hodgson, Paul; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Holbrook, Michael (NIH/NIAID) [C]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Honko, Anna; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); y.jacob.hou@unc.edu; REIRELAND (REIRELAND@mail.dstl.gov.uk); tomeri (tomeri@iibr.gov.il); mito@ciea.or.jp; Jayashankar, Lakshmi (OS/ASPR/BARDA); dustin.johnson (dustin.johnson@canada.ca); ajones; kandeil_a (kandeil_a@hotmail.com); Amelia Karlsson (amelia.karlsson@duke.edu); KAZI, Fatema; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); Nadia KHELEF (nadia.khelef@pasteur.fr); alankhoo.imr; sekim (sekim@krict.re.kr); Hwan K Kim (hwan.kim@stonybrook.edu); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); anja.kipar@uzh.ch; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); KNEZEVIC, Ivana; darwyn.kobasa@canada.ca; Kobie, James J; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); fkoide (fkoide@southernresearch.org); jeroen.kortekaas (jeroen.kortekaas@wur.nl); Krammer, Florian; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); Krause, Philip; kupke (kupke@staff.uni-marburg.de); Paul.Lambert (Paul.Lambert@unige.ch); mary.lane@nih.gov; langermans (langermans@bprc.nl); Lee-Parritz, David; Luis.Lugo.mil@afrims.org; Roger Le Grand (roger.le-grand@cea.fr); LESELLIER Sandrine (sandrine.lesellier@anses.fr); MSLEVER (MSLEVER@dstl.gov.uk); Levis, Robin; mlewis (mlewis@bioqual.com); sean.li (sean.li@canada.ca); grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; Little, James (OS/ASPR/BARDA); ldenisy (ldenisy@yahoo.com); anice.lowen; Kristine Macartney (kristine.macartney@health.nsw.gov.au); MacGill, Tracy; ramadany; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); Karen Makar (Karen.Makar@gatesfoundation.org); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); ivan.marazzi; IVMARTINEZ; daniel.martinez-arguelles; LMartinez@txbiomed.org; marzia; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); paul-mccray (paul-mccray@uiowa.edu); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); dmissiak (dmissiak@bsd.uchicago.edu); Kayvon Modjarrad (kmodjarrad@eidresearch.org); bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; Munir, Muhammad; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; nnagata@niid.go.jp; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); MNELSON@mail.dstl.gov.uk; johan.neyts (johan.neyts@kuleuven.be); SHELBY L O'CONNOR; DAVID H O'CONNOR (dhoconno@wisc.edu); horer@ku.edu.tr; Oreshkova, Nadia; mto@umn.edu; Mark Page (Mark.Page@nibsc.org); gustavo.palacios (gustavo.palacios@gmail.com); peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp (nirp@iibr.gov.il); Perlman, Stanley; Andrew.Phipps; bradley.pickering (bradley.pickering@canada.ca); Pickett, Thames (NIH/NIAID) [E]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR (JLPRIOR@dstl.gov.uk); qinchuan (qinchuan@pumc.edu.cn); troyrandall (troyrandall@uabmc.edu); angierasmussen@gmail.com; ravetch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; David Revelli (drevelli@lovelacebiomedical.org); Juergen Richt (jricht@vet.k-state.edu); RIVEROS BALTA, Ximena; B.H.G. Rockx (b.rockx@erasmusmc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); Nicola Rose (Nicola.Rose@nibsc.org); croy (croy@tulane.edu); Riccardo Russo; rkiatchula (rkiatchula@gmail.com);

Sabourin, Carol (OS/ASPR/BARDA); esulkowska@rics.bwh.harvard.edu; SALAMI, Kolawole; salgampa (salgampa@njms.rutgers.edu); Javier Salguero (Javier.Salguero@phe.gov.uk); erica (erica@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); Tony.Schountz@colostate.edu; res2025; Segales, Joaquim; snumouse (snumouse@snu.ac.kr); Seungtaek Kim (seungtaek.kim@ip-korea.org); shanchao (shanchao@wh.iov.cn); Sally Sharpe (Sally.Sharpe@phe.gov.uk); sheahan; Shi, Pei yong; Schotsaert, Michael; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Sivko, Gloria S; dean.smith (dean.smith@canada.ca); Manki Song (mksong@ivi.int); SPERGEL@email.chop.edu; Stemmy, Erik (NIH/NIAID) [E]; Stewart, James; stittelaar (stittelaar@viroclinics.com); lawton.stubbert@canada.ca; kanta.subbarao (kanta.subbarao@influenzacentre.org); sutter (sutter@micro.vetmed.uni-muenchen.de); tcs38@psu.edu; Tadaki (tksuzuki@nih.go.jp); SWAMINATHAN, Soumya; Techakitiroj Chatkul (tverakit@gmail.com); tenoever@gmail.com; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; Treanor, John (OS/ASPR/BARDA) (CTR); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Tseng, Chien-Te K.; Chi Van Dang (cdang@lcr.org); Vandenberghe, Luk; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Vergara, Julia; verschoor (verschoor@bprc.nl); verstrepen@bprc.nl; caroline.melo@rivm.nl; Romain Volmer (romain.volmer@envt.fr); Asisa.Volz (Asisa.Volz@tiho-hannover.de); WaickmaA@upstate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); wenchun0617; White, Alexander G; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; ZHU, Jin; bosioc@niaid.nih.gov; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); kyle.rosenke; caroline.foo; t.sulpice; gabriella.worwa; Yusibov, Vidadi (OS/ASPR/BARDA); f.briand

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From: JUDY.HUBBARD@gatesfoundation.org[JUDY.HUBBARD@gatesfoundation.org]

Attendees: tom@vaxxinity.com; David Vaughn; michael.schotsaert@mssm.edu; daraporn.p@bionet-asia.com; aetyang@kemri-wellcome.org; juan.moliva@nih.gov; yuri.vasiliev@hotmail.com; janet.lathey@nih.gov; elizabethleakey@gmail.com; may@vakzine-manager.de; daniel.martinez-arguelles@canada.ca; jinalb@nicd.ac.za; dr.annie.degroot@gmail.com; Fyezah Jehan; igor.smolenov@cloverbiopharma.com; k.j.von.eije@umcg.nl; amandacabralsilva@yahoo.com.br; tamala.mallettmoore@sanofi.com; imran@phcglobal.org; SGalloway@cdc.gov; Jeeninga@viroclinics.com; leid@who.int; tong.wu@canada.ca; jose.luis.di.fabio@cepi.net; D.Shah@wellcome.org; elizabeth.daglish@astrazeneca.com; Ockenhouse, Chris; Keith Klugman; vryab@mail.ru; William Dowling; sian.jones@pfizer.com; cuchip@who.int; THOMAS.JAENISCH@CUANSCHUTZ.EDU; jennifer@immunoprecise.com; marcelo.koike@gmail.com; grantr@who.int; lecoest@gmail.com; Mihaela.Nosca@Seqirus.com; sabinoec@gmail.com; harin.l@bionet-asia.com; chenhongyin@walvax.com; david.montefiori@duke.edu; Tom Mooney; Philip.Minor2@gmail.com; lindy.durrant@nottingham.ac.uk; jailal.ablack@entospharma.com; alcantaraluiz42@gmail.com; kelly.taylor@cihr-irsc.gc.ca; Lethanhtuyet@vabiotech.com.vn; michael.wiseman@health.gov.au; robert.j.oconnell.mil@mail.mil; federica.mori@reithera.com; lode.schuerman@gsk.com; andrew.pollard@paediatrics.ox.ac.uk; ji-hong.kim@sk.com; cookee@who.int; REIRELAND@mail.dstl.gov.uk; jane.s@bionet-asia.com; munoz-fontela@bnitm.de; sktseng@UTMB.EDU; preziosim@who.int; SUyoga@kemri-wellcome.org; Stephen.Savarino@sanofi.com; kishore.turaga@biologicale.com; sarah.frise@astrazeneca.com; paola.stefanelli@iss.it; vfa3@cdc.gov; tim.spector@kcl.ac.uk; claudioc@gsespa.cl; sanchezg@une.net.co; Corinne.Jouquelet-Royer@sanofi.com; lidia.oostvogels@curevac.com; dorits@imbm.org; leejooyeon@korea.kr; marc.veldhoen@medicina.ulisboa.pt; huruoyu@walvax.com; joaquim.segales@irta.cat; kandeil_a@hotmail.com; Deborah King; mff7@cdc.gov; inho.cheong@sk.com; sutter@micro.vetmed.uni-muenchen.de; annapurnavyakarnam@gmail.com; marion.vermeulen@sanbs.org.za; moncef.m.slaoui59@gmail.com; narcisa.x.mesaros@gsk.com; Elliot.Lilley@nc3rs.org.uk; teodora.aktas@folkhalsomyndigheten.se; Jin.gao@fda.hhs.gov; linfa.wang@duke-nus.edu.sg; liya.wassie@ahri.gov.et; thomazella16@gmail.com; achidi.eric@gmail.com; kovac@axon-neuroscience.eu; tom.monath@crozetbiopharma.com; nadirkocak@yahoo.com; rajeev.dhere@seruminstitute.com; kathleen.victoir@pasteur.fr; farah.qamar@aku.edu; sastanley@berkeley.edu; brosen@novavax.com; wilsonp@uchicago.edu; iman.satti@ndm.ox.ac.uk; raburn.mallory@astrazeneca.com; kathytai@medigenvac.com; twosned@googlemail.com; EShumba@aslm.org; HRees@wrhi.ac.za; stephanie.longet@phe.gov.uk; martin.bexon@bexonclinical.com; kate.broderick@inovio.com; Mark_Ic_Chen@ncid.sg; mlewis@bioqual.com; pereyaslovd@who.in; leli@who.int; liupengfei@zhifeishengwu.com; carole.verhoeven@seqirus.com; tianyuan1@sinopharm.com; vgarg@altimmune.com; bo_zhong@sinocelltech.com; guy.vernet@pasteur.fr; nhuskins@completegenomics.com; shuping_xu@sinocelltech.com; Stanley Plotkin; Padmini Srikantiah; llena@globalhealthstrategies.com; BBrande1@its.jnj.com; jean.patterson@nih.gov; adams_andrew_charles@lilly.com; Alena.Khromava@sanofi.com; iowusu@noguchi.ug.edu.gh; wenchun0617@gate.sinica.edu.tw; dapengzhoulab@tongji.edu.cn; xuefeng.yu@cansinotech.com; Norio.tamura@shionogi.co.jp; anita.suresh@finddx.org; joanne.langley@dal.ca; vrezelj@its.jnj.com; pieter.neels@vaccine-advice.be; renuka.kumar@gladstone.ucsf.edu; giorgio.fedele@iss.it; natalie.anosova@sanofi.com; fms2@cdc.gov; hana.golding@fda.hhs.gov; SofoniasT@africa-union.org; sudhirbabji@cmcvellore.ac.in; fderrar@pasteur.dz; kjambo@mlw.mw; s.saikrishna@indimmune.com; Kaitlyn.dambach@nih.gov; Jwilbur@mesoscale.com; Jason.Kindrachuk@umanitoba.ca; mimidarko66; rama.akondy@ashoka.edu.in; bottazzi@bcm.edu; slfeinberg@wisc.edu; seguina@medicago.com; gustavo.f.palacios.civ@mail.mil; saranya.sridhar@sanofi.com; n.okba@erasmusmc.nl; jeanie.jacquet@cepi.net; drbdmore@gmail.com; Brown ScD, Elizabeth R; Nick Andrews; Curcio, Daniel; supaporn.p@dmsc.mail.go.th; romain.volmer@envt.fr; magnus.ysander@astrazeneca.com; yabdiche@immunoprecise.com; dancohen@tauex.tau.ac.i; wangyc@nifdc.org.cn; dsantororosa@gmail.com; ofrinr@who.int; pieter.pannus@sciensano.be; coleman@codagenix.com; xavier.de-lamballerie@univ-amu.fr; alex@lji.org; rfaden@jhu.edu; MRabeh@dha.gov.ae; najwa.khuri@gmail.com; Chan_Cheng_Leng@hsa.gov.sg; krystian.jazdzewski@warsawgenomics.pl; Agnes_Chan@hsa.gov.sg; y.m.vasiliev@spbniivs.ru; AFO@ssi.dk; anja.kipar@uzh.ch; Madhavi.Yadavalli@astrazeneca.com; stephen.p.lockhart@pfizer.com; Susan.Mather@pfizer.com; Gerald Voss; sylvie.van-der-werf@pasteur.fr; dnkhong@sk.com; rjanssen@dynavax.com; emmerich@bnitm.de; alena.dabrazhynetskaya@fda.hhs.gov; creanywo@hku.hk; Stephan.Harbarth@hcuge.ch; kizzmekia.corbett@nih.gov; magdalena.spolnicka@policja.gov.pl; maria.salomao@butantan.gov.br; intl@ibto.ir; Pearl.Bamford@health.gov.au; galter@partners.org; rhonda.kuolee@nrc-cnrc.gc.ca; ADriscoll@som.umaryland.edu; John.Forde@phe.gov.uk; MWFREEMAN@mgh.harvard.edu; mayra.moura@butantan.gov.br; rscharf@path.org; JAYANTHI.WOLF@MERCK.COM; Christine.bruce@phe.gov.uk; chien@vabiotech.com.vn; ztq9@cdc.gov; Georgia Tomaras, Ph.D.; charu.sabharwal@pfizer.com; dpark@broadinstitute.org; ydm9@cdc.gov; fdubovsky@novavax.com; bernadettemrg5@gmail.com; mike.fisher@oncimmune.com; salgampa@njms.rutgers.edu; jean-luc.gala@uclouvain.be; jccastellanos@husi.org.co; ulrike.jaegle@curevac.com; amhashem@kau.edu.sa; rolf.fendel@uni-tuebingen.de; kpancer@pzh.gov.pl; chad.irwin@canada.ca; joser.arribas@salud.madrid.org; elizabeth.gabitzsch@immunitybio.com; cgomez@javeriana.edu.co; fangxing@zhifeishengwu.com;

irenenor@usp.br; beatriz.lucchesi@butantan.gov.br; vivek.rao@igib.res.in; horer@ku.edu.tr; AP.AlmeidaAranha@cepi.net; maksyutov_ra@vector.nsc.ru; ross.upshur@gmail.com; p.kellam@imperial.ac.uk; Lewis, Kristen; marciela.degrace@nih.gov; Helen.mao@cansinotech.com; whausdorff@path.org; iad7@cdc.gov; Ajoke Sobanjo-ter Meulen; m.addo@uke.de; leila.luheshi@nanoporetech.com; lwelch@iavi.org; farshad@vaxxinity.com; Steve Hadley; gingras@lunenfeld.ca; amenezes@globalhealthstrategies.com; kmohan@bharatbiotech.com; karin.vandenberg@sanbs.org.za; bob.small@cepi.net; Shitong Huan; s.borregaard@ctc-north.com; maina.lazou.jackson@cepi.net; gcanuel@osivax.com; sethc@africa-union.org; angeliki.melidou@ecdc.europa.eu; shahid.jameel@ashoka.edu.in; barbara.schnierle@pei.de; Giada.mattiuzzo@nibsc.org; annev@nicd.ac.za; Audrey Hutter; adam.hacker@cepi.net; araki-yasuhiro@pmda.go.jp; sjp97@medschl.cam.ac.uk; anzj@chinacdc.cn; enakouney@gmail.com; Kaslow, David; pebodyr@who.int; oliver.schoenborn-kellenberger@curevac.com; antonella.folgori@reithera.com; cyrus.yang@sbc-biotech.com; Brasel, Trevor; demooij@viroclinics.com; tksuzuki@niid.go.jp; Maria.Syrochkina@pfizer.com; Diana_Koh@hsa.gov.sg; nicole.gilberger@bnitm.de; cooldrdax@gmail.com; AAgweyu@kemri-wellcome.org; ckrubiner@CGDEV.ORG; Guang Li; giulianaxm@gmail.com; PScott@eidresearch.org; mesteban@cnb.csic.es; lili53@sinopharm.com; david.stewart@csl.com.au; philippa.matthews@ndm.ox.ac.uk; xhatzi@med.uth.gr; mario.christodoulou@cepi.net; ruoyuhu@walvax.com; POndoa@aslm.org; ullas@tifr.res.in; MAHIPALAP@who.int; xdv3@cdc.gov; Susan.Hopkins@phe.gov.uk; grode@vakzine-manager.de; pauline.maisonnasse@cea.fr; petra.budde@oncimmune.com; kaijie.pan@pfizer.com; Gary.Kobinger@crchudequebec.ulaval.ca; helen.thompson@bristol.ac.uk; manisha.tirvassen@cepi.net; nataliapasternak@gmail.com; prasadsd@bharatbiotech.com; Jyoti.logani@nic.in; norah.fu@walvax.com; wangxiludev@126.com; michelle.hoffmann@axon-neuroscience.eu; apinya.k@bionet-asia.com; joanna-trees.merckx@mcgill.ca; affrade@yahoo.com.br; helga.junker@curevac.com; slamola@path.org; Yyue315@vip.126.com; Kayla Laserson; ycwu@cde.org.tw; sungskim63@gmail.com; renald.gilbert@cnrc-nrc.gc.ca; christian.taucher@valneva.com; jwolf@heatbio.com; sebastian.ols@ki.se; ladda.s@bionet-asia.com; doug.holtzman@icosavax.com; lfries@novavax.com; ephcicm@nus.edu.sg; gll9@cdc.gov; atila@usp.br; roy.duncan@dal.ca; m.pryor@360biolabs.com; drkim@ivi.int; andrew.gorringe@phe.gov.uk; belll@who.int; aysegul.nalca.civ@mail.mil; catherine.whittaker@phe.gov.uk; marykate.morris@cdph.ca.gov; vfumado@hsjdbcn.org; akbulut@medicine.ankara.edu.tr; jen.gommerman@utoronto.ca; Luis.Lugo.mil@afrims.org; KKoram@noguchi.ug.edu.gh; yang_wang@sinocelltech.com; chhsu296@cde.org.tw; sunL@antibodychina.com; ping_zhan@sinocelltech.com; ttbiozyc@aliyun.com; Farid.Khan2@Pfizer.com; justins@microsoft.com; xinqq@sinovac.com; imaginapolo@gmail.com; frank.rockhold@duke.edu; huong72us@yahoo.com; xiedeying@sinopharm.com; therese.solstad@legemiddelverket.no; pardis@broadinstitute.org; Eduard.Salakhov@gmail.com; michael.malison@gmail.com; julia.vergara@irta.cat; ploemen@viroclinics.com; wangjz@nifdc.org.cn; epstein@ecohealthalliance.org; MStanford@imv-inc.com; alef.costa@saude.gov.br; CVHerst@flowpharma.com; Romain.Martischang@hcuge.ch; Cheryl@iliadbio.com; rajatonirinas@who.int; molho@viroclinics.com; liguifan@biominhai.com; Clare.Morris@nibsc.org; walter_straus@merck.com; CKeech@Novavax.com; PNorris@vitalant.org; vrunda.parikh@pfizer.com; cleide.garcez@fiocruz.br; sekim@krict.re.kr; FRIEDE, Martin Howell; 13718415635@163.com; lanqinying@walvax.com; limhy0919@korea.kr; raul.andino@ucsf.edu; hsaeb@phcc.gov.qa; sergey.kozhin@rdif.ru; avillarreal@indicasat.org.pa; heather.rubino@pfizer.com; albert.jan.van.hoek@rivm.nl; t.brehm@uke.de; christoph.rademacher@mpikg.mpg.de; jessica.lee@gmail.com; langermans@bprc.nl; srashid@atcc.org; annied@epivax.com; ekagucia@kemri-wellcome.org; nicolew@nicd.ac.za; Raj Ghosh; vera.gattas@butantan.giv.br; aleksandra.wesolowska@wum.edu.pl; patricia.braga@butantan.gov.br; FStruyf@ITS.JNJ.com; nymyung@sk.com; peter.palese@mssm.edu; costaa@who.int; elana_jaffe@med.unc.edu; dean.follmann@nih.gov; caroline.melo@rivm.nl; thatziio@rockefeller.edu; sayamrym@niid.go.jp; George Siber; wassana.w@bionet-asia.com; bwilliams@who.int; vittoria.offeddu@ird.global; tapia@mpi-magdeburg.mpg.de; Christina.Bareja@health.gov.au; jzejda@sum.edu.pl; ustjugov@biocad.ru; mlipsitc@hsph.harvard.edu; chaber@modernatx.com; fernando.p.polack@vanderbilt.edu; Tong-ming.Fu@sanofi.com; Susie.dunachie@ndm.ox.ac.uk; chuxiafei@zhifeishengwu.com; Stefania.Capone@reithera.com; Barbara Mahon; jqt8@cdc.gov; shabir.madhi@wits.ac.za; suchinda.m@chula.ac.th; ThomasC.Mettenleiter@fli.de; jim.buttery@monash.edu; david.rhew@microsoft.com; Kwasi.amfo@cepi.net; hstaines@sgul.ac.uk; nicholas.kitchin@pfizer.com; vrasolof@pasteur.mg; dingfan@zhifeishengwu.com; freidlg@who.int; vekemansj@who.int; hombachj@who.int; zengming@biominhai.com; ghkim33@korea.kr; John.Treanor@hhs.gov; tlying@fudan.edu.cn; dbarouch@bidmc.harvard.edu; brian.greenwood@lshtm.ac.uk; jeff_sachs@merck.com; hartka@bluewin.ch; Brooke Peetz (AgileOne); jprice@greffex.com; peshi@UTMB.EDU; lingyi.zheng@sanofi.com; msalit@stanford.edu; gaofu@chinacdc.cn; mlegars@its.jnj.com; katarina.prosenc@nlzoh.si; Vernon_LEE@moh.gov.sg; Emilio Emini; liu.michael222@gmail.com; daniela@lji.org; alan.kimura@curevac.com; taolifeng@zhifeishengwu.com; balaji.more@zyduscadila.com; carlos.diazgranados@sanofi.com; sgupta@iavi.org; judy.wen@icosavax.com; daniel.larremore@colorado.edu; lmoise@epivax.com; shinjini.bhatnagar@thsti.res.in; william.lee@health.ny.gov; sharris@altimmune.com; yjs199307@163.com; greanggrai.h@bionet-asia.com; annagiulia.stigliano@reithera.com; fchowdhury@icddrb.org; ajones@rockefeller.edu; dthea@bu.edu; saowanee.s@bionet-asia.com; valentina.bernasconi@cepi.net; jilian.sacks@finddx.org;

glynnsa@nhlbi.nih.gov; Gopa.Raychaudhuri@fda.hhs.gov; veronica.suarez@seqirus.com; samanthapaston@gmail.com; jill_gilmour@hotmail.co.uk; francesco.x.berlandascorza@gsk.com; dboyle@path.org; c.dahlke@uke.de; Anushri Singhvi; alexander.precioso@butantan.gov.br; nfaria@ic.ac.uk; paul.kristiansen; roland.tschismarov@themisbio.com; devan_mehrotra@merck.com; linsen.du@bravovax.com; miock.kim@sk.com; amelia.karlsson@duke.edu; yoshiyama1962@yahoo.co.jp; SPortillo@som.umaryland.edu; lhampton@gavi.org; connie.cai@gatesfoundation.org; TranBaQuang.Truong@sanofi.com; almonther@hotmail.com; soninov@rosminzdrav.ru; tonya.villafana@astrazeneca.com; min.dong@cloverbiopharma.com; pisano@vakzine-manager.de; wei.tu@fda.hhs.gov; gnorheim@vaccibody.com; nhj1114@mogam.re.kr; darwyn.kobasa@canada.ca; syeum10@korea.kr; Phil.yang@immunitybio.com; cassandra.overking@fda.hhs.gov; gmeller@iavi.org; faiz.ahmadkhan@mcgill.ca; christian.cao@ucalgary.ca; lucas.ribeiro@saude.gov.br; MBxVend-1@yahoo.co.uk; Julia.Tree@phe.gov.uk; bo_long@sinocelltech.com; sujan@lji.org; xuzhu@ucas.ac.cn; nigel.crawford@mcri.edu.au; mayara_bastos@yahoo.com.br; darryl.falzarano@usask.ca; ercument.karasulu@ege.edu.tr; david.vallo@astrazeneca.com; karineamicis@gmail.com; wangling@niaid.nih.gov; cecile.artaud@pasteur.fr; liz.miller@lshtm.ac.uk; Ajoke Sobanjo-ter Meulen; monica.conde@butantan.gov.br; juliana.viscondi@butantan.gov.br; CHOONG_May_Ling@hsa.gov.sg; amol.chaudhari@cepi.net; IVMARTINEZ@hsc.wvu.edu; zobstfeld@wesleyan.edu; jimin@walvax.com; mawiddowson@itg.be; Darin.Edwards@modernatx.com; brian.zabel@lakepharma.com; Elena.Matveeva@rdif.ru; Rolando.pajon@modernatx.com; Email:jplested@novavax.com; helen.thomas@cepi.net; zhout@who.int; Kai Dallmeier; lny1@cdc.gov; sheahan@email.unc.edu; helena.wilcox@ndm.ox.ac.uk; michael.wall@canada.ca; wangkai1@genomics.cn; Matthew.Reed.mil@afrims.org; d.watterson@uq.edu.au; mihaelacarla.nosca@seqirus.com; Mallory.Shriver@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; wrastawicki@pzh.gov.pl; lixin_yan@sinocelltech.com; guy.gorochov@sorbonne-universite.fr; Padeshpa@gmail.com; stroheru@who.int; Tom Kariuki; lydie.marcelon@sanofi.com; nirp@iibr.gov.il; mubangizid; tom@covaxx.com; douglas_fox@berkeley.edu; Ted.Tsai@Takeda.com; kwright@iavi.org; christine.colvis@nih.gov; ajones@mail.rockefeller.edu; maggie.luo@cloverbiopharma.com; Jer-Ming Chia; pawinee.k@redcross.or.th; hromadka@axon-neuroscience.eu; a.pan@asst-cremona.it; alariqil@who.int; peter.smith@lshtm.ac.uk; SlackCa@ukzn.ac.za; tom.tipton@phe.gov.uk; vankerkhovem@who.int; jwilbur@meso-scale.com; dr.rakesh3105@gmail.com; hlchen@hku.hk; Holger.Martinius@neovii.com; xing.li@fda.hhs.gov; winnie.x.janssens@gsk.com; cristina.tato@czbiohub.org; daclark@sgul.ac.uk; miriam.onishi@anvisa.gov.br; quliang@sinopharm.com; philipp.mann@curevac.com; Peter Patriarca; adriane.oliveira@anvisa.gov.br; sebastianms@gisaid.org; In-Kyu Yoon; mbo2@cdc.gov; mpernice@dynavax.com; dotuandat@vabiotech.com.vn; jacob@cmcsph.org; Lakshmi.Jayashankar@hhs.gov; nicole.roth@curevac.com; pickettte@niaid.nih.gov; Carol.Sabourin@hhs.gov; croy@tulane.edu; samiah.kanwar@aku.edu; Harish Iyer; richard.webby@stjude.org; dyu@dynavax.com; haylee@sk.com; Jean Lang; anahita.fathi.us@gmail.com; jessica.lee@inovio.com; jerry.weir@fda.hhs.gov; may.chu@cuanschutz.edu; anthony.macaluso@tonixpharma.com; macalvo@uach.cl; PFast@iavi.org; deoliveira@ukzn.ac.za; gdt@duke.edu; mmsiq@ioc.fiocruz.br; p.smith@lshtm.ac.uk; r.heyderman@ucl.ac.uk; zhangw@who.int; tasker@codagenix.com; azimt@who.int; christopher.da.costa@cepi.net; mksong@ivi.int; carniel@pasteur-yaounde.org; woodd@who.int; melanie.saville@cepi.net; vmoeder@illumina.com; sameer.parekh@seruminstitute.com; alex.sigal@ahri.org; mark.page@nibsc.org; melanie.ott@gladstone.ucsf.edu; karen.goldenthal@gmail.com; nadia.ansari@aku.edu; mt2f@virginia.edu; Kirsty Le Doare; amit.k.srivastava@pfizer.com; Supriya Kumar; res2025@med.cornell.edu; breeze.cavell@phe.gov.uk; horikoshiy@who.int; christian.drosten@charite.de; lydaespitia@unisinu.edu.co; smihwang@sk.com; liub@cde.org.cn; dave.boyle@lakepharma.com; 195046403@qq.com; william.windsor@cuanschutz.edu; anja.schiel@noma.no; giovanetti.marta@gmail.com; madhis@rmpru.co.za; Arnaud.Marchant@ulb.be; scordo@qb.fcen.uba.ar; desteo.ch@gmail.com; Youyi Fong; cwchou476@cde.org.tw; descherm@bni-hamburg.de; Jessica.liu@tigermedgrp.com; Mpasetti@som.umaryland.edu; leanne.robinson@burnet.edu.au; mazhari@wehi.edu.au; christina.henderson@uq.edu.au; noel.tordo@pasteur.fr; ploeman@viroclinics.com; RChikwamba@csir.co.za; zhangyuting@zhifeishengwu.com; monika.lindemann@uk-essen.de; martinbexon@yahoo.co.uk; karen.martins@hhs.gov; Asisa.Volz@tiho-hannover.de; dmissiak@bsd.uchicago.edu; gmackenzie@mrc.gm; marciabarbosavs@gmail.com; zhaozhimei89@163.com; a.a.khazaeli@gmail.com; reveizl@paho.org; mary.marovich@nih.gov; librada.f@bionet-asia.com; cdigermanio@vitalant.org; anh.wartel@ivi.int; allenlien@medigenvac.com; larry.wolfraim@nih.gov; robert.chen@cepi.net; zryn@walvax.com; Ashley.Smith1@hhs.gov; zhaoyuping@medleader.com.cn; tomwhite42450@gmail.com; brosen@novavax.net; agoodridge@indicasat.org.pa; mceuppe1@its.jnj.com; sunil.shewale@seruminstitute.com; dayejung@eubiologics.com; maghsoodlu@yahoo.com; rkoup@mail.nih.gov; freedmanne@mail.nih.gov; julie.joseph@canada.ca; vanessa.infante@butantan.gov.br; Liz.Miller@phe.gov.uk; LMeyers@epivax.com; John N. Nkengasong; GSimmons@vitalant.org; carolina.pingret@anvisa.gov.br; mehmet.ozturk@ibg.edu.tr; ruben.rizzi@biontech.de; lawton.stubbert@canada.ca; mcjm.sturkenboom@gmail.com; roberto.camerini@reithera.com; shanchao@wh.iov.cn; r.kobbe@uke.edu; xywang@shmu.edu.cn; lori.newman@nih.gov; patricia.garcia@upch.pe; mariella.zaroni@anvisa.gov.br; Matthew.Bonaparte@sanofi.com; Ragini.Shivji@ema.europa.eu; MNELSON@dstl.gov.uk; jcsedrik@path.org; imwei1@163.com; lea.sewell@pfizer.com; esulkowska@rics.bwh.harvard.edu; david.spiro@nih.gov; Karl.Erlandson@hhs.gov;

evan.sturtevant@hhs.gov; john.c.trefry.civ@mail.mil; sarina@instem.res.in; Abbie.Bown@phe.gov.uk; tj.chen@chanzuckerberg.com; avandebo@its.jnj.com; wangpw@ivdc.chinacdc.cn; OumaE@africa-union.org; dkim22@its.jnj.com; allergypk@gmail.com; dipyaman.iicb@gmail.com; pujingster@163.com; ebolakim@sk.com; shashikanth4257@bharatbiotech.com; eric.vangieson@darpa.mil; YenewK@africa-union.org; ygrad@hsph.harvard.edu; seongeun@sk.com; FOO_Yang_Tong@hsa.gov.sg; mit666666@pitt.edu; yangfeng@chazenbio.com; livia.vinhal@saude.gov.br; Ann.Rawkins@phe.gov.uk; cdang@lcr.org; mafarodriguez@unisalle.edu.co; zhangj@xmu.edu.cn; colwill@lunenfeld.ca; alan.liss@cepi.net; verstrepen@bprc.nl; 308041407@qq.com; christian.brechot@pasteur.fr; liyl@cde.org.cn; sonja.henne@cepi.net; mona.mohsen@saiba-biotech.com; jmcelrat@fredhutch.org; brian.ward@mcgill.ca; dong.shen@rnaimmune.com; hyl01@tsinghua.org.cn; r.kobbe@uke.de; Phanhonghoa@vabiotech.com.vn; Adam.Finn@bristol.ac.uk; igor.balashov@vaxine.net; hopr@uaem.mx; robert.wawrzinek@mpikg.mpg.de; mengx@sinovac.com; wdj@adaptvac.com; Cblish@stanford.edu; tyzhang1003@163.com; linjinzhong@fudan.edu.cn; gregory.d.gromowski.civ@mail.mil; sheetal.gandotra@igib.res.in; lei.shi@walvax.com; dustin.johnson@canada.ca; Tony.Schountz@colostate.edu; s.a.arakelov@spbniivs.ru; jason.fernandes@canada.ca; wildersmitha@who.int; pdeshpande@indimmune.com; verschoor@bprc.nl; Mike Whelan; James.Milligan@seqirus.com; ben.miller.13@ucl.ac.uk; pgilbert@fredhutch.org; aleksander.masny@policja.gov.pl; roice.fulton@cepi.net; silviacosta@usp.br; baihe@nmpa.gov.cn; Nicole Frahm; pilailuk.o@dmsc.mail.go.th; katom@who.int; Poonepalli_ANURADHA@hsa.gov.sg; tanakat@who.int; sheetal.gandotra@igib.in; zhiping.ye@fda.hhs.gov; savino@ioc.fiocruz.br; CCassetti@niaid.nih.gov; Wenfeng Gong; s.mccormack@ucl.ac.uk; rtchen1135@gmail.com; xumingjue0922@126.com; fred@imophoron.com; tdcarroll@ucdavis.edu; TSmith@inovio.com; lja2002@qatar-med.cornell.edu; drevelli@lovelacebiomedical.org; zhangyan@ivdc.chinacdc.cn; Abena.Amoah@lshtm.ac.uk; Vanessa.Fontana@curevac.com; arimoin@ucla.edu; rafael.delgado@salud.madrid.org; ricardo.palacios@butantan.gov.br; satyajit@iiserpune.ac.in; Rong.Xu@sabin.org; mary@mwuconsulting.com; susanne.rauch@curevac.com; lisa@amicitiam.com; cgast@path.org; Dong, Haiyan; Pillets@medicago.com; katharina.hartmann@cepi.net; kraehliv@staff.uni-marburg.de; Carlos.GuzmanQuilo@sanofi.com; Lynda Stuart; simon.funnell@phe.gov.uk; bernhard.kerscher@pei.de; Toher, Margaret; mgursel@metu.edu.tr; pennym@nicd.ac.za; bernadette.murgue@inserm.fr; olaf-oliver.wolz@curevac.com; mariann.bringsvaerd@cepi.net; Kriti Arora; dparmar@zydustherapeutics.com; M.Whittaker@wellcome.ac.uk; alejandra.gurtman@pfizer.com; jing_jiang201906@sina.com; jennifer.bath99@yahoo.com; RZahn@its.jnj.com; somchaiya@gpo.or.th; lawrence.reiter@providencetherapeutics.com; rbaric@email.unc.edu; Jacqueline.Miller@modernatx.com; dnovack@dynavax.com; david.lee-parritz@tufts.edu; Kathryn Rutkowski; bernadette.hendrickx@cepi.net; ytakahas@niid.go.jp; Rebecca.Harris@sanofi.com; Elizabeth Butler; angel@wedo-projects.com; wardmi@who.int; brooke.bozick@nih.gov; Jin.Zhu@health.gov.au; derrick.crook@ndcls.ox.ac.uk; mvinge@vaccibody.com; r.shattock@imperial.ac.uk; ramadany@sfda.gov.sa; Farah_MOHAMED_HANIFF@ncid.sg; enwereg@who.int; maria.cassia@hc.fm.usp.br; kum.ungchusak@gmail.com; Jeff.Yang@cloverbiopharma.com; ldunkle@novavax.com; mdohmd@snu.ac.kr; jeff.sachs@merck.com; msavoia@usp.br; fguirakhoo@geovax.com; sh@stemcro.com; k.chappell@uq.edu.au; fkoide@southernresearch.org; jlh66@cam.ac.uk; jmarien@itg.be; marmorato.mariana@gmail.com; drsahoo@indimmune.com; melanie.l.delannoy@gsk.com; paul.licciardi@mcri.edu.au; heather.gidding@sydney.edu.au; ravetch@mail.rockefeller.edu; Tom.Pilcher@dhsc.gov.uk; kwonseoyeon@sk.com; landryn@medicago.com; tomeri@iibr.gov.il; makwenyao@gmail.com; michael.holbrook@nih.gov; Zepp@mail.uni-mainz.de; richard.siggers@canada.ca; lbmulenga@yahoo.com; xin.fang@cloverbiopharma.com; Klaus.Cichutek@pei.de; pe_shu_ai@hsa.gov.sg; Anya Asuncion (Opus); lisa.hensley@nih.gov; raafat.fahim@cepi.net; liweihua8@sinopharm.com; jricht@vet.k-state.edu; shoubai.chao@cansinotech.com; nelias@nimr-mmrc.org; luc.gagnon@nexelis.com; Giovanni Della Cioppa; tijsma@viroclinics.com; sophiev@hku.hk; Arun Kumar; anna.may@joinzoe.com; nussen; esthel.vanbrackel@kuleuven.be; gustavo.santos@anvisa.gov.br; Susanne.EDER-LINGELBACH@valneva.com; HKaranja@kemri-wellcome.org; trvrb; mfkung@cde.org.tw; guido.grandi@unitn.it; alan@sanbi.ac.za; florian.krammer@mssm.edu; Sarah Mudrak, Ph.D.; jpattyn@gavi.org; marco.krieger@fiocruz.br; marilia.santini@ini.fiocruz.br; amishahbrown@inovio.com; chantal.veira@cepi.net; inbanathanf@who.int; geert.lerouxroels@ugent.be; olga.rovira@cepi.net; cori@chanzuckerberg.com; kcyau@hku.hk; huangenqi@zhifeishengwu.com; tracey.thue@usask.ca; lcho@novavax.com; marzia@niaid.nih.gov; d.dunn@ucl.ac.uk; robbert.x.van-der-most@gsk.com; mariangela.cavarelli@cea.fr; wuzy@263.net; john.talian@curevac.com; djernigan@cdc.gov; Andrew.Phipps@hhs.gov; jing.sun@cansinotech.com; carolina.blades@anvisa.gov.br; bertozzi@stanford.edu; hwan.kim@stonybrook.edu; natalie.marchevsky@paediatrics.ox.ac.uk; qasimattock@gmail.com; afrozaakter@icddrb.org; cassia.cearley@icosavax.com; dhoconno@wisc.edu; rgonzalez@uaem.mx; eunlyeong.park@ivi.int; imam.tauheed@icddrb.org; omar.sued@huesped.org.ar; nsalisch@its.jnj.com; kwonseoyeon@skdiscovery.com; teresa.lambe@ndm.ox.ac.uk; pramod.pujari@seruminstitute.com; giselle.castillo@pfizer.com; tesfaye.gelanew@ahri.gov.et; fqadri@icddrb.org; robertcoffman121@outlook.com; farshad@covaxx.com; lmercer@path.org; clemens.ralf@outlook.com; Tony.Wang@fda.hhs.gov; yoonyeong@sk.com; gtapiaca@its.jnj.com; kazif@who.int; Chelsea Bond (Opus); kmodjarrad@eidresearch.org; anissa.cheung@fda.hhs.gov; Gustavo.palacios@gmail.com; natalia@providencetherapeutics.com; ranga.cs@cdsco.nic.in; bologa.monica@gmail.com; jricht@ksu.edu; stanley-perlman@uiowa.edu; Celeste.Marsh@health.gov.au; chantal.reusken@rivm.nl;

paul.fine@lshtm.ac.uk; binuphilip@zyduscadila.com; fywu658@cde.org.tw; lapujadeo@who.int; karin.bok@nih.gov; clint.florence; gsellp@who.int; Shailesh.DEWASTHALY@valneva.com; Hongquan.wan@fda.hhs.gov; tasnuva.ahmed@icddrb.org; maria.baca-estrada@canada.ca; matthias.klose@curevac.com; amy.fix@scendea.com; mhasanul.kaisar@icddrb.org; kim.mulholland@lshtm.ac.uk; zengbing@sinopharm.com; indrajeet@bionet-asia.com; pcahn@huesped.org.ar; christian.bottomley@lshtm.ac.uk; taufiqur@icddrb.org; elizabeth.patino@butantan.gov.br; Surender.Khurana@fda.hhs.gov; franck.touret@univ-amu.fr; revans@who.int; ndiayesire@hotmail.fr; phil.yang@nantworks.com; juleen.gayed@pfizer.com; hychen@cde.org.tw; maaroufi@pasteur.ma; tingting.yan@mail.utoronto.ca; sabinoec@usp.br; malik@hku.hk; stephen.lockhart@pfizer.com; ruoyu.hu@walvax.com; bcowling@hku.hk; tkh4@cdc.gov; zhongkaishi28@gmail.com; aottosen@unicef.org; barnorj@who.int; nadia.oreshkova@wur.nl; adebola.olayinka@ncdc.gov.ng; joan@joinzoe.com; nadia.tornieporth@cepi.net; gftsai@cde.org.tw; 1531287517@qq.com; vongs@who.int; bond.court@gmail.com; rkiatchula@gmail.com; ywsohn09@gmail.com; JLPRIOR@dstl.gov.uk; snumouse@snu.ac.kr; kingpfph@sina.com; yjlee@eubiologics.com; robert.bailer@q2labsolutions.com; bronwyn@broadinstitute.org; khirullin@mail.ru; moorthyv; anice.lowen@emory.edu; dguyongellin@osivax.com; liliana.brown@nih.gov; fanxin7@sinopharm.com; katrin.ramsauer@themisbio.com; dean.smith@canada.ca; kate81@korea.kr; judith.absalon@pfizer.com; Christophe.Gregoire@sanofi.com; yangyunkai@sinopharm.com; 57667504@innovax.cn; juzdias@gmail.com; Todd.Suscovich@seromyx.com; gromova@biopharma-excellence.com; fguirakhoo@unitedneuroscience.com; anand.drk@gmail.com; eric.osoro@wsu.edu; zengxizi@kangtai.com; stephane.bancel@modernatx.com; zhongzaixin@zhifeishengwu.com; dsz@imbcams.com.cn; a.luttick@360biolabs.com; Gerald.Kovacs@hhs.gov; Zhanghua_Lan@sinocelltech.com; hutiny@Who.int; solomon.yimer@cepi.net; paul-mccray@uiowa.edu; nuno.faria@zoo.ox.ac.uk; J.P.Stewart@liverpool.ac.uk; sbrowne@altimmune.com; jins.park@sk.com; matthew.snape@paediatrics.ox.ac.uk; jkonyndyk@usaid.gov; maria-angeles.x.ceregido@gsk.com; lmartinez@txbiomed.org; robin.levis@fda.hhs.gov; stig.tollefsen@cepi.net; thyde@cdc.gov; matthew.hohenboken@seqirus.com; bergerii@who.int; sameeullah@bs.qau.edu.pk; rehman.zaira@yahoo.com; james.huleatt@sanofi.com; Molly.Lamb@cuanschutz.edu; jldeen@up.edu.ph; sandsa@who.int; vincent.munster@nih.gov; Holger Kanzler; jinbo.gou@cansinotech.com; acope@iavi.org; rosemaryaudu@yahoo.com; rodrigo.correa@fiocruz.br; irahetar@who.int; arandhaw@fredhutch.org; shaumik.islam@icddrb.org; Sophie Mathewson; paul@medigenvac.com; pgarg@thsti.res.in; pamela.proud@phe.gov.uk; carolina.argondizo@usp.br; loy@who.int; asmronger@gmail.com; wbrooks3@jhu.edu; schwartz@pasteur.fr; Jakob Cramer; hanwx@sinovac.com; paul.hodgson@usask.ca; Hang.Xie@fda.hhs.gov; jorge.osorio@wisc.edu; Hendrik Jan Thibaut; adamou.rafiou@gmail.com; tdelossantos@path.org; brett.barnett@cepi.net; danielbrasseur@gmail.com; ASiyer@mgh.harvard.edu; robert.paris@modernatx.com; raquel.guiomar@insa.min-saude.pt; Ali.Mirazimi@folkhalsomyndigheten.se; diane.descamps@aphp.fr; jschindler@imv-inc.com; Johan Neyts; brangelp@who.int; javadi11@hzdr.de; MCELROYA@pitt.edu; eric@providencetherapeutics.com; ggj2@cdc.gov; wangyilin@medleader.com.cn; swaminathans@who.int; chr.vin@web.de; erich.tauber@themisbio.com; jeroen.kortekaas@wur.nl; joshua.liang@cloverbiopharma.com; kristy.tomas@health.gov.au; hjanes@fredhutch.org; agw13@pitt.edu; ihsangursel@bilkent.edu.tr; Anthony.Scott@lshtm.ac.uk; kevinkumarkansagra@zyduscadila.com; Anna.JefferySmith@phe.gov.uk; Harry Kleanthous; freire@bio.fiocruz.br; jkalil@pq.cnpq.br; jlehrman@iavi.org; mcortese@vaxart.com; tranminhn@who.int; troyrandall@uabmc.edu; m.koopmans@erasmusmc.nl; anu.raghunathan@ncl.res.in; Eeva.Broberg@ecdc.europa.eu; yoos@who.int; senta.walton@usz.ch; Nieuwburg@viroclinics.com; julianna.pieknik@fda.hhs.gov; mdjjh@nmc.or.kr; andrew.p.hollands.civ@mail.mil; cwonodi1@jhu.edu; Mia.Crampin@lshtm.ac.uk; Charlie Weller; wuting@xmu.edu.cn; wangruyue@zhifeishengwu.com; svein.rune.andersen@legemiddelverket.no; bhagwat.gunale@seruminstitute.com; pingping.zhang@pfizer.com; Bev.Menner@csl.com.au; rodriguezhernandezc@who.int; daniel.brasseur@cepi.net; WaickmaA@upstate.edu; clsilva@fmrp.usp.br; Isis Kanevsky; joanna.zmurko@q2labsolutions.com; Lloyd.Mulenga@moh.gov.zm; Julie.Lobjeois@sanofi.com; xumiaobj@126.com; agartlan@fredhutch.org; Khadija.Jarik@international.gc.ca; ann.eakin@nih.gov; jeff@stabilitech.com; annap@auth.gr; liuying@medleader.com.cn; tedross@uga.edu; varma.bhupathiraju@biologicale.com; paul.lambert@unige.ch; marc.eloit@pasteur.fr; wdj@expres2ionbio.com; SMalhotra@iavi.org; dj56wood@gmail.com; yuho74@hotmail.com; barney.graham@nih.gov; nadege.ripley@modernatx.com; charles.chiu@ucsf.edu; sumitbhushan@panaceabiotec.com; tom@covaxx.xom; gasparr@who.int; bgraham@mail.nih.gov; nb@rdif.ru; rodewaldl@chinacdc.cn; lorna.mcinroy@phe.gov.uk; beatrice.n.laupeze@gsk.com; muldersm@who.int; rkiat@chula.ac.th; Jorge Kalil; kim.brolin@ecdc.europa.eu; cherylc@nicd.ac.za; STorhaug@vaccibody.com; Lienanhha.do@mcri.edu.au; katrin.leitmeyer@ecdc.europa.eu; rahul.arora@balliol.ox.ac.uk; marion.gruber@fda.hhs.gov; donna.ambrosino1@gmail.com; David Blazes; Imran Nisar; dlggpp@gmail.com; shimian.zou@nih.gov; marisol.simoes@bio.fiocruz.br; carl.hanson@cdph.ca.gov; shinj@who.int; MAFRANCO@JAVERIANA.EDU.CO; rebecca.klein1@merck.com; a.agrawal@igib.in; miyazakikrauser@who.int; eliana.barros@butantan.gov.br; stephanie.longet@well.ox.ac.uk; sihindawi@yahoo.com; luk_vandenberghe@meei.harvard.edu; rmallory@novavax.com; CHOO_Qiuyi@hsa.gov.sg; dginete@sciphil.org; reinel120305@gmail.com; mayor@ncbs.res.in; medeiros@bio.fiocruz.br; brian.greewood@lshtm.ac.uk; pbieniasz@mail.rockefeller.edu; marta.diaz@salud.madrid.org; Suellen.Nicholson@vidrl.org.au; rodrigueza@paho.org; Gilbert, Peter B;

mireilledosso@yahoo.fr; okeibunorj@who.int; cindy.x.gutzeit@gsk.com; rawleigh.howe@ahri.gov.et; Jacqueline.Shea@inovio.com; eyangoh@pasteur-yaounde.org; boulayi@medicago.com; jokim@ivi.int; carla.brichesi@anvisa.gov.br; songqiaoqiao@ystwt.com; nbhat@path.org; ravindra.gupta@ucl.ac.uk; lizhigang@biominhai.com; russori@njms.rutgers.edu; mirajw@who.int; dsreed@cvr.pitt.edu; Heather.Whitaker@phe.gov.uk; nbaylor@biologicsconsulting.com; wim.vanderpoel@wur.nl; Tracy.MacGill@fda.hhs.gov; James.Little@hhs.gov; alka.dbt@nic.in; Bogdana.Coudsy@sanofi.com; elliot@stabilitech.com; cbstauft@gmail.com; Tamala.MallettMoore@sanofipasteur.com; alyson.kelvin@usask.ca; perkinsm@who.int; thall@sgul.ac.uk; niklas.bobrovitz@mail.utoronto.ca; sroberts@altimmune.com; Bethany_Gauthier@hms.harvard.edu; GWeiding@its.jnj.com; deven.parmar@zydusdiscovery.ae; dr.petrov_jordan@yahoo.com; Antonia.Ho@glasgow.ac.uk; zoeteweij@viroclinics.com; dlaufer@iavi.org; alessandro.torelli@vismederi.com; stoback@novavax.com; francois.p.roman@gsk.com; roberta.piorelli@butantan.gov.br; dailp@biols.ac.cn; gweiss@uci.edu; Keith.Peden@fda.hhs.gov; rachna.gupta@sanofi.com; priti.shah@astrazeneca.com; Joe Rininger; nax3@cdc.gov; kristine.rose@cepi.net; martin.plante@nrc-cnrc.gc.ca; Nupur.Sengupta@biologicale.com; Frieman, Matthew; alemseged.abdissa@ahri.gov.et; srinivas.murthy; joe@czbiohub.org; csv@ssi.dk; hironorinakagami@gmail.com; ckchew@crc.gov.my; Piyush.patel@providencetherapeutics.com; sapan4252@bharatbiotech.com; Buitendijk@viroclinics.com; fmarks@ivi.int; wanxilu@zhifeishengwu.com; Bassam.Hallis@phe.gov.uk; changguili@aliyun.com; sot1@cdc.gov; jenifer.healy@abbott.com; tuliodna@gmail.com; qinjian_zhao@xmu.edu.cn; merryn.voysey@paediatrics.ox.ac.uk; payden@who.int; matthew.cheng@mcgill.ca; liujiankai@biominhai.com; keiko.simon@inovio.com; geldmacher@lrz.uni-muenchen.de; m.noursadeghi@ucl.ac.uk; brenda.valente@anvisa.gov.br; nnagata@niid.go.jp; tksuzuki@nih.go.jp; patrick.reid@unmc.edu; pogueg1@RJRT.com; Robin Mogg; lvrizzo@einstein.br; ls.shashidhara@ashoka.edu.in; Marco.Cavaleri@ema.europa.eu; mto@umn.edu; sue.costa@unisi.it; Pasi.Penttinen@ecdc.europa.eu; crowcroftn@who.int; joseph.chiu@nih.gov; mueller@wehi.edu.au; jguthmiller@uchicago.edu; Kristen Earle; tzyyyuin.chong@cloverbiopharma.com; gayle.pulle@canada.ca; Hisham.Fyyaz@sanofi.com; rachel.park@eubiologics.com; tinaoneko@gmail.com; c.weller@wellcome.org; tenoever@gmail.com; kalisvar_marimuthu@ttsh.com.sg; yumei_huang@sinocelltech.com; ellar@bharatbiotech.com; koningsf@who.int; carolyn.clark@cepi.net; Jordan Tappero; oliver.schoenborn-kellenberger@cogitars.com; h.skirrow@imperial.ac.uk; Scott Dowell; Georgina Murphy; Judy Hubbard

Sent: Tue 4/13/2021 1:01:52 AM (UTC-05:00)

Subject: UPDATED: Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

COVAX ES Workshop April 16th draft Agenda v1.pdf

Dear All,

Final agenda COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants attached.

Friendly reminder if you have not yet registered please use highlighted link by Wednesday, April 14th EOD.

Thank you.
Judy

Dear all,

We are emailing to invite you to a webinar workshop led by the COVAX Enabling Sciences SWAT Team on April 16, 2021, from 6:00-9:00 PT / 14:00-17:00 CET.

The topic of the workshop is "**Global and local approaches to detect and interpret SARS-CoV-2 variants**". The goal of the workshop is to discuss how to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. This requires connecting local pathogen genomic sequencing and epidemiology with high quality virology and immunology. There will also be a discussion of how immunological knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making.

This workshop is organized by the COVAX Enabling SWAT team co-led by CEPI and the Bill & Melinda Gates Foundation.

To attend the workshop, please register here by Wednesday, April 14th EOD. This workshop will be held on Zoom and you will find the Zoom link within the registration portal a couple of days before the event. Once you have registered, there will be an option to add this event to your calendar. In addition to the Zoom link being in your registration portal, our systems will also email you the Zoom link information on three occasions (the day before the event, one hour before the event, and once we go-live). *Please ensure our emails are not going into the junk folder.*

As email lists are imperfect, please forward this email invite to the appropriate contact(s) in your organization and contact Judy Hubbard at the Gates Foundation (Judy.Hubbard@gatesfoundation.com) to indicate who from your group should be invited. Please note that anyone who was forwarded the original calendar save the date may not have necessarily received this email, but may register using the same link provided above.

We look forward to your participation at the workshop.

Thank you.
Judy Hubbard, sent on behalf of

Karen Makar, PhD (BMGF)
William Dowling, PhD (CEPI)
COVAX Enabling Sciences SWAT Team Co-Leads

COVAX

CEPI Gavi unicef World Health Organization

Workshop Agenda

Global and local approaches to detect and interpret SARS-CoV2 variants

DATE	TIME	LOCATION
Friday, April 16th, 2021	06:00 – 9:00 PT/ 15:00 – 18:00 CET	Zoom Webinar

We all share a common goal to develop safe and effective vaccines. The Enabling Sciences SWAT team aims to provide cross-cutting product-agnostic support to COVID-19 vaccine developers in the area of diagnostics, standards and animal models.

Rapid assessment of the biological impacts of new variants of SARS-CoV-2 requires the collaboration of epidemiologists, virologists and immunologists at the local and global level. However, these efforts are often disconnected from one another, resulting in delays and an incomplete picture of the implications for vaccines and diagnostics.

The objective of this workshop is to share information on how to efficiently connect local pathogen genomic sequencing, epidemiology, virology and immunology to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. There will be a discussion of how knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making. We will discuss ideas for best practices for assessing virus neutralization activity, and approaches to standardizing assays and protocols to improve interpretation of results generated in different labs and geographies

This workshop is convened by the COVAX Enabling Sciences SWAT team, which is co-led by CEPI and the WHO and includes members from the Bill & Melinda Gates Foundation, NIAID and industry. COVAX is the vaccines pillar of the Access to COVID-19 Tools (ACT) Accelerator, co-led by Gavi, the Coalition for Epidemic Preparedness Innovations (CEPI) and WHO. COVAX aims to accelerate the development and manufacture of COVID-19 vaccines, and to guarantee fair and equitable access to appropriate, safe and efficacious vaccines for all countries.

Time (CET)	Presentation Title *(TBD)*	Speaker(s)
15:00-15:05	Welcome and meeting objectives	*TBC, ES SWAT*
15:05-15:20	South Africa Pathogen Genomics Sequencing & AfCDC PGI program	**Tulio DeOliveira,** KRISP
15:20-15:30	Assessing immunological implications of VoCs in South Africa	**Penny Moore,** NICD

15:30-15:40	Immune escape and evidence for re-infection with P.1 in Brazil	**Ester Sabino**, U. Sao Paulo
15:40-15:50	Impact of B.1.1.7 on vaccine induced immune responses	**Ravi Gupta,** Cambridge
15:50-16:00	India Consortium for COVID-19 genomics	**Anurag Agrawal**, CSIR/IGIB
16:00-16:25	**Panel Discussion**	Moderated by **Karen Makar**, BMGF
16:25-16:30	*BREAK*	
16:30-16:40	WHO framework for response to new COVID vaccines	**Sylvie Briand,** WHO
16:40-16:50	Pulling it all together in the COG-UK	**Sharon Peacock,** COG-UK
16:50-17:00	CEPI's Agility program: a centralised approach to evaluate VoCs	**Simon Funnell**, PHE
17:00-17:10	Virus stock and sequencing QC- best practices & available resources	**Sujatha Rashid**, BEI
17:10-17:20	SARS-CoV-2 Interagency Group (SIG) Variant Assessment/Characterization	*TBC, NIAID*
17:20-17:30	ACTIV/TRACE OpenData portal	**Christine Colvis,** NIH/NCATS
17:30-17:55	**Panel Discussion**	Moderated by**: Bill Dowling,** CEPI
17:55-18:00	Wrap up & Next Steps	*TBC, ES SWAT*

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Albrecht, Randy; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Alyson Kelvin; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); JOHN JAMES BACZENAS; BAMFORD, Pearl; rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); sinabavari@comcast.net; Martin.Beer (Martin.Beer@fli.de); Neil Berry (Neil.Berry@nibsc.org); terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); dbolton@hivresearch.org; mopargal (mopargal@rams.colostate.edu); SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion (rcarrion@TxBiomed.org); Miles.Carroll (Miles.Carroll@phe.gov.uk); Cartner, Samuel Corbin; Cassels, Fred; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); lisa.chakrabarti@pasteur.fr; jfwchan (jfwchan@hku.hk); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); hlchen (hlchen@hku.hk); Carolyn Clark (carolyn.clark@cepi.net); yu.cong@nih.gov; scordo (scordo@qb.fcen.uba.ar); lisette.cornelissen; Crozier, Ian (NIH) [C]; kai.dallmeier (kai.dallmeier@kuleuven.be); Damron, Fredrick; que.dang@nih.gov; sodas; sharon.daye2.mil@mail.mil; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); De wit, Emmie (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mdiamond (mdiamond@wustl.edu); dgdiel@cornell.edu; CDillen@som.umaryland.edu; Dohm, Erik Daniel; Donis, Ruben (OS/ASPR/BARDA); William Dowling (william.dowling@cepi.net); mariette.ducatez@envt.fr; Duprex, Paul; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson (Karl.Erlandson@hhs.gov); marlene.espinozamoraga; mesteban (mesteban@cnb.csic.es); Falzarano, Darryl; feldmannh@niaid.nih.gov; Florence, Clint (NIH/NIAID) [E]; Flynn, Joanne L; thomasf@primate.wisc.edu; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Juan García Arriaza (jfgarcia@cnb.csic.es); Garcia-Sastre, Adolfo; Olinger, Gene; anna (anna@thsti.res.in); Volker.gerdts (Volker.gerdts@usask.ca); Gerhards, Nora; Christiane Gerke (christiane.gerke@pasteur.fr); Golding, Hana; Graham, Barney (NIH/VRC) [E]; lgralins@email.unc.edu; GREY Finn (fgrey@exseed.ed.ac.uk); Griffiths, Anthony; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); B.L. Haagmans (b.haagmans@erasmusmc.nl); rhakami@gmu.edu; Yper.Hall (Yper.Hall@phe.gov.uk); kevinharrod (kevinharrod@uabmc.edu); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; S. Herfst; seos@cnu.ac.kr; Hild, Sheri (NIH/OD) [E]; Hodgson, Paul; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Holbrook, Michael (NIH/NIAID) [C]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Honko, Anna; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); y.jacob.hou@unc.edu; REIRELAND (REIRELAND@mail.dstl.gov.uk); tomeri (tomeri@iibr.gov.il); mito@ciea.or.jp; Jayashankar, Lakshmi (OS/ASPR/BARDA); dustin.johnson (dustin.johnson@canada.ca); ajones; kandeil_a (kandeil_a@hotmail.com); Amelia Karlsson (amelia.karlsson@duke.edu); KAZI, Fatema; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); Nadia KHELEF (nadia.khelef@pasteur.fr); alankhoo.imr; sekim (sekim@krict.re.kr); Hwan K Kim (hwan.kim@stonybrook.edu); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); anja.kipar@uzh.ch; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); KNEZEVIC, Ivana; darwyn.kobasa@canada.ca; Kobie, James J; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); fkoide (fkoide@southernresearch.org); jeroen.kortekaas (jeroen.kortekaas@wur.nl); Krammer, Florian; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); Krause, Philip; kupke (kupke@staff.uni-marburg.de); Paul.Lambert (Paul.Lambert@unige.ch); mary.lane@nih.gov; langermans (langermans@bprc.nl); Lee-Parritz, David; Luis.Lugo.mil@afrims.org; Roger Le Grand (roger.le-grand@cea.fr); LESELLIER Sandrine (sandrine.lesellier@anses.fr); MSLEVER (MSLEVER@dstl.gov.uk); Levis, Robin; mlewis (mlewis@bioqual.com); sean.li (sean.li@canada.ca); grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; Little, James (OS/ASPR/BARDA); ldenisy (ldenisy@yahoo.com); anice.lowen; Kristine Macartney (kristine.macartney@health.nsw.gov.au); MacGill, Tracy; ramadany; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); Karen Makar (Karen.Makar@gatesfoundation.org); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); ivan.marazzi; IVMARTINEZ; daniel.martinez-arguelles; LMartinez@txbiomed.org; marzia; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); paul-mccray (paul-mccray@uiowa.edu); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); dmissiak (dmissiak@bsd.uchicago.edu); Kayvon Modjarrad (kmodjarrad@eidresearch.org); bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; Munir, Muhammad; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; nnagata@niid.go.jp; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); MNELSON@mail.dstl.gov.uk; johan.neyts (johan.neyts@kuleuven.be); SHELBY L O'CONNOR; DAVID H O'CONNOR (dhoconno@wisc.edu); horer@ku.edu.tr; Oreshkova, Nadia; mto@umn.edu; Mark Page (Mark.Page@nibsc.org); gustavo.palacios (gustavo.palacios@gmail.com); peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp (nirp@iibr.gov.il); Perlman, Stanley; Andrew.Phipps; bradley.pickering (bradley.pickering@canada.ca); Pickett, Thames (NIH/NIAID) [E]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR (JLPRIOR@dstl.gov.uk); qinchuan (qinchuan@pumc.edu.cn); troyrandall (troyrandall@uabmc.edu); angierasmussen@gmail.com; ravetch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; David Revelli (drevelli@lovelacebiomedical.org); Juergen Richt (jricht@vet.k-state.edu); RIVEROS BALTA, Ximena; B.H.G. Rockx (b.rockx@erasmusmc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); Nicola Rose (Nicola.Rose@nibsc.org); croy (croy@tulane.edu); Riccardo Russo; rkiatchula (rkiatchula@gmail.com);

Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; SALAMI, Kolawole; salgampa (salgampa@njms.rutgers.edu); Javier Salguero (Javier.Salguero@phe.gov.uk); erica (erica@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); Tony.Schountz@colostate.edu; res2025; Segales, Joaquim; snumouse (snumouse@snu.ac.kr); Seungtaek Kim (seungtaek.kim@ip-korea.org); shanchao (shanchao@wh.iov.cn); Sally Sharpe (Sally.Sharpe@phe.gov.uk); sheahan; Shi, Pei yong; Schotsaert, Michael; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Sivko, Gloria S; dean.smith (dean.smith@canada.ca); Manki Song (mksong@ivi.int); SPERGEL@email.chop.edu; Stemmy, Erik (NIH/NIAID) [E]; Stewart, James; stittelaar (stittelaar@viroclinics.com); lawton.stubbert@canada.ca; kanta.subbarao (kanta.subbarao@influenzacentre.org); sutter (sutter@micro.vetmed.uni-muenchen.de); tcs38@psu.edu; Tadaki (tksuzuki@nih.go.jp); SWAMINATHAN, Soumya; Techakitiroj Chatkul (tverakit@gmail.com); tenoever@gmail.com; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; Treanor, John (OS/ASPR/BARDA) (CTR); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Tseng, Chien-Te K.; Chi Van Dang (cdang@lcr.org); Vandenberghe, Luk; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Vergara, Julia; verschoor (verschoor@bprc.nl); verstrepen@bprc.nl; caroline.melo@rivm.nl; Romain Volmer (romain.volmer@envt.fr); Asisa.Volz (Asisa.Volz@tiho-hannover.de); WaickmaA@upstate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); wenchun0617; White, Alexander G; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; ZHU, Jin; bosioc@niaid.nih.gov

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Albrecht, Randy; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Alyson Kelvin; danielle.anderson (danielle.anderson@duke-nus.edu.sg); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); JOHN JAMES BACZENAS; BAMFORD, Pearl; rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); sinabavari@comcast.net; Martin.Beer (Martin.Beer@fli.de); Neil Berry (Neil.Berry@nibsc.org); terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); dbolton@hivresearch.org; mopargal (mopargal@rams.colostate.edu); SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion (rcarrion@TxBiomed.org); Miles.Carroll (Miles.Carroll@phe.gov.uk); Cartner, Samuel Corbin; Cassels, Fred; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); lisa.chakrabarti@pasteur.fr; jfwchan (jfwchan@hku.hk); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); hlchen (hlchen@hku.hk); Carolyn Clark (carolyn.clark@cepi.net); yu.cong@nih.gov; scordo (scordo@qb.fcen.uba.ar); lisette.cornelissen; Crozier, Ian (NIH) [C]; kai.dallmeier (kai.dallmeier@kuleuven.be); Damron, Fredrick; que.dang@nih.gov; sodas; sharon.daye2.mil@mail.mil; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); De wit, Emmie (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mdiamond (mdiamond@wustl.edu); dgdiel@cornell.edu; CDillen@som.umaryland.edu; Dohm, Erik Daniel; Donis, Ruben (OS/ASPR/BARDA); William Dowling (william.dowling@cepi.net); mariette.ducatez@envt.fr; Duprex, Paul; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson (Karl.Erlandson@hhs.gov); marlene.espinozamoraga; mesteban (mesteban@cnb.csic.es); Falzarano, Darryl; feldmannh@niaid.nih.gov; Florence, Clint (NIH/NIAID) [E]; Flynn, Joanne L; thomasf@primate.wisc.edu; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Juan García Arriaza (jfgarcia@cnb.csic.es); Garcia-Sastre, Adolfo; Olinger, Gene; anna (anna@thsti.res.in); Volker.gerdts (Volker.gerdts@usask.ca); Gerhards, Nora; Christiane Gerke (christiane.gerke@pasteur.fr); Golding, Hana; Graham, Barney (NIH/VRC) [E]; lgralins@email.unc.edu; GREY Finn (fgrey@exseed.ed.ac.uk); Griffiths, Anthony; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); B.L. Haagmans (b.haagmans@erasmusmc.nl); rhakami@gmu.edu; Yper.Hall (Yper.Hall@phe.gov.uk); kevinharrod (kevinharrod@uabmc.edu); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; S. Herfst; seos@cnu.ac.kr; Hild, Sheri (NIH/OD) [E]; Hodgson, Paul; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Holbrook, Michael (NIH/NIAID) [C]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Honko, Anna; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); y.jacob.hou@unc.edu; REIRELAND (REIRELAND@mail.dstl.gov.uk); tomeri (tomeri@iibr.gov.il); mito@ciea.or.jp; Jayashankar, Lakshmi (OS/ASPR/BARDA); dustin.johnson (dustin.johnson@canada.ca); ajones; kandeil_a (kandeil_a@hotmail.com); Amelia Karlsson (amelia.karlsson@duke.edu); KAZI, Fatema; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); Nadia KHELEF (nadia.khelef@pasteur.fr); alankhoo.imr; sekim (sekim@krict.re.kr); Hwan K Kim (hwan.kim@stonybrook.edu); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); anja.kipar@uzh.ch; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); KNEZEVIC, Ivana; darwyn.kobasa@canada.ca; Kobie, James J; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); fkoide (fkoide@southernresearch.org); jeroen.kortekaas (jeroen.kortekaas@wur.nl); Krammer, Florian; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); Krause, Philip; kupke (kupke@staff.uni-marburg.de); Paul.Lambert (Paul.Lambert@unige.ch); mary.lane@nih.gov; langermans (langermans@bprc.nl); Lee-Parritz, David; Luis.Lugo.mil@afrims.org; Roger Le Grand (roger.le-grand@cea.fr); LESELLIER Sandrine (sandrine.lesellier@anses.fr); MSLEVER (MSLEVER@dstl.gov.uk); Levis, Robin; mlewis (mlewis@bioqual.com); sean.li (sean.li@canada.ca); grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; Little, James (OS/ASPR/BARDA); ldenisy (ldenisy@yahoo.com); anice.lowen; Kristine Macartney (kristine.macartney@health.nsw.gov.au); MacGill, Tracy; ramadany; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); Karen Makar (Karen.Makar@gatesfoundation.org); Suchinda Malaivijitnond (suchinda.m@chula.ac.th); ivan.marazzi; IVMARTINEZ; daniel.martinez-arguelles; LMartinez@txbiomed.org; marzia; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); paul-mccray (paul-mccray@uiowa.edu); ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); dmissiak (dmissiak@bsd.uchicago.edu); Kayvon Modjarrad (kmodjarrad@eidresearch.org); bobomok@hku.hk; SATHIYAMOORTHY, Vaseeharan; Munir, Muhammad; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; nnagata@niid.go.jp; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); MNELSON@mail.dstl.gov.uk; johan.neyts (johan.neyts@kuleuven.be); SHELBY L O'CONNOR; DAVID H O'CONNOR (dhoconno@wisc.edu); horer@ku.edu.tr; Oreshkova, Nadia; mto@umn.edu; Mark Page (Mark.Page@nibsc.org); gustavo.palacios (gustavo.palacios@gmail.com); peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp (nirp@iibr.gov.il); Perlman, Stanley; Andrew.Phipps; bradley.pickering (bradley.pickering@canada.ca); Pickett, Thames (NIH/NIAID) [E]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR (JLPRIOR@dstl.gov.uk); qinchuan (qinchuan@pumc.edu.cn); troyrandall (troyrandall@uabmc.edu); angierasmussen@gmail.com; ravetch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; David Revelli (drevelli@lovelacebiomedical.org); Juergen Richt (jricht@vet.k-state.edu); RIVEROS BALTA, Ximena; B.H.G. Rockx (b.rockx@erasmusmc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); Nicola Rose (Nicola.Rose@nibsc.org); croy (croy@tulane.edu); Riccardo Russo; rkiatchula (rkiatchula@gmail.com);

Sabourin, Carol (OS/ASPR/BARDA); esulkowska@rics.bwh.harvard.edu; SALAMI, Kolawole; salgampa (salgampa@njms.rutgers.edu); Javier Salguero (Javier.Salguero@phe.gov.uk); erica (erica@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); Tony.Schountz@colostate.edu; res2025; Segales, Joaquim; snumouse (snumouse@snu.ac.kr); Seungtaek Kim (seungtaek.kim@ip-korea.org); shanchao (shanchao@wh.iov.cn); Sally Sharpe (Sally.Sharpe@phe.gov.uk); sheahan; Shi, Pei yong; Schotsaert, Michael; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Sivko, Gloria S; dean.smith (dean.smith@canada.ca); Manki Song (mksong@ivi.int); SPERGEL@email.chop.edu; Stemmy, Erik (NIH/NIAID) [E]; Stewart, James; stittelaar (stittelaar@viroclinics.com); lawton.stubbert@canada.ca; kanta.subbarao (kanta.subbarao@influenzacentre.org); sutter (sutter@micro.vetmed.uni-muenchen.de); tcs38@psu.edu; Tadaki (tksuzuki@nih.go.jp); SWAMINATHAN, Soumya; Techakitiroj Chatkul (tverakit@gmail.com); tenoever@gmail.com; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; Treanor, John (OS/ASPR/BARDA) (CTR); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Tseng, Chien-Te K.; Chi Van Dang (cdang@lcr.org); Vandenberghe, Luk; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Vergara, Julia; verschoor (verschoor@bprc.nl); verstrepen@bprc.nl; caroline.melo@rivm.nl; Romain Volmer (romain.volmer@envt.fr); Asisa.Volz (Asisa.Volz@tiho-hannover.de); WaickmaA@upstate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); wenchun0617; White, Alexander G; WOOD, David John; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; ZHOU, Tiequn; ZHU, Jin; bosioc@niaid.nih.gov; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); kyle.rosenke; caroline.foo; t.sulpice; gabriella.worwa; Yusibov, Vidadi (OS/ASPR/BARDA); f.briand

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+1 651 372 8299 US (Minnesota)
+1 786 635 1003 US (Miami)
+1 267 831 0333 US (Philadelphia)
+1 301 715 8592 US (Washington D.C)
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207.226.132.110 (Japan)
Meeting ID: 361 256 8290

From: JUDY.HUBBARD@gatesfoundation.org[JUDY.HUBBARD@gatesfoundation.org]

Attendees: Harry Kleanthous; Holger Kanzler; Max Silverman; David Vaughn; Anastazia Older Aguilar; Colleen Woods; Kriti Arora; Susan Barnett; Ajoke Sobanjo-ter Meulen; Anna DU; Emilio Emini; Judy Hubbard; David Robinson; Nina Russell; Anushri Singhvi; Chris Karp; Peter Dull; Scott Dowell; Vivian Hsu; Kristen Earle; Julia Kuhn; Steve Hadley; Janet White; Heather Ann Brauer; Jacqueline Kirchner; Max Silverman; Kavita Malling (Camber Collective); Natalie Revelle; Chris Chen; Vidya Vasu-Devan; Ros Hollingsworth; Laura Powell; Email Recovery Approval; randy.albrecht@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; AKelvin@dal.ca; danielle.anderson@duke-nus.edu.sg; s.a.arakelov@spbniivs.ru; baczenas@wisc.edu; Pearl.Bamford@health.gov.au; rbaric@email.unc.edu; dbarouch@bidmc.harvard.edu; sinabavari@comcast.net; Martin.Beer@fli.de; Neil.Berry@nibsc.org; terry.k.besch.ctr@mail.mil; dbolton@hivresearch.org; mopargal@rams.colostate.edu; SBradfute@salud.unm.edu; BRANGEL, Polina; Brasel, Trevor; lisambrosseau@gmail.com; Bukreyev, Alexander; rcarrion@txbiomed.org; Miles.Carroll@phe.gov.uk; scartner@uab.edu; fcassels@path.org; Marco.Cavaleri@ema.europa.eu; lisa.chakrabarti@pasteur.fr; jfwchan@hku.hk; Monalisa Chatterji; hlchen@hku.hk; carolyn.clark@cepi.net; yu.cong@nih.gov; scordo@qb.fcen.uba.ar; lisette.cornelissen@wur.nl; ian.crozier@nih.gov; Kai Dallmeier; Damron, Fredrick; que.dang@nih.gov; Das, Soumita; sharon.daye2.mil@mail.mil; jorgen.de.jonge@rivm.nl; xavier.de-lamballerie@univ-amu.fr; emmie.dewit@nih.gov; Delgado Vazquez.Rafael; mdiamond@wustl.edu; dgdiel@cornell.edu; Dillen, Carly; edohm@uab.edu; Ruben.Donis@hhs.gov; William Dowling; mariette.ducatez@envt.fr; pduprex@pitt.edu; Eitzen, Melissa M.; l.enjuanes@cnb.csic.es; Karl.Erlandson@hhs.gov; marlene.espinozamoraga@mssm.edu; mesteban@cnb.csic.es; darryl.falzarano@usask.ca; feldmannh@niaid.nih.gov; clint.florence; joanne@pitt.edu; thomasf@primate.wisc.edu; Frieman, Matthew; Simon.Funnell@phe.gov.uk; jfgarcia@cnb.csic.es; Garcia-Sastre, Adolfo; golinger@mriglobal.org; anna@thsti.res.in; Volker.gerdts@usask.ca; nora.gerhards@wur.nl; christiane.gerke@pasteur.fr; Hana.Golding@fda.hhs.gov; barney.graham@nih.gov; lgralins@email.unc.edu; fgrey@exseed.ed.ac.uk; ahgriff@bu.edu; CarlosAlberto.Guzman@helmholtz-hzi.de; b.haagmans@erasmusmc.nl; rhakami@gmu.edu; Yper.Hall@phe.gov.uk; kevinharrod@uabmc.edu; henaorestrepoa@who.int; lisa.hensley@nih.gov; S. Herfst; seos@cnu.ac.kr; sheri.hild@nih.gov; paul.hodgson@usask.ca; christian.c.hofer.mil@mail.mil; jhogan@uga.edu; Michael.holbrook@nih.gov; Anthony Holmes - NC3Rs; Honko, Anna; jay.w.hooper.civ@mail.mil; y.jacob.hou@unc.edu; REIRELAND@mail.dstl.gov.uk; tomeri@iibr.gov.il; mito@ciea.or.jp; Lakshmi.Jayashankar@hhs.gov; dustin.johnson@canada.ca; ajones@mail.rockefeller.edu; kandeil_a@hotmail.com; amelia.karlsson@duke.edu; kazif@who.int; Bernhard.Kerscher@pei.de; nadia.khelef@pasteur.fr; alankhoo.imr@gmail.com; sekim@krict.re.kr; hwan.kim@stonybrook.edu; Jason.Kindrachuk@umanitoba.ca; anja.kipar@uzh.ch; Jacqueline Kirchner; knezevici; darwyn.kobasa@canada.ca; jjkobie@uabmc.edu; Gary.Kobinger@crchudequebec.ulaval.ca; fkoide@southernresearch.org; jeroen.kortekaas@wur.nl; florian.krammer@mssm.edu; i.v.krasilnikov@spbniivs.ru; philip.krause@fda.hhs.gov; kupke@staff.uni-marburg.de; Paul.Lambert@unige.ch; mary.lane@nih.gov; langermans@bprc.nl; david.lee-parritz@tufts.edu; Luis.Lugo.mil@afrims.org; Roger Le Grand; sandrine.lesellier@anses.fr; MSLEVER@dstl.gov.uk; robin.levis@fda.hhs.gov; mlewis@bioqual.com; sean.li@canada.ca; grace.m.lidl.mil@mail.mil; Elliot Lilley - NC3Rs; James.Little@hhs.gov; ldenisy@yahoo.com; Lowen, Anice; kristine.macartney@health.nsw.gov.au; Tracy.MacGill@fda.hhs.gov; Rana A. Al Madany; pauline.maisonnasse@cea.fr; suchinda.m@chula.ac.th; ivan.marazzi@mssm.edu; Martinez, Ivan; daniel.martinez-arguelles@canada.ca; LMartinez@txbiomed.org; Marzi, Andrea (NIH/NIAID) [E; Giada.Mattiuzzo@nibsc.org; paul-mccray@uiowa.edu; ThomasC.Mettenleiter@fli.de; cjmiller@ucdavis.edu; philip.minor2@gmail.com; Ali.Mirazimi@folkhalsomyndigheten.se; dmissiak@bsd.uchicago.edu; kmodjarrad@eidresearch.org; bobomok@hku.hk; moorthyv; muhammad.munir@lancaster.ac.uk; munoz-fontela@bnitm.de; vincent.munster@nih.gov; nnagata@niid.go.jp; aysegul.nalca.civ@mail.mil; MNELSON@mail.dstl.gov.uk; Johan Neyts; slfeinberg@wisc.edu; dhoconno@wisc.edu; horer@ku.edu.tr; nadia.oreshkova@wur.nl; mto@umn.edu; Mark.Page@nibsc.org; gustavo.palacios@gmail.com; peter.palese@mssm.edu; mitchell.palmer@usda.gov; nirp@iibr.gov.il; stanley-perlman@uiowa.edu; Andrew.Phipps@hhs.gov; bradley.pickering@canada.ca; pickettte@niaid.nih.gov; margaret.l.pitt.civ@mail.mil; Mark Prescott - NC3Rs; PREZIOSI, Marie-pierre; JLPRIOR@dstl.gov.uk; qinchuan@pumc.edu.cn; troyrandall@uabmc.edu; angierasmussen@gmail.com; ravetch@mail.rockefeller.edu; Ann.Rawkins@phe.gov.uk; Russell.Ray@bcm.edu; Matthew.Reed.mil@afrims.org; dsreed@cvr.pitt.edu; patrick.reid@unmc.edu; drevelli@lovelacebiomedical.org; jricht@vet.k-state.edu; lauriex@who.int; b.rockx@erasmusmc.nl; estefania.rodriguez@bnitm.de; Nicola.Rose@nibsc.org; croy@tulane.edu; russori@njms.rutgers.edu; rkiatchula@gmail.com; Carol.Sabourin@hhs.gov; esulkowska@rics.bwh.harvard.edu; salamik@who.int; salgampa@njms.rutgers.edu; Javier.Salguero@phe.gov.uk; Erica Ollmann Saphire; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; Tony.Schountz@colostate.edu; schwartzl@who.int; res2025@med.cornell.edu; joaquim.segales@irta.cat; snumouse@snu.ac.kr; seungtaek.kim@ip-korea.org; shanchao@wh.iov.cn; Sally.Sharpe@phe.gov.uk; Sheahan, Timothy Patrick; Shi, Pei yong; michael.schotsaert@mssm.edu; amy.c.shurtleff@cepi.net; yoos@who.int; sivkog@battelle.org; dean.smith@canada.ca; mksong@ivi.int; SPERGEL@email.chop.edu; erik.stemmy@nih.gov; J.P.Stewart@liverpool.ac.uk; stittelaar@viroclinics.com; lawton.stubbert@canada.ca; kanta.subbarao@influenzacentre.org; sutter@micro.vetmed.uni-muenchen.de; tcs38@psu.edu; tksuzuki@nih.go.jp; swaminathans@who.int; tverakit@gmail.com; tenoever@gmail.com; nax3@cdc.gov;

JTorrelles@txbiomed.org; franck.TOURET@univ-amu.fr; John.Treanor@hhs.gov; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Tseng, Chien-Te K.; cdang@lcr.org; luk_vandenberghe@meei.harvard.edu; wim.vanderpoel@wur.nl; neeltje.vandoremalen@nih.gov; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David Vaughn; julia.vergara@irta.cat; verschoor@bprc.nl; verstrepen@bprc.nl; caroline.melo@rivm.nl; romain.volmer@envt.fr; Asisa.Volz@tiho-hannover.de; WaickmaA@upstate.edu; tony.wang@fda.hhs.gov; wenchun0617@gate.sinica.edu.tw; agw13@pitt.edu; woodd@who.int; tyamamoto@ciea.or.jp; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; zhout@who.int; Jin.Zhu@health.gov.au; alex.sigal@ahri.org; rawcraig@yahoo.com; Gerald.Kovacs@hhs.gov; Ashley.Smith1@hhs.gov; fjc37@cam.ac.uk; SGalloway@cdc.gov; lny1@cdc.gov; gll9@cdc.gov; mbo2@cdc.gov; sot1@cdc.gov; angeliki.melidou@ecdc.europa.eu; liyl@cde.org.cn; liub@cde.org.cn; zuz4@cdc.gov; htq4@cdc.gov; lad7@cdc.gov; bhx1@cdc.gov; ilj2@cdc.gov; rzh7@cdc.gov; tkh4@cdc.gov; djernigan@cdc.gov; map1@cdc.gov; xdv3@cdc.gov; valentina.bernasconi@cepi.net; elwyn.griffiths@cepi.net; celine.gurry@cepi.net; johan.holst@cepi.net; Arun Kumar; solomon.yimer@cepi.net; christian.drosten@charite.de; MAY.CHU@CUANSCHUTZ.EDU; eric.vangieson@darpa.mil; MNELSON@dstl.gov.uk; Georgia Tomaras, Ph.D.; david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang@duke-nus.edu.sg; Eeva Broberg; epstein@ecohealthalliance.org; daszak@ecohealthalliance.org; emmanuelle.charton@edqm.eu; BUDA Mihaela; Ragini.Shivji@ema.europa.eu; m.koopmans@erasmusmc.nl; n.okba@erasmusmc.nl; Mayra.Garcia@fda.hhs.gov; Todd.Myers@fda.hhs.gov; Keith.Peden@fda.hhs.gov; Jerry.Weir@fda.hhs.gov; Jilian.Sacks@finddx.org; jmcelrat@fredhutch.org; tlying@fudan.edu.cn; cheryl@gisaid.org; christian.brechot@pasteur.fr; ASiyer@mgh.harvard.edu; maria.baca-estrada@canada.ca; jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik@hku.hk; r.tedder@imperial.ac.uk; vyusibov@indianabiosciences.org; guy.gorochov@sorbonne-universite.fr; sylvie.van-der-werf@pasteur.fr; supaporn.p@dmsc.mail.go.th; jokim@ivi.int; qiang.pan-hammarstrom@ki.se; katie.doores@kcl.ac.uk; leejooyeon@korea.kr; limhy0919@korea.kr; shane@lji.org; Sharon Schendel; alex@lji.org; sujan@lji.org; daniela@lji.org; liz.miller@lshtm.ac.uk; Luc.Gagnon@nexelis.com; Greg.Kulnis@nexelis.com; brooke.bozick@nih.gov; marciela.degrace@nih.gov; janet.lathey@nih.gov; larry.wolfraim@nih.gov; johnsonreed@niaid.nih.gov; karin.bok@nih.gov; kizzmekia.corbett@nih.gov; adrian.mcdermott@nih.gov; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; pennym@nicd.ac.za; changguili@aliyun.com; lyhchengdu@163.com; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; xumiaobj@126.com; pilailuk.o@dmsc.mail.go.th; baihe@nmpa.gov.cn; william.lee@health.ny.gov; dboyle@path.org; tdelossantos@path.org; bleader@path.org; Christine.bruce@phe.gov.uk; Mary.Matheson@phe.gov.uk; galter@partners.org; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; dancohen@tauex.tau.ac.il; jma@sgul.ac.uk; msalit@stanford.edu; pawinee.k@redcross.or.th; shinjini.bhatnagar@thsti.res.in; gmedigeshi@thsti.res.in; gweiss@uci.edu; arimoin@g.ucla.edu; jmclellan@austin.utexas.edu; wilsonp@uchicago.edu; Nick.Gilbert@ed.ac.uk; diane.descamps@aphp.fr; Goldblatt, David; mit666666@pitt.edu; jwm1@pitt.edu; Kelvin, Alyson; teresa.lambe@ndm.ox.ac.uk; ydm9@cdc.gov; gustavo.f.palacios.civ@mail.mil; scott.napper@usask.ca; tracey.thue@usask.ca; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ@mail.mil; skrebs@hivresearch.org; sheila.a.peel2.civ@mail.mil; PScott@eidresearch.org; costaa@who.int; omorgan@who.int; perkinsm@who.int; subissil@who.int; dj56wood@gmail.com; STRÖHER, Ute; sandsa@who.int; irahetar@who.int; zlshi@wh.iov.cn; Youngmee Jee; thatziio@rockefeller.edu; mafranco@javeriana.edu.co; Jiae Kim; a.luttick@360biolabs.com; renuka.kumar@gladstone.ucsf.edu; melanie.ott@gladstone.ucsf.edu; arjun.rustagi@stanford.edu; sastanley@berkeley.edu; Pillai, Satish; joe@czbiohub.org; raul.andino@ucsf.edu; charles.chiu@ucsf.edu; GSimmons@vitalant.org; MaryKate.Morris@cdph.ca.gov; amy.kistler@czbiohub.org; cblish@stanford.edu; bertozzi@stanford.edu; tdcarroll@ucdavis.edu; douglas_fox@berkeley.edu; Debra.Wadford@cdph.ca.gov; Carl.Hanson@cdph.ca.gov; fernando.p.polack@vanderbilt.edu; Celeste.Marsh@health.gov.au; kim.Mulholland@lshtm.ac.uk; achidi.eric@gmail.com; macalvo@uach.cl; rodewaldl@chinacdc.cn; AFO@ssi.dk; hutiny@Who.int; sylvain.baize@pasteur.fr; mariangela.cavarelli@cea.fr; alariqil@who.int; may@bnitm.de; Jakob Cramer; Harish Iyer; Gagandeep Kang; Kayla Laserson; alemseged.abdissa@ahri.gov.et; azimt@who.int; cawthornea@who.int; adane.mihret@ahri.gov.et; ephcicm@nus.edu.sg; Vernon_LEE@moh.gov.sg; cherylc@nicd.ac.za; madhis@rmpru.co.za; mdohmd@snu.ac.kr; joser.arribas@salud.madrid.org; marta.diaz@salud.madrid.org; Katrin.Leitmeyer@ecdc.europa.eu; bergerii@who.int; feikind@who.int; grantr@who.int; Stephan.Harbarth@hcuge.ch; vankerkhovem@who.int; kum.ungchusak@gmail.com; albert.jan.van.hoek@rivm.nl; chantal.reusken@rivm.nl; mawiddowson@itg.be; Gayatri.Amirthalingam@phe.gov.uk; Nick Andrews; Andrew.Gorringe@phe.gov.uk; Bassam.Hallis@phe.gov.uk; Liz.Miller@phe.gov.uk; ccassetti@niaid.nih.gov; glynnsa@nhlbi.nih.gov; Graham, Barney (NIH/VRC) [E]; kdk6@cdc.gov; Barbara Mahon; MCELROYA@pitt.edu; ztq9@cdc.gov; Padmini Srikantiah; Jordan Tappero; jqt8@cdc.gov; rgonzalez@uaem.mx; hopr@uaem.mx; m.addo@uke.de; Mark_Ic_Chen@ncid.sg; Romain.Martischang@hcuge.ch; shimian.zou@nih.gov; Christina.Bareja@health.gov.au; John.Forde@phe.gov.uk; JinalB@nicd.ac.za; vekemansj@who.int; paola.stefanelli@iss.it; liya.wassie@ahri.gov.et; vongs@who.int; starkullaj@who.int; mahamuda@who.int; reveizl@paho.org; rodrigueza@paho.org; leitejul@paho.org; vicarian@paho.org; pebodyr@who.int; rawleigh.howe@ahri.gov.et; THOMAS.JAENISCH@CUANSCHUTZ.EDU; ayola-akim.adegnika@medizin.uni-tuebingen.de; t.brehm@uke.de; adamou.rafiou@gmail.com; bernadettemrg5@gmail.com; bernadette.murgue@inserm.fr; gmackenzie@mrc.gm; Anthony.Scott@lshtm.ac.uk; SUyoga@kemri-wellcome.org; atanuri1@gmail.com; ggj2@cdc.gov; wbrooks3@jhu.edu; kkotloff@som.umaryland.edu;

ADriscoll@som.umaryland.edu; ehi.igumbor@ncdc.gov.ng; SHakre@eidresearch.org; derrick.crook@ndcls.ox.ac.uk; csv@ssi.dk; schwartz@pasteur.fr; marc.eloit@pasteur.fr; srinivas.murthy; matthew.cheng@mcgill.ca; nymadawa@gyals.mn; wuzy@263.net; gaofu@chinacdc.cn; Mpasetti@som.umaryland.edu; aleksandra.wesolowska@wum.edu.pl; cuchip@who.int; per.ashorn@tuni.fi; kwatrag@rmpru.co.za; jmarien@itg.be; KArien@itg.be; adebola.olayinka@ncdc.gov.ng; bcowling@hku.hk; Suellen.Nicholson@vidrl.org.au; paul.licciardi@mcri.edu.au; lienanhha.do@mcri.edu.au; marc-alexandre.lafrance.1@ulaval.ca; paul.fine@lshtm.ac.uk; krystian.jazdzewski@warsawgenomics.pl; jzejda@sum.edu.pl; freidlg@who.int; taufiqur@icddrb.org; fqadri@icddrb.org; r.heyderman@ucl.ac.uk; mff7@cdc.gov; Heather.Whitaker@phe.gov.uk; tonoletej@who.int; annev@nicd.ac.za; shinj@who.int; johnvparry@ntlworld.com; leli@who.int; krishnanv@who.int; revans@who.int; belll@who.int; juneja@tifr.res.in; violetafonsecaocampos@gmail.com; twosned@googlemail.com; alain.townsend@imm.ox.ac.uk; sanchezg@une.net.co; muldersm@who.int; pereyaslovd@who.in; mueller@wehi.edu.au; leanne.robinson@burnet.edu.au; claudioc@gsespa.cl; drmlaman@yahoo.com; ffntoumi@hotmail.com; rajatonirinas@who.int; Kirsty Le Doare; Joe.Fitchett@mologic.co.uk; hstaines@sgul.ac.uk; thall@sgul.ac.uk; okeibunorj@who.int; barnorj@who.int; heather.gidding@sydney.edu.au; mayara_bastos@yahoo.com.br; faiz.ahmadkhan@mcgill.ca; louis.patrick.haraoui@usherbrooke.ca; yuemei.fan@tuni.fi; almonther@hotmail.com; philippa.matthews@ndm.ox.ac.uk; Abbie.Bown@phe.gov.uk; hsaeb@phcc.gov.qa; intl@ibto.ir; dorits@imbm.org; dthea@bu.edu; yoshiyama1962@yahoo.co.jp; ullas@tifr.res.in; jsshastri@gmail.com; Audrey Hutter; cooldrdax@gmail.com; inbanathanf@who.int; muhammadqasim.qasim@otago.ac.nz; ofrinr@who.int; payden@who.int; vokatya@who.int; tranminhn@who.int; cgomez@javeriana.edu.co; jccastellanos@husi.org.co; katom@who.int; snsmarlowe@doctors.org.uk; arashirot@who.int; lOwusu@noguchi.ug.edu.gh; eric.osoro@wsu.edu; HarbiNa2@NGHA.MED.SA; amhashem@kau.edu.sa; bwilliams@who.int; radegbola@hotmail.com; jean-luc.gala@uclouvain.be; rosemaryaudu@yahoo.com; sandeepdogra@gmail.com; allergypk@gmail.com; maghsoodlu@yahoo.com; peshghi64@gmail.com; a.a.khazaeli@gmail.com; Bethany_Gauthier@hms.harvard.edu; vittoria.offeddu@ird.global; MAHIPALAP@who.int; ian.marr@menzies.edu.au; Abena.Amoah@lshtm.ac.uk; Mia.Crampin@lshtm.ac.uk; Antonia.Ho@glasgow.ac.uk; javadi11@hzdr.de; asmronger@gmail.com; Kaitlyn.Vette@health.nsw.gov.au; magdalena.spolnicka@policja.gov.pl; aleksander.masny@policja.gov.pl; marc.veldhoen@medicina.ulisboa.pt; MRabeh@dha.gov.ae; susie.dunachie@ndm.ox.ac.uk; necla.tulek@atilim.edu.tr; sophiev@hku.hk; koningsf@who.int; Lloyd.Mulenga@moh.gov.zm; lbmulenga@yahoo.com; mastershakil@hotmail.com; rahul.arora@balliol.ox.ac.uk; christian.cao@ucalgary.ca; liu.michael222@gmail.com; niklas.bobrovitz@mail.utoronto.ca; tingting.yan@mail.utoronto.ca; a.pan@asst-cremona.it; s.testa@asst-cremona.it; alessia.zoncada@tin.it; nicolew@nicd.ac.za; GWarimwe@kemri-wellcome.org; HKaranja@kemri-wellcome.org; dancohen@tauex.tau.ac.i; sabinoec@usp.br; patricia.garcia@upch.pe; zobstfeld@wesleyan.edu; amyjanel@gmail.com; liliana.brown@nih.gov; lori.newman@nih.gov; descherm@bni-hamburg.de; emmerich@bnitm.de; charlotte.thalin@sll.se; voneijek@who.int; avillarreal@indicasat.org.pa; agoodridge@indicasat.org.pa; r.a.mckendry@ucl.ac.uk; jint@ustc.edu.cn; Email; monika.lindemann@uk-essen.de; ygrad@hsph.harvard.edu; KHerbst@ahri.org; daniel.larremore@colorado.edu; william.windsor@cuanschutz.edu; Molly.Lamb@cuanschutz.edu; rolf.fendel@uni-tuebingen.de; jguthmiller@uchicago.edu; mzrein@infynity-biomarkers.com; mike.fisher@oncimmune.com; kjambo@mlw.mw; petra.budde@oncimmune.com; oon_tek_ng@ncid.sg; kalisvar_marimuthu@ttsh.com.sg; Farah_MOHAMED_HANIFF@ncid.sg; a.t.decruz.20@ucl.ac.uk; ben.miller.13@ucl.ac.uk; mafarodriguez@unisalle.edu.co; Anna.JefferySmith@phe.gov.uk; keti.glonti@gmail.com; imaginapolo@gmail.com; Maria.Zambon@phe.gov.uk; Jennifer.Yates@health.ny.gov; gingras@lunenfeld.ca; jen.gommerman@utoronto.ca; lewish@who.int; daclark@sgul.ac.uk; omar.nyabi@uclouvain.be; giorgio.fedele@iss.it; Rachel.Halkerston@phe.gov.uk; pamela.proud@phe.gov.uk; kpancer@pzh.gov.pl; wegene.borena@i-med.ac.at; wrastawicki@pzh.gov.pl; sungskim63@gmail.com; vfa3@cdc.gov; teodora.aktas@folkhalsomyndigheten.se; Email: jplested@novavax.com; bkhatri@lunenfeld.ca; tesfaye.gelanew@ahri.gov.et; juan.moliva@nih.gov; anne.werner@nih.gov; gabriela.alvarado@nih.gov; Breeze Cavell; wangling@niaid.nih.gov; eunsung.yang@nih.gov; yi.zhang3@nih.gov; nicole.doriarose@nih.go; lorna.mcinroy@phe.gov.uk; mazhari@wehi.edu.au; zhuna@ivdc.chinacdc.cn; maony@ivdc.chinacdc.cn; zhuzhen@ivdc.chinacdc.cn; zhangyan@ivdc.chinacdc.cn; wangpw@ivdc.chinacdc.cn; sanghwan.seo@ivi.int; vfumado@hsjdbcn.org; xhatzi@med.uth.gr; tatjana.vilibic-cavlek@hzjz.hr; annap@auth.gr; andargachew.mulu@ahri.gov.et; viki.indenbaum@sheba.health.gov.il; colwill@lunenfeld.ca; ytakahas@niid.go.jp; sayamrym@niid.go.jp; tksuzuki@niid.go.jp; raquel.guiomar@insa.min-saude.pt; merit.melin@thl.fi; katarina.prosenc@nlzoh.si; jwilbur@meso-scale.com; Celine.Parsy-Kowalska@oncimmune.com; Imran Nisar; Fyezah Jehan; lcorey@fredhutch.org; m.noursadeghi@ucl.ac.uk; fabienne.brilot@sydney.edu.au; lja2002@qatar-med.cornell.edu; mdjjh@nmc.or.kr; AAgweyu@kemri-wellcome.org; katherine.gallagher@lshtm.ac.uk; AEtyang@kemri-wellcome.org; ekagucia@kemri-wellcome.org; Christian.Bottomley@LSHTM.ac.uk; SPortillo@som.umaryland.edu; nicole.gilberger@bnitm.de; sudhirbabji@cmcvellore.ac.in; Mallory.Shriver@som.umaryland.edu; freedmanne@mail.nih.gov; galter@mgh.harvard.edu; kristian@andersen-lab.com; trvrb; pbieniasz@rockefeller.edu; Bjorkman, Pamela J.; jbloom@fredhutch.org; burton@scripps.edu; mmdavis@stanford.edu; deoliveira@ukzn.ac.za; gd312@cam.ac.uk; embrya@niaid.nih.gov; katie.ewer@ndm.ox.ac.uk; agartlan@fredhutch.org; r.fouchier@erasmusmc.nl; ggaiha@mgh.harvard.edu; dh2994@cumc.columbia.edu; Nick Jackson; yoshihiro.kawaoka@wisc.edu;

akiko.iwasaki@yale.edu; paul.kellam@kymab.com; neil@ipd.uw.edu; btk@lanl.gov; karin.lore@ki.se; J. Christopher Love; darrenpatrickmartin@gmail.com; monte@duke.edu; felipe.naveca@fiocruz.br; nussen@mail.rockefeller.edu; Erica Ollmann Saphire; sjp97@medschl.cam.ac.uk; mpepper@uw.edu; bpulend@stanford.edu; rino.r.rappuoli@gsk.com; sabinoec@gmail.com; senjutisaha@gmail.com; schief@scripps.edu; gideon.schreiber@weizmann.ac.il; gavin.screaton@medsci.ox.ac.uk; djs200@cam.ac.uk; varadar; dveesler@uw.edu; bwalker@mgh.harvard.edu; andrew@scripps.edu; wilson@scripps.edu; wyatt@scripps.edu

Sent: Mon 3/29/2021 9:55:05 PM (UTC-05:00)

Subject: Save the date COVAX Enabling Sciences Workshop: Global and local approaches to detect and interpret SARS-CoV-2 variants

Dear All

The goal of the workshop is to discuss how to rapidly generate actionable information on the immunological consequences of emerging SARS-CoV-2 variants. This requires connecting local pathogen genomic sequencing and epidemiology with high quality virology and immunology. There will also be a discussion of how immunological knowledge gained in one country or region can feed into, and benefit from, large international efforts and inform global and local decision making.

Agenda and registration link forthcoming.

Thank you.
Karen

From: Dalder-Alpher, Erin [edalder-alpher@asmusa.org]
Sent: 5/28/2021 9:19:28 AM
To: Kristen Bernard [kristen.bernard@wisc.edu]; zlshi@wh.iov.cn; Menachery, Vineet [vimenach@UTMB.EDU]; Bloom PhD, Jesse D [jbloom@fredhutch.org]
CC: Spindler, Katherine [krspin@umich.edu]; American Society for Virology (asv@asv.org) [asv@asv.org]; volker.thiel@vetsuisse.unibe.ch
Subject: RE: Speaker information update for ASM World Microbe

Greetings everyone!

If you haven't booked a recording already, you can do so at this link: http://projectionnet.com/wmf2021/Login.aspx. Recording appointments are available through June 11 but I encourage you to book soon. We have also coordinated some additional recording appointments on June 14 and 15 and my colleague, Kellen Bagnoli can assist you with making those appointments.

Best regards,
Erin

Erin Dalder-Alpher | Program Manager, ASM Microbe
American Society for Microbiology
1752 N Street, NW | Washington, DC 20036
202.942.9382 direct | 202.737.3600 main | 202.942.9340 fax

From: Kristen Bernard <kristen.bernard@wisc.edu>
Sent: Thursday, May 27, 2021 1:50 PM
To: zlshi@wh.iov.cn; Menachery, Vineet <vimenach@UTMB.EDU>; Bloom PhD, Jesse D <jbloom@fredhutch.org>
Cc: krspin@umich.edu; American Society for Virology (asv@asv.org) <asv@asv.org>; Dalder-Alpher, Erin <edalder-alpher@asmusa.org>; volker.thiel@vetsuisse.unibe.ch
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We will have a **LIVE** "After Chat" panel discussion with myself and Volker Thiel as your hosts on **June 21, 3:45-4:30 pm EST**. Please let us know if you cannot attend the discussion panel.

The talk order for the session will be:

Zhengli Shi
Vineet Menarchy
Jesse Bloom

Please let us know if you have any questions.

Best regards,
Kristen and Volker

Kristen Bernard, DVM, PhD
Professor of Virology
Department of Pathobiological Sciences
School of Veterinary Medicine
University of Wisconsin-Madison
2015 Linden Dr.
Madison, WI 53706

Pronouns: she/her
Why pronouns matter https://lgbt.wisc.edu/education/pronouns-matter/

Email: kristen.bernard@wisc.edu
Phone: 608-263-7114
Office room #: 4270C
Lab room #: 4240A

Twitter @UWbernardLab

From: Kristen Bernard [kristen.bernard@wisc.edu]
Sent: 5/28/2021 10:50:01 AM
To: Menachery, Vineet [vimenach@UTMB.EDU]; zlshi@wh.iov.cn; Bloom PhD, Jesse D [jbloom@fredhutch.org]
CC: Spindler, Katherine [krspin@umich.edu]; American Society for Virology (asv@asv.org) [asv@asv.org]; Dalder-Alpher, Erin [edalder-alpher@asmusa.org]; volker.thiel@vetsuisse.unibe.ch
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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, May 28, 2021 9:34 AM
To: Kristen Bernard <kristen.bernard@wisc.edu>; zlshi@wh.iov.cn; Bloom PhD, Jesse D <jbloom@fredhutch.org>
Cc: Spindler, Katherine <krspin@umich.edu>; American Society for Virology (asv@asv.org) <asv@asv.org>; Dalder-Alpher, Erin <edalder-alpher@asmusa.org>; volker.thiel@vetsuisse.unibe.ch
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Thanks

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Kristen Bernard <kristen.bernard@wisc.edu>
Sent: Thursday, May 27, 2021 12:50 PM
To: zlshi@wh.iov.cn <zlshi@wh.iov.cn>; Menachery, Vineet <vimenach@UTMB.EDU>; Bloom PhD, Jesse D <jbloom@fredhutch.org>
Cc: Spindler, Katherine <krspin@umich.edu>; American Society for Virology (asv@asv.org) <asv@asv.org>; Dalder-

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2015 Linden Dr.
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Why pronouns matter https://lgbt.wisc.edu/education/pronouns-matter/

Email: kristen.bernard@wisc.edu
Phone: 608-263-7114
Office room #: 4270C
Lab room #: 4240A

Twitter @UWbernardLab

From: Bloom PhD, Jesse D [jbloom@fredhutch.org]
Sent: 5/28/2021 5:57:26 PM
To: Kristen Bernard [kristen.bernard@wisc.edu]; Menachery, Vineet [vimenach@UTMB.EDU]; zlshi@wh.iov.cn
CC: Spindler, Katherine [krspin@umich.edu]; American Society for Virology (asv@asv.org) [asv@asv.org]; Dalder-Alpher, Erin [edalder-alpher@asmusa.org]; volker.thiel@vetsuisse.unibe.ch
Subject: Re: Speaker information update for ASM World Microbe

Hi Kristen,

Thanks for coordinating all of this.

As far as the AfterChat, can I be a *maybe*? I would like to do this and have blocked out the time, but I was just called for jury duty the week of June 21 and it's unclear if I'll be required to show up on June 21 itself. I can do the AfterChat if I don't have to be on a jury then, but may not know until shortly beforehand.

Also (and I apologize if I missed this in an earlier e-mail), how exactly do we upload and record our talks? If instructions just haven't been sent yet that's fine, but I wanted to make sure I didn't miss them.

Thanks,
Jesse

Jesse Bloom
Associate Professor, Fred Hutch Cancer Research Center
Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington
Investigator, Howard Hughes Medical Institute

From: Kristen Bernard <kristen.bernard@wisc.edu>
Date: Friday, May 28, 2021 at 8:50 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>, zlshi@wh.iov.cn <zlshi@wh.iov.cn>, Bloom PhD, Jesse D <jbloom@fredhutch.org>
Cc: Spindler, Katherine <krspin@umich.edu>, American Society for Virology (asv@asv.org) <asv@asv.org>, Dalder-Alpher, Erin <edalder-alpher@asmusa.org>, volker.thiel@vetsuisse.unibe.ch <volker.thiel@vetsuisse.unibe.ch>
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University of Texas Medical Branch, Galveston, Texas
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Cc: Spindler, Katherine <krspin@umich.edu>; American Society for Virology (asv@asv.org) <asv@asv.org>; Dalder-Alpher, Erin <edalder-alpher@asmusa.org>; volker.thiel@vetsuisse.unibe.ch <volker.thiel@vetsuisse.unibe.ch>
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School of Veterinary Medicine
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Why pronouns matter https://lgbt.wisc.edu/education/pronouns-matter/

Email: kristen.bernard@wisc.edu
Phone: 608-263-7114
Office room #: 4270C
Lab room #: 4240A

Twitter @UWbernardLab

To: Xie, Xuping[xuxie@UTMB.EDU]; chenxw@wh.iov.cn[chenxw@wh.iov.cn]; Shi, Pei yong[peshi@UTMB.EDU]
From: onmedic[info@onmedic.com]
Sent: Fri 4/23/2021 2:29:32 AM (UTC-05:00)
Subject: Hoping to help

Dear Xuping,
We just read your article published in mBio (http://www.ncbi.nlm.nih.gov/pubmed/31662457), and, first of all, congrats, it's very interesting. We are writing to the email we found in affiliation. Sorry if our English is not perfect, we are data scientists, not grammar experts.
We are contacting you to present our services. We are known for our ehealth products, like websites, big data, machine learning, Gsuite resellers - now called Google Workspace (e.g. automate pdf report creation from google sheets), etc - but today we want to offer you a service to help you in the social media field for researchers, especially Twitter. Lots of scientists have asked us about managing their online profilesWe can help you to improve your social presence. Please reply if you are interested in having hundreds or thousands of followers, and we can discuss by email or teleconference.
Kind regards,
onmedic team

From: Zhengli SHI [onbehalfof@manuscriptcentral.com]
Sent: 1/14/2021 4:29:11 AM
To: Shi, Pei yong [peshi@UTMB.EDU]
CC: editorial@virosin.org;vs@wh.iov.cn
Subject: Invitation for Manuscript Review, Virologica Sinica VS-2021-5454

VS-2021-5454 - "Ozone Water is an Effective Disinfectant for SARS-CoV-2" .

14-Jan-2021

Dear Prof. Shi,

Manuscript ID VS-2021-5454 entitled "Ozone Water is an Effective Disinfectant for SARS-CoV-2" with Dr. Yun Wang as corresponding author has been submitted to Virologica Sinica.

I invite you to review this manuscript. The author list and abstract are appended below, plus more detailed information about Virologica Sinica and its editorial criteria.

To respond automatically, click below:

*** PLEASE NOTE: This is a two-step process. After clicking on the link, you will be directed to a webpage to confirm. ***

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https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fmc03.manuscriptcentral.com%2Fvs%3FURL_MASK%3Df8d3f617d9bb42929dd33e8fb67e52e4&data=04%7C01%7Cpeshi%40UTMB.edu%7Cac70f900a85742d5601608d8b8773cb4%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637462169573017547%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=OJ13ltFdEm%2Bo1VRi6Okl6YWhq1FFWqVwC%2FRNQ9bqpzQ%3D&reserved=0

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I would appreciate receiving your review comment within 14 calendar days of your acceptance.

Once you accept my invitation to review this manuscript, an e-mail will be sent to you (within 10min) about how to access Manuscript Central, our online review system. You will then have access to the manuscript and reviewer instructions in your Reviewer Center.

If you are unable to review at this time, I would appreciate you recommending another expert reviewer.

Thank you for your participation. If you have any questions or concerns, please do not hesitate to contact me, or the VS editorial office at editorial@virosin.org.

Sincerely,

Zhengli SHI
Editor, Virologica Sinica
zhengli.shi@virosin.org

MANUSCRIPT DETAILS

TITLE: Ozone Water is an Effective Disinfectant for SARS-CoV-2

AUTHORS: Hu, Xiao; Chen, Xinwen; Yang, Qi; Li, Pan; Ma, Jun; Guan, Wuxiang; Wang, Yun; Pei, Rongjuan; Chen, Zhen; Su, Zhengyuan; Deng, Fei; Chen, Quanjiao

ABSTRACT: The severe acute respiratory syndrome coronavirus (SARS-CoV-2) can reportedly survive on various materials for days. This property of SARS-CoV-2 probably plays a vital role in the materials-to-human transmission pathway, which accounts for a significant fraction of new infection cases in China

nowadays. Therefore, there is an urgent need to develop safe and effective environmental disinfectants for SARS-CoV-2. Ozone water has been shown to inactivate a broad spectrum of viral pathogens. Therefore, in this study, we aimed to test its effectiveness in inactivating SARS-CoV-2. We showed that ozone water with ozone concentrations greater than 18 mg/L could effectively inactivate SARS-CoV-2, with complete viral inactivation occurring within 1 min. Compared to traditional chemical disinfectants, ozonated water is safe and readily available as a low-cost disinfectant. Therefore, it can be considered for use in the elimination of SARS-CoV-2 contamination in public areas and facilities.

About Virologica Sinica

Virologica Sinica is an academic journal which aims at presenting the cutting-edge research on viruses all over the world. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including the research on animal, plant and microbe viruses. The journal welcomes studies on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related bio-techniques.

Virologica Sinica, the official journal of the Chinese Society for Microbiology, holds an editorial board of experts from a broad range of research fields worldwide, and will serve as a platform for the communication and exchange of academic information and ideas in an international context. The journal is published by Springer-Verlag Press, and abstracted/indexed in: Science Citation Index Expanded (SCIE), Journal Citaton Reports (JCR), PubMed/Medline, Pubmed Central, Scopus, BIOSIS Previews, EMBASE, Google Scholar, and etc.

To be accepted for publication in Virologica Sinica, research articles must satisfy the following criteria:

1. The study presents novel findings and results have not been published elsewhere.
2. Experiments, statistics, and other analyses are performed to a high technical standard and dataset and figures are in good quality.
3. Conclusions are well supported by the data, and significance is well defined.
4. The research meets all the ethics of experimentation and research integrity.
5. If the article is not presented in good English, we will have it polished before the final acceptance.

To find more information about Virologica Sinica, please visit:
https://nam11.safelinks.protection.outlook.com/?url=http%3A%2F%2Fwww.virosin.org%2F&data=04%7C01%7Cpeshi%40UTMB.edu%7Cac70f900a85742d5601608d8b8773cb4%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637462169573017547%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=YxHjMC1MF6ik6ma9iF9XZWutpYonhcfjrtk8lsGThnA%3D&reserved=0
https://nam11.safelinks.protection.outlook.com/?url=http%3A%2F%2Flink.springer.com%2Fjournal%2F12250&data=04%7C01%7Cpeshi%40UTMB.edu%7Cac70f900a85742d5601608d8b8773cb4%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637462169573027542%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=dVqD9EjFn98jWe4uGZTzyWrv5LEpflZYAGhIKukTAxA%3D&reserved=0
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From: Zhengli SHI [onbehalfof@manuscriptcentral.com]
Sent: 1/16/2021 11:22:11 PM
To: Shi, Pei yong [peshi@UTMB.EDU]
CC: vs@wh.iov.cn
Subject: Reminder: Invitation for Manuscript Review, Virologica Sinica

17-Jan-2021

VS-2021-5454 - "Ozone Water is an Effective Disinfectant for SARS-CoV-2" .

Dear Prof. Shi:

Three days ago, an invitation was sent to you to review Manuscript ID VS-2021-5454, entitled "Ozone Water is an Effective Disinfectant for SARS-CoV-2." The author list and abstract are appended below, plus more detailed information about Virologica Sinica and its editorial criteria.

This is a gentle reminder that the link to the invitation is below:

To respond automatically, click below:

*** PLEASE NOTE: This is a two-step process. After clicking on the link, you will be directed to a webpage to confirm. ***

Agreed:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fmc03.manuscriptcentral.com%2Fvs%3FURL_MASK%3Dc7f3ab454ff647cdb413618fad81b1f4&data=04%7C01%7Cpeshi%40UTMB.edu%7C4d3b8209cc584e6bbe8c08d8baa7d853%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637464577358654953%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=faLdYXN%2Fo501tcm8R07G4u%2B8i3UMGoOv2bUl3uX8%2FMU%3D&reserved=0

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If you are unable to review at this time, I would appreciate you recommending another expert reviewer.

Thank you for your participation. If you have any questions or concerns, please do not hesitate to contact me, or the VS editorial office at editorial@virosin.org.

Sincerely,

Zhengli SHI
Editor, Virologica Sinica
zhengli.shi@virosin.org

MANUSCRIPT DETAILS

TITLE: Ozone Water is an Effective Disinfectant for SARS-CoV-2

AUTHORS: Hu, Xiao; Chen, Xinwen; Yang, Qi; Li, Pan; Ma, Jun; Guan, Wuxiang; Wang, Yun; Pei, Rongjuan; Chen, Zhen; Su, Zhengyuan; Deng, Fei; Chen, Quanjiao

ABSTRACT: The severe acute respiratory syndrome coronavirus (SARS-CoV-2) can reportedly survive on various materials for days. This property of SARS-CoV-2 probably plays a vital role in the materials-to-human transmission pathway, which accounts for a significant fraction of new infection cases in China nowadays. Therefore, there is an urgent need to develop safe and effective environmental disinfectants for SARS-CoV-2. Ozone water has been shown to inactivate a broad spectrum of viral pathogens. Therefore, in this study, we aimed to test its effectiveness in inactivating SARS-CoV-2. We showed that ozone water with ozone concentrations greater than 18 mg/L could effectively inactivate SARS-CoV-2, with complete viral inactivation occurring within 1 min. Compared to traditional chemical disinfectants, ozonated water is safe and readily available as a low-cost disinfectant. Therefore, it can be considered for use in the elimination of SARS-CoV-2 contamination in public areas and facilities.

About Virologica Sinica

Virologica Sinica is an academic journal which aims at presenting the cutting-edge research on viruses all over the world. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including the research on animal, plant and microbe viruses. The journal welcomes studies on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related bio-techniques.

Virologica Sinica, the official journal of the Chinese Society for Microbiology, holds an editorial board of experts from a broad range of research fields worldwide, and will serve as a platform for the communication and exchange of academic information and ideas in an international context. The journal is published by Springer-Verlag Press, and abstracted/indexed in: Science Citation Index Expanded (SCIE), Journal Citaton Reports (JCR), PubMed/Medline, Pubmed Central, Scopus, BIOSIS Previews, EMBASE, Google Scholar, and etc.

Please visit the following websites for more information about Virologica Sinica.
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From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]

Location: zoom mtg

Importance: Normal

Subject: US-China dialogue on gene ediing

Start Time: Tue 7/14/2020 8:00:00 PM (UTC-05:00)

End Time: Tue 7/14/2020 10:00:00 PM (UTC-05:00)

Required Attendees: LeDuc, James W.

U.S. China Gene Editing Technologies to Detect and Respond to Viral Pathogens - workshop - July 14 and July 16

Final information for Gene Editing Workshop

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; LeDuc, James W.[jwleduc@UTMB.EDU]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; Sharples, Fran[FSharples@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Sat 7/4/2020 6:27:59 PM (UTC-05:00)
Subject: U.S. China Gene Editing Technologies to Detect and Respond to Viral Pathogens - workshop - July 14 and July 16

Greetings,

I wanted to let you all know that as a follow on to our bio dialogue discussions NASEM is holding a small invitation only virtual workshop on ***Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens***. The virtual workshop will take place over Zoom on the evenings on **Tuesday, July 14 and Thursday, July 16 for U.S. participants (6-8 PM U.S. PT / 9-11 PM U.S. ET on both evenings)** and the mornings of Wednesday July 15 and Friday July 17 for Chinese participants (9-11 AM Beijing time)**.**

The workshop will explore the use of genome editing technologies, such as those based on CRISPR-Cas systems, to understand and combat viral pathogens. Issues to be discussed include the use of genome editing as a research tool to better understand the basic biology of viral infection and interactions with the immune system; the development of rapid CRISPR-based diagnostic systems to detect viral pathogens; and the potential to use genome editing as an innovative anti-viral strategy as well as best practices for biosafety and biosecurity. Diane Griffin and George Gao will co-chair and Nancy Connell is organizing with help from Katie Bowman, Fran Sharples and Hui Sun from CAS. We expect that the workshop will include approximately 6 or 7 invited speakers with about 30 total participants split between the U.S. and China. The preliminary agenda is below. The first day will focus on the development of CRISPR-based diagnostic systems to detect viral pathogens such as SARS-CoV2. The second day will focus on the potential to use genome editing as an innovative anti-viral strategy, as well as best practices for biosafety and biosecurity.

We hope that you can participate in some or all of the workshop. If you plan to participate please RSVP, and we will send the Zoom link to you before the call.

Happy to answer any questions that you have. Hope you have a great July 4th.

PS as we discussed at the end of the 3rd bio dialogue Zoom meeting last month we plan to hold another bio dialogue meeting in August. I will be back in touch to start planning that meeting after the gene editing workshop.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Virtual Workshop on Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens
Agenda

Day 1: **Evening of July 14 in US (Tuesday) and Morning of July 15 in Beijing (Wednesday)**

- Welcome
  - US welcome and focus of the 2 sessions and how they extend the topics of the 3 bio dialogue meetings held in May/June *[5min]* – **Diane Griffin**, NASEM
  - China welcome *[5 min]* – **George Gao**, China CDC

- Opening Presentation: Introduction to how CRISPR-based technologies can be applied to diagnosis and treatment of disease *[10 min]*
  Nancy Connell, Johns Hopkins University

- Detecting Viral Pathogens *[75 min] – 3 presentations x 15 min each followed by panel discussion*
  Session moderator: **David Walt**, Harvard University
  - **Feng Zhang** [invited], Massachusetts Institute of Technology*: Development of CRISPR/Cas-based systems to detect viral pathogens)*
  - **Chunbo Lou** [invited]**,** Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences: *Paired Design of dCas9 as a Systematic Platform for the Detection of Featured Nucleic Acid Sequences in Pathogenic Strains*
  - **Charles Chiu** [invited]*,* University of California San Francisco: *Detection of SARS-CoV-2 using CRISPR/Cas-based systems)*
  - Moderated Discussion *[30 min]*

- Looking ahead to session 2 – **Nancy Connell**, Johns Hopkins University *[5 min]*
- Adjourn until second session

Day 2: **Evening of July 16 in US (Thursday) and Morning of July 17 in Beijing (Friday)**

- Welcome – **Nancy Connell**, Johns Hopkins University [*5min]*

- Responding to viral pathogens [60 min] - *3 presentations x 15 min each followed by panel discussion.*
  Session moderator: **Nancy Connell**, Johns Hopkins University
  - **Deyin Guo** [invited], School of Medicine (Shenzhen), Sun Yat-sen University: *CRISPR-Cas Targeting of Host Genes as an Antiviral Strategy*
  - **Xin Zhao** [invited]**,** Institute of Microbiology, Chinese Academy of Sciences: *Receptor hunting of Enterovirus B by CRISPR screening*
  - **Stanley Qi** [invited, recommended colleague]*,* Stanford University: *Development of CRISPR as an Antiviral Strategy to Combat SARS-CoV-2 and Influenza")*
  - Moderated Discussion *[30 min]*

- Capturing the opportunities through responsible development *[30 min]*
  - **Weiwen Zhang** [invited], Tianjin University: The importance of promoting responsible development around technologies such as gene editing, including following good biosafety/biosecurity practices) [15 min]
  - Discussion among all participants *[20 min]*

- Thanks to all speakers and participants and adjourn virtual workshop

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

To: cb.lou@siat.ac.cn[cb.lou@siat.ac.cn]; zhaoxin@im.ac.cn[zhaoxin@im.ac.cn]; liwei@ioz.ac.cn[liwei@ioz.ac.cn]; wanghaoyi@ioz.ac.cn[wanghaoyi@ioz.ac.cn]; shiyi@im.ac.cn[shiyi@im.ac.cn]; wangj01@hotmail.com[wangj01@hotmail.com]; gaof@im.ac.cn[gaof@im.ac.cn]; guodeyin@mail.sysu.edu.cn[guodeyin@mail.sysu.edu.cn]; Diane Griffin[dgriffi6@jhmi.edu]; Walt, David[dwalt@bwh.harvard.edu]; Zhang_F@mit.edu[Zhang_F@mit.edu]; mlarussa@stanford.edu[mlarussa@stanford.edu]; Wayne Deng[wayne.deng09@gmail.com]; relman@stanford.edu[relman@stanford.edu]; peggy@hbfam.net[peggy@hbfam.net]; harvey.fineberg@moore.org[harvey.fineberg@moore.org]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; LeDuc, James W.[jwleduc@UTMB.EDU]; davidrfranz@gmail.com[davidrfranz@gmail.com]; racharo@wisc.edu[racharo@wisc.edu]; jeanloz@berkeley.edu[jeanloz@berkeley.edu]; kristian@andersen-lab.com[kristian@andersen-lab.com]; trevor@bedford.io[trevor@bedford.io]; ssawyer@colorado.edu[ssawyer@colorado.edu]
Cc: Rusek, Benjamin[BRusek@nas.edu]; Bowman, Katherine[KBowman@nas.edu]; Nancy Connell[NancyConnell@jhu.edu]
From: Sharples, Fran[FSharples@nas.edu]
Sent: Mon 7/13/2020 2:42:31 PM (UTC-05:00)
Subject: Final information for Gene Editing Workshop
Agenda_Virtual Workshop on Gene Editing Technologies to Detect and Respond to Viral Pathogens (2).docx
Participant List_Virtual Workshop on Gene Editing Technologies to Detect and Respond to Viral Pathogens (3).docx

Greetings,

Thank you again for agreeing to participate in the *US-China Virtual Workshop on Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens.* **The final workshop agenda and participant list is attached.** The workshop will take place over Zoom, the Zoom link to connect the day 1 and day 2 sessions are below:

Day 1: The development of CRISPR-based diagnostic systems to detect viral pathogens such as SARS-CoV2.

Evening of July 14 in the U.S. (Tuesday from 6-8PM PT and 9-11PM ET) and Morning of July 15 in China (Wednesday from 9-11AM)

Morning of July 15 in China (Wednesday from 9-11AM) *Evening of July 14 in the U.S. (Tuesday from 6-8PM PT and 9-11PM ET) and*

Zoom Link: https://nasem.zoom.us/j/91842954740?pwd= **552.136**
(Meeting ID: 918 4295 4740 and Password: **552.136**)

Day 2: The potential to use genome editing as an innovative anti-viral strategy, as well as best practices for biosafety and biosecurity.

Evening of July 16 in the U.S. (Thursday from 6-8PM PT and 9-11PM ET) and Morning of July 17 in China (Friday from 9-11AM)

Morning of July 17 in China (Friday from 9-11AM) *and evening of July 16 in the U.S. (Thursday from 6-8PM PT and 9-11PM ET)*

Link: https://nasem.zoom.us/j/93050757697?pwd= **552.136**
(Meeting ID: 930 5075 7697 and Password: **552.136**)

As noted on the agenda, at the end of each session there will be time for Q&A and discussion. All discussions will be off the record and not-for-attribution, and no public written product will be prepared.

Thank you again for your interest in this workshop. Please let us know if you have any questions or concerns, and we look forward to a very interesting and productive two days.

Best regards,

Katie Bowman and Ben Rusek, US National Academies

Fran Sharples, PhD
Board on Life Sciences
National Academy of Sciences
500 Fifth St. NW
Washington, DC 20001
202-334-2187

Virtual Workshop on Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens

AGENDA

Day 1: Evening of July 14 in US (Tuesday from 6-8PM PT and 9-11PM ET) and Morning of July 15 in Beijing (Wednesday from 9-11AM)

Day 2: Evening of July 16 in US (Thursday from 6-8PM PT and 9-11PM ET) and Morning of July 17 in Beijing (Friday from 9-11AM)

Day 1 (July 14 US / July 15 China)

Welcome Remarks
- **Diane Griffin**, U.S. National Academies of Sciences, Engineering, and Medicine *[5 min]*
- **George Gao**, Chinese Center for Disease Control and Prevention *[5 min]*

Opening Presentation
- **Nancy Connell**, Johns Hopkins University: *Introduction to how CRISPR-based technologies can be applied to diagnosis and treatment of disease [10 min]*

Detecting Viral Pathogens
- Session moderator: **David Walt**, Harvard University
- Speakers:
  - **Feng Zhang**, Massachusetts Institute of Technology: *Development of CRISPR/Cas-based systems to detect viral pathogens [15 min]*
  - **Chunbo Lou**, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences and **Jin Wang**, Shenzhen Second People's Hospital, Shenzhen University: *Paired design of dCas9 as a systematic platform for the detection of featured nucleic acid sequences in pathogenic strains [20 min]*
  - **Wayne Xianding Deng**, University of California San Francisco: *Detection of SARS-CoV-2 using CRISPR/Cas-based systems [15 min]*
- Moderated Discussion *[30 min]*

Looking Ahead to Day 2
- **Nancy Connell**, Johns Hopkins University *[5 min]*

Adjourn until Second Session

Day 2 (July 16 US / July 17 China)

Welcome Remarks
- **Nancy Connell**, Johns Hopkins University *[5 min]*

Responding to Viral Pathogens
- Session moderator: **Nancy Connell**, Johns Hopkins University
- Speakers:

- **Deyin Guo**, School of Medicine (Shenzhen), Sun Yat-sen University: *CRISPR-Cas targeting of host genes as an antiviral strategy [15 min]*
- **Xin Zhao**, Institute of Microbiology, Chinese Academy of Sciences: *Receptor hunting of Enterovirus B by CRISPR screening [15 min]*
- **Marie La Russa**, Stanford University: *Development of CRISPR as an antiviral strategy to combat SARS-CoV-2 and influenza [15 min]*

– Moderated Discussion *[30 min]*

Capturing the Opportunities through Responsible Development

– Discussion moderator: **Nancy Connell**, Johns Hopkins University
– Exchange of views and discussion among all participants *[30 min]*

Adjourn Virtual Workshop

Virtual Workshop on Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens: Speakers and Participants

PARTICIPANT LIST

July 14/15 and July 16/17, 2020

Speakers from China

1. **George F. Gao**, Director-General, China Centers for Disease Control
2. **Chunbo Lou**, Principal Investigator, Shenzhen Institutes of Advanced Technology
3. **Xin Zhao**, Associate Research Fellow, Institute of Microbiology, Chinese Academy of Sciences (CAS)
4. **Deyin Guo**, School of Medicine (Shenzhen), Sun Yat-sen University

Speakers from the U.S.

5. **Diane Griffin**, Vice President, U.S. National Academy of Sciences
6. **Nancy Connell,** Senior Scholar, Center for Health Security, Johns Hopkins University
7. **David Walt,** Hansjörg Wyss Professor of Biologically Inspired Engineering and Professor of Pathology, Harvard University; Institute Professor, Howard Hughes Medical Institute
8. **Feng Zhang,** James and Patricia Poitras Professor of Neuroscience and Professor, Brain and Cognitive Sciences and Biological Engineering, Massachusetts Institute of Technology; Investigator, Howard Hughes Medical Institute
9. **Marie La Russa,** Research Associate, Stanford University
10. **Wayne Xianding Deng**, Postdoctoral Fellow, University of California San Francisco

Participants from China

11. **Wei Li**, PI, Deputy Director, State Key Laboratory of Stem Cell and Reproductive Biology, Institute of Zoology, CAS
12. **Haoyi Wang**, PI, Group leader of Genome Engineering Technology, Institute of Zoology, CAS
13. **Yi Shi, PI,** Deputy Director of CAS Key laboratory of Pathogenic Microbiology & Immunology, Institute of Microbiology, CAS
14. **Jin Wang**, Professor, Shenzhen Second People's Hospital, the First Affiliated Hospital of Shenzhen University
15. **Zhengli Shi**, Wuhan Institute of Virology
16. **Zhigao Bu,** Harbin Veterinary Research Institute [invited]
17. **Zhiming Yuan**, Wuhan Institute of Virology [invited]

Participants from the U.S.

18. **David Relman**, [HYPERLINK "https://en.wikipedia.org/wiki/Stanford_University_School_of_Medicine" \o "Stanford University School of Medicine"].
19. **Peggy Hamburg,** Foreign Secretary, U.S. National Academy of Medicine
20. **Harvey Fineberg,** President, Gordon and Betty Moore Foundation
21. **Stanley Perelman**, University of Iowa Health Care
22. **Jim LeDuc**, [HYPERLINK "https://www.utmb.edu/gnl" \t "_blank"], University of Texas Medical Branch
23. **Dave Franz**, U.S. Army Medical Research and Materiel Command, retired
24. **Alta Charo,** University of Wisconsin, Madison

25. **Raymond Jeanloz,** [HYPERLINK "https://en.wikipedia.org/wiki/University_of_California,_Berkeley" \o "University of California, Berkeley"]
26. **Kristian Andersen,** Scripps Research [invited]
27. **Trevor Bedford**, Fred Hutchinson Cancer Research Center [invited]
28. **Sara L. Sawyer,** University of Colorado Boulder [invited]

NAS and CAS staff:

29. **Katie Bowman**, Board on Life Sciences (BLS), U.S. National Academies of Sciences, Engineering, and Medicine (NASEM)
30. **Fran Sharples**, BLS, NASEM
31. **Ben Rusek**, Policy and Global Affairs Division (PGA), NASEM
32. **Hui Sun**, Chinese Academy of Sciences
33. **Micah Lowenthal**, PGA, NASEM
34. **Communications support**, NASEM

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch@bidmc.harvard.edu; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; jmclellan@austin.utexas.edu; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; mehul.s.suthar@emory.edu; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; 'Krammer, Florian' (florian.krammer@mssm.edu); jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Webby, Richard; adolfo.garcia-sastre@mssm.edu; malik@hku.hk; Andrew B. Ward; Ellebedy, Ali; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; David Montefiori, Ph.D.; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Nelson Michael; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Douek, Daniel (NIH/VRC) [E]; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Donis, Ruben (OS/ASPR/BARDA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Sullivan, Nancy (NIH/VRC) [E]; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Alter, Galit; Ho, David D.; Luo, Yang; Wolf, Josh; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Debbie.Bratt@nih.gov; Luis Martinez; Tomer Hertz; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA)

Location: https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 2/12/2021 7:30:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 8:30:00 AM (UTC-06:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch@bidmc.harvard.edu; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; jmclellan@austin.utexas.edu; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; mehul.s.suthar@emory.edu; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; 'Krammer, Florian' (florian.krammer@mssm.edu); jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Webby, Richard; adolfo.garcia-sastre@mssm.edu; malik@hku.hk; Andrew B. Ward; Ellebedy, Ali; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Alter, Galit; Wolf, Josh; Tomer Hertz

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		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal
Start Time: Fri 3/12/2021 1:30:00 PM (UTC)
End Time: Fri 3/12/2021 2:30:00 PM (UTC)
Research Update Template.xlsx

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		B.1.351
		P.1
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	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
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	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
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	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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-	Deposited in BEI, available in 1-2 weeks
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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Start Time: Fri 5/28/2021 12:30:00 PM (UTC)

End Time: Fri 5/28/2021 1:30:00 PM (UTC)

Required Attendees: Graham, Barney (NIH/VRC) [E]; Garcia-Sastre, Adolfo; Menachery, Vineet; Shi, Pei yong; stacey schultz-cherry; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, JoshMaciel, Milton (NIH/NIAID) [E]stevens@anl.gov

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		Description of study
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Other updates	Other	

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Start Time: Fri 6/18/2021 12:30:00 PM (UTC)

End Time: Fri 6/18/2021 1:30:00 PM (UTC)

Required Attendees: Graham, Barney (NIH/VRC) [E]; Garcia-Sastre, Adolfo; Menachery, Vineet; Shi, Pei yong; stacey schultz-cherry; Degrace, Marciela (NIH/NIAID) [E]; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; dbarouch; McDermott, Adrian (NIH/VRC) [E]; Douek, Daniel (NIH/VRC) [E]Vincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]stevens@anl.gov

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		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Start Time: Fri 6/4/2021 12:30:00 PM (UTC)

End Time: Fri 6/4/2021 1:30:00 PM (UTC)

Required Attendees: Wentworth, David E. (CDC/DDID/NCIRD/ID); Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, JoshVincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]stevens@anl.gov; Wentworth, David E. (CDC/DDID/NCIRD/ID)

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis MartinezHo, David D.

Research Update Template.xlsx

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Meeting ID: 160 266 4950
Passcode: **552.136**
One tap mobile
+16692545252,,1602664950#,,,, **552.136** # US (San Jose)

+16468287666,,1602664950#,,,,552.136US (New York)

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
833 568 8864 US Toll-free
Meeting ID: 160 266 4950
Passcode: 552.136
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP
1602664950@sip.zoomgov.com

Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: **552.136**

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 6/25/2021 12:30:00 PM (UTC)
End Time:	Fri 6/25/2021 1:30:00 PM (UTC)
Required Attendees:	Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; McDermott, Adrian (NIH/VRC) [E]Vincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]stevens@anl.gov
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Doria-Rose, Nicole (NIH/NIAID) [E]Ho, David D.

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
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	Plasmids	
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		Description of study
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		Description of study
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BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 6/11/2021 12:30:00 PM (UTC)
End Time:	Fri 6/11/2021 1:30:00 PM (UTC)
Required Attendees:	Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Pei yong. Shi; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer HertzVincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]stevens@anl.gov
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]Ho, David D.

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		Description of study
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Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]

Attendees: cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Gabi Neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; Simon, Viviana; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; kalthoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; Mejias, Asuncion; etmartin@umich.edu; alauring@med.umich.edu; Beaubien, Candice (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason

(CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif; Warner, Blake (NIH/NIDCR) [E]; Joseph, Paule (NIH/NIAAA) [E]; Kim, Sonnie (NIH/NIAID) [E]; otienojr@yahoo.com; Dyall, Julie (NIH/NIAID) [E]

Sent: Tue 2/9/2021 8:13:02 AM (UTC-06:00)

Subject: SARS-CoV-2 Weekly Investigators Meeting

Hi Everyone,

As a reminder, I will be sending out a brief introduction to the following weeks presenter. Please join if you are interested in listening to this week's presentation. *

Also, if you have any interest in presenting, please reach out to me so I can put you on the schedule.

Thanks,
Rebecca

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Importance: Normal
Subject: SARS-CoV-2 Weekly Investigators Meeting
Start Time: Tue 2/9/2021 8:00:00 AM (UTC-06:00)
End Time: Tue 2/9/2021 9:00:00 AM (UTC-06:00)
Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; Weaver, Scott; Plante, Kenneth S.; Weaver, Scott; Plante, Kenneth S.

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Hi Everyone,

We will be incorporating COVID-19 Cohort presentations to our arsenal of talks. As a reminder, the goal for the weekly SARS-CoV-2 Investigators meeting is to provide a platform that is informative and encourages collaboration.

If you would like to present your research, please let me know. *

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 2/23/2021 2:00:00 PM (UTC)
End Time:	Tue 2/23/2021 3:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Wentworth, David E. (CDC/DDID/NCIRD/ID); cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; 'adolfo.garcia-sastre@mssm.edu'; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; stacey schultz-cherry; 'david_topham@urmc.rochester.edu'; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; Menachery, Vineet; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID)

[E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; Plante, Kenneth S.; McDonald, David (NIH/NIAID) [E]; Krafft, Amy (NIH/NIAID) [E]; Duprex, Paul; Graham, Rachel; Ferguson, Stacy (NIH/NIAID) [E]; Davis, Mindy (NIH/NIAID) [E]; Goldstein, Jason (CDC/DDID/NCEZID/DSR); cobeywork@gmail.com; Lockmuller, Jane (NIH/NIAID) [E]; Timothy Burgess; Martin Blaser; Gergen, Peter (NIH/NIAID) [E]; ZHANG, JIAJIA; Thompson, Mark (CDC/DDID/NCIRD/ID); Staat, Mary Allen; Robien, Mark (NIH/NIAID) [E]; Monica McNeal; Siriruk Changrob; Asturias, Edwin; Fulkerson, Patricia (NIH/NIAID) [E]; Halasa, Natasha; Nayak, Seema (NIH/NIAID) [E]; Baqar, Shahida (NIH/NIAID [E]; Rogier van Doorn; Lee, Marina (NIH/NIAID) [E]; Whelan, Sean; Haslam, David; Gordon, Robin (Robin Gordon); Lerner, Andrea (NIH/NIAID) [E]; Alaa Abdel Latif

Importance: Normal

Start Time: Tue 6/15/2021 1:00:00 PM (UTC)

End Time: Tue 6/15/2021 2:00:00 PM (UTC)

Required Attendees: Stevens, Rick L.; Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; marcjohnson@missouri.edu; Stevens, Laura J; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; Mejias, Asuncion; etmartin@umich.edu; alauring@med.umich.edu; McDonald, David (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Sabra Klein; Logue, James; Isabelle.Phan@seattlechildrens.org; Van bakel, Harm; Jennifer Hyde; Thomas Friedrich; Pickett, Thames (NIH/NIAID) [E]; Breen, Joseph (NIH/NIAID) [E]; McKenzie, Pamela; paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); Hoffman, James; WVanVoorhis@medicine.washington.edu; Ghazi Kayali; tenOever, Benjamin; rebecca.dutch@uky.edu; amushegian@gmail.com; viviana.simon; fullerdh@uw.edu; cpage001@umaryland.edu; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; Munster, Vincent (NIH/NIAID) [E]; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. 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mshukla@anl.gov; rscheuermann@jcvi.org; samantha.l.grimes@vanderbilt.edu; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Bratt, Debbie (NIH/NIAID) [C]; Patterson, Jean (NIH/NIAID) [E]; Priya Luthra; Malloy, Allison; ckabengele@rzhrg-mail.org

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If you have any questions, please feel free to reach out.

Stay safe,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 2089
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

Importance:	Normal
Start Time:	Tue 5/25/2021 1:00:00 PM (UTC)
End Time:	Tue 5/25/2021 2:00:00 PM (UTC)
Required Attendees:	Stevens, Rick L.; Jesse ErasmusLampley, Rebecca (NIH/NIAID) [C]; Lockmuller, Jane (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Katzelnick, Leah (NIH/NIAID) [E]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Isabelle.Phan@seattlechildrens.org; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID)

[E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Cammarata, Sue (OS/ASPR/IO) (CTR); Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Eva Harris; Fausto Bustos; Ricotta, Emily (NIH/NIAID) [E]; Coughlan, Lynda

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Start Time: Tue 6/22/2021 1:00:00 PM (UTC)

End Time: Tue 6/22/2021 2:00:00 PM (UTC)

Required Attendees: Jennifer Rebecca German; Stevens, Rick L.; Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy

(NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; ksplante@UTMB.EDU; marcjohnson@missouri.edu; mshukla@anl.gov; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Bratt, Debbie (NIH/NIAID) [C]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; Mejias, Asuncion; etmartin@umich.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Patterson, Jean (NIH/NIAID) [E]; Nelson, Martha (NIH/NIAID) [C]; Coughlan, Lynda; Midgley, Claire (CDC/DDID/NCIRD/DVD); Miller, Benjamin; Priya Luthra; Weaver, Scott; Lowen, Anice; Pickett, Thames (NIH/NIAID) [E]; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela; Rogan Grant; McDonald, David (NIH/NIAID) [E]; alauring@med.umich.edu

Importance:	Normal
Start Time:	Tue 8/17/2021 1:00:00 PM (UTC)
End Time:	Tue 8/17/2021 2:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Mejias, Asuncion; etmartin@umich.edu; mmoonga@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); cmichelo@rzhrg-mail.org; Roberts, Chris (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Priya Luthra; Sabra Klein; Ghazi Kayali; WVanVoorhis@medicine.washington.edu; Cammarata, Sue (OS/ASPR/IO) (CTR); paul-mccray@uiowa.edu; marlene.espinozamoraga@mssm.edu; rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; Malloy, Allison; fullerdh@uw.edu; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina;

David.Renner@pennmedicine.upenn.edu; Fremont, Daved; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Feldstein, Leora (CDC/DDID/NCIRD/DVD); Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Coughlan, Lynda; Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; alauring@med.umich.edu

Importance:	Normal
Start Time:	Tue 6/29/2021 1:00:00 PM (UTC)
End Time:	Tue 6/29/2021 2:00:00 PM (UTC)
Required Attendees:	Lampley, Rebecca (NIH/NIAID) [C]; Richard Webby; Stacey Schultz-Cherry; Aubree Gordon; Florian Krammer; Midgley, Claire (CDC/DDID/NCIRD/DVD); Aneesh Mehta; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); gabriele.neumann; Kanta Subbarao; Matthew Frieman; Ryan A. Langlois; Holbrook, Michael (NIH/NIAID) [C]; Nelson, Martha (NIH/NIAID) [C]; Karla Satchell; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Sarah Cobey; Jennifer Kishimori; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Roder, Allison (NIH/NIAID) [F]; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Huyen.cao@hhs.gov; Mejias, Asuncion; etmartin@umich.edu; Seema Lakdawala; Weaver, Scott; Ghazi Kayali; WVanVoorhis@medicine.washington.edu; Pickett, Thames (NIH/NIAID) [E]; Cammarata, Sue (OS/ASPR/IO) (CTR); rebecca.dutch@uky.edu; Thomas Friedrich; Brooke, Christopher Byron; Jennifer Hyde; andrzejj@anl.gov; fullerdh@uw.edu; cmichelo@rzhrg-mail.org; ckabengele@rzhrg-mail.org; McKenzie, Pamela; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; malik; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Robert E. Schwartz; PETERPALESE; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Wrammert, Jens; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-

mccray@uiowa.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald, Theresa; Nguyen, Phuong; Jesse Erasmus; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Olson, Daniel; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; mmoonga@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Nanishi, Etsuro; Borriello, Francesco; Dowling, David; alauring@med.umich.edu

Importance: Normal

Start Time: Tue 11/2/2021 1:00:00 PM (UTC)

End Time: Tue 11/2/2021 2:00:00 PM (UTC)

Required Attendees: Lampley, Rebecca (NIH/NIAID) [C]; cpage001@umaryland.edu; Hoffman, James; Leo Poon; Hou, Yixuan Jacob; Richard Webby; malik; Ghazi Kayali; Yoshi Kawaoka; R.A.M. Fouchier; yguan@hku.hk; cthio@jhmi.edu; Richard Rothman; Pekosz, Andrew S.; Simons, Mark; Stacey Schultz-Cherry; Orenstein, Walter; Lowen, Anice; Baric, Ralph; 'Perlman, Stanley'; daszak@ecohealthalliance.org; zhu huachen; Aubree Gordon; Robert E. Schwartz; PETERPALESE; Florian Krammer; Esona, Mathew D. (CDC/DDID/NCIRD/DVD); Ben Cowling; larry.anderson@emory.edu; Midgley, Claire (CDC/DDID/NCIRD/DVD); Wrammert, Jens; Aneesh Mehta; antoinette_baric; MASATO HATTA; Hendricks, Tanya J; Brooke, Christopher Byron; pduprex@cvr.pitt.edu; McElroy, Anita Katherine; Prabhudas, Mercy (NIH/NIAID) [E]; Marta Gaglia; Williams, Mark (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hsu, Christopher (CDC/DDID/NCIRD/DVD); Kirking, Hannah L. (CDC/DDID/NCIRD/DVD); Plumb, Ian (CDC/DDID/NCEZID/DFWED); Zendt, Mackenzie (NIH/NIAID) [E]; Logue, James; jheath@systemsbiology.org; Gordon, Jennifer (NIH/NIAID) [E]; Hauguel, Teresa (NIH/NIAID) [E]; gabriele.neumann; Kanta Subbarao; Mathur, Punam (NIH/NIAID) [E]; Jason McLellan; Mark Denison; Matthew Frieman; vimenach@UTMB.EDU; Johnson, Reed (NIH/NIAID) [E]; Hensley, Lisa (NIH/NIAID) [E]; gavin.smith@duke-nus.edu.sg; Stemple, Kimberly (NIH/NIAID) [E]; Sutton, Troy Clavell; marlene.espinozamoraga@mssm.edu; viviana.simon; Van bakel, Harm; McKenzie, Pamela; Deckhut, Alison (NIH/NIAID) [E]; Donald K. Milton; Hensley, Scott; Degrace, Marciela (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Fry, Alicia (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/OD); Hall, Aron (CDC/DDID/NCIRD/DVD); Post, Diane (NIH/NIAID) [E]; Embry, Alan (NIH/NIAID) [E]; Andy Pekosz; Topham, David; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED); zhuhuachen@gmail.com; Bozick, Brooke (NIH/NIAID) [E]; martin.linster@duke-nus.edu.sg; Schmaljohn, Connie (NIH/NIAID) [E]; Wentworth, David E. (CDC/DDID/NCIRD/ID); Charles Russell; Cooper, Michael (NIH/NIAID) [E]; Weiss, Susan; bushman@pennmedicine.upenn.edu; bencowling88@gmail.com; Sun, Weina; Roberts, Chris (NIH/NIAID) [E]; S. Mark Tompkins; Uccellini, Melissa; Paul Thomas; B.H.G. Rockx; Michael Chan; S. Herfst; Lane, Chelsea (NIH/NIAID) [E]; Park, Eun-Chung (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Andrea Sant; Ali Ellebedy; maureen.Mcgargill@stjude.org; Read, Sarah (NIH/NIAID) [E]; Finzi, Diana (NIH/NIAID) [E]; Turpin, Jim (NIH/NIAID) [E]; jae jung (jaeujung@med.usc.edu); SAMANTHA LOEBER; Cherry, Sara; akuki@trudeauinstitute.org; Hui-Ling Yen; Andrew Mesecar; Jonsson, Colleen Beth; Strome, Scott Eric; Fitzpatrick, Elizabeth A; Ryan A. Langlois; Seema Lakdawala; amesecar@gmail.com; Runstadler, Jonathan A.; Pruijssers, Ardina; David.Renner@pennmedicine.upenn.edu; Fremont, Daved; paul-mccray@uiowa.edu; WVanVoorhis@medicine.washington.edu; Piantadosi, Anne L.; Richt, Juergen; Khurana, Surender (FDA/CBER); Neu, Donna; Golding, Hana (FDA/CBER); Gaur, Aditya; hlarman1@jhmi.edu; Mary Rode; 'lsauer2@jhmi.edu'; Kathryn Shaw-Saliba; Andino, Raul; Peter Halfmann; Shiho Chiba; Brown, Liliana (NIH/NIAID) [E]; Miller, Benjamin; lhughes@scripps.edu; asu@scripps.edu; andersen@scripps.edu; mmcgraw@scripps.edu; Shabman, Reed (NIH/NIAID) [E]; Chandramouliswaran, Ishwar (NIH/NIAID) [E]; Evans, Jared D.; Chaves, Francisco; Lambert, Kris; Reilly, Emma C (CVBI); Fitzgerald,

Theresa; Nguyen, Phuong; Jesse Erasmus; fullerdh@uw.edu; Anthony, Simon J.; Katherine Fenstermacher; Zhou, Bin (CDC/DDID/NCIRD/ID); alr2105@cumc.columbia.edu; Dillen, Carly; Sabra Klein; Koelle, Katharina V.; Holbrook, Michael (NIH/NIAID) [C]; Blocker, Wendy (NIH/NIAID) [E]; Suthar, Mehul; Andrea Cox; Cong, Yu (NIH/NIAID) [C]; Jain, Sanjay; Alvaro Ordonez; Joseph Mankowski; Hildebrand, Kristen; rebecca.dutch@uky.edu; Breen, Joseph (NIH/NIAID) [E]; Newman, Lori (NIH/NIAID) [E]; Williams, Carolyn (NIH/NIAID) [E]; Jim Heath; Nelson, Martha (NIH/NIAID) [C]; Jennifer Hyde; Marshall Strome; RDBViral; Marazzi, Ivan; Trovao, Nidia (NIH/FIC) [F]; Ray, Russell Scott; tenOever, Benjamin; Pickett, Thames (NIH/NIAID) [E]; andrzejj@anl.gov; Michael J Gale; Sheahan, Timothy Patrick; Sheldon Shih-han Tai; Jennifer Rebecca German; Paul Jacob Bueno de Mesquita; Oluwasanmi Oladapo Adenaiye; Lafont, Bernard (NIH/NIAID) [E]; Martinez, David Rafael; Karla Satchell; Rutvisuttinunt, Wiriya (NIH/NIAID) [E]; Saydah, Sharon (CDC/DDID/NCIRD/DVD); Olson, Daniel; Sarah Cobey; Qifang Bi; Emma Hodcroft; Becker, Patrice (NIH/NIAID) [E]; Denis Nash; Dutta, Jayeeta; Ramilo, Octavio; Keri Althoff; Jennifer Kishimori; Thomas Friedrich; Biggins, Julia E CTR (USA); Katarina Braun; Gage Moreno; DAVID H O'CONNOR; SHELBY L O'CONNOR; Bruno, Robert (OS/ASPR/BARDA) (CTR); Eisnor, Derek (OS/ASPR/BARDA); Walker, Robert (OS/ASPR/BARDA); ns2@medicine.wisc.edu; jon.temte@fammed.wisc.edu; Katie Mulka; Richard G Wunderink; Alexander Misharin; Rogan Grant; james.mancuso@usuhs.edu; Ghedin, Elodie (NIH/NIAID) [E]; Roder, Allison (NIH/NIAID) [F]; amushegian@gmail.com; Mcgugan, Glen (NIH/NIAID) [E]; abdullah.syed@gladstone.ucsf.edu; Weaver, Scott; ksplante@UTMB.EDU; McDonald, David (NIH/NIAID) [E]; marcjohnson@missouri.edu; mshukla@anl.gov; Stevens, Rick L.; rscheuermann@jcvi.org; Stevens, Laura J; samantha.l.grimes@vanderbilt.edu; jordan.m.anderson-daniels.1@vumc.org; jennifer.gribble@vanderbilt.edu; Priya Luthra; Santosh Dhakal; Mclendon, Molly (OS/ASPR/BARDA); Kevin.Messacar@childrenscolorado.org; pcreish1@jhmi.edu; cmichelo@rzhrg-mail.org; mmoonga@rzhrg-mail.org; ckabengele@rzhrg-mail.org; cchanda@rzhrg-mail.org; smwangelwa@rzhrg-mail.org; chimukumbwa@rzhrg-mail.org; kmumba@rzhrg-mail.org; Lee, John (OS/ASPR/BARDA); Feldstein, Leora (CDC/DDID/NCIRD/DVD); Malloy, Allison; Otieno, James (NIH/FIC) [G]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US); alrouth@utmb.edu; Jones, Jefferson (CDC/DDID/NCIRD/DVD); Patterson, Jean (NIH/NIAID) [E]; Bratt, Debbie (NIH/NIAID) [C]; Coughlan, Lynda; Briggs-Hagen, Melissa (CDC/DDPHSIS/CGH/DGHT); Nanishi, Etsuro; Borriello, Francesco; Dowling, David; Huyen.cao@hhs.gov; Mejias, Asuncion; etmartin@umich.edu; alauring@med.umich.edu

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott

Location: https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 2/12/2021 7:30:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 8:30:00 AM (UTC-06:00)

Required Attendees: dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott

Research Update Template.xlsx

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd=552.136

Meeting ID: 160 266 4950
Passcode: 552.136
One tap mobile
+16692545252,,1602664950#,,,,*552.136 US (San Jose)
+16468287666,,1602664950#,,,,*552.136 US (New York)

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
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Passcode: 552.136
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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: 552.136

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

From: Vincent, Leah (NIH/NIAID) [E][leah.vincent@nih.gov]

Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Ho, David D.

Location: https://nih.zoomgov.com/j/1619922848?pwd=bzUxRXErSFJ6STNSZklpYXU4cWNIdz09

Importance: Normal

Subject: Leah Vincent (NIAID)'s Zoom Meeting

Start Time: Fri 4/30/2021 7:30:00 AM (UTC-05:00)

End Time: Fri 4/30/2021 8:30:00 AM (UTC-05:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Ho, David D.

Good morning,

Please use this link for today's meeting only. Apologies for issues this morning.

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov;

Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Krogan, Nevan; stevens@anl.gov

Leah

Leah Vincent (NIAID) is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://nih.zoomgov.com/j/1619922848?pwd=bzUxRXErSFJ6STNSZklpYXU4cWNIdz09

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Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 161 992 2848
Passcode: 799349

From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]

Location: telecon

Importance: Normal

Subject: Hold for US NAS-CAS dialogue

Start Time: Tue 6/9/2020 8:00:00 PM (UTC-05:00)

End Time: Tue 6/9/2020 10:00:00 PM (UTC-05:00)

Required Attendees: LeDuc, James W.

RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET

Immunity topics plus Gao for 3rd China U.S. Dialogue v2.docx

RE: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET

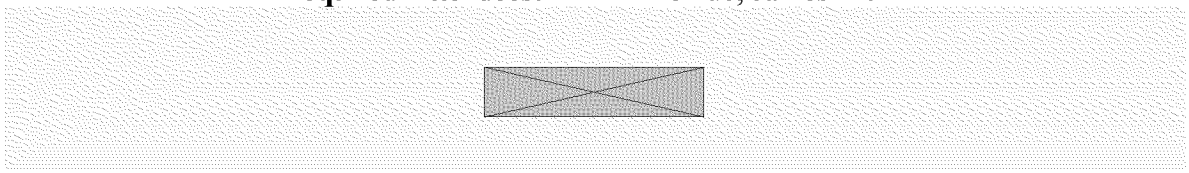
Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection (Le Duc)
  - How is immune response being measured?
  - Was there standardization of testing tools?

Required Attendees: LeDuc, James W.



Meeting link: https://nasem.zoom.us/j/95921551654?pwd= **552.136**

552.136

Meeting Topic: **Third Virtual U.S. China Bio Dialogue Meeting**

Meeting Time: **Jun 9, 2020 9:00 - 11:00 PM Eastern Time**

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Meeting ID: 959 2155 1654

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Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; 'Nancy Connell'[NancyConnell@jhu.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Thur 6/4/2020 12:24:31 PM (UTC-05:00)
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Immunity topics plus Gao for 3rd China U.S. Dialogue v2.docx

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

Questions:

Immune Response and Immunotherapy

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection (Le Duc)
  - How is immune response being measured?
  - Was there standardization of testing tools?
- **What is the overall situation of serologic investigation in the US? (Fineberg)**
- What can be said about the characterization of the (Perlman)
  - Innate immune responses?
  - humoral immune response?
  - cellular immune response?
- What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection? (Hamburg)
  - Is the use of immune plasma effective?
  - Have there been any complications?
- What has been China's experience with human monoclonal antibodies for treatment and prevention? (Hamburg)
  - Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?
- What immunopathologies are evident in the patients with COVID-19? (Relman)
  - Are there any biomarkers in patients who develop systemic inflammation?
  - What is the most effective treatment for patients who develop a cytokine storm?

Immunity

- After recovery, what types of antiviral immune responses are present? (Saif)
  - Do these immune responses protect from re-infection?
  - What is known about the durability of neutralizing antibody and longevity of protective immunity?

  Did recovery from SARS provide any protection from infection with SARS-CoV-2?
- **Progress in the development of vaccine in the U.S. especially mRNA vaccine? (Baric)**

Reactivation or Reinfection of Recovered Patients/Fall resurgence

- Has reactivation of latent virus or re-infection been seen among survivors? (Shi)
- Is reactivation/reinfection a concern with respect to a fall resurgence?
- What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)

- **What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the U.S.? (Fineberg)**

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

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To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; 'Nancy Connell'[NancyConnell@jhu.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 6/8/2020 11:02:00 PM (UTC-05:00)
Subject: RE: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET
Immunity topics plus Gao for 3rd China U.S. Dialogue v2.docx
Chinese Participants-0610.docx

Greetings,

I have attached the list of Chinese participants for the meeting tomorrow (that I just received). There will be fewer people on their side this time (at our request). **Please let me know if you are not planning to participate.**

I have also attached the **American version** of the agenda / list of questions. Recall that their version lists Harvey Fineberg and Ralph Baric as discussants to answer Dr. Gao's questions but not the other names.

FYI the Zoom link for the meeting is:
https://nasem.zoom.us/j/95921551654?pwd= **552.136**

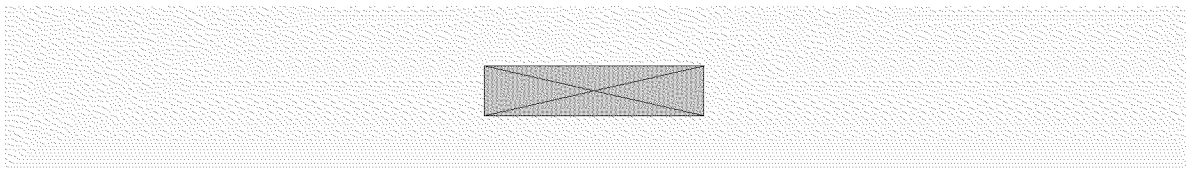
Please let me know if you have any questions or concerns. Thanks again for taking the time to participate in these meetings.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 11:28 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET



Meeting link:
https://nasem.zoom.us/j/95921551654?pwd=552.136
552.136

Meeting Topic: **Third Virtual U.S. China Bio Dialogue Meeting**

Meeting Time: **Jun 9, 2020 9:00 - 11:00 PM Eastern Time**

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For higher quality, dial a number based on your current location.

Dial: US : +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or +1 213 338 8477 or +1 253 215 8782 or 877 853 5257 (Toll Free) or 888 475 4499 (Toll Free)

Meeting ID: 959 2155 1654

Password: **552.136**

International numbers

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103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)

Meeting ID: 959 2155 1654

Password: **552.136**

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-The Zoom Team

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

Questions:

Immune Response and Immunotherapy

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection (Le Duc)
  - How is immune response being measured?
  - Was there standardization of testing tools?
- **What is the overall situation of serologic investigation in the US? (Fineberg)**
- What can be said about the characterization of the (Perlman)
  - Innate immune responses?
  - humoral immune response?
  - cellular immune response?
- What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection? (Hamburg)
  - Is the use of immune plasma effective?
  - Have there been any complications?
- What has been China's experience with human monoclonal antibodies for treatment and prevention? (Hamburg)
  - Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?
- What immunopathologies are evident in the patients with COVID-19? (Relman)
  - Are there any biomarkers in patients who develop systemic inflammation?
  - What is the most effective treatment for patients who develop a cytokine storm?

Immunity

- After recovery, what types of antiviral immune responses are present? (Saif)
  - Do these immune responses protect from re-infection?
    - What is known about the durability of neutralizing antibody and longevity of protective immunity?

  Did recovery from SARS provide any protection from infection with SARS-CoV-2?
- **Progress in the development of vaccine in the U.S. especially mRNA vaccine? (Baric)**

Reactivation or Reinfection of Recovered Patients/Fall resurgence

- Has reactivation of latent virus or re-infection been seen among survivors? (Shi)
- Is reactivation/reinfection a concern with respect to a fall resurgence?
- What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)

- **What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the U.S.? (Fineberg)**

Chinese Participants

Ling Chen: Dr. Ling Chen is a professor and founding director of CAS Guangzhou Institute of Biomedicine and Health, former deputy director of State Key Lab of Respiratory Disease.

Chen Dong: Dr. Chen Dong is Director and a professor of the Institute for Immunology, Dean of the School of Medicine at Tsinghua University, CAS member.

George F. Gao: Dr. George F. Gao is Director-General of CCDC, a professor at the CAS Institute of Microbiology, CAS member.

Qihan Li: Dr. Qihan Li is a professor of the Institute of Medical Biology, Chinese Academy of Medical Science, Peking Union Medical College. His research focuses on viral vaccine and viral immunology.

Wenjie Tan: Dr. Wenjie Tan is Chief and a professor of the Biotech Center for Viral Disease Emergency, National Institute for Viral Disease Control and Prevention, CCDC.

Jianqing Xu: Dr. Jianqing Xu is a professor of the Institutes of Biomedical Sciences, Fudan University.

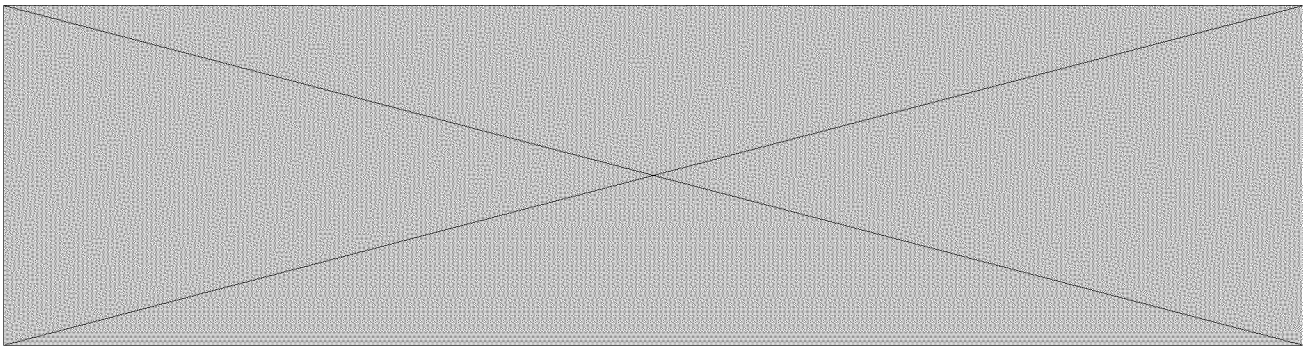
Zhiming Yuan: Dr. Zhiming Yuan is a professor of CAS Wuhan Institute of Virology, Director of Wuhan P4 lab.

To: zengli Shi[zlshi@wh.iov.cn]; Yuan Zhiming[yzm@wh.iov.cn]; Shi, Pei yong[peshi@UTMB.EDU]
From: jwleduc@UTMB.EDU[jwleduc@UTMB.EDU]
Sent: Fri 7/24/2020 8:22:39 PM (UTC-05:00)
Subject: Fwd: Weekly Roundup of AJTMH COVID-19 Articles, 7/24

You May find the first two papers of special interest.
Best wishes. Jim
Sent from my iPhone

Begin forwarded message:

From: ASTMH <info@astmh.org>
Date: July 24, 2020 at 4:04:55 PM CDT
To: "LeDuc, James W." <jwleduc@UTMB.EDU>
Subject: Weekly Roundup of AJTMH COVID-19 Articles, 7/24
Reply-To: info@astmh.org



Weekly Roundup of COVID-19 Articles

Journal Editor-in-Chief Philip Rosenthal, Managing Editor Cathi Siegel, and Editorial Assistant Alison Jaeb are giving high priority to all COVID-19 manuscripts. Accepted manuscripts are posted to the Journal website almost immediately and are open to all. To keep you apprised of the latest research, we are sending a weekly roundup of the newly published articles on Friday.

We extend our deep thanks to the *Journal*'s Editors and staff who are working together to review and publish all accepted articles as quickly as possible.

► **Keep Politics out of Funding Decisions for Medical Research and Public Health**

Philip J. Rosenthal, Daniel G. Bausch, Karen A. Goraleski, David R. Hill, Julie A. Jacobson, Chandy C. John and Joel G. Breman

► **The Origin of COVID-19 and Why It Matters**

David M. Morens, Joel G. Breman, Charles H. Calisher, Peter C. Doherty, Beatrice H. Hahn, Gerald T. Keusch, Laura D. Kramer, James W. LeDuc, Thomas P. Monath and Jeffery K. Taubenberger

► **More Studies are Needed on the Link between Metformin and Decreased Mortality in Diabetic COVID-19 Patients**

Marinos Fysekidis, Régis Cohen and Abdallah Al-Salameh

► **Artemisia Spp. Derivatives for COVID-19 Treatment: Anecdotal Use, Political Hype, Treatment Potential, Challenges, and Road Map to Randomized Clinical Trials**

Paulin M. Kapepula, Jimmy K. Kabengele, Micheline Kingombe, Françoise Van Bambeke, Paul M. Tulkens, Antoine Sadiki Kishabongo, Eric Decloedt, Adam Zumla, Simon Tiberi, Fatima Suleman, Léon Tshilolo, Jean-Jacques Muyembe-TamFum, Alimuddin Zumla and Jean B. Nachega

► **Case Report: Pneumothorax and Pneumomediastinum as Uncommon Complications of COVID-19 Pneumonia—Literature Review**

Alvaro Quincho-Lopez, Dania L. Quincho-Lopez and Fernando D. Hurtado-Medina

► **Predicting the Impact of COVID-19 and the Potential Impact of the Public Health Response on Disease Burden in Uganda**

David Bell, Kristian Schultz Hansen, Agnes N. Kiragga, Andrew Kambugu, John Kissa and Anthony K. Mbonye

► **Incident SARS-CoV-2 Infection and a Shared Latrine**

Oscar H. Del Brutto, Aldo F. Costa and Héctor H. García

► **A University-Wide Preparedness Effort in the Alert Phase of COVID-19 Incorporating Community Mental Health and Task-Shifting Strategies: Experience from a Bornean Institute of Higher Learning**

Mohamad Hafiz Mukhsam, Mohammad Saffree Jeffree, Nicholas Tze Ping Pang, Syed Sharizman Syed Abdul Rahim, Azizan Omar, Muhammad Syafiq Abdullah, Khamisah Awang Lukman, Nelbon Giloi, Loganathan Salvaraji, Mohd Rahimie Abd Karim, Sahipudin Saupin, Yeap Boon Tat, Mohd Firdaus Mohd Hayati, Mohd Yusof Ibrahim, Assikin Muhamad and Syaza Putri Zainudin

All COVID-19 articles are being made freely available on the *Journal* website. Click here for the most up-to-date list of what's been published.

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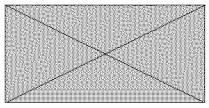

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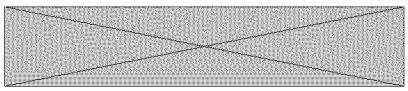

From: Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Location: GoToMeeting
Importance: Normal
Subject: Canceled: A38 Task Order Bi-weekly Call
Start Time: Fri 6/18/2021 9:30:00 AM (UTC-05:00)
End Time: Fri 6/18/2021 11:00:00 AM (UTC-05:00)
Required Attendees: Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]
Optional Attendees: Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Taylor, Ebony (NIH/NIAID) [E]

****UPDATE: Canceling our bi-weekly check-in tomorrow due to Juneteenth holiday.**
Chelsea

Dear A38 Task Order Team,

Please find below the GoToMeeting information for the biweekly A38 task order teleconferences. Please forward the meeting to those on your team that you wish to attend (should they not be on this meeting invite).

Best,
Erik & Chelsea

Join ZoomGov Meeting
https://www.zoomgov.com/j/1618871310?pwd= **552.136**

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Meeting ID: 161 887 1310
Password: **552.136**

From:	Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]
Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]; Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Taylor, Ebony (NIH/NIAID) [E]
Location:	GoToMeeting
Importance:	Normal
Subject:	A38 Task Order Bi-weekly Call
Start Time:	Fri 6/18/2021 9:30:00 AM (UTC-05:00)
End Time:	Fri 6/18/2021 11:00:00 AM (UTC-05:00)
Required Attendees:	Julie Harvey; Bowen, Richard; Chandra Caldwell; Victoria Moore; Baric, Ralph; Taylor Bray, Christy J.; Viner, Rebekah L.; Beasley, David W.; Devin Hansen; Jennipher Hulse; bart.tarbet; Katie Dana; Adams, Miranda (NIH/NIAID) [E]; Pickett, Thames (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; antoinette_baric; Liz.grinstead@colostate.edu; Graham, Rachel; Menachery, Vineet; Brett Hurst; LeGros, Erika; Schilling, Beth A.; Tseng, Chien-Te K.; McNees, Andrew G.; Florence, Clint (NIH/NIAID) [E]; Bryan, Jonathan (NIH/NIAID) [E]; Jackson, Charles (NIH/NIAID) [E]; Zhongde Wang; Lampley, Rebecca (NIH/NIAID) [C]; Massey, Christopher; Davis, Mindy (NIH/NIAID) [E]
Optional Attendees:	Richard Bowen; Bouvier, Nicole; Eakin, Ann (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Hewitt, Judith (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Young, Jennifer (AE); Vily, Aytaj (NIH/NIAID) [E]; Palin, Amy (NIH/NIAID) [E]; Sciotti, Rick (NIH/NIAID) [E]; Venkatraman Siddharthan; Taylor, Ebony (NIH/NIAID) [E]

To: Jennifer Rebecca German[jgerman@umd.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Weaver, Scott[sweaver@UTMB.EDU]; Lowen, Anice[anice.lowen@emory.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; Jennifer Hyde[jlhyde4@uw.edu]; fullerdh@uw.edu[fullerdh@uw.edu]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; Rogan Grant[rogangrant2022@u.northwestern.edu]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; Stevens, Rick L.[stevens@anl.gov]; alauring@med.umich.edu[alauring@med.umich.edu]; Wrammert, Jens[jwramme@emory.edu]; Aubree Gordon[gordonal@umich.edu]; Sasha W Tilles[swtilles@uw.edu]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Ghazi Kayali[ghazi@human-link.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; Seema Lakdawala[seemal@pitt.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Piantadosi, Anne

L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Karla Satchell[k-satchell@northwestern.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]; Mejias, Asuncion[Asuncion.Mejias@nationwidechildrens.org]; etmartin@umich.edu[etmartin@umich.edu]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]

Cc: Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Graham, Rachel[rlgraham@ad.unc.edu]; cobeywork@gmail.com[cobeywork@gmail.com]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Haslam, David[David.Haslam@cchmc.org]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan,

Sean[spjwhelan@wustl.edu]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Alaa Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]; Luke, Catherine (NIH/NIAID) [E][catherine.luke@nih.gov]; Cassetti, Cristina (NIH/NIAID) [E][ccassetti@niaid.nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Mon 6/21/2021 10:12:43 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - June 22nd

Good evening!

Thank you Dr. Krammer and those who attended last week's presentation titled "**Antibody responses to SARS-CoV-2 vaccination**". This week we have Dr. Sara Cherry who will be speak on "**SARS-CoV-2 and antiviral therapeutics**".

See all of your names in the morning!

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

To: Seema Lakdawala[seemal@pitt.edu]; Eisnor, Derek (OS/ASPR/BARDA)[Derek.Eisnor@hhs.gov]; Weaver, Scott[sweaver@UTMB.EDU]; Isabelle.Phan@seattlechildrens.org[Isabelle.Phan@seattlechildrens.org]; Ghazi Kayali[ghazi@human-link.org]; Karla Satchell[k-satchell@northwestern.edu]; WVanVoorhis@medicine.washington.edu[WVanVoorhis@medicine.washington.edu]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; Cammarata, Sue (OS/ASPR/IO) (CTR)[Sue.Cammarata@hhs.gov]; rebecca.dutch@uky.edu[rebecca.dutch@uky.edu]; Thomas Friedrich[tfriedri@wisc.edu]; Brooke, Christopher Byron[cbrooke@illinois.edu]; Jennifer Hyde[jlhyde4@uw.edu]; andrzejj@anl.gov[andrzejj@anl.gov]; fullerdh@uw.edu[fullerdh@uw.edu]; cmichelo@rzhrg-mail.org[cmichelo@rzhrg-mail.org]; ckabengele@rzhrg-mail.org[ckabengele@rzhrg-mail.org]; McKenzie, Pamela[Pamela.McKenzie@STJUDE.ORG]; cpage001@umaryland.edu[cpage001@umaryland.edu]; Hoffman, James[James.Hoffman@STJUDE.ORG]; Leo Poon[llmpoon@hku.hk]; Hou, Yixuan Jacob[y.jacob.hou@unc.edu]; Richard Webby[richard.webby@stjude.org]; malik[malik@hku.hk]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; yguan@hku.hk[yguan@hku.hk]; cthio@jhmi.edu[cthio@jhmi.edu]; 'adolfo.garcia-sastre@mssm.edu'['adolfo.garcia-sastre@mssm.edu']; Richard Rothman[rrothma1@jhmi.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Simons, Mark[mark.simons@usuhs.edu]; stacey schultz-cherry[stacey.schultz-cherry@stjude.org]; 'david_topham@urmc.rochester.edu'['david_topham@urmc.rochester.edu']; Orenstein, Walter[worenst@emory.edu]; Lowen, Anice[anice.lowen@emory.edu]; Baric, Ralph[rbaric@email.unc.edu]; 'Perlman, Stanley'[stanley-perlman@uiowa.edu]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; zhu huachen[zhuhch@hku.hk]; Aubree Gordon[gordonal@umich.edu]; Robert E. Schwartz[res2025@med.cornell.edu]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; PETERPALESE[peter.palese@mssm.edu]; Florian Krammer[florian.krammer@mssm.edu]; Esona, Mathew D. (CDC/DDID/NCIRD/DVD)[mdi4@CDC.GOV]; Ben Cowling[bcowling@hku.hk]; larry.anderson@emory.edu[larry.anderson@emory.edu]; Midgley, Claire (CDC/DDID/NCIRD/DVD)[ydk5@cdc.gov]; Wrammert, Jens[jwramme@emory.edu]; Aneesh Mehta[aneesh.mehta@emory.edu]; antoinette_baric[antoinette_baric@med.unc.edu]; MASATO HATTA[masato.hatta@wisc.edu]; Hendricks, Tanya J[thendr19@uthsc.edu]; pduprex@cvr.pitt.edu[pduprex@cvr.pitt.edu]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prabhudas, Mercy (NIH/NIAID) [E][mprabhudas@niaid.nih.gov]; Marta Gaglia[Marta.Gaglia@tufts.edu]; Williams, Mark (NIH/NIAID) [E][mark.williams4@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; Hsu, Christopher (CDC/DDID/NCIRD/DVD)[ydh2@cdc.gov]; Kirking, Hannah L. (CDC/DDID/NCIRD/DVD)[hrj7@cdc.gov]; Plumb, Ian (CDC/DDID/NCIRD/DVD)[ydk9@cdc.gov]; Zendt, Mackenzie (NIH/NIAID) [E][mackenzie.zendt@nih.gov]; Logue, James[James.Logue@som.umaryland.edu]; jheath@systemsbiology.org[jheath@systemsbiology.org]; Gordon, Jennifer (NIH/NIAID) [E][jennifer.gordon2@nih.gov]; Hauguel, Teresa (NIH/NIAID) [E][teresa.hauguel@nih.gov]; Gabi Neumann[gabriele.neumann@wisc.edu]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Mathur, Punam (NIH/NIAID) [E][mathurpu@niaid.nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Mark Denison[mark.denison@vumc.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Johnson, Reed (NIH/NIAID) [E][johnsonreed@niaid.nih.gov]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; gavin.smith@duke-nus.edu.sg[gavin.smith@duke-nus.edu.sg]; Stemple, Kimberly (NIH/NIAID) [E][kstemple@niaid.nih.gov]; Sutton, Troy Clavell[tcs38@psu.edu]; marlene.espinozamoraga@mssm.edu[marlene.espinozamoraga@mssm.edu]; Simon, Viviana[viviana.simon@MSSM.EDU]; Van bakel, Harm[harm.vanbakel@mssm.edu]; Deckhut, Alison (NIH/NIAID) [E][augustine@niaid.nih.gov]; Donald K. Milton[dmilton@umd.edu]; Hensley, Scott[hensley@pennmedicine.upenn.edu]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Fry, Alicia (CDC/DDID/NCIRD/ID)[agf1@CDC.GOV]; Pallansch, Mark A. (CDC/DDID/NCIRD/OD)[map1@CDC.GOV]; Hall, Aron (CDC/DDID/NCIRD/DVD)[esg3@CDC.GOV]; Post, Diane (NIH/NIAID) [E][postd@niaid.nih.gov]; Embry, Alan (NIH/NIAID) [E][embrya@niaid.nih.gov]; Andy Pekosz[apekosz1@jhu.edu]; Topham, David[David_Topham@URMC.Rochester.edu]; Gerber, Susan I. (CDC/DDID/NCEZID/DFWED)[bhx1@cdc.gov]; zhuhuachen@gmail.com[zhuhuachen@gmail.com]; Bozick, Brooke (NIH/NIAID) [E][brooke.bozick@nih.gov]; martin.linster@duke-nus.edu.sg[martin.linster@duke-nus.edu.sg]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Wentworth, David E. (CDC/DDID/NCIRD/ID)[gll9@cdc.gov]; Charles Russell[charles.russell@stjude.org]; Cooper, Michael (NIH/NIAID) [E][michael.cooper3@nih.gov]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; bushman@pennmedicine.upenn.edu[bushman@pennmedicine.upenn.edu]; bencowling88@gmail.com[bencowling88@gmail.com]; Sun, Weina[weina.sun@mssm.edu]; Roberts, Chris (NIH/NIAID) [E][paul.roberts@nih.gov]; S. Mark Tompkins[smt@uga.edu]; Uccellini, Melissa[melissa.uccellini@mssm.edu]; Paul Thomas[paul.thomas@stjude.org]; B.H.G. Rockx[b.rockx@erasmusmc.nl]; Michael Chan[mchan@hku.hk]; S. Herfst[s.herfst@erasmusmc.nl]; Lane, Chelsea (NIH/NIAID) [E][mary.lane@nih.gov]; Park, Eun-Chung (NIH/NIAID) [E][epark@niaid.nih.gov]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Andrea Sant[andrea_sant@urmc.rochester.edu]; Ali Ellebedy[ellebedy@wustl.edu]; maureen.Mcgargill@stjude.org[maureen.Mcgargill@stjude.org]; Read, Sarah (NIH/NIAID) [E][readsa@niaid.nih.gov]; Finzi, Diana (NIH/NIAID) [E][dfinzi@niaid.nih.gov]; Turpin, Jim (NIH/NIAID) [E][JTurpin@niaid.nih.gov]; jae jung (jaeujung@med.usc.edu)[jaeujung@med.usc.edu]; SAMANTHA LOEBER[sloeber@wisc.edu]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; akuki@trudeauinstitute.org[akuki@trudeauinstitute.org]; Hui-Ling Yen[hyen@hku.hk]; Andrew Mesecar[amesecar@purdue.edu]; Jonsson, Colleen Beth[cjonsson@uthsc.edu]; Strome, Scott Eric[sstrome@uthsc.edu]; Fitzpatrick, Elizabeth A[efitzpat@uthsc.edu]; Ryan A. Langlois[langlois@umn.edu]; amesecar@gmail.com[amesecar@gmail.com]; Runstadler, Jonathan A.[Jonathan.Runstadler@tufts.edu]; Pruijssers, Ardina[ardina.pruijssers@vumc.org]; David.Renner@pennmedicine.upenn.edu[David.Renner@pennmedicine.upenn.edu]; Fremont, Daved[fremont@wustl.edu]; paul-mccray@uiowa.edu[paul-mccray@uiowa.edu]; Piantadosi, Anne L.[anne.piantadosi@emory.edu]; Richt, Juergen[jricht@vet.k-state.edu]; Khurana, Surender (FDA/CBER)[Surender.Khurana@fda.hhs.gov]; Neu, Donna[Donna_Neu@URMC.Rochester.edu]; Golding, Hana (FDA/CBER)[Hana.Golding@fda.hhs.gov]; Gaur, Aditya[Aditya.Gaur@STJUDE.ORG]; hlarman1@jhmi.edu[hlarman1@jhmi.edu]; Mary Rode[mrode4@jhmi.edu]; 'lsauer2@jhmi.edu'[lsauer2@jhmi.edu]; Kathryn Shaw-Saliba[kshaw15@jhu.edu]; Andino, Raul[Raul.Andino@ucsf.edu]; Peter Halfmann[peter.halfmann@wisc.edu]; Shiho

Chiba[shiho.chiba@wisc.edu]; Brown, Liliana (NIH/NIAID) [E][liliana.brown@nih.gov]; Miller, Benjamin[Benjamin_Miller@URMC.Rochester.edu]; lhughes@scripps.edu[lhughes@scripps.edu]; asu@scripps.edu[asu@scripps.edu]; andersen@scripps.edu[andersen@scripps.edu]; mmcgraw@scripps.edu[mmcgraw@scripps.edu]; Shabman, Reed (NIH/NIAID) [E][reed.shabman@nih.gov]; Chandramouliswaran, Ishwar (NIH/NIAID) [E][ishwar.chandramouliswaran@nih.gov]; Evans, Jared D.[Jared.Evans@jhuapl.edu]; Chaves, Francisco[Francisco_Chaves@URMC.Rochester.edu]; Lambert, Kris[Kris_Lambert@URMC.Rochester.edu]; Reilly, Emma C (CVBI)[Emma_Reilly@URMC.Rochester.edu]; Fitzgerald, Theresa[Theresa_Fitzgerald@URMC.Rochester.edu]; Nguyen, Phuong[Phuong_Nguyen@URMC.Rochester.edu]; Jesse Erasmus[jerasmus@uw.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; Katherine Fenstermacher[kfenste1@jhu.edu]; Zhou, Bin (CDC/DDID/NCIRD/ID)[nmb7@cdc.gov]; alr2105@cumc.columbia.edu[alr2105@cumc.columbia.edu]; Dillen, Carly[CDillen@som.umaryland.edu]; Sabra Klein[sklein2@JHU.EDU]; Koelle, Katharina V.[katia.koelle@emory.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Blocker, Wendy (NIH/NIAID) [E][wendy.blocker@nih.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; Andrea Cox[acox@JHMI.EDU]; Cong, Yu (NIH/NIAID) [C][yu.cong@nih.gov]; Jain, Sanjay[sjain5@jhmi.edu]; Alvaro Ordonez[aordone2@jhmi.edu]; Joseph Mankowski[jmankows@jhmi.edu]; Hildebrand, Kristen[Kristen.Hildebrand@STJUDE.ORG]; Breen, Joseph (NIH/NIAID) [E][jbreen@niaid.nih.gov]; Newman, Lori (NIH/NIAID) [E][lori.newman@nih.gov]; Williams, Carolyn (NIH/NIAID) [E][cwilliams@niaid.nih.gov]; Jim Heath[jim.heath@isbscience.org]; Nelson, Martha (NIH/NIAID) [C][nelsonma@mail.nih.gov]; Marshall Strome[stromemhnsg@gmail.com]; RDBViral[NIAIDRDBViral@mail.nih.gov]; Marazzi, Ivan[ivan.marazzi@mssm.edu]; Trovao, Nidia (NIH/FIC) [F][nidia.trovao@nih.gov]; Ray, Russell Scott[Russell.Ray@bcm.edu]; tenOever, Benjamin[benjamin.tenoever@mssm.edu]; Michael J Gale[mgale@uw.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Sheldon Shih-han Tai[stai1@umd.edu]; Jennifer Rebecca German[jgerman@umd.edu]; Paul Jacob Bueno de Mesquita[jbueno@umd.edu]; Oluwasanmi Oladapo Adenaiye[adenaiye@umd.edu]; Lafont, Bernard (NIH/NIAID) [E][blafont@niaid.nih.gov]; Martinez, David Rafael[davidmar@email.unc.edu]; Rutvisuttinunt, Wiriya (NIH/NIAID) [E][wiriya.rutvisuttinunt@nih.gov]; Saydah, Sharon (CDC/DDID/NCIRD/DVD)[zle0@CDC.GOV]; Olson, Daniel[Daniel.Olson@childrenscolorado.org]; Sarah Cobey[cobey@uchicago.edu]; Qifang Bi[qbi@uchicago.edu]; Emma Hodcroft[emmahodcroft@gmail.com]; Becker, Patrice (NIH/NIAID) [E][patrice.becker@nih.gov]; Denis Nash[Denis.Nash@sph.cuny.edu]; Dutta, Jayeeta[jayeeta.dutta@mssm.edu]; Ramilo, Octavio[Octavio.Ramilo@nationwidechildrens.org]; kalthoff[kalthoff@jhu.edu]; Jennifer Kishimori[Jennifer.M.Kishimori.mil@mail.mil]; Biggins, Julia E CTR (USA)[julia.e.biggins.ctr@mail.mil]; Katarina Braun[kmbraun2@wisc.edu]; Gage Moreno[gkmoreno@wisc.edu]; DAVID H O'CONNOR[dhoconno@wisc.edu]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Bruno, Robert (OS/ASPR/BARDA) (CTR)[Robert.Bruno@hhs.gov]; Walker, Robert (OS/ASPR/BARDA)[Robert.Walker@hhs.gov]; ns2@medicine.wisc.edu[ns2@medicine.wisc.edu]; jon.temte@fammed.wisc.edu[jon.temte@fammed.wisc.edu]; Katie Mulka[kmulka1@jhmi.edu]; Richard G Wunderink[r-wunderink@northwestern.edu]; Alexander Misharin[a-misharin@northwestern.edu]; Rogan Grant[rogangrant2022@u.northwestern.edu]; james.mancuso@usuhs.edu[james.mancuso@usuhs.edu]; Ghedin, Elodie (NIH/NIAID) [E][elodie.ghedin@nih.gov]; Roder, Allison (NIH/NIAID) [E][allison.roder@nih.gov]; amushegian@gmail.com[amushegian@gmail.com]; Mcgugan, Glen (NIH/NIAID) [E][gmcgugan@niaid.nih.gov]; abdullah.syed@gladstone.ucsf.edu[abdullah.syed@gladstone.ucsf.edu]; Plante, Kenneth S.[ksplante@UTMB.EDU]; McDonald, David (NIH/NIAID) [E][david.mcdonald@nih.gov]; marcjohnson@missouri.edu[marcjohnson@missouri.edu]; mshukla@anl.gov[mshukla@anl.gov]; Stevens, Rick L.[stevens@anl.gov]; rscheuermann@jcvi.org[rscheuermann@jcvi.org]; Stevens, Laura J[laura.j.stevens@vumc.org]; samantha.l.grimes@vanderbilt.edu[samantha.l.grimes@vanderbilt.edu]; jordan.m.anderson-daniels.1@vumc.org[jordan.m.anderson-daniels.1@vumc.org]; jennifer.gribble@vanderbilt.edu[jennifer.gribble@vanderbilt.edu]; Priya Luthra[pluthra@trudeauinstitute.org]; Santosh Dhakal[sdhakal3@jhmi.edu]; Mclendon, Molly (OS/ASPR/BARDA)[Molly.Mclendon@hhs.gov]; Kevin.Messacar@childrenscolorado.org[Kevin.Messacar@childrenscolorado.org]; pcreish1@jhmi.edu[pcreish1@jhmi.edu]; mmoonga@rzhrg-mail.org[mmoonga@rzhrg-mail.org]; cchanda@rzhrg-mail.org[cchanda@rzhrg-mail.org]; smwangelwa@rzhrg-mail.org[smwangelwa@rzhrg-mail.org]; chimukumbwa@rzhrg-mail.org[chimukumbwa@rzhrg-mail.org]; kmumba@rzhrg-mail.org[kmumba@rzhrg-mail.org]; Lee, John (OS/ASPR/BARDA)[John.Lee@hhs.gov]; Feldstein, Leora (CDC/DDID/NCIRD/DVD)[nqw5@cdc.gov]; Malloy, Allison[allison.malloy@usuhs.edu]; Otieno, James (NIH/FIC) [G][james.otieno@nih.gov]; Bishop-Lilly, Kimberly A CIV USN NAVMEDRSCHCEN SVS MD (US)[kimberly.a.bishop-lilly.civ@mail.mil]; Routh, Andrew L.[alrouth@UTMB.EDU]; Jones, Jefferson (CDC/DDID/NCIRD/DVD)[ioe8@cdc.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Bratt, Debbie (NIH/NIAID) [C][debbie.bratt@nih.gov]; Coughlan, Lynda[LCoughlan@som.umaryland.edu]; Briggs-Hagen, Melissa (CDC/DDID/NCIRD/DVD)[VKA5@cdc.gov]; Nanishi, Etsuro[Etsuro.Nanishi@childrens.harvard.edu]; Borriello, Francesco[Francesco.Borriello@childrens.harvard.edu]; Dowling, David[David.Dowling@childrens.harvard.edu]; alauring@med.umich.edu[alauring@med.umich.edu]; Sasha W Tilles[swtilles@uw.edu]; jwasserh@uw.edu[jwasserh@uw.edu]; Huyen.cao@hhs.gov[Huyen.cao@hhs.gov]; Mejias, Asuncion[Asuncion.Mejias@nationwidechildrens.org]; etmartin@umich.edu[etmartin@umich.edu]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; Renee Ireton[rireton@uw.edu]; lwhitmo@uw.edu[lwhitmo@uw.edu]

Cc: Graham, Rachel[rlgraham@ad.unc.edu]; Lerner, Andrea (NIH/NIAID) [E][andrea.lerner@nih.gov]; Haslam, David[David.Haslam@cchmc.org]; Martin Blaser[martin.blaser@cabm.rutgers.edu]; Krafft, Amy (NIH/NIAID) [E][kraffta@niaid.nih.gov]; Duprex, Paul[pduprex@pitt.edu]; Ferguson, Stacy (NIH/NIAID) [E][fergusonst@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Goldstein, Jason (CDC/DDID/NCEZID/DSR)[fex0@CDC.GOV]; cobeywork@gmail.com[cobeywork@gmail.com]; Lockmuller, Jane (NIH/NIAID) [E][lockj@niaid.nih.gov]; Timothy Burgess[timothy.burgess@usuhs.edu]; Gergen, Peter (NIH/NIAID) [E][pgergen@niaid.nih.gov]; ZHANG, JIAJIA[JZHANG@mailbox.sc.edu]; Thompson, Mark (CDC/DDID/NCIRD/ID)[isq8@cdc.gov]; Staat, Mary Allen[Mary.Staat@cchmc.org]; Robien, Mark (NIH/NIAID) [E][mark.robien@nih.gov]; Monica McNeal[monica.mcneal@cchmc.org]; Siriruk Changrob[siriruk@uchicago.edu]; Asturias, Edwin[Edwin.Asturias@childrenscolorado.org]; Fulkerson, Patricia (NIH/NIAID) [E][patricia.fulkerson@nih.gov]; Halasa, Natasha[natasha.halasa@vumc.org]; Nayak, Seema (NIH/NIAID) [E][seema.nayak@nih.gov]; Baqar, Shahida (NIH/NIAID [E][shahida.baqar@nih.gov]; Rogier van Doorn[rvandoorn@oucru.org]; Lee, Marina (NIH/NIAID) [E][marina.lee@nih.gov]; Whelan, Sean[spjwhelan@wustl.edu]; Gordon, Robin (Robin Gordon)[Robin.Gordon@cchmc.org]; Alaa

Abdel Latif[aabdellatif@scripps.edu]; kga1978@gmail.com[kga1978@gmail.com]; Warner, Blake (NIH/NIDCR) [E][blake.warner@nih.gov]; Joseph, Paule (NIH/NIAAA) [E][paule.joseph@nih.gov]; Kim, Sonnie (NIH/NIAID) [E][sonnie.kim@nih.gov]; otienojr@yahoo.com[otienojr@yahoo.com]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]; Aleta Elliott[aletae@uw.edu]; Luke, Catherine (NIH/NIAID) [E][catherine.luke@nih.gov]; Cassetti, Cristina (NIH/NIAID) [E][ccassetti@niaid.nih.gov]
From: Lampley, Rebecca (NIH/NIAID) [C][rebecca.lampley@nih.gov]
Sent: Thur 6/24/2021 2:41:10 PM (UTC-05:00)
Subject: SARS-CoV-2 Weekly Investigators Meeting - June 29th

Hi All!

On Tuesday, June 22nd, Dr. Sara Cherry presented on "**SARS-CoV-2 and antiviral therapeutics**." Thank you Dr. Cherry and everyone who was able to make it.

Next Tuesday, June 29th, Dr. Seema Lakdawala will be presenting on "**PHIGHT COVID: Public Health Interventions aGainst Human Transmission of COVID-19**". Hope you all can make it!

We are in need of presenters starting in mid-July. If you are interested in presenting, please let me know.

Best,
Rebecca

Rebecca M. Lampley M.S. [C]
Program Manager
Respiratory Diseases Branch
DMID/NIAID/NIH/DHHS
5601 Fishers Lane Desk 8A17
Rockville, MD 20892
Direct: 301.761.6384
Cell: 240.385.2331
E-mail: Rebecca.lampley@nih.gov

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Location: https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Importance: Normal

Subject: Canceled: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 6/18/2021 7:30:00 AM (UTC-05:00)

End Time: Fri 6/18/2021 8:30:00 AM (UTC-05:00)

Required Attendees: stevens@anl.gov; dbarouch; McDermott, Adrian (NIH/VRC) [E]; Douek, Daniel (NIH/VRC) [E]; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz

Optional Attendees: Boritz, Eli (NIH/NIAID) [E]; Doria-Rose, Nicole (NIH/NIAID) [E]; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Erlandson, Karl (OS/ASPR/BARDA)

Research Update Template.xlsx

Cancelling tomorrow's meeting due to the new federal holiday.

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting

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Join by H.323
161.199.138.10 (US West)
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		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

To: Baric, Toni C[antoinette_baric@med.unc.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Berhorst, Jackie[jdao@uw.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Ferris, Martin Thomas[mtferris@email.unc.edu]; Fischer, William A. II[william_fischer@med.unc.edu]; Graham, Jessica [jgraham@fhcrc.org]; Graham, Rachel[rlgraham@ad.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]; Heise, Mark T[mark_heisem@med.unc.edu]; Ireton, Renee[rireton@u.washington.edu]; Kathleen Voss[katvoss@uw.edu]; Klaus Schughart (kschugha@uthsc.edu)[kschugha@uthsc.edu]; Leist, Sarah Rebecca[leist@email.unc.edu]; Linnertz, Colton[colton_linnertz@med.unc.edu]; Lund, Jennifer[jlund@fredhutch.org]; Shannon McWeeney[mcweeney@ohsu.edu]; mgale@u.washington.edu[mgale@u.washington.edu]; Michael Davis[madphd@uw.edu]; Miller, Darla[darla_miller@med.unc.edu]; Michael Mooney[mooneymi@ohsu.edu]; Pardo Manuel de Villena, Fernando[fernando_pardo-manuel@med.unc.edu]; Schaefer, Alexandra[aschaefe@email.unc.edu]; Schughart, Klaus[Klaus.Schughart@helmholtz-hzi.de]; Shaw, Ginger[ginger_shaw@med.unc.edu]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Suthar, Mehul S. (mehul.s.suthar@emory.edu)[mehul.s.suthar@emory.edu]; Swarts, Jessica[jswarts@fredhutch.org]; West, Ande[westande@email.unc.edu]
From: Baric, Toni C[antoinette_baric@med.unc.edu]
Sent: Wed 6/23/2021 4:46:41 PM (UTC-05:00)
Subject: SIG U19 monthly call

Hi Everyone,
We will have our monthly SIG u19 call tomorrow. The only change is that we will be starting 30 minutes later, for a brief call. I sent out a revised invitation.
Thank you

Toni Baric

Dept of Microbiology & Immunology

9025 Burnett Womack Bldg CB# 7292

Chapel Hill, NC 27599-7292

919-966-3507

tcbaric@med.unc.edu

From: Baric, Toni C[antoinette_baric@med.unc.edu]

Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande; Ralph Baric; Graham PhD, Jessica B; Michael J Gale

Location: https://zoom.us/j/99380423092?pwd= **552.136**

Importance: Normal

Subject: SIG U19 Monthly Meeting

Start Time: Thur 6/24/2021 1:00:00 PM (UTC-05:00)

End Time: Thur 6/24/2021 2:00:00 PM (UTC-05:00)

Required Attendees: Baric, Ralph S; Berhorst, Jackie; Menachery, Vineet; Ferris, Martin Thomas; Fischer, William A. II; Graham, Jessica ; Graham, Rachel; Gralinski, Lisa E; Heise, Mark T; Ireton, Renee; Kathleen Voss; Klaus Schughart (kschugha@uthsc.edu); Leist, Sarah Rebecca; Linnertz, Colton; Lund, Jennifer; Shannon McWeeney; mgale@u.washington.edu; Michael Davis; Miller, Darla; Michael Mooney; Pardo Manuel de Villena, Fernando; Schaefer, Alexandra; Schughart, Klaus; Shaw, Ginger; Sheahan, Timothy Patrick; Suthar, Mehul S. (mehul.s.suthar@emory.edu); Swarts, Jessica; West, Ande

Optional Attendees: Ralph Baric; Graham PhD, Jessica B; Michael J Gale

This call will start 30 minutes later than usual and will be brief.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); SACKS, Jilian; SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo;

tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); ym.vasilev; David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; Amy Chung; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont; MULDERS, Mick; diana.molino; Merryn Voysey (merryn.voysey@paediatrics.ox.ac.uk)

Sent: Sun 6/27/2021 4:31:34 PM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assay

Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER,

Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont; MULDERS, Mick

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To: rahmed[rahmed@emory.edu]; Alter, Galit[galter@partners.org]; raul.andino[raul.andino@ucsf.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; bertozzi[bertozzi@stanford.edu]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish[cblish@stanford.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; tdcarroll[tdcarroll@ucdavis.edu]; Cassels, Fred[fcassels@path.org]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Meera Chand[Meera.Chand@phe.gov.uk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; charles.chiu[charles.chiu@ucsf.edu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; t.desilva[t.desilva@sheffield.ac.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; joe[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Camille Escadafal[Camille.Escadafal@finddx.org]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; douglas_fox[douglas_fox@berkeley.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Karen Gooch[karen.gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Griffiths, Anthony[ahgriff@bu.edu]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; William James[william.james@path.ox.ac.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj[kemptj@mail.nih.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; jakim[jakim@hivresearch.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler[amy.kistler@czbiohub.org]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Krammer, Florian[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; a.luttick[a.luttick@360biolabs.com]; jma[jma@sgul.ac.uk]; MacGill,

Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Paxton, Bill[w.a.paxton@liverpool.ac.uk]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol[pintol@mail.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; arjun.rustagi[arjun.rustagi@stanford.edu]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; Jilian Sacks (Jilian.sacks@finddx.org)[Jilian.sacks@finddx.org]; SALAMI, Kolawole[salamik@who.int]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; SANDS, Anita[sandsa@who.int]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons[GSimmons@vitalant.org]; viviana.simon[viviana.simon@mssm.edu]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; sastanley[sastanley@berkeley.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; SUBISSI, Lorenzo[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; sid.byrareddy[sid.byrareddy@unmc.edu]; awchung@unimelb.edu.au[awchung@unimelb.edu.au]; Breeze.Cavell[Breeze.Cavell@phe.gov.uk]; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP)[gbu3@cdc.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; LDumont[LDumont@vitalant.org]; MULDERS, Mick[muldersm@who.int]

Cc: Towers, Greg[g.towers@ucl.ac.uk]; Krogan, Nevan[nevan.krogan@ucsf.edu]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 6/22/2021 3:15:24 PM (UTC-05:00)
Subject: RE: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 23 2:30PM CET (Geneva Time)

1. Nevan Krogan (UCSF) & Greg Towers (UCL) - *A multidisciplinary approach to studying SARS-CoV-2 evolution and innate immune responses*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, June 20, 2021 8:54 AM
To: rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; a.luttick@360biolabs.com; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; ramadany@sfda.gov.sa; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; angeliki.melidou@ecdc.europa.eu; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; cjmiller@UCDAVIS.EDU; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris@cdph.ca.gov; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se; w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena;

Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan@phe.gov.uk; Carol.Sabourin@hhs.gov; Jilian.Sacks@finddx.org; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; sid.byrareddy@unmc.edu; awchung@unimelb.edu.au; Breeze.Cavell@phe.gov.uk; gbu3@cdc.gov; mehul.s.suthar@emory.edu; LDumont@vitalant.org; MULDERS, Mick
Subject: WHO Working Group on COVID-19 Assays
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Agenda to follow.

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Meeting ID: 361 256 8290

To: rahmed[rahmed@emory.edu]; Alter, Galit[galter@partners.org]; raul.andino[raul.andino@ucsf.edu]; Maria Baca Estrada (maria.baca-estrada@canada.ca)[maria.baca-estrada@canada.ca]; baihe (baihe@nmpa.gov.cn)[baihe@nmpa.gov.cn]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; ellie.barnes[ellie.barnes@ndm.ox.ac.uk]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; cheryl (cheryl@gisaid.org)[cheryl@gisaid.org]; valentina.bernasconi@cepi.net[valentina.bernasconi@cepi.net]; bertozzi[bertozzi@stanford.edu]; Kevin Bewley (Kevin.bewley@phe.gov.uk)[Kevin.bewley@phe.gov.uk]; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in)[shinjini.bhatnagar@thsti.res.in]; pbieniasz@mail.rockefeller.edu[pbieniasz@mail.rockefeller.edu]; cblish[cblish@stanford.edu]; karin.bok (karin.bok@nih.gov)[karin.bok@nih.gov]; Boyle, David[dboyle@path.org]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; BRANGEL, Polina[brangelp@who.int]; Aodhan.Breathnach[Aodhan.Breathnach@stgeorges.nhs.uk]; christian.brechot (christian.brechot@pasteur.fr)[christian.brechot@pasteur.fr]; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu)[Eeva.Broberg@ecdc.europa.eu]; Christine Bruce (Christine.bruce@phe.gov.uk)[Christine.bruce@phe.gov.uk]; Mihaela BUDA[Mihaela.BUDA@edqm.eu]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; zuz4 (zuz4@cdc.gov)[zuz4@cdc.gov]; tdcarroll[tdcarroll@ucdavis.edu]; Cassels, Fred[fcassels@path.org]; Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; Meera Chand[Meera.Chand@phe.gov.uk]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Emmanuelle Charton (emmanuelle.charton@edqm.eu)[emmanuelle.charton@edqm.eu]; charles.chiu[charles.chiu@ucsf.edu]; Chu, May[MAY.CHU@CUANSCHUTZ.EDU]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; Daniel Cohen (dancohen@tauex.tau.ac.il)[dancohen@tauex.tau.ac.il]; kizzmekia.corbett@nih.gov[kizzmekia.corbett@nih.gov]; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co)[mafranco@javeriana.edu.co]; COSTA, Alejandro Javier[costaa@who.int]; Coughlin, Melissa (CDC/DDID/NCIRD/DVD)[htq4@cdc.gov]; shane@lji.org[shane@lji.org]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@cdc.gov]; Lisa@amicitiam.com[Lisa@amicitiam.com]; Peter Daszak[daszak@ecohealthalliance.org]; de los Santos, Tala[tdelossantos@path.org]; t.desilva[t.desilva@sheffield.ac.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; joe[joe@czbiohub.org]; diane.descamps@aphp.fr[diane.descamps@aphp.fr]; mit666666 (mit666666@pitt.edu)[mit666666@pitt.edu]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; katie.doores (katie.doores@kcl.ac.uk)[katie.doores@kcl.ac.uk]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; christian.drosten (christian.drosten@charite.de)[christian.drosten@charite.de]; lny1@cdc.gov[lny1@cdc.gov]; susie.dunachie[susie.dunachie@ndm.ox.ac.uk]; epstein@ecohealthalliance.org[epstein@ecohealthalliance.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Camille Escadafal[Camille.Escadafal@finddx.org]; Falzarano, Darryl[darryl.falzarano@usask.ca]; jason.fernandes@canada.ca[jason.fernandes@canada.ca]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; douglas_fox[douglas_fox@berkeley.edu]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Jacqueline.Fryer[Jacqueline.Fryer@nibsc.org]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; Luc.Gagnon (Luc.Gagnon@nexelis.com)[Luc.Gagnon@nexelis.com]; SGalloway@cdc.gov[SGalloway@cdc.gov]; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov)[Mayra.Garcia@fda.hhs.gov]; bhx1 (bhx1@cdc.gov)[bhx1@cdc.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; GILBERT Nick[Nick.Gilbert@ed.ac.uk]; Goldblatt, David[d.goldblatt@ich.ucl.ac.uk]; Karen Gooch[karen.gooch@phe.gov.uk]; guy.gorochov@sorbonne-universite.fr[guy.gorochov@sorbonne-universite.fr]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; elwyn.griffiths@cepi.net[elwyn.griffiths@cepi.net]; Griffiths, Anthony[ahgriff@bu.edu]; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil)[gregory.d.gromowski.civ@mail.mil]; ilj2 (ilj2@cdc.gov)[ilj2@cdc.gov]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; Victoria.Hall[Victoria.Hall@phe.gov.uk]; Carl.Hanson[Carl.Hanson@cdph.ca.gov]; Theodora Hatziioannou[thatziio@rockefeller.edu]; Helfand, Rita (CDC/DDID/NCEZID/OD)[rzh7@cdc.gov]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; Hodgson, Paul[paul.hodgson@usask.ca]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; johan.holst@cepi.net[johan.holst@cepi.net]; rawcraig@yahoo.com[rawcraig@yahoo.com]; Hyde, Terri (CDC/DDPHSIS/CGH/GID)[thyde@cdc.gov]; IRAHETA SIGUENZA, Raul Emilio[irahetar@who.int]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Iturriza-Gomara, Miren[miturrizagomara@path.org]; ASiyer@mgh.harvard.edu[ASiyer@mgh.harvard.edu]; William James[william.james@path.ox.ac.uk]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; Youngmee Jee (jeey62@gmail.com)[jeey62@gmail.com]; Jernigan, Daniel B. (CDC/DDID/NCIRD/ID)[djernigan@cdc.gov]; johnsonreed@niaid.nih.gov[johnsonreed@niaid.nih.gov]; ydm9@cdc.gov[ydm9@cdc.gov]; KAZI, Fatema[kazif@who.int]; Kelvin, Alyson[alyson.kelvin@usask.ca]; kemptj[kemptj@mail.nih.gov]; alankhoo.imr[alankhoo.imr@gmail.com]; jakim[jakim@hivresearch.org]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; amy.kistler[amy.kistler@czbiohub.org]; paul.klenerman[paul.klenerman@medawar.ox.ac.uk]; KNEZEVIC, Ivana[knezevici@who.int]; M.P.G. Koopmans (m.koopmans@erasmusmc.nl)[m.koopmans@erasmusmc.nl]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Krammer, Florian[florian.krammer@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Shelly Krebs (skrebs@hivresearch.org)[skrebs@hivresearch.org]; Greg Kulnis (Greg.Kulnis@nexelis.com)[Greg.Kulnis@nexelis.com]; Arun Kumar (arun.kumar@cepi.net)[arun.kumar@cepi.net]; renuka.kumar[renuka.kumar@gladstone.ucsf.edu]; pawinee.k@redcross.or.th[pawinee.k@redcross.or.th]; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk)[teresa.lambe@ndm.ox.ac.uk]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Leader, Troy[bleader@path.org]; leejooyeon (leejooyeon@korea.kr)[leejooyeon@korea.kr]; Lee, William T (HEALTH)[william.lee@health.ny.gov]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; liyl (liyl@cde.org.cn)[liyl@cde.org.cn]; changguili (changguili@aliyun.com)[changguili@aliyun.com]; lyhchengdu (lyhchengdu@163.com)[lyhchengdu@163.com]; limhy0919 (limhy0919@korea.kr)[limhy0919@korea.kr]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; liub (liub@cde.org.cn)[liub@cde.org.cn]; a.luttick[a.luttick@360biolabs.com]; jma[jma@sgul.ac.uk]; MacGill,

Tracy[Tracy.MacGill@fda.hhs.gov]; ramadany[ramadany@sfda.gov.sa]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; jmclellan (jmclellan@austin.utexas.edu)[jmclellan@austin.utexas.edu]; adrian.mcdermott (adrian.mcdermott@nih.gov)[adrian.mcdermott@nih.gov]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; gmedigeshi (gmedigeshi@thsti.res.in)[gmedigeshi@thsti.res.in]; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu)[angeliki.melidou@ecdc.europa.eu]; jwm1 (jwm1@pitt.edu)[jwm1@pitt.edu]; Liz Miller (Liz.Miller@lshtm.ac.uk)[Liz.Miller@lshtm.ac.uk]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; david.montefiori@duke.edu[david.montefiori@duke.edu]; pennym@nicd.ac.za[pennym@nicd.ac.za]; kaitlyn.dambach@nih.gov[kaitlyn.dambach@nih.gov]; Clare.Morris@nibsc.org[Clare.Morris@nibsc.org]; MaryKate.Morris[MaryKate.Morris@cdph.ca.gov]; Sarah Mudrak, Ph.D.[sarah.mudrak@duke.edu]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Myers, Todd[Todd.Myers@fda.hhs.gov]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; scott.napper (scott.napper@usask.ca)[scott.napper@usask.ca]; MNELSON (MNELSON@dstl.gov.uk)[MNELSON@dstl.gov.uk]; PNorris@vitalant.org[PNorris@vitalant.org]; mbo2@cdc.gov[mbo2@cdc.gov]; pilailuk.o (pilailuk.o@dmsc.mail.go.th)[pilailuk.o@dmsc.mail.go.th]; n.okba@erasmusmc.nl[n.okba@erasmusmc.nl]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; engeong.ooi[engeong.ooi@duke-nus.edu.sg]; melanie.ott[melanie.ott@gladstone.ucsf.edu]; Jae Ouk Kim (jokim@ivi.int)[jokim@ivi.int]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil)[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP)[xdv3@cdc.gov]; qiang.pan-hammarstrom@ki.se[qiang.pan-hammarstrom@ki.se]; Paxton, Bill[w.a.paxton@liverpool.ac.uk]; Peden, Keith[keith.peden@fda.hhs.gov]; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil)[sheila.a.peel2.civ@mail.mil]; malik (malik@hku.hk)[malik@hku.hk]; PERKINS, Mark[perkinsm@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th)[supaporn.p@dmsc.mail.go.th]; Pillai, Satish[Satish.Pillai@ucsf.edu]; pintol[pintol@mail.nih.gov]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; mireille.plamondon@canada.ca[mireille.plamondon@canada.ca]; Pollakis, Georgios[g.pollakis@liverpool.ac.uk]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; arimoin (arimoin@g.ucla.edu)[arimoin@g.ucla.edu]; RIVEROS BALTA, Ximena[lauriex@who.int]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; arjun.rustagi[arjun.rustagi@stanford.edu]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; SACKS, Jilian[sacksj@who.int]; SALAMI, Kolawole[salamik@who.int]; Marc L Salit (msalit@stanford.edu)[msalit@stanford.edu]; SANDS, Anita[sandsa@who.int]; erica (erica@lji.org)[erica@lji.org]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Sharon Schendel (schendel@lji.org)[schendel@lji.org]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; PScott (PScott@eidresearch.org)[PScott@eidresearch.org]; alex@lji.org[alex@lji.org]; Shi, Pei yong[peshi@UTMB.EDU]; Shivji Ragini (Ragini.Shivji@ema.europa.eu)[Ragini.Shivji@ema.europa.eu]; sujan@lji.org[sujan@lji.org]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; YOO, Si Hyung[yoos@who.int]; alex.sigal@ahri.org[alex.sigal@ahri.org]; GSimmons[GSimmons@vitalant.org]; viviana.simon[viviana.simon@mssm.edu]; Smith, Ashley (OS/ASPR/BARDA)[Ashley.Smith1@hhs.gov]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; sastanley[sastanley@berkeley.edu]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; STRÖHER, Ute[stroheru@who.int]; SUBISSI, Lorenzo[subissil@who.int]; tcs38@psu.edu[tcs38@psu.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; r.tedder@imperial.ac.uk[r.tedder@imperial.ac.uk]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; tracey.thue (tracey.thue@usask.ca)[tracey.thue@usask.ca]; georgia.tomaras (georgia.tomaras@duke.edu)[georgia.tomaras@duke.edu]; sot1@cdc.gov[sot1@cdc.gov]; alain.townsend (alain.townsend@imm.ox.ac.uk)[alain.townsend@imm.ox.ac.uk]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; Turtle, Lance[Lance.Turtle@liverpool.ac.uk]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; eric.vangieson@darpa.mil[eric.vangieson@darpa.mil]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au]; ym.vasilev[ym.vasilev@rpharm.ru]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; Wadford, Debra@CDPH[Debra.Wadford@cdph.ca.gov]; wangjz (wangjz@nifdc.org.cn)[wangjz@nifdc.org.cn]; wangyc (wangyc@nifdc.org.cn)[wangyc@nifdc.org.cn]; linfa.wang (linfa.wang@duke-nus.edu.sg)[linfa.wang@duke-nus.edu.sg]; Weir, Jerry P.[jerry.weir@fda.hhs.gov]; gweiss@uci.edu[gweiss@uci.edu]; Wentworth, David E. (CDC/OID/NCIRD)[gll9@cdc.gov]; daniela@lji.org[daniela@lji.org]; tomwhite42450@gmail.com[tomwhite42450@gmail.com]; KurtW[KurtW@nicd.ac.za]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Wolfraim, Larry (NIH/NIAID) [E][larry.wolfraim@nih.gov]; David Wood (dj56wood@gmail.com)[dj56wood@gmail.com]; xumiaobj (xumiaobj@126.com)[xumiaobj@126.com]; solomon.yimer@cepi.net[solomon.yimer@cepi.net]; tlying (tlying@fudan.edu.cn)[tlying@fudan.edu.cn]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Vidadi Yusibov (vyusibov@indianabiosciences.org)[vyusibov@indianabiosciences.org]; zlshi (zlshi@wh.iov.cn)[zlshi@wh.iov.cn]; ZHOU, Tiequn[ZhouT@who.int]; sid.byrareddy[sid.byrareddy@unmc.edu]; Amy Chung[awchung@unimelb.edu.au]; Breeze.Cavell[Breeze.Cavell@phe.gov.uk]; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP)[gbu3@cdc.gov]; Suthar, Mehul[mehul.s.suthar@emory.edu]; LDumont[LDumont@vitalant.org]; MULDERS, Mick[muldersm@who.int]; diana.molino[diana.molino@inserm.fr]; Merryn Voysey (merryn.voysey@paediatrics.ox.ac.uk)[merryn.voysey@paediatrics.ox.ac.uk]

Cc: Javier Castillo-Olivares Pallardo[fjc37@cam.ac.uk]; Merryn Voysey (merryn.voysey@paediatrics.ox.ac.uk)[merryn.voysey@paediatrics.ox.ac.uk]

From: SCHWARTZ, Lauren[schwartzl@who.int]

Sent: Mon 6/28/2021 11:56:00 AM (UTC-05:00)

Subject: RE: WHO Working Group on COVID-19 Assay

Dear All,

Please find below the agenda for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday June 30 2:30PM CET (Geneva Time)

1. Javier Castillo-Olivares Pallardo (Cambridge) - *Defining correlates of humoral immunity to COVID-19 using samples from patients and healthcare workers'*
2. Merryn Voysey (U Oxford) - *Correlates of protection against symptomatic and asymptomatic SARS-CoV-2 infection*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, June 27, 2021 2:31 PM
To: rahmed@emory.edu; galter@partners.org; raul.andino@ucsf.edu; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; ellie.barnes@ndm.ox.ac.uk; dbarouch@bidmc.harvard.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; bertozzi@stanford.edu; Kevin.Bewley@phe.gov.uk; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; cblish@stanford.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach@stgeorges.nhs.uk; christian.brechot@pasteur.fr; Eeva Broberg; Christine.bruce@phe.gov.uk; BUDA Mihaela; Miles.Carroll@phe.gov.uk; zuz4@cdc.gov; tdcarroll@ucdavis.edu; fcassels@path.org; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; Meera.Chand@phe.gov.uk; MONALISA.CHATTERJI@gatesfoundation.org; emmanuelle.charton@edqm.eu; charles.chiu@ucsf.edu; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; dancohen@tauex.tau.ac.il; kizzmekia.corbett@nih.gov; mafranco@javeriana.edu.co; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; t.desilva@sheffield.ac.uk; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; joe@czbiohub.org; diane.descamps@aphp.fr; mit666666@pitt.edu; Ruben.Donis@hhs.gov; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; lny1@cdc.gov; susie.dunachie@ndm.ox.ac.uk; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; Camille.Escadafal@finddx.org; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; douglas_fox@berkeley.edu; MFrieman@som.umaryland.edu; Jacqueline.Fryer@nibsc.org; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; SGalloway@cdc.gov; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; Nick.Gilbert@ed.ac.uk; d.goldblatt@ucl.ac.uk; karen.gooch@phe.gov.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; elwyn.griffiths@cepi.net; ahgriff@bu.edu; gregory.d.gromowski.civ@mail.mil; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; Victoria.Hall@phe.gov.uk; Carl.Hanson@cdph.ca.gov; thatziio@rockefeller.edu; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; IRAHETA SIGUENZA, Raul Emilio; REIRELAND@mail.dstl.gov.uk; miturrizagomara@path.org; ASiyer@mgh.harvard.edu; william.james@path.ox.ac.uk; Lakshmi.Jayashankar@hhs.gov; Youngmee Jee; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj@mail.nih.gov; alankhoo.imr@gmail.com; Jiae Kim; Jacqueline.Kirchner@gatesfoundation.org; amy.kistler@czbiohub.org; paul.klenerman@medawar.ox.ac.uk; 'KNEZEVIC, Ivana'; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; renuka.kumar@gladstone.ucsf.edu; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; william.lee@health.ny.gov; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; a.luttick@360biolabs.com; jma@sgul.ac.uk; Tracy.MacGill@fda.hhs.gov; ramadany@sfda.gov.sa; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; angeliki.melidou@ecdc.europa.eu; jwm1@pitt.edu; Liz.Miller@lshtm.ac.uk; cjmiller@UCDAVIS.EDU; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris@cdph.ca.gov; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; engeong.ooi@duke-nus.edu.sg; melanie.ott@gladstone.ucsf.edu; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; qiang.pan-hammarstrom@ki.se;

w.a.paxton@liverpool.ac.uk; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; stanley-perlman@uiowa.edu; supaporn.p@dmsc.mail.go.th; satish.pillai@ucsf.edu; pintol@mail.nih.gov; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; g.pollakis@liverpool.ac.uk; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; arjun.rustagi@stanford.edu; Kathryn.ryan@phe.gov.uk; Carol.Sabourin@hhs.gov; SACKS, Jilian; 'SALAMI, Kolawole'; msalit@stanford.edu; SANDS, Anita; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; SCHWARTZ, Lauren; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; sujan@lji.org; amy.c.shurtleff@cepi.net; YOO, Si Hyung; alex.sigal@ahri.org; GSimmons@vitalant.org; viviana.simon@mssm.edu; Ashley.Smith1@hhs.gov; mksong@ivi.int; sastanley@berkeley.edu; erik.stemmy@nih.gov; STRÖHER, Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; sot1@cdc.gov; alain.townsend@imm.ox.ac.uk; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; Lance.Turtle@liverpool.ac.uk; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; ym.vasilev@rpharm.ru; David.Vaughn@gatesfoundation.org; Debra.Wadford@cdph.ca.gov; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; linfa.wang@duke-nus.edu.sg; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; gll9@cdc.gov; daniela@lji.org; tomwhite42450@gmail.com; KurtW@nicd.ac.za; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi.Yusibov@hhs.gov; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; sid.byrareddy@unmc.edu; awchung@unimelb.edu.au; Breeze.Cavell@phe.gov.uk; gbu3@cdc.gov; mehul.s.suthar@emory.edu; LDumont@vitalant.org; MULDERS, Mick; diana.molino@inserm.fr; merryn.voysey@paediatrics.ox.ac.uk
Subject: WHO Working Group on COVID-19 Assay
When: Wednesday, June 30, 2021 2:30 PM-3:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson; Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); Idenisy (Idenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; D.A.J. van Riel; Cherry, Sara; mohamad.taha; Mariana.Baz

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To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson[danielle.anderson@unimelb.edu.au]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jmkperrine[jmkperrine@gmail.com]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara,

Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au];

SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru)[y.m.vasiliev@spbniivs.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]; lok-yinroy-wong[lok-yinroy-wong@uiowa.edu]; julia.port[julia.port@nih.gov]; Benjamin Murrell[benjamin.murrell@ki.se]; D.A.J. van Riel[d.vanriel@erasmusmc.nl]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; mohamad.taha[mohamad.taha@canada.ca]; Mariana.Baz[Mariana.Baz@influenzacentre.org]
Cc: rineke.jong@wur.nl[rineke.jong@wur.nl]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Tue 6/22/2021 12:08:16 PM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday June 24 3PM CET (Geneva time)

1. Rineke de Jonge (Wageningen Bioveterinary Research) - *Vaccine-mediated enhanced disease in a SARS-CoV-2 hamster model?*
2. Julia Port (NIH) - *Western diet increases COVID-19 disease severity in the Syrian hamster*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, June 20, 2021 8:57 AM
To: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@unimelb.edu.au; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru;

ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jmkperrine@gmail.com; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; y.m.vasiliev@spbniivs.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; julia.port@nih.gov; benjamin.murrell@ki.se; d.vanriel@erasmusmc.nl; cherrys@pennmedicine.upenn.edu; mohamad.taha@canada.ca; Baz, Mariana

Subject: WHO COVID-19 Animal Models Group Call

When: Thursday, June 24, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.

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Agenda to follow.

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To: WaickmaA@upstate.edu[WaickmaA@upstate.edu]; Garcia-Sastre, Adolfo[adolfo.garcia-sastre@mssm.edu]; kandeil_a (kandeil_a@hotmail.com)[kandeil_a@hotmail.com]; alankhoo.imr[alankhoo.imr@gmail.com]; Bukreyev, Alexander[abukreye@UTMB.EDU]; White, Alexander G[agw13@pitt.edu]; kupke (kupke@staff.uni-marburg.de)[kupke@staff.uni-marburg.de]; Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se)[Ali.Mirazimi@folkhalsomyndigheten.se]; Amelia Karlsson (amelia.karlsson@duke.edu)[amelia.karlsson@duke.edu]; Amy C. Shurtleff (amy.c.shurtleff@cepi.net)[amy.c.shurtleff@cepi.net]; HENAO RESTREPO, Ana Maria[henaorestrepoa@who.int]; marzia[marzia@niaid.nih.gov]; Andrew.Phipps[Andrew.Phipps@hhs.gov]; ajones[ajones@mail.rockefeller.edu]; mopargal (mopargal@rams.colostate.edu)[mopargal@rams.colostate.edu]; angierasmussen@gmail.com[angierasmussen@gmail.com]; anice.lowen[anice.lowen@emory.edu]; anja.kipar@uzh.ch[anja.kipar@uzh.ch]; Ann Rawkins (Ann.Rawkins@phe.gov.uk)[Ann.Rawkins@phe.gov.uk]; Honko, Anna[honko@bu.edu]; anna (anna@thsti.res.in)[anna@thsti.res.in]; Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk)[Anthony.Holmes@nc3rs.org.uk]; Griffiths, Anthony[ahgriff@bu.edu]; Asisa.Volz (Asisa.Volz@tiho-hannover.de)[Asisa.Volz@tiho-hannover.de]; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil)[aysegul.nalca.civ@mail.mil]; verstrepen@bprc.nl[verstrepen@bprc.nl]; Barbara.Schnierle (Barbara.Schnierle@pei.de)[Barbara.Schnierle@pei.de]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; B.H.G. Rockx (b.rockx@erasmusmc.nl)[b.rockx@erasmusmc.nl]; B.L. Haagmans (b.haagmans@erasmusmc.nl)[b.haagmans@erasmusmc.nl]; tenoever@gmail.com[tenoever@gmail.com]; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de)[bernhard.kerscher@pei.de]; bobomok@hku.hk[bobomok@hku.hk]; bradley.pickering (bradley.pickering@canada.ca)[bradley.pickering@canada.ca]; CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de)[CarlosAlberto.Guzman@helmholtz-hzi.de]; CDillen@som.umaryland.edu[CDillen@som.umaryland.edu]; Sabourin, Carol (OS/ASPR/BARDA)[Carol.Sabourin@hhs.gov]; caroline.foo[caroline.foo@kuleuven.be]; caroline.melo@rivm.nl[caroline.melo@rivm.nl]; Carolyn Clark (carolyn.clark@cepi.net)[carolyn.clark@cepi.net]; bosioc@niaid.nih.gov[bosioc@niaid.nih.gov]; Cesar Munoz-Fontela (munoz-fontela@bnitm.de)[munoz-fontela@bnitm.de]; croy (croy@tulane.edu)[croy@tulane.edu]; shanchao (shanchao@wh.iov.cn)[shanchao@wh.iov.cn]; Techakitiroj Chatkul (tverakit@gmail.com)[tverakit@gmail.com]; mary.lane@nih.gov[mary.lane@nih.gov]; Chi Van Dang (cdang@lcr.org)[cdang@lcr.org]; Chris Miller (cjmiller@ucdavis.edu)[cjmiller@ucdavis.edu]; christian.c.hofer.mil@mail.mil[christian.c.hofer.mil@mail.mil]; Christiane Gerke (christiane.gerke@pasteur.fr)[christiane.gerke@pasteur.fr]; qinchuan (qinchuan@pumc.edu.cn)[qinchuan@pumc.edu.cn]; wenchun0617[wenchun0617@gate.sinica.edu.tw]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][connie.schmaljohn@nih.gov]; dbarouch (dbarouch@bidmc.harvard.edu)[dbarouch@bidmc.harvard.edu]; daniel.martinez-arguelles[daniel.martinez-arguelles@canada.ca]; danielle.anderson[danielle.anderson@unimelb.edu.au]; Falzarano, Darryl[darryl.falzarano@usask.ca]; darwyn.kobasa@canada.ca[darwyn.kobasa@canada.ca]; DAVID H O'CONNOR (dhoconno@wisc.edu)[dhoconno@wisc.edu]; David Vaughn (David.Vaughn@gatesfoundation.org)[David.Vaughn@gatesfoundation.org]; David Revelli (drevelli@lovelacebiomedical.org)[drevelli@lovelacebiomedical.org]; Lee-Parritz, David[david.lee-parritz@tufts.edu]; WOOD, David John[woodd@who.int]; dean.smith (dean.smith@canada.ca)[dean.smith@canada.ca]; ldenisy (ldenisy@yahoo.com)[ldenisy@yahoo.com]; dbolton@hivresearch.org[dbolton@hivresearch.org]; dgdiel@cornell.edu[dgdiel@cornell.edu]; dmissiak (dmissiak@bsd.uchicago.edu)[dmissiak@bsd.uchicago.edu]; dsreed@cvr.pitt.edu[dsreed@cvr.pitt.edu]; dustin.johnson (dustin.johnson@canada.ca)[dustin.johnson@canada.ca]; esulkowska@rics.bwh.harvard.edu[esulkowska@rics.bwh.harvard.edu]; Elliot Lilley - NC3Rs[elliot.lilley@nc3rs.org.uk]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; erica (erica@lji.org)[erica@lji.org]; Stemmy, Erik (NIH/NIAID) [E][erik.stemmy@nih.gov]; Dohm, Erik Daniel[edohm@uab.edu]; verschoor (verschoor@bprc.nl)[verschoor@bprc.nl]; estefania.rodriguez (estefania.rodriguez@bnitm.de)[estefania.rodriguez@bnitm.de]; KAZI, Fatema[kazif@who.int]; GREY Finn (fgrey@exseed.ed.ac.uk)[fgrey@exseed.ed.ac.uk]; Krammer, Florian[florian.krammer@mssm.edu]; franck.TOURET@univ-amu.fr[franck.TOURET@univ-amu.fr]; f.briand[f.briand@physiogenex.com]; Cassels, Fred[fcassels@path.org]; fkoide (fkoide@southernresearch.org)[fkoide@southernresearch.org]; gabriella.worwa[gabriella.worwa@nih.gov]; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca)[Gary.Kobinger@crchudequebec.ulaval.ca]; sutter (sutter@micro.vetmed.uni-muenchen.de)[sutter@micro.vetmed.uni-muenchen.de]; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org)[Giada.Mattiuzzo@nibsc.org]; Sivko, Gloria S[sivkog@battelle.org]; grace.m.lidl.mil@mail.mil[grace.m.lidl.mil@mail.mil]; gustavo.palacios (gustavo.palacios@gmail.com)[gustavo.palacios@gmail.com]; horer@ku.edu.tr[horer@ku.edu.tr]; Golding, Hana[Hana.Golding@fda.hhs.gov]; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org)[Harry.Kleanthous@gatesfoundation.org]; Damron, Fredrick[fdamron@hsc.wvu.edu]; feldmannh@niaid.nih.gov[feldmannh@niaid.nih.gov]; hlchen (hlchen@hku.hk)[hlchen@hku.hk]; Hwan K Kim (hwan.kim@stonybrook.edu)[hwan.kim@stonybrook.edu]; Crozier, Ian (NIH) [C][ian.crozier@nih.gov]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru)[i.v.krasilnikov@spbniivs.ru]; ivan.marazzi[ivan.marazzi@mssm.edu]; KNEZEVIC, Ivana[knezevici@who.int]; IVMARTINEZ[IVMARTINEZ@hsc.wvu.edu]; y.jacob.hou@unc.edu[y.jacob.hou@unc.edu]; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org)[Jacqueline.Kirchner@gatesfoundation.org]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Kobie, James J[jjkobie@uabmc.edu]; Stewart, James[J.P.Stewart@liverpool.ac.uk]; langermans (langermans@bprc.nl)[langermans@bprc.nl]; Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca)[Jason.Kindrachuk@umanitoba.ca]; jfwchan (jfwchan@hku.hk)[jfwchan@hku.hk]; Javier Salguero (Javier.Salguero@phe.gov.uk)[Javier.Salguero@phe.gov.uk]; jay.w.hooper.civ (jay.w.hooper.civ@mail.mil)[jay.w.hooper.civ@mail.mil]; snumouse (snumouse@snu.ac.kr)[snumouse@snu.ac.kr]; jhogan@uga.edu[jhogan@uga.edu]; ravetch[ravetch@mail.rockefeller.edu]; jmkperrine[jmkperrine@gmail.com]; jeroen.kortekaas (jeroen.kortekaas@wur.nl)[jeroen.kortekaas@wur.nl]; ZHU, Jin[Jin.Zhu@health.gov.au]; JLPRIOR (JLPRIOR@dstl.gov.uk)[JLPRIOR@dstl.gov.uk]; Flynn, Joanne L[joanne@pitt.edu]; Segales, Joaquim[joaquim.segales@irta.cat]; johan.neyts (johan.neyts@kuleuven.be)[johan.neyts@kuleuven.be]; Treanor, John (OS/ASPR/BARDA) (CTR)[John.Treanor@hhs.gov]; john.c.trefry.civ (john.c.trefry.civ@mail.mil)[john.c.trefry.civ@mail.mil]; JOHN JAMES BACZENAS[baczenas@wisc.edu]; SPERGEL@email.chop.edu[SPERGEL@email.chop.edu]; JTorrelles@txbiomed.org[JTorrelles@txbiomed.org]; Jorgen de Jonge (jorgen.de.jonge@rivm.nl)[jorgen.de.jonge@rivm.nl]; Juan García Arriaza (jfgarcia@cnb.csic.es)[jfgarcia@cnb.csic.es]; Juergen Richt (jricht@vet.k-state.edu)[jricht@vet.k-state.edu]; Vergara,

Julia[julia.vergara@irta.cat]; Julia Tree (Julia.Tree@phe.gov.uk)[Julia.Tree@phe.gov.uk]; kai.dallmeier (kai.dallmeier@kuleuven.be)[kai.dallmeier@kuleuven.be]; kanta.subbarao (kanta.subbarao@influenzacentre.org)[kanta.subbarao@influenzacentre.org]; Karen Makar (Karen.Makar@gatesfoundation.org)[Karen.Makar@gatesfoundation.org]; Karl.Erlandson (Karl.Erlandson@hhs.gov)[Karl.Erlandson@hhs.gov]; Kayvon Modjarrad (kmodjarrad@eidresearch.org)[kmodjarrad@eidresearch.org]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Alyson Kelvin[AKelvin@dal.ca]; kevinharrod (kevinharrod@uabmc.edu)[kevinharrod@uabmc.edu]; rkiatchula (rkiatchula@gmail.com)[rkiatchula@gmail.com]; Seungtaek Kim (seungtaek.kim@ip-korea.org)[seungtaek.kim@ip-korea.org]; stittelaar (stittelaar@viroclinics.com)[stittelaar@viroclinics.com]; SALAMI, Kolawole[salamik@who.int]; Kristine Macartney (kristine.macartney@health.nsw.gov.au)[kristine.macartney@health.nsw.gov.au]; kyle.rosenke[kyle.rosenke@nih.gov]; Jayashankar, Lakshmi (OS/ASPR/BARDA)[Lakshmi.Jayashankar@hhs.gov]; lawton.stubbert@canada.ca[lawton.stubbert@canada.ca]; lisambrosseau@gmail.com[lisambrosseau@gmail.com]; lisa.chakrabarti@pasteur.fr[lisa.chakrabarti@pasteur.fr]; Hensley, Lisa (NIH/NIAID) [E][lisa.hensley@nih.gov]; lgralins@email.unc.edu[lgralins@email.unc.edu]; lisette.cornelissen[lisette.cornelissen@wur.nl]; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil)[margaret.l.pitt.civ@mail.mil]; Luis.Lugo.mil@afrims.org[Luis.Lugo.mil@afrims.org]; l.enjuanes@cnb.csic.es[l.enjuanes@cnb.csic.es]; LMartinez@txbiomed.org[LMartinez@txbiomed.org]; Vandenberghe, Luk[luk_vandenberghe@meei.harvard.edu]; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD)[ibz1@cdc.gov]; mito@ciea.or.jp[mito@ciea.or.jp]; Manki Song (mksong@ivi.int)[mksong@ivi.int]; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu)[Marco.Cavaleri@ema.europa.eu]; mesteban (mesteban@cnb.csic.es)[mesteban@cnb.csic.es]; PREZIOSI, Marie-pierre[preziosim@who.int]; mariette.ducatez@envt.fr[mariette.ducatez@envt.fr]; mlewis (mlewis@bioqual.com)[mlewis@bioqual.com]; Mark Page (Mark.Page@nibsc.org)[Mark.Page@nibsc.org]; Mark Prescott - NC3Rs[Mark.Prescott@nc3rs.org.uk]; marlene.espinozamoraga[marlene.espinozamoraga@mssm.edu]; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu)[Martha.Alexander-Miller@wakehealth.edu]; Martin.Beer (Martin.Beer@fli.de)[Martin.Beer@fli.de]; Matthew.Reed.mil@afrims.org[Matthew.Reed.mil@afrims.org]; Frieman, Matthew[MFrieman@som.umaryland.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Schotsaert, Michael[michael.schotsaert@mssm.edu]; mdiamond (mdiamond@wustl.edu)[mdiamond@wustl.edu]; MNELSON@mail.dstl.gov.uk[MNELSON@mail.dstl.gov.uk]; mto@umn.edu[mto@umn.edu]; Holbrook, Michael (NIH/NIAID) [C][michael.holbrook@nih.gov]; Hevey, Michael (CTR)[michael.hevey@ST.DHS.GOV]; Miles.Carroll (Miles.Carroll@phe.gov.uk)[Miles.Carroll@phe.gov.uk]; mitchell.palmer@usda.gov[mitchell.palmer@usda.gov]; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org)[MONALISA.CHATTERJI@gatesfoundation.org]; Munir, Muhammad[muhammad.munir@lancaster.ac.uk]; Nadia KHELEF (nadia.khelef@pasteur.fr)[nadia.khelef@pasteur.fr]; Oreshkova, Nadia[nadia.oreshkova@wur.nl]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; neeltje.vandoremalen@nih.gov[neeltje.vandoremalen@nih.gov]; Neil Berry (Neil.Berry@nibsc.org)[Neil.Berry@nibsc.org]; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU[Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU]; Nicola Rose (Nicola.Rose@nibsc.org)[Nicola.Rose@nibsc.org]; nirp (nirp@iibr.gov.il)[nirp@iibr.gov.il]; Gerhards, Nora[nora.gerhards@wur.nl]; nnagata@niid.go.jp[nnagata@niid.go.jp]; Olinger, Gene[golinger@MRIGLOBAL.ORG]; salgampa (salgampa@njms.rutgers.edu)[salgampa@njms.rutgers.edu]; patrick.reid@unmc.edu[patrick.reid@unmc.edu]; Duprex, Paul[pduprex@pitt.edu]; Paul.Lambert (Paul.Lambert@unige.ch)[Paul.Lambert@unige.ch]; paul-mccray (paul-mccray@uiowa.edu)[paul-mccray@uiowa.edu]; Hodgson, Paul[paul.hodgson@usask.ca]; Paul.Dabisch[Paul.Dabisch@ST.DHS.GOV]; Pauline Maisonnasse (pauline.maisonnasse@cea.fr)[pauline.maisonnasse@cea.fr]; BAMFORD, Pearl[Pearl.Bamford@health.gov.au]; Shi, Pei yong[peshi@UTMB.EDU]; peter.palese@mssm.edu[peter.palese@mssm.edu]; Krause, Philip[philip.krause@fda.hhs.gov]; Philip Minor (Philip.Minor2@gmail.com)[Philip.Minor2@gmail.com]; BRANGEL, Polina[brangelp@who.int]; que.dang@nih.gov[que.dang@nih.gov]; REIRELAND (REIRELAND@mail.dstl.gov.uk)[REIRELAND@mail.dstl.gov.uk]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org)[rafael.delgado@salud.madrid.org]; rbaric (rbaric@email.unc.edu)[rbaric@email.unc.edu]; rhakami@gmu.edu[rhakami@gmu.edu]; ramadany[ramadany@sfda.gov.sa]; Albrecht, Randy[randy.albrecht@mssm.edu]; Riccardo Russo[russori@njms.rutgers.edu]; rcarrion (rcarrion@TxBiomed.org)[rcarrion@TxBiomed.org]; res2025[res2025@med.cornell.edu]; Levis, Robin[robin.levis@fda.hhs.gov]; Roger Le Grand (roger.le-grand@cea.fr)[roger.le-grand@cea.fr]; Romain Volmer (romain.volmer@envt.fr)[romain.volmer@envt.fr]; Donis, Ruben (OS/ASPR/BARDA)[ruben.donis@hhs.gov]; Russell.Ray@bcm.edu[Russell.Ray@bcm.edu]; Sally Sharpe (Sally.Sharpe@phe.gov.uk)[Sally.Sharpe@phe.gov.uk]; Cartner, Samuel Corbin[scartner@uab.edu]; S. Herfst[s.herfst@erasmusmc.nl]; scordo (scordo@qb.fcen.uba.ar)[scordo@qb.fcen.uba.ar]; LESELLIER Sandrine (sandrine.lesellier@anses.fr)[sandrine.lesellier@anses.fr]; seos@cnu.ac.kr[seos@cnu.ac.kr]; sean.li (sean.li@canada.ca)[sean.li@canada.ca]; sekim (sekim@krict.re.kr)[sekim@krict.re.kr]; Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru)[s.a.arakelov@spbniivs.ru]; sharon.daye2.mil@mail.mil[sharon.daye2.mil@mail.mil]; SHELBY L O'CONNOR[slfeinberg@wisc.edu]; Hild, Sheri (NIH/OD) [E][sheri.hild@nih.gov]; Simon Funnell (simon.funnell@phe.gov.uk)[simon.funnell@phe.gov.uk]; sinabavari@comcast.net[sinabavari@comcast.net]; YOO, Si Hyung[yoos@who.int]; sodas[sodas@health.ucsd.edu]; SWAMINATHAN, Soumya[swaminathans@who.int]; Perlman, Stanley[stanley-perlman@uiowa.edu]; MSLEVER (MSLEVER@dstl.gov.uk)[MSLEVER@dstl.gov.uk]; SBradfute@salud.unm.edu[SBradfute@salud.unm.edu]; sbournazos@mail.rockefeller.edu[sbournazos@mail.rockefeller.edu]; Suchinda Malaivijitnond (suchinda.m@chula.ac.th)[suchinda.m@chula.ac.th]; Tadaki (tksuzuki@nih.go.jp)[tksuzuki@nih.go.jp]; tyamamoto@ciea.or.jp[tyamamoto@ciea.or.jp]; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil)[terry.k.besch.ctr@mail.mil]; Pickett, Thames (NIH/NIAID) [E][pickettte@niaid.nih.gov]; t.sulpice[t.sulpice@physiogenex.com]; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de)[ThomasC.Mettenleiter@fli.de]; thomasf@primate.wisc.edu[thomasf@primate.wisc.edu]; ZHOU, Tiequn[ZhouT@who.int]; sheahan[sheahan@email.unc.edu]; tomeri (tomeri@iibr.gov.il)[tomeri@iibr.gov.il]; Tony.Schountz@colostate.edu[Tony.Schountz@colostate.edu]; Tony.Wang (Tony.Wang@fda.hhs.gov)[Tony.Wang@fda.hhs.gov]; MacGill, Tracy[Tracy.MacGill@fda.hhs.gov]; Brasel, Trevor[trbrasel@UTMB.EDU]; tcs38@psu.edu[tcs38@psu.edu]; troyrandall (troyrandall@uabmc.edu)[troyrandall@uabmc.edu]; Vasan, Vasan (H&B, Geelong ACDP)[Vasan.Vasan@csiro.au];

SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; Victoria.Wahl[Victoria.Wahl@ST.DHS.GOV]; Yusibov, Vidadi (OS/ASPR/BARDA)[Vidadi.Yusibov@hhs.gov]; Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]; Volker.gerdts (Volker.gerdts@usask.ca)[Volker.gerdts@usask.ca]; William Dowling (william.dowling@cepi.net)[william.dowling@cepi.net]; wim.vanderpoel@wur.nl[wim.vanderpoel@wur.nl]; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr)[xavier.de-lamballerie@univ-amu.fr]; RIVEROS BALTA, Ximena[lauriex@who.int]; Yper.Hall (Yper.Hall@phe.gov.uk)[Yper.Hall@phe.gov.uk]; yu.cong@nih.gov[yu.cong@nih.gov]; ym.vasilev[ym.vasilev@rpharm.ru]; sanath.rao[sanath.rao@canada.ca]; Jason.Mott[Jason.Mott@hhs.gov]; antoine.nougairede[antoine.nougairede@univ-amu.fr]; ygoez[ygoez@txbiomed.org]; Karen Gooch[karen.gooch@phe.gov.uk]; Kathryn Ryan[Kathryn.ryan@phe.gov.uk]; sid.byrareddy[sid.byrareddy@unmc.edu]; lok-yinroy-wong[lok-yinroy-wong@uiowa.edu]; julia.port[julia.port@nih.gov]; Benjamin Murrell[benjamin.murrell@ki.se]; D.A.J. van Riel[d.vanriel@erasmusmc.nl]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; mohamad.taha[mohamad.taha@canada.ca]; Mariana.Baz[Mariana.Baz@influenzacentre.org]; d.muller4[d.muller4@uq.edu.au]; hellopragya22 (hellopragya22@gmail.com)[hellopragya22@gmail.com]
Cc: kyle.rosenke[kyle.rosenke@nih.gov]; d.muller4[d.muller4@uq.edu.au]
From: SCHWARTZ, Lauren[schwartzl@who.int]
Sent: Mon 6/28/2021 2:57:31 PM (UTC-05:00)
Subject: RE: WHO COVID-19 Animal Models Group Call

Dear All,

Please find below the agenda for this week's WHO COVID-19 Animal Models group call.

Best,
Lauren – César, Simon, and Bill

Agenda WHO COVID-19 Animal Models group call Thursday July 1 3PM CET (Geneva time)

1. David Muller (U. Queensland) - *Complete protection by a single dose skin patch delivered SARS-CoV-2 spike vaccine in mice*
2. Kyle Rosenke (NIAID/RML) - *UK B.1.1.7 variant exhibits increased respiratory replication and shedding in nonhuman primates*

-----Original Appointment-----
From: SCHWARTZ, Lauren
Sent: Sunday, June 27, 2021 2:34 PM
To: SCHWARTZ, Lauren; WaickmaA@upstate.edu; Adolfo.Garcia-Sastre@mssm.edu; kandeil_a@hotmail.com; alankhoo.imr@gmail.com; abukreye@utmb.edu; agw13@pitt.edu; kupke@staff.uni-marburg.de; Ali.Mirazimi@folkhalsomyndigheten.se; amelia.karlsson@duke.edu; amy.c.shurtleff@cepi.net; HENAO RESTREPO, Ana Maria; Marzi, Andrea (NIH/NIAID) [E; Andrew.Phipps@hhs.gov; ajones@mail.rockefeller.edu; mopargal@rams.colostate.edu; angierasmussen@gmail.com; Lowen, Anice; anja.kipar@uzh.ch; Ann.Rawkins@phe.gov.uk; Honko, Anna; anna@thsti.res.in; Anthony Holmes - NC3Rs; ahgriff@bu.edu; Asisa.Volz@tiho-hannover.de; aysegul.nalca.civ@mail.mil; verstrepen@bprc.nl; Barbara.Schnierle@pei.de; barney.graham@nih.gov; b.rockx@erasmusmc.nl; b.haagmans@erasmusmc.nl; tenoever@gmail.com; Bernhard.Kerscher@pei.de; bobomok@hku.hk; bradley.pickering@canada.ca; CarlosAlberto.Guzman@helmholtz-hzi.de; CDillen@som.umaryland.edu; Carol.Sabourin@hhs.gov; caroline.foo@kuleuven.be; caroline.melo@rivm.nl; carolyn.clark@cepi.net; bosioc@niaid.nih.gov; munoz-fontela@bnitm.de; croy@tulane.edu; shanchao@wh.iov.cn; tverakit@gmail.com; mary.lane@nih.gov; cdang@lcr.org; cjmiller@ucdavis.edu; christian.c.hofer.mil@mail.mil; christiane.gerke@pasteur.fr; qinchuan@pumc.edu.cn; wenchun0617@gate.sinica.edu.tw; clint.florence@nih.gov; connie.schmaljohn@nih.gov; dbarouch@bidmc.harvard.edu; daniel.martinez-arguelles@canada.ca; danielle.anderson@unimelb.edu.au; darryl.falzarano@usask.ca; darwyn.kobasa@canada.ca; dhoconno@wisc.edu; David.Vaughn@gatesfoundation.org; drevelli@lovelacebiomedical.org; david.lee-parritz@tufts.edu; WOOD, David John; dean.smith@canada.ca; ldenisy@yahoo.com; dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak@bsd.uchicago.edu; dsreed@cvr.pitt.edu; dustin.johnson@canada.ca; esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; emmie.dewit@nih.gov; erica@lji.org; erik.stemmy@nih.gov; edohm@uab.edu; verschoor@bprc.nl; estefania.rodriguez@bnitm.de; KAZI, Fatema; fgrey@exseed.ed.ac.uk; florian.krammer@mssm.edu; franck.TOURET@univ-amu.fr; f.briand@physiogenex.com; fcassels@path.org; fkoide@southernresearch.org; gabriella.worwa@nih.gov; Gary.Kobinger@crchudequebec.ulaval.ca; sutter@micro.vetmed.uni-muenchen.de; Giada.Mattiuzzo@nibsc.org; sivkog@battelle.org; grace.m.lidl.mil@mail.mil; gustavo.palacios@gmail.com; horer@ku.edu.tr; Hana.Golding@fda.hhs.gov; Harry.Kleanthous@gatesfoundation.org; Damron,

Fredrick; feldmannh@niaid.nih.gov; hlchen@hku.hk; hwan.kim@stonybrook.edu; ian.crozier@nih.gov; i.v.krasilnikov@spbniivs.ru; ivan.marazzi@mssm.edu; 'KNEZEVIC, Ivana'; Martinez, Ivan; y.jacob.hou@unc.edu; Jacqueline.Kirchner@gatesfoundation.org; James.Little@hhs.gov; jjkobie@uabmc.edu; J.P.Stewart@liverpool.ac.uk; langermans@bprc.nl; Jason.Kindrachuk@umanitoba.ca; jfwchan@hku.hk; Javier.Salguero@phe.gov.uk; jay.w.hooper.civ@mail.mil; snumouse@snu.ac.kr; jhogan@uga.edu; ravetch@mail.rockefeller.edu; jmkperrine@gmail.com; jeroen.kortekaas@wur.nl; Jin.Zhu@health.gov.au; JLPRIOR@dstl.gov.uk; joanne@pitt.edu; joaquim.segales@irta.cat; johan.neyts (johan.neyts@kuleuven.be); John.Treanor@hhs.gov; john.c.trefry.civ@mail.mil; baczenas@wisc.edu; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; jorgen.de.jonge@rivm.nl; jfgarcia@cnb.csic.es; jricht@vet.k-state.edu; julia.vergara@irta.cat; Julia.Tree@phe.gov.uk; kai.dallmeier@kuleuven.be; kanta.subbarao@influenzacentre.org; Karen.Makar@gatesfoundation.org; Karl.Erlandson@hhs.gov; kmodjarrad@eidresearch.org; sktseng@UTMB.EDU; AKelvin@dal.ca; kevinharrod@uabmc.edu; rkiatchula@gmail.com; seungtaek.kim@ip-korea.org; stittelaar@viroclinics.com; 'SALAMI, Kolawole'; kristine.macartney@health.nsw.gov.au; kyle.rosenke@nih.gov; Lakshmi.Jayashankar@hhs.gov; SCHWARTZ, Lauren; lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; lisa.hensley@nih.gov; lgralins@email.unc.edu; lisette.cornelissen@wur.nl; margaret.l.pitt.civ@mail.mil; Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; luk_vandenberghe@meei.harvard.edu; ibz1@cdc.gov; mito@ciea.or.jp; mksong@ivi.int; Marco.Cavaleri@ema.europa.eu; mesteban@cnb.csic.es; PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis@bioqual.com; Mark.Page@nibsc.org; Mark Prescott - NC3Rs; marlene.espinozamoraga@mssm.edu; Martha.Alexander-Miller@wakehealth.edu; Martin.Beer@fli.de; Matthew.Reed.mil@afrims.org; MFrieman@som.umaryland.edu; mmeitzen@utmb.edu; michael.schotsaert@mssm.edu; mdiamond@wustl.edu; MNELSON@mail.dstl.gov.uk; mto@umn.edu; Michael.holbrook@nih.gov; michael.hevey@ST.DHS.GOV; Miles.Carroll@phe.gov.uk; mitchell.palmer@usda.gov; MONALISA.CHATTERJI@gatesfoundation.org; muhammad.munir@lancaster.ac.uk; nadia.khelef@pasteur.fr; nadia.oreshkova@wur.nl; nax3@cdc.gov; neeltje.vandoremalen@nih.gov; Neil.Berry@nibsc.org; Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola.Rose@nibsc.org; nirp@iibr.gov.il; nora.gerhards@wur.nl; nnagata@niid.go.jp; golinger@mriglobal.org; salgampa@njms.rutgers.edu; patrick.reid@unmc.edu; pduprex@pitt.edu; Paul.Lambert@unige.ch; paul-mccray@uiowa.edu; paul.hodgson@usask.ca; Paul.Dabisch@ST.DHS.GOV; pauline.maisonnasse@cea.fr; Pearl.Bamford@health.gov.au; peshi@UTMB.EDU; peter.palese@mssm.edu; philip.krause@fda.hhs.gov; philip.minor2@gmail.com; BRANGEL, Polina; que.dang@nih.gov; REIRELAND@mail.dstl.gov.uk; Delgado Vazquez.Rafael; rbaric@email.unc.edu; rhakami@gmu.edu; Rana A. Al Madany; randy.albrecht@mssm.edu; russori@njms.rutgers.edu; rcarrion@txbiomed.org; res2025@med.cornell.edu; robin.levis@fda.hhs.gov; roger.le-grand@cea.fr; romain.volmer@envt.fr; Ruben.Donis@hhs.gov; Russell.Ray@bcm.edu; Sally.Sharpe@phe.gov.uk; scartner@uab.edu; S. Herfst; scordo@qb.fcen.uba.ar; sandrine.lesellier@anses.fr; seos@cnu.ac.kr; sean.li@canada.ca; sekim@krict.re.kr; s.a.arakelov@spbniivs.ru; sharon.daye2.mil@mail.mil; slfeinberg@wisc.edu; sheri.hild@nih.gov; Simon.Funnell@phe.gov.uk; sinabavari@comcast.net; YOO, Si Hyung; Das, Soumita; SWAMINATHAN, Soumya; stanley-perlman@uiowa.edu; MSLEVER@dstl.gov.uk; SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; suchinda.m@chula.ac.th; tksuzuki@nih.go.jp; tyamamoto@ciea.or.jp; terry.k.besch.ctr@mail.mil; pickettte@niaid.nih.gov; t.sulpice@physiogenex.com; ThomasC.Mettenleiter@fli.de; thomasf@primate.wisc.edu; ZHOU, Tiequn; Sheahan, Timothy Patrick; tomeri@iibr.gov.il; Tony.Schountz@colostate.edu; tony.wang@fda.hhs.gov; Tracy.MacGill@fda.hhs.gov; trbrasel@UTMB.EDU; tcs38@psu.edu; troyrandall@uabmc.edu; Vasan.Vasan@csiro.au; SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl@ST.DHS.GOV; Vidadi.Yusibov@hhs.gov; vincent.munster@nih.gov; Volker.gerdts@usask.ca; william.dowling@cepi.net; wim.vanderpoel@wur.nl; xavier.de-lamballerie@univ-amu.fr; RIVEROS BALTA, Ximena; Yper.Hall@phe.gov.uk; yu.cong@nih.gov; ym.vasilev@rpharm.ru; sanath.rao@canada.ca; Jason.Mott@hhs.gov; antoine.nougairede@univ-amu.fr; ygoez@txbiomed.org; karen.gooch@phe.gov.uk; Kathryn.ryan@phe.gov.uk; sid.byrareddy@unmc.edu; lok-yinroy-wong@uiowa.edu; julia.port@nih.gov; benjamin.murrell@ki.se; d.vanriel@erasmusmc.nl; cherrys@pennmedicine.upenn.edu; mohamad.taha@canada.ca; Mariana.Baz@influenzacentre.org; d.muller4@uq.edu.au; hellopragya22@gmail.com

Subject: WHO COVID-19 Animal Models Group Call
When: Thursday, July 1, 2021 3:00 PM-4:30 PM (UTC+01:00) Amsterdam, Berlin, Bern, Rome, Stockholm, Vienna.
Where: https://who.zoom.us/j/3612568290

Agenda to follow.

Join Zoom Meeting
https://who.zoom.us/j/3612568290

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+41225910005,,3612568290# Switzerland
+41225910156,,3612568290# Switzerland

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+41 22 591 00 05 Switzerland
+41 22 591 01 56 Switzerland
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+41 43 210 70 42 Switzerland
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+1 253 215 8782 US (Tacoma)
+1 720 928 9299 US (Denver)
+1 971 247 1195 US (Portland)
+1 213 338 8477 US (Los Angeles)
+1 346 248 7799 US (Houston)
+1 602 753 0140 US (Phoenix)
+1 669 219 2599 US (San Jose)
+1 669 900 9128 US (San Jose)
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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: WaickmaA@upstate.edu; Garcia-Sastre, Adolfo; kandeil_a (kandeil_a@hotmail.com); alankhoo.imr; Bukreyev, Alexander; White, Alexander G; kupke (kupke@staff.uni-marburg.de); Ali.Mirazimi (Ali.Mirazimi@folkhalsomyndigheten.se); Amelia Karlsson (amelia.karlsson@duke.edu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); HENAO RESTREPO, Ana Maria; marzia; Andrew.Phipps; ajones; mopargal (mopargal@rams.colostate.edu); angierasmussen@gmail.com; anice.lowen; anja.kipar@uzh.ch; Ann Rawkins (Ann.Rawkins@phe.gov.uk); Honko, Anna; anna (anna@thsti.res.in); Anthony Holmes - NC3Rs (Anthony.Holmes@nc3rs.org.uk); Griffiths, Anthony; Asisa.Volz (Asisa.Volz@tiho-hannover.de); aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); verstrepen@bprc.nl; Barbara.Schnierle (Barbara.Schnierle@pei.de); Graham, Barney (NIH/VRC) [E]; B.H.G. Rockx (b.rockx@erasmusmc.nl); B.L. Haagmans (b.haagmans@erasmusmc.nl); tenoever@gmail.com; Bernhard Kerscher (PEI-DE) (bernhard.kerscher@pei.de); bobomok@hku.hk; bradley.pickering (bradley.pickering@canada.ca); CarlosAlberto.Guzman (CarlosAlberto.Guzman@helmholtz-hzi.de); CDillen@som.umaryland.edu; Sabourin, Carol (OS/ASPR/BARDA); caroline.foo; caroline.melo@rivm.nl; Carolyn Clark (carolyn.clark@cepi.net); bosioc@niaid.nih.gov; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); croy (croy@tulane.edu); shanchao (shanchao@wh.iov.cn); Techakitiroj Chatkul (tverakit@gmail.com); mary.lane@nih.gov; Chi Van Dang (cdang@lcr.org); Chris Miller (cjmiller@ucdavis.edu); christian.c.hofer.mil@mail.mil; Christiane Gerke (christiane.gerke@pasteur.fr); qinchuan (qinchuan@pumc.edu.cn); wenchun0617; Florence, Clint (NIH/NIAID) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; dbarouch (dbarouch@bidmc.harvard.edu); daniel.martinez-arguelles; danielle.anderson; Falzarano, Darryl; darwyn.kobasa@canada.ca; DAVID H O'CONNOR (dhoconno@wisc.edu); David Vaughn (David.Vaughn@gatesfoundation.org); David Revelli (drevelli@lovelacebiomedical.org); Lee-Parritz, David; WOOD, David John; dean.smith (dean.smith@canada.ca); Idenisy (Idenisy@yahoo.com); dbolton@hivresearch.org; dgdiel@cornell.edu; dmissiak (dmissiak@bsd.uchicago.edu); dsreed@cvr.pitt.edu; dustin.johnson (dustin.johnson@canada.ca); esulkowska@rics.bwh.harvard.edu; Elliot Lilley - NC3Rs; De wit, Emmie (NIH/NIAID) [E]; erica (erica@lji.org); Stemmy, Erik (NIH/NIAID) [E]; Dohm, Erik Daniel; verschoor (verschoor@bprc.nl); estefania.rodriguez (estefania.rodriguez@bnitm.de); KAZI, Fatema; GREY Finn (fgrey@exseed.ed.ac.uk); Krammer, Florian; franck.TOURET@univ-amu.fr; f.briand; Cassels, Fred; fkoide (fkoide@southernresearch.org); gabriella.worwa; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); sutter (sutter@micro.vetmed.uni-muenchen.de); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Sivko, Gloria S; grace.m.lidl.mil@mail.mil; gustavo.palacios (gustavo.palacios@gmail.com); horer@ku.edu.tr; Golding, Hana; Harry Kleanthous (Harry.Kleanthous@gatesfoundation.org); Damron, Fredrick; feldmannh@niaid.nih.gov; hlchen (hlchen@hku.hk); Hwan K Kim (hwan.kim@stonybrook.edu); Crozier, Ian (NIH) [C]; i.v.krasilnikov (i.v.krasilnikov@spbniivs.ru); ivan.marazzi; KNEZEVIC, Ivana; IVMARTINEZ; y.jacob.hou@unc.edu; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Little, James (OS/ASPR/BARDA); Kobie, James J; Stewart, James; langermans (langermans@bprc.nl); Jason Kindrachuk (Jason.Kindrachuk@umanitoba.ca); jfwchan (jfwchan@hku.hk); Javier Salguero (Javier.Salguero@phe.gov.uk); jay.w.hooper.civ (jay.w.hooper.civ@mail.mil); snumouse (snumouse@snu.ac.kr); jhogan@uga.edu; ravetch; jmkperrine; jeroen.kortekaas (jeroen.kortekaas@wur.nl); ZHU, Jin; JLPRIOR (JLPRIOR@dstl.gov.uk); Flynn, Joanne L; Segales, Joaquim; johan.neyts (johan.neyts@kuleuven.be); Treanor, John (OS/ASPR/BARDA) (CTR); john.c.trefry.civ (john.c.trefry.civ@mail.mil); JOHN JAMES BACZENAS; SPERGEL@email.chop.edu; JTorrelles@txbiomed.org; Jorgen de Jonge (jorgen.de.jonge@rivm.nl); Juan García Arriaza (jfgarcia@cnb.csic.es); Juergen Richt (jricht@vet.k-state.edu); Vergara, Julia; Julia Tree (Julia.Tree@phe.gov.uk); kai.dallmeier (kai.dallmeier@kuleuven.be); kanta.subbarao (kanta.subbarao@influenzacentre.org); Karen Makar (Karen.Makar@gatesfoundation.org); Karl.Erlandson (Karl.Erlandson@hhs.gov); Kayvon Modjarrad (kmodjarrad@eidresearch.org); Tseng, Chien-Te K.; Alyson Kelvin; kevinharrod (kevinharrod@uabmc.edu); rkiatchula (rkiatchula@gmail.com); Seungtaek Kim (seungtaek.kim@ip-korea.org); stittelaar (stittelaar@viroclinics.com); SALAMI, Kolawole; Kristine Macartney (kristine.macartney@health.nsw.gov.au); kyle.rosenke; Jayashankar, Lakshmi (OS/ASPR/BARDA); lawton.stubbert@canada.ca; lisambrosseau@gmail.com; lisa.chakrabarti@pasteur.fr; Hensley, Lisa (NIH/NIAID) [E]; lgralins@email.unc.edu; lisette.cornelissen; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Luis.Lugo.mil@afrims.org; l.enjuanes@cnb.csic.es; LMartinez@txbiomed.org; Vandenberghe, Luk; Atherton, Lydia J. (CDC/DDID/NCIRD/DVD); mito@ciea.or.jp; Manki Song (mksong@ivi.int); Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); mesteban (mesteban@cnb.csic.es); PREZIOSI, Marie-pierre; mariette.ducatez@envt.fr; mlewis (mlewis@bioqual.com); Mark Page (Mark.Page@nibsc.org); Mark Prescott - NC3Rs; marlene.espinozamoraga; Martha Alexander-Miller (Martha.Alexander-Miller@wakehealth.edu); Martin.Beer (Martin.Beer@fli.de); Matthew.Reed.mil@afrims.org; Frieman, Matthew; Eitzen, Melissa M.; Schotsaert, Michael; mdiamond (mdiamond@wustl.edu); MNELSON@mail.dstl.gov.uk; mto@umn.edu; Holbrook, Michael (NIH/NIAID) [C]; Hevey, Michael (CTR); Miles.Carroll (Miles.Carroll@phe.gov.uk); mitchell.palmer@usda.gov; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Munir, Muhammad; Nadia KHELEF (nadia.khelef@pasteur.fr); Oreshkova, Nadia; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); neeltje.vandoremalen@nih.gov; Neil Berry (Neil.Berry@nibsc.org); Nerea_ZabaletaLasarte@MEEI.HARVARD.EDU; Nicola Rose (Nicola.Rose@nibsc.org); nirp (nirp@iibr.gov.il); Gerhards, Nora; nnagata@niid.go.jp; Olinger, Gene; salgampa (salgampa@njms.rutgers.edu); patrick.reid@unmc.edu; Duprex, Paul; Paul.Lambert

(Paul.Lambert@unige.ch); paul-mccray (paul-mccray@uiowa.edu); Hodgson, Paul; Paul.Dabisch; Pauline Maisonnasse (pauline.maisonnasse@cea.fr); BAMFORD, Pearl; Shi, Pei yong; peter.palese@mssm.edu; Krause, Philip; Philip Minor (Philip.Minor2@gmail.com); BRANGEL, Polina; que.dang@nih.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); rbaric (rbaric@email.unc.edu); rhakami@gmu.edu; ramadany; Albrecht, Randy; Riccardo Russo; rcarrion (rcarrion@TxBiomed.org); res2025; Levis, Robin; Roger Le Grand (roger.le-grand@cea.fr); Romain Volmer (romain.volmer@envt.fr); Donis, Ruben (OS/ASPR/BARDA); Russell.Ray@bcm.edu; Sally Sharpe (Sally.Sharpe@phe.gov.uk); Cartner, Samuel Corbin; S. Herfst; scordo (scordo@qb.fcen.uba.ar); LESELLIER Sandrine (sandrine.lesellier@anses.fr); seos@cnu.ac.kr; sean.li (sean.li@canada.ca); sekim (sekim@krict.re.kr); Аракелов Сергей Александрович (s.a.arakelov@spbniivs.ru); sharon.daye2.mil@mail.mil; SHELBY L O'CONNOR; Hild, Sheri (NIH/OD) [E]; Simon Funnell (simon.funnell@phe.gov.uk); sinabavari@comcast.net; YOO, Si Hyung; sodas; SWAMINATHAN, Soumya; Perlman, Stanley; MSLEVER (MSLEVER@dstl.gov.uk); SBradfute@salud.unm.edu; sbournazos@mail.rockefeller.edu; Suchinda Malaivijitnond (suchinda.m@chula.ac.th); Tadaki (tksuzuki@nih.go.jp); tyamamoto@ciea.or.jp; terry.k.besch.ctr (terry.k.besch.ctr@mail.mil); Pickett, Thames (NIH/NIAID) [E]; t.sulpice; ThomasC.Mettenleiter (ThomasC.Mettenleiter@fli.de); thomasf@primate.wisc.edu; ZHOU, Tiequn; sheahan; tomeri (tomeri@iibr.gov.il); Tony.Schountz@colostate.edu; Tony.Wang (Tony.Wang@fda.hhs.gov); MacGill, Tracy; Brasel, Trevor; tcs38@psu.edu; troyrandall (troyrandall@uabmc.edu); Vasan, Vasan (H&B, Geelong ACDP); SATHIYAMOORTHY, Vaseeharan; Victoria.Wahl; Yusibov, Vidadi (OS/ASPR/BARDA); Munster, Vincent (NIH/NIAID) [E]; Volker.gerdts (Volker.gerdts@usask.ca); William Dowling (william.dowling@cepi.net); wim.vanderpoel@wur.nl; NICOLAS DE LAMBALLERIE Xavier (xavier.de-lamballerie@univ-amu.fr); RIVEROS BALTA, Ximena; Yper.Hall (Yper.Hall@phe.gov.uk); yu.cong@nih.gov; Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); sanath.rao; Jason.Mott; antoine.nougairede; ygoez; Karen Gooch; Kathryn Ryan; sid.byrareddy; lok-yinroy-wong; julia.port; Benjamin Murrell; D.A.J. van Riel; Cherry, Sara; mohamad.taha; Mariana.Baz

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To: Menachery, Vineet[vimenach@UTMB.EDU]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; volker.thiel@vetsuisse.unibe.ch[volker.thiel@vetsuisse.unibe.ch]; kristen.bernard@wisc.edu[kristen.bernard@wisc.edu]
From: Dalder-Alpher, Erin[edalder-alpher@asmusa.org]
Sent: Mon 6/21/2021 2:36:52 PM (UTC-05:00)
Subject: Let's try this again--today's after chat

For today's After Chat

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Erin Dalder-Alpher | Senior Program Officer, ASM Microbe
American Society for Microbiology
1752 N Street, NW | Washington, DC 20036
202.942.9382 direct | 202.737.3600 main | 202.942.9340 fax

To: zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Menachery, Vineet[vimenach@UTMB.EDU]; Bloom PhD, Jesse D[jbloom@fredhutch.org]
Cc: volker.thiel@vetsuisse.unibe.ch[volker.thiel@vetsuisse.unibe.ch]; Spindler, Katherine[krspin@umich.edu]
From: Kristen Bernard[kristen.bernard@wisc.edu]
Sent: Mon 6/21/2021 3:54:46 PM (UTC-05:00)
Subject: Thanks for the great session

Dear Zhengli, Vineet, and Jesse,

Thanks so much for your very interesting talks for the World Microbe Forum. I was so impressed with the science, and your recordings were really polished.

I hope to see you in person in the future. Take care!

Best,
Kristen

Kristen Bernard, DVM, PhD
Professor of Virology
Department of Pathobiological Sciences
School of Veterinary Medicine
University of Wisconsin-Madison
2015 Linden Dr.
Madison, WI 53706

Pronouns: she/her
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Email: kristen.bernard@wisc.edu
Phone: 608-263-7114
Office room #: 4270C
Lab room #: 4240A

Twitter @UWbernardLab

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); SACKS, Jilian; SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER, Ute; SUBISSI, Lorenzo;

tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); ym.vasilev; David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; Amy Chung; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont; MULDERS, Mick; diana.molino; Merryn Voysey (merryn.voysey@paediatrics.ox.ac.uk)

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: rahmed; Alter, Galit; raul.andino; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); ellie.barnes; dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; bertozzi; Kevin Bewley (Kevin.bewley@phe.gov.uk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; cblish; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; Aodhan.Breathnach; christian.brechot (christian.brechot@pasteur.fr); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); Christine Bruce (Christine.bruce@phe.gov.uk); Mihaela BUDA; Miles.Carroll (Miles.Carroll@phe.gov.uk); zuz4 (zuz4@cdc.gov); tdcarroll; Cassels, Fred; Javier Castillo-Olivares Pallardo; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Meera Chand; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); charles.chiu; Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; Crozier, Ian (NIH) [C]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; t.desilva; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); joe; diane.descamps@aphp.fr; mit666666 (mit666666@pitt.edu); Donis, Ruben (OS/ASPR/BARDA); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); lny1@cdc.gov; susie.dunachie; epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Camille Escadafal; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; douglas_fox; Frieman, Matthew; Jacqueline.Fryer; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); SGalloway@cdc.gov; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; Karen Gooch; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; elwyn.griffiths@cepi.net; Griffiths, Anthony; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Victoria.Hall; Carl.Hanson; Theodora Hatziioannou; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); Iturriza-Gomara, Miren; ASiyer@mgh.harvard.edu; William James; Jayashankar, Lakshmi (OS/ASPR/BARDA); Youngmee Jee (jeey62@gmail.com); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; KAZI, Fatema; Kelvin, Alyson; kemptj; alankhoo.imr; jakim; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); amy.kistler; paul.klenerman; KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Krammer, Florian; Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); renuka.kumar; pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); a.luttick; jma; MacGill, Tracy; ramadany; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Chris Miller (cjmiller@ucdavis.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; Clare.Morris@nibsc.org; MaryKate.Morris; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; mbo2@cdc.gov; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; engeong.ooi; melanie.ott; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Paxton, Bill; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Pillai, Satish; pintol; margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; Pollakis, Georgios; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); arjun.rustagi; Kathryn Ryan; Sabourin, Carol (OS/ASPR/BARDA); Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; Marc L Salit (msalit@stanford.edu); SANDS, Anita; erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; GSimmons; viviana.simon; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); sastanley; Stemmy, Erik (NIH/NIAID) [E]; STRÖHER,

Ute; SUBISSI, Lorenzo; tcs38@psu.edu; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); sot1@cdc.gov; alain.townsend (alain.townsend@imm.ox.ac.uk); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); Turtle, Lance; Vandenberghe, Luk; Sylvie VAN DER WERF; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); Wadford, Debra@CDPH; wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); linfa.wang (linfa.wang@duke-nus.edu.sg); Weir, Jerry P.; gweiss@uci.edu; Wentworth, David E. (CDC/OID/NCIRD); daniela@lji.org; tomwhite42450@gmail.com; KurtW; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Yusibov, Vidadi (OS/ASPR/BARDA); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; sid.byrareddy; awchung@unimelb.edu.au; Breeze.Cavell; Townsend, Michael B. (CDC/DDID/NCEZID/DHCPP); Suthar, Mehul; LDumont; MULDERS, Mick

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From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; 'jjdavis@anl.gov'; Richard Scheuermann; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; 'adam.godzik@ucr.edu'; Jason McLellan; Bette Korber; 'lmwoga@fredhutch.org'; 'monte@duke.edu'; 'spjwhelan@wustl.edu'; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; 'jbloom@fredhutch.org'; Julie McElrath; 'kawaokay@svm.vetmed.wisc.edu'; 'vimenach@utmb.edu'; 'noah.sather@seattlechildrens.org'; Matthew Frieman; Morgane Rolland; Baric, Ralph; Richard Webby; Adolfo García-Sastre; 'malik@hku.hk'; Andrew B. Ward; Ali Ellebedy; 'mdiamond@wustl.edu'; Derek J. Smith; 'jboon@wustl.edu'; Aubree Gordon; 'stanley-perlman@uiowa.edu'; 'harm.vanbakel@mssm.edu'; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; 'Alessandro Sette'; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Michael Schotsaert; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; 'gregory.d.gromowski.civ@mail.mil'; 'irina.maljkovicberry.ctr@mail.mil'; 'jeffrey.r.currier.civ@mail.mil'; 'tbedford@fredhutch.org'; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; 'Tomer Hertz'; agrifoni; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; sweaver; 'Lidl, Grace M LTC USARMY FUTURES COMMAND (USA)'; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Carly Dillen; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S. (apekosz@jhsph.edu); Andy Pekosz; lemieux@broadinstitute.org; Ardanuy, Jeremy; leah.katzelnick@niaid.nih.gov; Katzelnick, Leah (NIH/NIAID) [E]; Marlene Espinoza-Moraga; Burnham, Andrew (NIH/NIAID) [C]; Stephan Bour; aburnham@gryphonscientific.com; 'stevens@anl.gov'; Vincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]

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Subject: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 2/12/2021 7:30:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 8:30:00 AM (UTC-06:00)

Required Attendees: Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni'stevens@anl.gov'; Vincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]

Optional Attendees: David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S.

(apekosz@jhsph.edu); Andy Pekosz; lemieux@broadinstitute.org; Ardanuy, Jeremy; leah.katzelnick@niaid.nih.gov; Katzelnick, Leah (NIH/NIAID) [E]; Marlene Espinoza-Moraga; Burnham, Andrew (NIH/NIAID) [C]; Stephan Bour; aburnham@gryphonscientific.com

Research Update Template.xlsx

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd= **552.136**

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161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: **552.136**

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
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	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
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	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 5/28/2021 12:30:00 PM (UTC)
End Time:	Fri 5/28/2021 1:30:00 PM (UTC)
Required Attendees:	Graham, Barney (NIH/VRC) [E]; Garcia-Sastre, Adolfo; Menachery, Vineet; stevens@anl.gov; stacey schultz-cherry; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh
Optional Attendees:	Weaver, ScottDavid Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
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	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
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		Description of assay
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	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
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Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Subject: Canceled: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 6/18/2021 12:30:00 PM (UTC)

End Time: Fri 6/18/2021 1:30:00 PM (UTC)

Required Attendees: Stacey Schultz-Cherry; vimenach@utmb.edu; Adolfo García-Sastre; Graham, Barney (NIH/VRC) [E]Degrace, Marciela (NIH/NIAID) [E]; stevens@anl.gov; dbarouch; McDermott, Adrian (NIH/VRC) [E]; Douek, Daniel (NIH/VRC) [E]; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz

Optional Attendees: Weaver, ScottBoritz, Eli (NIH/NIAID) [E]; Doria-Rose, Nicole (NIH/NIAID) [E]; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Erlandson, Karl (OS/ASPR/BARDA)

Research Update Template.xlsx

Cancelling tomorrow's meeting due to the new federal holiday.

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Join ZoomGov Meeting
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+1 646 828 7666 US (New York)
+1 551 285 1373 US
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Meeting ID: 160 266 4950
Passcode: **552.136**
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161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: **552.136**

		Description of resource
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		Description of assay
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	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 6/4/2021 12:30:00 PM (UTC)
End Time:	Fri 6/4/2021 1:30:00 PM (UTC)
Required Attendees:	Wentworth, David E. (CDC/DDID/NCIRD/ID); stevens@anl.gov; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez

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Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 6/25/2021 12:30:00 PM (UTC)
End Time:	Fri 6/25/2021 1:30:00 PM (UTC)
Required Attendees:	stevens@anl.gov; mdiamond@wustl.edu; Stacey Schultz-Cherry; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; McDermott, Adrian (NIH/VRC) [E]
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Doria-Rose, Nicole (NIH/NIAID) [E]; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA)

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 6/11/2021 12:30:00 PM (UTC)
End Time:	Fri 6/11/2021 1:30:00 PM (UTC)
Required Attendees:	stevens@anl.gov; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz
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Research Update Template.xlsx

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		B.1.351
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	Plasmids	
	RG virus	
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	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
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	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
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	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Subject: Canceled: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 7/2/2021 12:30:00 PM (UTC)

End Time: Fri 7/2/2021 1:30:00 PM (UTC)

Required Attendees: Stacey Schultz-Cherry; vimenach@utmb.edu; Adolfo García-Sastre; Graham, Barney (NIH/VRC) [E]Degrace, Marciela (NIH/NIAID) [E]; McDermott, Adrian (NIH/VRC) [E]; dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz

Optional Attendees: Weaver, ScottDavid Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA)

Research Update Template.xlsx

****Cancelling due to the holiday weekend*****

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Meeting ID: 160 266 4950
Passcode: 552.136
One tap mobile
+16692545252,,1602664950#,,,,* 552.136 US (San Jose)
+16468287666,,1602664950#,,,,* 552.136 US (New York)

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
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Meeting ID: 160 266 4950
Passcode: 552.136
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP
1602664950@sip.zoomgov.com

Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: **552.136**

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 7/16/2021 12:30:00 PM (UTC)
End Time:	Fri 7/16/2021 1:30:00 PM (UTC)
Required Attendees:	stevens@anl.gov; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni; Ghedin, Elodie (NIH/NIAID) [E]; McDermott, Adrian (NIH/VRC) [E]
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Gordon, Jennifer (NIH/NIAID) [E]

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
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		Description (ms strain, number available, etc.)
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		Description of assay
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		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 7/9/2021 12:30:00 PM (UTC)
End Time:	Fri 7/9/2021 1:30:00 PM (UTC)
Required Attendees:	R.A.M. Fouchier; Wentworth, David E. (CDC/DDID/NCIRD/ID); Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz
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		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 7/30/2021 12:30:00 PM (UTC)
End Time:	Fri 7/30/2021 1:30:00 PM (UTC)
Required Attendees:	Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni; McDermott, Adrian (NIH/VRC) [E]
Optional Attendees:	Boritz, Eli (NIH/NIAID) [E]; Corbett, Kizzmekia SDavid Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S. (apekosz@jhsph.edu); Andy Pekosz

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
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	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
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	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 8/6/2021 12:30:00 PM (UTC)
End Time:	Fri 8/6/2021 1:30:00 PM (UTC)
Required Attendees:	mdiamond@wustl.edu; Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni; McDermott, Adrian (NIH/VRC) [E]
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S. (apekosz@jhsph.edu); Andy Pekosz; lemieux@broadinstitute.org; Ardanuy, Jeremy; leah.katzelnick@niaid.nih.gov; Katzelnick, Leah (NIH/NIAID) [E]; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA)

Research Update Template.xlsx

		Description of resource
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		B.1.351
		P.1
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	NHP	

		Description of assay
	Binding	

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	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 7/23/2021 12:30:00 PM (UTC)
End Time:	Fri 7/23/2021 1:30:00 PM (UTC)
Required Attendees:	Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni
Optional Attendees:	Doria-Rose, Nicole (NIH/NIAID) [E]David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Lerner, Andrea (NIH/NIAID) [E]

Research Update Template.xlsx

		Description of resource
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		B.1.351
		P.1
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		Description (ms strain, number available, etc.)
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		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

Importance: Normal

Subject: Canceled: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 8/13/2021 12:30:00 PM (UTC)

End Time: Fri 8/13/2021 1:30:00 PM (UTC)

Required Attendees: Stacey Schultz-Cherry; vimenach@utmb.edu; Adolfo García-Sastre; Graham, Barney (NIH/VRC) [E]Degrace, Marciela (NIH/NIAID) [E]; mdiamond@wustl.edu; Wentworth, David E. (CDC/DDID/NCIRD/ID); dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]; tbedford@fredhutch.org; Patrick C. Wilson; R.A.M. Fouchier; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni

Optional Attendees: Weaver, ScottDoria-Rose, Nicole (NIH/NIAID) [E]; David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Ho, David D.; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S. (apekosz@jhsph.edu); Andy Pekosz; lemieux@broadinstitute.org; Ardanuy, Jeremy; leah.katzelnick@niaid.nih.gov; Katzelnick, Leah (NIH/NIAID) [E]

Research Update Template.xlsx

Hi everyone,

We are cancelling tomorrow's meeting due to a conflict with the WHO Consultation on COVID-19 vaccine research. If you would like to attend please find information here: https://www.who.int/news-room/events/detail/2021/08/13/default-calendar/who-consultation-on-covid-19-vaccines-research-13-august-2021

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd=552.136

Meeting ID: 160 266 4950
Passcode: 552.136
One tap mobile
+16692545252,,1602664950#,,,,*552.136 US (San Jose)
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Dial by your location
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833 568 8864 US Toll-free
Meeting ID: 160 266 4950
Passcode: 552.136
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP
1602664950@sip.zoomgov.com

Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: 552.136

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Importance:	Normal
Start Time:	Fri 8/27/2021 12:30:00 PM (UTC)
End Time:	Fri 8/27/2021 1:30:00 PM (UTC)
Required Attendees:	Degrace, Marciela (NIH/NIAID) [E]; dbarouch; Krogan, Nevan; Paul Thomas; Stacey Schultz-Cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; vimenach@utmb.edu; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Adolfo García-Sastre; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; tbedford@fredhutch.org; Patrick C. Wilson; Douek, Daniel (NIH/VRC) [E]; Donis, Ruben (OS/ASPR/BARDA); Hauguel, Teresa (NIH/NIAID) [E]; D'Souza, Patricia (NIH/NIAID) [E]; Galloway, Summer (CDC/DDID/NCIRD/ID); Oberste, Steve (CDC/DDID/NCIRD/DVD); Sullivan, Nancy (NIH/VRC) [E]; Galit Alter; Wolf, Josh; Tomer Hertz; agrifoni; Florian Krammer'stevens@anl.gov'; Vincent, Leah (NIH/NIAID) [E]; Maciel, Milton (NIH/NIAID) [E]; McDermott, Adrian (NIH/VRC) [E]; R.A.M. Fouchier; Wentworth, David E. (CDC/DDID/NCIRD/ID)
Optional Attendees:	David Montefiori, Ph.D.; Michael, Nelson; Zhou, Bin (CDC/DDID/NCIRD/ID); Peter Halfmann; Holbrook, Michael (NIH/NIAID) [C]; Hensley, Lisa (NIH/NIAID) [E]; Gardner, Meredith Elizabeth Davis; Weaver, Scott; Lidl, Grace M LTC USARMY FUTURES COMMAND (USA); Friberg-Robertson, Heather L CIV USARMY FUTURES COMMAND (USA); Simon, Viviana; sxshen@duke.edu; Doria-Rose, Nicole (NIH/NIAID) [E]; Logue, James; Dillen, Carly; Johnson, Robert; Shabman, Reed (NIH/NIAID) [E]; Hui-Ling Yen; Luo, Yang; Guido Ferrari, M.D.; Georgia Tomaras, Ph.D.; Kuhn, Jens (NIH/NIAID) [C]; Bratt, Debbie (NIH/NIAID) [C]; Luis Martinez; Boritz, Eli (NIH/NIAID) [E]; Erlandson, Karl (OS/ASPR/BARDA); Gordon, Jennifer (NIH/NIAID) [E]; Corbett, Kizzmekia S; Erbelding, Emily (NIH/NIAID) [E]; Pekosz, Andrew S. (apekosz@jhsph.edu); Andy Pekosz; lemieux@broadinstitute.org; Ardanuy, Jeremy; leah.katzelnick@niaid.nih.gov; Katzelnick, Leah (NIH/NIAID) [E]; Ho, David D.

Research Update Template.xlsx

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
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Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

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		B.1.351
		P.1
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Animal Models	Mice	
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		Description of assay
	Binding	

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	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

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BLUF Variant Data to date	Relevant pre-print(s)	

Importance:	Normal
Start Time:	Fri 9/3/2021 12:30:00 PM (UTC)
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		Description of study
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		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

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Data source (country, etc.)	Resources needed/ potential bottlenecks

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Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

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BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

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Sent: Sun 4/18/2021 3:31:06 PM (UTC-05:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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From: Macoubray, Aaron[amacoubray@rti.org]

Attendees: Garry, Robert F; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; Pardis Sabeti; Kristian Andersen; Bronwyn MacInnis; mmgraw; Kevin Olival; Peter Daszak; Quiner, Claire; Patterson, Jean (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]; Linde, Amber (NIH/NIAID) [E]; julie.dyall@nih.gov; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan; kga1978@gmail.com

Location: https://rtiorg.zoom.us/j/98355183025?pwd= **552.136**

Importance: Normal

Subject: CREID EBOV Discussion

Start Time: Fri 4/23/2021 2:00:00 PM (UTC-05:00)

End Time: Fri 4/23/2021 3:00:00 PM (UTC-05:00)

Required Attendees: Garry, Robert F; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; Pardis Sabeti; Kristian Andersen; Bronwyn MacInnis; mmgraw; Kevin Olival; Peter Daszak; Quiner, Claire; Patterson, Jean (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]; Linde, Amber (NIH/NIAID) [E]; julie.dyall@nih.gov; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan

Optional Attendees: kga1978@gmail.com

Hi all,

I've added others from your Research Centers to this invite. Please feel free to forward this invitation to the most appropriate representative on the topic from your RC, and to other CREID Network members as you see fit.

Thank you very much,

Aaron

Required Attendees: Garry, Robert F; Cross, Robert W.; Weaver, Scott; MacDonald, Pia; Pardis Sabeti; Kristian Andersen; Bronwyn MacInnis; mmgraw; Kevin Olival; Peter Daszak; Quiner, Claire; Patterson, Jean (NIH/NIAID) [E]; Woodson, Sara (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]; Linde, Amber (NIH/NIAID) [E]; julie.dyall@nih.gov; Weldon, Caroline; Hongying Li; Cadhla Firth; linfa.wang; Eric Laing; rbaric@email.unc.edu; christopher.broder@usuhs.edu; Aleksei Chmura; Emily Hagan; Cross, Robert W.; Shi, Pei yong; McLellan, Susan; Paessler, Slobodan

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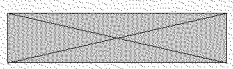

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From: The Journal of Infectious Diseases [jid@jidoffice.org]
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Subject: Revision Due

Start: 6/24/2021 4:00:00 AM
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Show Time As: Free

Recurrence: (none)

Revision of Report of the National Institutes of Health SARS-CoV-2 Antiviral Therapeutics Summit due to The Journal of Infectious Diseases

To: Whitley, Rich[rwhitley@peds.uab.edu]; Denison, Mark[mark.denison@vumc.org]; Tomas Cihlar[Tomas.Cihlar@gilead.com]; Elizabeth Campbell[elizabeth.campbell0@gmail.com]; Matthias Gotte[gotte@ualberta.ca]; Painter, George R.[george.r.painter@emory.edu]; Michael Sofia[msofia@arbutusbio.com]; Weller,Sandra K.[weller@uchc.edu]; Anderson, Annaliesa S[Annaliesa.Anderson@pfizer.com]; Lanteri, Charlotte A LTC USARMY FUTURES COMMAND (USA)[charlotte.a.lanteri.mil@mail.mil]; Andrew Mesecar[amesecar@purdue.edu]; Jen Nwankwo[jen@1910genetics.com]; Schiffer, Celia[Celia.Schiffer@umassmed.edu]; Kara Carter[Kara.Carter@evotec.com]; David Baker[dabaker@uw.edu]; Lillian Chiang[lillian@evrysbio.com]; Matthew Disney[disney@scripps.edu]; Singh Saikatendu, Kumar[kumar.saikatendu@takeda.com]; Weetall, Marla[mweetall@ptcbio.com]; Shi, Pei yong[peshi@UTMB.EDU]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; O'Rear, Julian (FDA/CDER)[Jules.ORear@fda.hhs.gov]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Smyth, Hugh D[hugh.smyth@austin.utexas.edu]; Hazuda, Daria J[daria_hazuda@merck.com]; Bradner, James[james.bradner@novartis.com]; Fletcher, Courtney V[cfletcher@unmc.edu]; Hayden, Frederick G (fgh)[fgh@virginia.edu]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]
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From: Hall, Matthew (NIH/NCATS) [E][hallma@mail.nih.gov]
Sent: Thur 6/3/2021 9:48:20 AM (UTC-05:00)
Subject: FW: MS #JID-73083R1, Report of the National Institutes of Health SARS-CoV-2 Antiviral Therapeutics Summit

Colleagues – quick turnaround and **approval** for the JID antiviral summit article. Will keep you posted on when a link appears for the article (we pre-requested a fast posting to their 'just accepted' section), and the final formatted article. Thanks,
Matt

On 6/3/21, 10:28 AM, "em.jid.0.73bb1a.070efb16@editorialmanager.com on behalf of The Journal of Infectious Diseases" <em.jid.0.73bb1a.070efb16@editorialmanager.com on behalf of em@editorialmanager.com> wrote:

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Dear Dr. Hall,

We are pleased to inform you that your revised manuscript has been accepted for publication in a supplement to The Journal of Infectious Diseases.

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Sincerely,

Martin Hirsch, MD
Editor

The Journal of Infectious Diseases
65 Landsdowne Street #412
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Phone: 617-367-1848
E-mail: jid@jidoffice.org

To: Whitley, Rich[rwhitley@peds.uab.edu]; Denison, Mark[mark.denison@vumc.org]; Tomas Cihlar[Tomas.Cihlar@gilead.com]; Elizabeth Campbell[elizabeth.campbell0@gmail.com]; Matthias Gotte[gotte@ualberta.ca]; Painter, George R.[george.r.painter@emory.edu]; Michael Sofia[msofia@arbutusbio.com]; Weller,Sandra K.[weller@uchc.edu]; Anderson, Annaliesa S[Annaliesa.Anderson@pfizer.com]; Lanteri, Charlotte A LTC USARMY FUTURES COMMAND (USA)[charlotte.a.lanteri.mil@mail.mil]; Andrew Mesecar[amesecar@purdue.edu]; Jen Nwankwo[jen@1910genetics.com]; Schiffer, Celia[Celia.Schiffer@umassmed.edu]; Kara Carter[Kara.Carter@evotec.com]; David Baker[dabaker@uw.edu]; Lillian Chiang[lillian@evrysbio.com]; Matthew Disney[disney@scripps.edu]; Singh Saikatendu, Kumar[kumar.saikatendu@takeda.com]; Weetall, Marla[mweetall@ptcbio.com]; Shi, Pei yong[peshi@UTMB.EDU]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; O'Rear, Julian (FDA/CDER)[Jules.ORear@fda.hhs.gov]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Smyth, Hugh D[hugh.smyth@austin.utexas.edu]; Hazuda, Daria J[daria_hazuda@merck.com]; Bradner, James[james.bradner@novartis.com]; Fletcher, Courtney V[cfletcher@unmc.edu]; Hayden, Frederick G (fgh)[fgh@virginia.edu]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]
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From: Hall, Matthew (NIH/NCATS) [E][hallma@mail.nih.gov]
Sent: Thur 6/10/2021 12:32:49 PM (UTC-05:00)
Subject: Re: MS #JID-73083R1, Report of the National Institutes of Health SARS-CoV-2 Antiviral Therapeutics Summit

All,

The accepted JID manuscript "**Report of the National Institutes of Health SARS-CoV-2 Antiviral Therapeutics Summit**" is now available available at: https://academic.oup.com/jid/advance-article/doi/10.1093/infdis/jiab305/6296018

Please do share, and cite ! We hope this article will be a useful reference point for antiviral drug development needs over the coming years.

Matt

Matthew D. Hall
Director, Early Translation Branch

National Center for Advancing Translational Sciences (NCATS)
National Institutes of Health
9800 Medical Center Drive
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https://ncats.nih.gov/staff/hallma

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From: Matthew Hall <hallma@mail.nih.gov>
Date: Thursday, June 3, 2021 at 10:48 AM

To: "Whitley, Rich" <rwhitley@peds.uab.edu>, "Denison, Mark" <mark.denison@vumc.org>, Tomas Cihlar <Tomas.Cihlar@gilead.com>, Elizabeth Campbell <elizabeth.campbell0@gmail.com>, Matthias Gotte <gotte@ualberta.ca>, "Painter, George R." <george.r.painter@emory.edu>, Michael Sofia <msofia@arbutusbio.com>, "Weller,Sandra K." <weller@uchc.edu>, "Anderson, Annaliesa S" <Annaliesa.Anderson@pfizer.com>, "Lanteri, Charlotte A LTC USARMY FUTURES COMMAND (USA)" <charlotte.a.lanteri.mil@mail.mil>, Andrew Mesecar <amesecar@purdue.edu>, Jen Nwankwo <jen@1910genetics.com>, "Schiffer, Celia" <Celia.Schiffer@umassmed.edu>, Kara Carter <Kara.Carter@evotec.com>, David Baker <dabaker@uw.edu>, Lillian Chiang <lillian@evrysbio.com>, Matthew Disney <disney@scripps.edu>, "Singh Saikatendu, Kumar" <kumar.saikatendu@takeda.com>, "Weetall, Marla" <mweetall@ptcbio.com>, "Pei yong. Shi" <peshi@UTMB.EDU>, "Cherry, Sara" <cherrys@pennmedicine.upenn.edu>, "De wit, Emmie (NIH/NIAID) [E]" <emmie.dewit@nih.gov>, "O'Rear, Julian (FDA/CDER)" <Jules.ORear@fda.hhs.gov>, "Sheahan, Timothy Patrick" <sheahan@email.unc.edu>, "Smyth, Hugh D" <hugh.smyth@austin.utexas.edu>, "Hazuda, Daria J" <daria_hazuda@merck.com>, "Bradner, James" <james.bradner@novartis.com>, "Fletcher, Courtney V" <cfletcher@unmc.edu>, "Hayden, Frederick G (fgh)" <fgh@virginia.edu>, "Marston, Hilary (NIH/NIAID) [E]" <hilary.marston@nih.gov>
Cc: "Anderson, James (NIH/OD) [E]" <james.anderson2@nih.gov>, "Davis, Mindy (NIH/NIAID) [E]" <mindy.davis@nih.gov>, "Conley, Tony (NIH/NIAID) [E]" <conleyto@niaid.nih.gov>, "Brimacombe, Kyle (NIH/NCATS) [E]" <kyle.brimacombe@nih.gov>, "Grossman, Abigail (NIH/NCATS) [C]" <abigail.grossman@nih.gov>, "Ford-Scheimer, Stephanie (NIH/NCATS) [C]" <stephanie.ford-scheimer@nih.gov>, "Austin, Christopher (NIH/NCATS) [V]" <austinc@mail.nih.gov>, "Fauci, Anthony (NIH/NIAID) [E]" <afauci@niaid.nih.gov>, "Collins, Francis (NIH/OD) [E]" <collinsf@od.nih.gov>
Subject: FW: MS #JID-73083R1, Report of the National Institutes of Health SARS-CoV-2 Antiviral Therapeutics Summit

Colleagues – quick turnaround and **approval** for the JID antiviral summit article. Will keep you posted on when a link appears for the article (we pre-requested a fast posting to their 'just accepted' section), and the final formatted article. Thanks,
Matt

On 6/3/21, 10:28 AM, "em.jid.0.73bb1a.070efb16@editorialmanager.com on behalf of The Journal of Infectious Diseases" <em.jid.0.73bb1a.070efb16@editorialmanager.com on behalf of em@editorialmanager.com> wrote:

CC: mshirsch@partners.org

Dear Dr. Hall,

We are pleased to inform you that your revised manuscript has been accepted for publication in a supplement to The Journal of Infectious Diseases.

In order to publish your article, our publisher, Oxford University Press (OUP), requires that you complete a license agreement online. A link to the online licensing system, and instructions on how to select and complete a license, will be provided to you by the Production Editor at Oxford University Press after your manuscript has been sent to the publisher for production.

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note: If you are a UK-based author and are looking to comply with the HEFCE policy on open access in the Research Excellence Framework, you should use the official acceptance date when depositing in your repository.)

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Sincerely,

Martin Hirsch, MD
Editor

The Journal of Infectious Diseases
65 Landsdowne Street #412
Cambridge, MA 02139
Phone: 617-367-1848
E-mail: jid@jidoffice.org

To: Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]; 'Erdman Dean'[derdman05@gmail.com]; Murphy, Frederick A.[famurphy@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; 'Denison Mark'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rollin Pierre'[pierrerollin2019@gmail.com]; 'Tesh Robert'[rbtesh22@gmail.com]; Weaver, Scott[sweaver@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Menachery, Vineet[vimenach@UTMB.EDU]; 'Folks Thomas'[Virusdoctom@aol.com]; 'Nichol Stuart'[stn1@CDC.GOV]; 'Spiropoulou Christina (CDC/CCID/NCZVED)'[ccs8@cdc.gov]; Keiser, Philip[phkeiser@UTMB.EDU]; Karl Johnson[microcaddis@gmail.com]; Doug Watts[dwatts2@utep.edu]; Ian Lipkin[wil2001@columbia.edu]
From: calisher@cybersafe.net[calisher@cybersafe.net]
Sent: Sun 4/26/2020 1:14:07 PM (UTC-05:00)
Subject: RE: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Want to weigh something large? Put it on one end of a teeter-totter (a seesaw). Then balance that with a large rock on the other end. Now all you need do is weight the rock.

One way to determine the quality of these newly developed assays is to (a) find someone who knows what the hell they are doing and have them (b) test by MACELISA and IgGelisa, then (c) test by NEUTRALIZATION. Without the latter, I ain't buying it. In the current situation, who cares whether a person has antibody, to SARS-CoV-2, unless that antibody is helpful in determining protection. Jordi Casals and Bob Shope must be turning in their graves.

Now W.H.O. is saying that the presence of antibody is not indicative of protection from a second exposure to SARS-CoV-2. No shit, Sherlock.

Charlie

-----Original Message-----
From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Saturday, April 25, 2020 10:42 PM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Erdman Dean <derdman05@gmail.com>; Murphy, Frederick A. <famurphy@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Denison Mark <mark.denison@vanderbilt.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Rollin Pierre <pierrerollin2019@gmail.com>; Tesh Robert <rbtesh22@gmail.com>; Weaver, Scott <sweaver@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Folks Thomas <Virusdoctom@aol.com>; Calisher Charles <calisher@cybersafe.net>; Nichol Stuart <stn1@CDC.GOV>; Spiropoulou Christina (CDC/CCID/NCZVED) <ccs8@cdc.gov>; Keiser, Philip <phkeiser@UTMB.EDU>
Subject: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Coronavirus Antibody Tests: Can You Trust the Results?
https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nytimes.com%2F2020%2F04%2F24%2Fhealth%2Fcoronavirus-antibody-tests.html%3Fre&data=02%7C01%7Cpeshi%40utmb.edu%7C6adc62f137904d62a5bc08d7ea0d9da4%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637235216518247057&sdata=rXoUrSQ%2FepcG9xTolMHpdEHsLq22V10ik%2F81UUGuT8c%3D&reserved=0

ferringSource=articleShare

Tom Ksiazek

Sent from a portable device

To: Motamedi, Massoud[mmotamed@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Brining, Douglas L.[dlbrinin@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Mire, Chad[chmire@UTMB.EDU]; Paessler, Slobodan[SLPAESSL@utmb.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]
Cc: McNees, Andrew G.[amcnees@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 4/29/2020 1:50:02 PM (UTC-05:00)
Subject: Re: Quantum GX2 lung imaging slide deck and bibliography

Here is a paper we did describing the system from few years ago.

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4482571/

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, April 29, 2020 1:44 PM
To: Motamedi, Massoud <mmotamed@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Brining, Douglas L. <dlbrinin@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Paessler, Slobodan <SLPAESSL@utmb.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Cc: McNees, Andrew G. <amcnees@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Subject: Re: Quantum GX2 lung imaging slide deck and bibliography

Find product info manual.

From: Motamedi, Massoud <mmotamed@UTMB.EDU>
Sent: Wednesday, April 29, 2020 12:15 PM
To: Weaver, Scott <sweaver@UTMB.EDU>; Brining, Douglas L. <dlbrinin@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Paessler, Slobodan <SLPAESSL@utmb.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Cc: McNees, Andrew G. <amcnees@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Subject: Fw: Quantum GX2 lung imaging slide deck and bibliography

Dear All,

I plan to use the attached file that I am sharing with you here in case that we encounter any issues with sharing my screen during our call later this afternoon.

Thanks

Massoud

Massoud Motamedi, Ph.D.
Charles H. and Mary Campbell Professor in Ophthalmology and Visual Sciences
Vice Chair for Research, Department of Ophthalmology and Visual Sciences
The University of Texas Medical Branch
301 University Boulevard
Galveston, TX 77555-0625
Phone: 409/772-8363

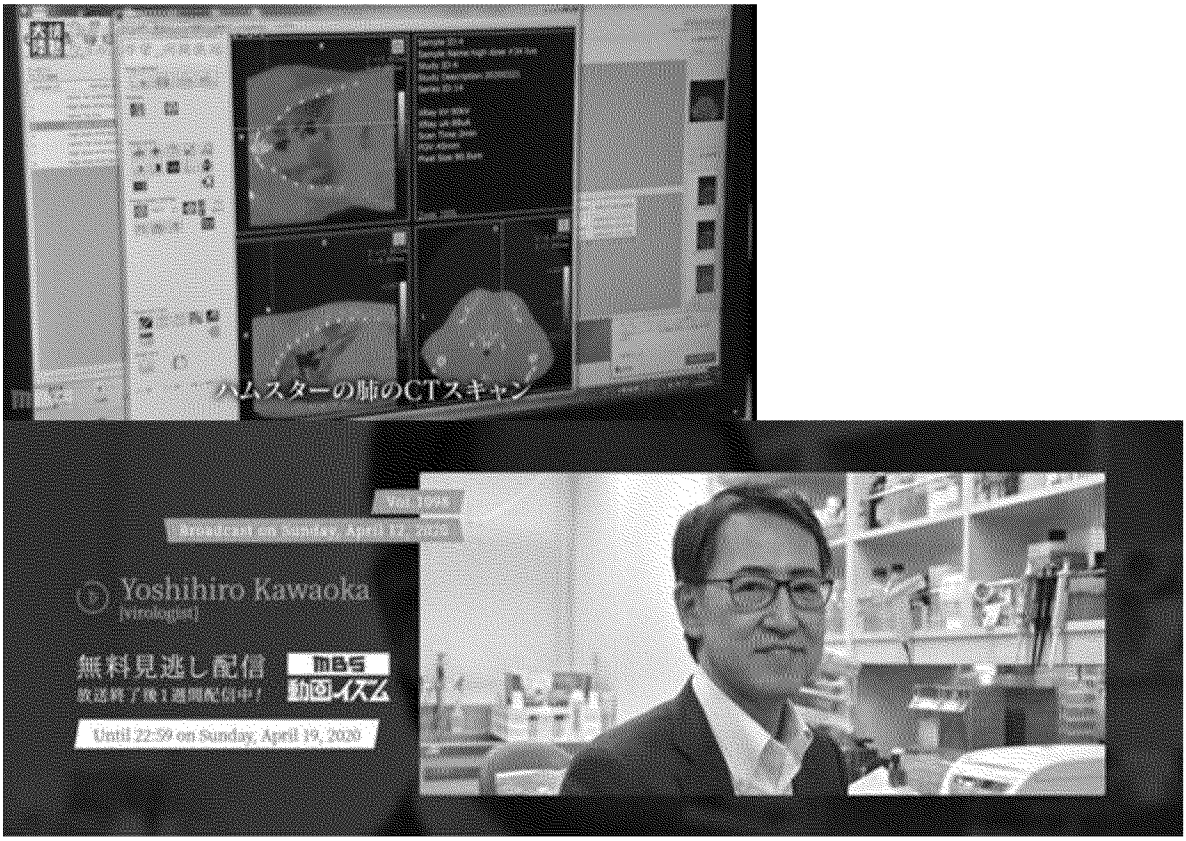
From: Kelada, Olivia <Olivia.Kelada@PERKINELMER.COM>
Sent: Friday, April 17, 2020 4:40 PM
To: Motamedi, Massoud <mmotamed@UTMB.EDU>
Cc: Gothelf, David <David.Gothelf@PERKINELMER.COM>; Weaver, Maurice <Maurice.Weaver@PERKINELMER.COM>
Subject: Quantum GX2 lung imaging slide deck and bibliography

Dear Massoud,

It was nice to finally speak with you today. Please find attached:

- A Quantum GX2 lung imaging slide deck
- A bibliography of all the Quantum lung imaging papers

Also, On Sunday April 12th 2020, Prof. Kawaoka's (University of Tokyo) research was highlighted on Japanese TV. Prof. Kawaoka is a virologist who used the Quantum to image COVID-19 in hamster lungs. He has also imaged ferrets. Find some screenshots below.
https://www.mbs.jp/jounetsu/



Have a great weekend.

Best,
Olivia

Olivia J. Kelada, PhD
Sr. Applications Scientist | Preclinical Imaging | PerkinElmer Inc.
Adjunct Researcher | Molecular Imaging Program | National Cancer Institute (NCI)
olivia.kelada@perkinelmer.com

To: Motamedi, Massoud[mmotamed@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Brining, Douglas L.[dlbrinin@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Mire, Chad[chmire@UTMB.EDU]; Paessler, Slobodan[SLPAESSL@utmb.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]
Cc: McNees, Andrew G.[amcnees@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]
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Sent: Wed 4/29/2020 1:44:48 PM (UTC-05:00)
Subject: Re: Quantum GX2 lung imaging slide deck and bibliography
FP WBP Application Manual (007898-001 Rev05).pdf

Find product info manual.

From: Motamedi, Massoud <mmotamed@UTMB.EDU>
Sent: Wednesday, April 29, 2020 12:15 PM
To: Weaver, Scott <sweaver@UTMB.EDU>; Brining, Douglas L. <dlbrinin@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Paessler, Slobodan <SLPAESSL@utmb.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Cc: McNees, Andrew G. <amcnees@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
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Massoud

Massoud Motamedi, Ph.D.
Charles H. and Mary Campbell Professor in Ophthalmology and Visual Sciences
Vice Chair for Research, Department of Ophthalmology and Visual Sciences
The University of Texas Medical Branch
301 University Boulevard
Galveston, TX 77555-0625
Phone: 409/772-8363

From: Kelada, Olivia <Olivia.Kelada@PERKINELMER.COM>
Sent: Friday, April 17, 2020 4:40 PM
To: Motamedi, Massoud <mmotamed@UTMB.EDU>
Cc: Gothelf, David <David.Gothelf@PERKINELMER.COM>; Weaver, Maurice <Maurice.Weaver@PERKINELMER.COM>
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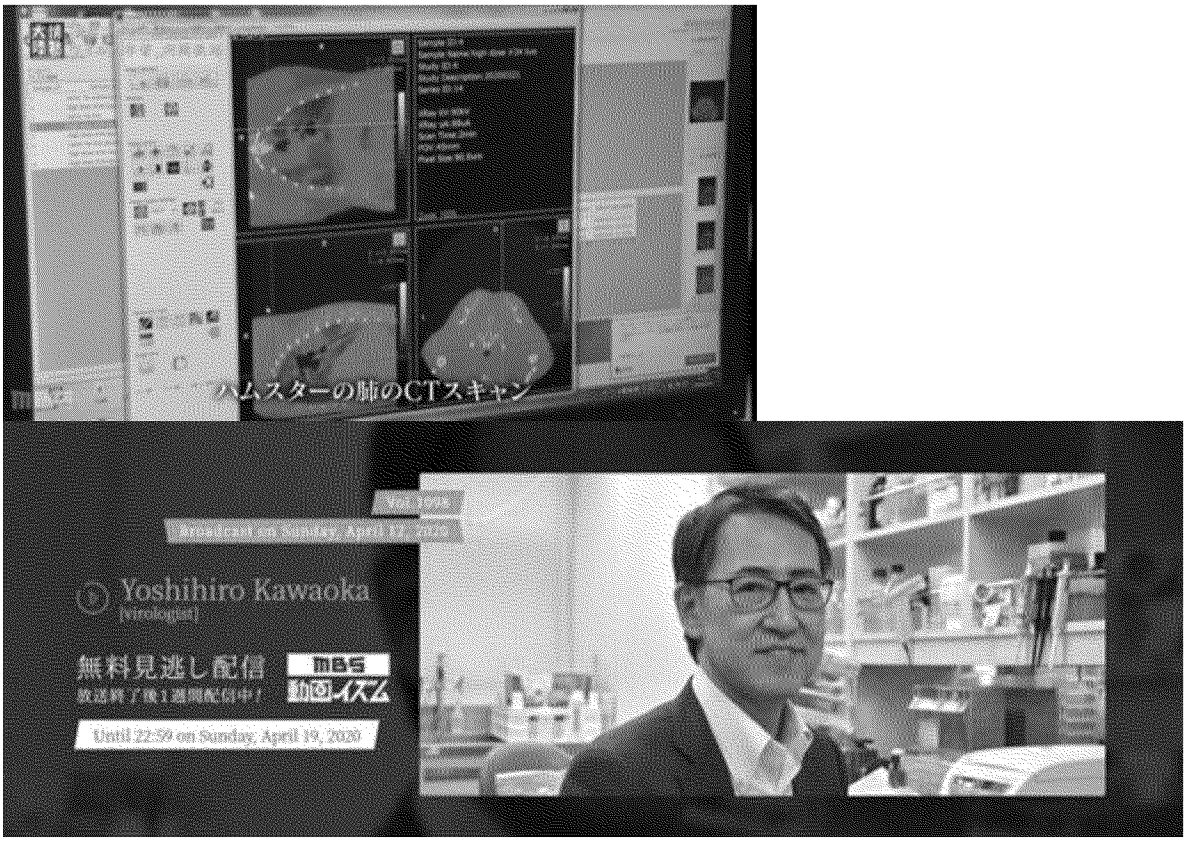
https://www.mbs.jp/jounetsu/



Have a great weekend.

Best,
Olivia

Olivia J. Kelada, PhD
Sr. Applications Scientist | Preclinical Imaging | PerkinElmer Inc.
Adjunct Researcher | Molecular Imaging Program | National Cancer Institute (NCI)
olivia.kelada@perkinelmer.com

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Fri 5/22/2020 2:54:38 PM (UTC-05:00)
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 20, 2020 11:44 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

As we discussed during our meeting on Monday we hope to hold a third virtual dialogue meeting with CAS and CCDC experts to discuss what is known about COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

We have proposed to CAS that this meeting take place on~~**Tuesday evening, May 26 from 9:00 -11:00 PM ET for the Americans**(and the morning of Wednesday, May 27 for the Chinese).~~ I have attached the list of questions on these topics we sent to CAS for your information. **Please let me know if you are interested and available to participate in the 3rd virtual dialogue meeting.**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 18, 2020 10:18 AM
To: Hare, Hope <HHare@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
3) Ideas for topics (and additional American experts) for future virtual dialogue sessions
4) Discussion of George Gao's joint statement idea
5) CAS idea to post a blurb about the meetings on the CAS website
6) Other issues, concerns

I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: https://nasem.zoom.us/j/99353621870?pwd

552.136

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 4:26 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org'

<daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Cc: Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
Here is the Zoom link for this meeting: https://nasem.zoom.us/j/99353621870?pwd
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

552.136

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
The National Academies of Sciences, Engineering, and Medicine
500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

The National Academies of
SCIENCES · ENGINEERING · MEDICINE

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 6/1/2020 9:03:07 AM (UTC-05:00)
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Wednesday, May 20, 2020 11:44 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

As we discussed during our meeting on Monday we hope to hold a third virtual dialogue meeting with CAS and CCDC experts to discuss what is known about COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

We have proposed to CAS that this meeting take place on~~**Tuesday evening, May 26 from 9:00 -11:00 PM ET for the Americans**(and the morning of Wednesday, May 27 for the Chinese).~~ I have attached the list of questions on these topics we sent to CAS for your information. **Please let me know if you are interested and available to participate in the 3rd virtual dialogue meeting.**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, May 18, 2020 10:18 AM
To: Hare, Hope <HHare@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org'

<andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Thought it would be helpful to send you a basic outline for the follow up call (**at 11:30 ET today**).

1) Intro
2) Comments on the Day 1 and Day 2 discussion
3) Ideas for topics (and additional American experts) for future virtual dialogue sessions
4) Discussion of George Gao's joint statement idea
5) CAS idea to post a blurb about the meetings on the CAS website
6) Other issues, concerns

I have attached the dialogue agenda (American version) for reference along with Jim's summaries of future collaboration ideas from the sessions.

I know a few people can't make it but I would be happy to follow up with you individually over the phone or email.

I look forward to talking to the group soon.
Zoom link: https://nasem.zoom.us/j/99353621870?pwd= **552.136**

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Hare, Hope <HHare@nas.edu>
Sent: Friday, May 15, 2020 4:26 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>
Cc: Rusek, Benjamin <BRusek@nas.edu>
Subject: RE: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

It is very difficult to find a time suitable for all—we apologize, but the one time that seemed to work is Monday, May 18th, at 11:30 AM. We understand that not all of you will be able to participate.
Here is the Zoom link for this meeting: https://nasem.zoom.us/j/99353621870?pwd= **552.136**
We look forward to seeing you on Monday at 11:30 am.
Best wishes,
Hope

From: Hare, Hope
Sent: Thursday, May 14, 2020 3:16 PM
Subject: Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19

Ben has asked me to contact you to schedule a time for the follow up call. We need to do this early next week, as there was not a time

that worked well for everyone this week. Please send me your availability for a one hour Zoom meeting between 9AM - 6PM ET, Monday - Wednesday next week.

Thank you and best wishes,

Hope Hare
Administrative Assistant
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500 Fifth Street, NW
Washington, DC 20001
Phone: 202-334-3435

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From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Thur 6/4/2020 12:24:31 PM (UTC-05:00)
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Immunity topics plus Gao for 3rd China U.S. Dialogue v2.docx

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
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- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

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We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

3rd U.S.-China Virtual Dialogue Conference Call

COVID-19 immunity, including the relationship between previous infection, antibody response, reinfection and convalescent plasma and preparing for a possible Fall 2020 resurgence of the virus.

Questions:

Immune Response and Immunotherapy

- Use of antibody assays in diagnosis of acute disease and as an indicator of protection (Le Duc)
  - How is immune response being measured?
  - Was there standardization of testing tools?
- **What is the overall situation of serologic investigation in the US? (Fineberg)**
- What can be said about the characterization of the (Perlman)
  - Innate immune responses?
  - humoral immune response?
  - cellular immune response?
- What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection? (Hamburg)
  - Is the use of immune plasma effective?
  - Have there been any complications?
- What has been China's experience with human monoclonal antibodies for treatment and prevention? (Hamburg)
  - Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?
- What immunopathologies are evident in the patients with COVID-19? (Relman)
  - Are there any biomarkers in patients who develop systemic inflammation?
  - What is the most effective treatment for patients who develop a cytokine storm?

Immunity

- After recovery, what types of antiviral immune responses are present? (Saif)
  - Do these immune responses protect from re-infection?
    - What is known about the durability of neutralizing antibody and longevity of protective immunity?

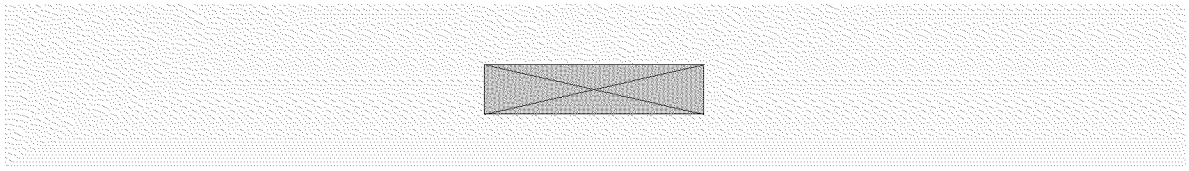
  Did recovery from SARS provide any protection from infection with SARS-CoV-2?
- **Progress in the development of vaccine in the U.S. especially mRNA vaccine? (Baric)**

Reactivation or Reinfection of Recovered Patients/Fall resurgence

- Has reactivation of latent virus or re-infection been seen among survivors? (Shi)
- Is reactivation/reinfection a concern with respect to a fall resurgence?
- What steps should be taken in anticipation of a fall resurgence in transmission? (Fineberg)

- **What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the U.S.? (Fineberg)**

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; 'Nancy Connell'[NancyConnell@jhu.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Thur 6/4/2020 10:27:47 PM (UTC-05:00)
Subject: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET



Meeting link:
https://nasem.zoom.us/j/95921551654?pwd= **552.136**
552.136

Meeting Topic: **Third Virtual U.S. China Bio Dialogue Meeting**

Meeting Time: **Jun 9, 2020 9:00 - 11:00 PM Eastern Time**

Add to Calendar Add to Google Calendar Add to Yahoo Calendar

Start Meeting

If the above button is not clickable, try copying and pasting the following link into the address bar of your web browser

https://nasem.zoom.us/s/95921551654

Or join meeting with the following methods

Phone one-tap

Phone one-tap: US: +14702509358,,95921551654# or +16465189805,,95921551654#

Join by Telephone

For higher quality, dial a number based on your current location.

Dial: **US : +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or +1 213 338 8477 or +1 253 215 8782 or 877 853 5257 (Toll Free) or 888 475 4499 (Toll Free)**

Meeting ID: **959 2155 1654**

Password: **552.136**

International numbers

Join from an H.323/SIP room system

H.323: 162.255.37.11 (US West)
162.255.36.11 (US East)
221.122.88.195 (China)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (EMEA)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)

Meeting ID: 959 2155 1654

Password: **552.136**

SIP: 95921551654@zoomcrc.com

Password: **552.136**

Skype for Business (Lync)

https://nasem.zoom.us/skype/95921551654

Would you like to test your Zoom connection? Please go to the URL below.
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Thank you for choosing Zoom.

-The Zoom Team

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

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1-202-334-3975

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CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

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We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

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From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Tue 6/9/2020 7:37:27 PM (UTC-05:00)
Subject: RE: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET
American Participants-0610.docx

Greetings,

When we do intros please introduce yourselves in alphabetical order (see attached pat list). Also here is the Zoom link again:
Meeting link: https://nasem.zoom.us/j/95921551654?pwd **552.136**

Talk to you soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Tuesday, June 9, 2020 12:02 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the list of Chinese participants for the meeting tomorrow (that I just received). There will be fewer people on their side this time (at our request). **Please let me know if you are not planning to participate.**

I have also attached the **American version** of the agenda / list of questions. Recall that their version lists Harvey Fineberg and Ralph Baric as discussants to answer Dr. Gao's questions but not the other names.

FYI the Zoom link for the meeting is:
https://nasem.zoom.us/j/95921551654?pwd= **552.136**

Please let me know if you have any questions or concerns. Thanks again for taking the time to participate in these meetings.

Kind regards,

Ben

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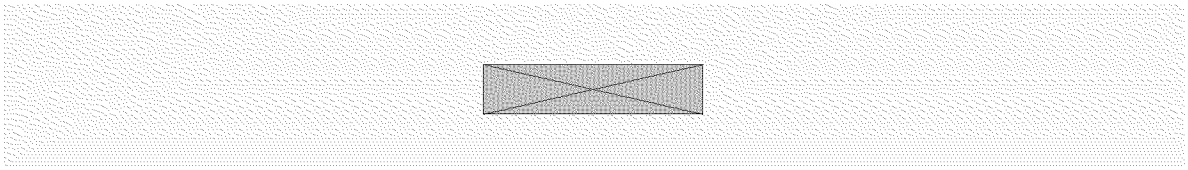
Subject: ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET



Meeting link:
https://nasem.zoom.us/j/95921551654?pwd= **552.136**

552.136

Meeting Topic: **Third Virtual U.S. China Bio Dialogue Meeting**

Meeting Time: **Jun 9, 2020 9:00 - 11:00 PM Eastern Time**

Add to Calendar Add to Google Calendar Add to Yahoo Calendar

Start Meeting

If the above button is not clickable, try copying and pasting the following link into the address bar of your web browser

https://nasem.zoom.us/s/95921551654

Or join meeting with the following methods

Phone one-tap

Phone one-tap: US: +14702509358,,95921551654# or +16465189805,,95921551654#

Join by Telephone

For higher quality, dial a number based on your current location.

Dial: US : +1 470 250 9358 or +1 646 518 9805 or +1 646 558 8656 or +1 651 372 8299 or +1 301 715 8592 or +1 312 626 6799 or +1 602 753 0140 or +1 669 219 2599 or +1 669 900 6833 or +1 720 928 9299 or +1 971 247 1195 or +1 213 338 8477 or +1 253 215 8782 or 877 853 5257 (Toll Free) or 888 475 4499 (Toll Free)

Meeting ID: 959 2155 1654

Password: **552.136**

International numbers

Join from an H.323/SIP room system

H.323: 162.255.37.11 (US West)
162.255.36.11 (US East)
221.122.88.195 (China)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (EMEA)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)

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Password: **552.136**

SIP: 95921551654@zoomcrc.com

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https://nasem.zoom.us/skype/95921551654

Would you like to test your Zoom connection? Please go to the URL below.
https://nasem.zoom.us/test
Thank you for choosing Zoom.
-The Zoom Team

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The U.S. National Academy of Sciences
1-202-334-3975

Ralph Baric: Dr. Ralph Baric, PhD, is a Professor in the Department of Epidemiology at the University of North Carolina's School of Public Health.

Nancy Connell: Nancy Connell, PhD, is a Senior Scholar at the Johns Hopkins Center for Health Security and a Professor in the Department of Environmental Health and Engineering at the Johns Hopkins Bloomberg School of Public Health.

Peter Daszak: Dr. Peter Daszak, PhD, is president of EcoHealth Alliance, a nonprofit non-governmental organization that supports various programs on global health.

Victor Dzau: Dr. Victor Dzau, MD, is currently president of the U.S. National Academy of Medicine of the U.S. National Academy of Sciences, Engineering and Medicine. He was previously the president and CEO of Duke University Medical Center.

David Franz: Dr. David R. Franz, DVM, PhD, is currently retired, but served in the U.S. Army Medical Research and Materiel Command for 23 of 27 years on active duty and as Commander of the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID).

Harvey Fineberg: Dr. Harvey Fineberg, MD**,** is currently president of the [HYPERLINK "https://www.moore.org/" \t "_blank"], immediately prior to which he was President of the [HYPERLINK "https://en.wikipedia.org/wiki/National_Academy_of_Medicine" \o "National Academy of Medicine"].

Diane Griffin: Dr. Diane Griffin, MD, PhD, is University Distinguished Service Professor in the W. Harry Feinstone Department of Molecular Microbiology and Immunology at Johns Hopkins Bloomberg School of Public Health and the current vice-president of the U.S. National Academy of Sciences.

Peggy Hamburg: Dr. Margaret (Peggy) Hamburg, MD, is an [HYPERLINK "https://en.wikipedia.org/wiki/Americans" \o "Americans"] physician and public health administrator. She served as the 21st Commissioner of the [HYPERLINK "https://en.wikipedia.org/wiki/Food and Drug Administration" \o "Food and Drug Administration"] from May 2009 to April 2015 and is currently foreign secretary for the U.S. National Academy of Medicine.

James Le Duc: Dr. James Le Duc, PhD, is the director of the [HYPERLINK "https://www.utmb.edu/gnl" \t "_blank"], professor, Microbiology and Immunology and the John Sealy Distinguished Chair in Tropical and Emerging Virology, University of Texas Medical Branch, Galveston Texas.

Stanley Perlman: Dr. Stanley Perlman, MD, PhD, is Professor of Microbiology and Immunology and of Pediatrics at the University of Iowa Health Care.

David Relman: Dr. David Relman, MD, PhD is a [HYPERLINK "https://en.wikipedia.org/wiki/Microbiologist" \o "Microbiologist"] and the Thomas C. and Joan M. Merigan Professor in Medicine and in Microbiology & Immunology at the [HYPERLINK "https://en.wikipedia.org/wiki/Stanford_University_School_of_Medicine" \o "Stanford University School of Medicine"].

Linda Saif: Dr. Linda J. Saif, PhD,[HYPERLINK "https://en.wikipedia.org/wiki/Linda_Saif" \l "cite_note-:0-3"] is Distinguished University Professor, [HYPERLINK "http://vet.osu.edu/preventive-medicine" \o "Preventive Medicine"], [HYPERLINK "http://www.oardc.ohio-state.edu/fahrp/" \t "_blank"], Ohio Agricultural Research and Development Center of the Ohio State University.

Pei-Yong Shi: Dr. Pei-Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas.

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; 'davidrfranz@gmail.com'[davidrfranz@gmail.com]; LeDuc, James W.[jwleduc@UTMB.EDU]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; Sharples, Fran[FSharples@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Sat 7/4/2020 6:27:59 PM (UTC-05:00)
Subject: U.S. China Gene Editing Technologies to Detect and Respond to Viral Pathogens - workshop - July 14 and July 16

Greetings,

I wanted to let you all know that as a follow on to our bio dialogue discussions NASEM is holding a small invitation only virtual workshop on ***Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens***. The virtual workshop will take place over Zoom on the evenings on **Tuesday, July 14 and Thursday, July 16 for U.S. participants (6-8 PM U.S. PT / 9-11 PM U.S. ET on both evenings)** and the mornings of Wednesday July 15 and Friday July 17 for Chinese participants (9-11 AM Beijing time)**.**

The workshop will explore the use of genome editing technologies, such as those based on CRISPR-Cas systems, to understand and combat viral pathogens. Issues to be discussed include the use of genome editing as a research tool to better understand the basic biology of viral infection and interactions with the immune system; the development of rapid CRISPR-based diagnostic systems to detect viral pathogens; and the potential to use genome editing as an innovative anti-viral strategy as well as best practices for biosafety and biosecurity. Diane Griffin and George Gao will co-chair and Nancy Connell is organizing with help from Katie Bowman, Fran Sharples and Hui Sun from CAS. We expect that the workshop will include approximately 6 or 7 invited speakers with about 30 total participants split between the U.S. and China. The preliminary agenda is below. The first day will focus on the development of CRISPR-based diagnostic systems to detect viral pathogens such as SARS-CoV2. The second day will focus on the potential to use genome editing as an innovative anti-viral strategy, as well as best practices for biosafety and biosecurity.

We hope that you can participate in some or all of the workshop. If you plan to participate please RSVP, and we will send the Zoom link to you before the call.

Happy to answer any questions that you have. Hope you have a great July 4th.

PS as we discussed at the end of the 3rd bio dialogue Zoom meeting last month we plan to hold another bio dialogue meeting in August. I will be back in touch to start planning that meeting after the gene editing workshop.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Virtual Workshop on Opportunities and Best Practices for Using Gene Editing Technologies to Detect and Respond to Viral Pathogens
Agenda

Day 1: **Evening of July 14 in US (Tuesday) and Morning of July 15 in Beijing (Wednesday)**

- Welcome
  - US welcome and focus of the 2 sessions and how they extend the topics of the 3 bio dialogue meetings held in May/June *[5min]* – **Diane Griffin**, NASEM
  - China welcome *[5 min]* – **George Gao**, China CDC

- Opening Presentation: Introduction to how CRISPR-based technologies can be applied to diagnosis and treatment of disease *[10 min]*
  Nancy Connell, Johns Hopkins University

- Detecting Viral Pathogens *[75 min] – 3 presentations x 15 min each followed by panel discussion*
  Session moderator: **David Walt**, Harvard University
  - **Feng Zhang** [invited], Massachusetts Institute of Technology*: Development of CRISPR/Cas-based systems to detect viral pathogens)*
  - **Chunbo Lou** [invited]**,** Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences: *Paired Design of dCas9 as a Systematic Platform for the Detection of Featured Nucleic Acid Sequences in Pathogenic Strains*
  - **Charles Chiu** [invited]*,* University of California San Francisco: *Detection of SARS-CoV-2 using CRISPR/Cas-based systems)*
  - Moderated Discussion *[30 min]*

- Looking ahead to session 2 – **Nancy Connell**, Johns Hopkins University *[5 min]*
- Adjourn until second session

Day 2: **Evening of July 16 in US (Thursday) and Morning of July 17 in Beijing (Friday)**

- Welcome – **Nancy Connell**, Johns Hopkins University [*5min]*

- Responding to viral pathogens [60 min] - *3 presentations x 15 min each followed by panel discussion.*
  Session moderator: **Nancy Connell**, Johns Hopkins University
  - **Deyin Guo** [invited], School of Medicine (Shenzhen), Sun Yat-sen University: *CRISPR-Cas Targeting of Host Genes as an Antiviral Strategy*
  - **Xin Zhao** [invited]**,** Institute of Microbiology, Chinese Academy of Sciences: *Receptor hunting of Enterovirus B by CRISPR screening*
  - **Stanley Qi** [invited, recommended colleague]*,* Stanford University: *Development of CRISPR as an Antiviral Strategy to Combat SARS-CoV-2 and Influenza")*
  - Moderated Discussion *[30 min]*

- Capturing the opportunities through responsible development *[30 min]*
  - **Weiwen Zhang** [invited], Tianjin University: The importance of promoting responsible development around technologies such as gene editing, including following good biosafety/biosecurity practices) [15 min]
  - Discussion among all participants *[20 min]*

- Thanks to all speakers and participants and adjourn virtual workshop

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

To: rbtesh22@gmail.com[rbtesh22@gmail.com]; calisher@cybersafe.net[calisher@cybersafe.net]; eharris@berkeley.edu[eharris@berkeley.edu]; hotez@bcm.edu[hotez@bcm.edu]; Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; vasilan@hotmail.com[vasilan@hotmail.com]; LeDuc, James W.[jwleduc@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Juares Simoes Quaresma[juarez.quaresma@gmail.com]; ltmfigue@fmrp.usp.br[ltmfigue@fmrp.usp.br]; Livia Caricio Martins[liviamartins@iec.gov.br]; Jannifer Oliveira Chiang[janniferchiang@iec.gov.br]; albert.ko@yale.edu[albert.ko@yale.edu]; wil2001@columbia.edu[wil2001@columbia.edu]; mauricio.nogueira@edu.famerp.br[mauricio.nogueira@edu.famerp.br]; mmtex.ufmg@gmail.com[mmtex.ufmg@gmail.com]; alcantaraluiz42@gmail.com[alcantaraluiz42@gmail.com]; flaviab@ioc.fiocruz.br[flaviab@ioc.fiocruz.br]; lourenco@ioc.fiocruz.br[lourenco@ioc.fiocruz.br]; bozza.fernando@gmail.com[bozza.fernando@gmail.com]; Raimunda do Socorro da Silva Azevedo[raimundaazevedo@iec.gov.br]; juliocroda@gmail.com[juliocroda@gmail.com]; Daniele Barbosa de Almeida Medeiros[danielemedeiros@iec.gov.br]; Shan, Chao[chshan@UTMB.EDU]; mbonaldo@ioc.fiocruz.br[mbonaldo@ioc.fiocruz.br]; eaneto@fmrp.usp.br[eaneto@fmrp.usp.br]; baldfons@fmrp.usp.br[baldfons@fmrp.usp.br]; atanuri1@gmail.com[atanuri1@gmail.com]; marques@pitt.edu[marques@pitt.edu]; peter.walker@ug.edu.au[peter.walker@ug.edu.au]; tom.monath@crotezbiopharma.com[tom.monath@crotezbiopharma.com]; shiggs@bri.ksu.edu[shiggs@bri.ksu.edu]; ccassetti@niaid.nih.gov[ccassetti@niaid.nih.gov]; akp7@cdc.gov[akp7@cdc.gov]; acbrault1@mac.com[acbrault1@mac.com]; amy.aegypti@gmail.com[amy.aegypti@gmail.com]; dwatts2@utep.edu[dwatts2@utep.edu]; michael.turell.civ@mail.mil[michael.turell.civ@mail.mil]; gustavo.f.palacios.ctr@mail.mil[gustavo.f.palacios.ctr@mail.mil]; remi.charrel@univ-amu.fr[remi.charrel@univ-amu.fr]; abispo@ioc.fiocruz.br[abispo@ioc.fiocruz.br]; miter@bahia.fiocruz.br[miter@bahia.fiocruz.br]; sinval@cpqam.fiocruz.br[sinval@cpqam.fiocruz.br]; felipe.naveca@fiocruz.br[felipe.naveca@fiocruz.br]; sergioluz@amazonia.fiocruz.br[sergioluz@amazonia.fiocruz.br]; fernandors@feevale.br[fernandors@feevale.br]
Cc: peralta@micro.ufrj.br[peralta@micro.ufrj.br]; Giselle Maria Rachid Viana[giselleviana@iec.gov.br]; pedrofc.vasconcelos@gmail.com[pedrofc.vasconcelos@gmail.com]
From: Pedro Fernando da Costa Vasconcelos[pedrovasconcelos@iec.gov.br]
Sent: Wed 7/22/2020 3:58:11 PM (UTC-05:00)
Subject: ENC: [Pathogens] (IF 3.018, ISSN 2076-0817) [Diagnostics and Surveillance of Arboviral Diseases] Website is Ready
arboviral_diseases.pdf
arboviral_diseases_horizontal_light.png

Dear colleagues,

This is to invite you to submit manuscripts to a (very) special issue of PATHOGENS (IF 3.018, ISSN 2076-0817) [Diagnostics and Surveillance of Arboviral Diseases]. This special number will be edited by Prof. José Mauro Peralta from Federal University of Rio de Janeiro and Pedro Fernando Vasconcelos. In the attached files you can find additional information. The deadline will be in April 2021, but we think that the issue can be complete before, perhaps by December/2020 or January/2021. I hope you can contribute. All the best,

José Mauro Peralta (peralta@micro.ufrj.br)
Pedro Fernando Vasconcelos (pedrovasconcelos@iec.gov.br); (pedrofc.vasconcelos@gmail.com)

---------- Forwarded message ---------
From: **Ms. Mejoe Wang/MDPI** <mejoe.wang@mdpi.com>
Date: Mon, Jul 20, 2020 at 5:19 AM
Subject: [Pathogens] (IF 3.018, ISSN 2076-0817) [Diagnostics and Surveillance of Arboviral Diseases] Website is Ready
To: Jose Mauro Peralta <peralta@micro.ufrj.br>, <pedrofcvasconcelos@gmail.com>
Cc: <pathogens@mdpi.com>

Dear Colleagues,

Thank you for your summary. The website of this special issue is ready now. Please check following link to see if any modifications needed:
https://www.mdpi.com/journal/pathogens/special_issues/arboviral_diseases

At this point, I would like to explain more details about the Special Issue:
1) Regarding the number of published papers

We expect to publish around 10 papers in this Special Issue; however, we do not have a limit for the number of papers, but encourage authors to publish high-quality papers in the Special Issue.

As guest editor, we hope you could help to invite some colleagues and experts in this field to contribute from your side. At the same time, we will also prepare a regular call for paper list, and once it is ready, we will ask you to check it. After receiving your approval, we will organize public call for papers from our official account.

For guest editor, you could publish one review paper and one article paper free of charge. For the feature papers invited by you, we could give a special discount (30-50%). Meanwhile, to attract more scholars with high reputation to publish with us, the editorial office would like to waive the charges of 3 papers invited by you. However, please send us the author list in advance as the editorial office needs to approve it before granting the waivers.

2) Promotion
I suggest promoting this Special Issue within your scientific network and reaching out to your collaborators to ask for submissions.

Enclosed are the banner and flyer we prepared for issue promotions, which you can publicize via social media, such as through Twitter and LinkedIn; we also encourage you to add the Special Issue as a project to your institute homepage or ResearchGate homepage.

I would be pleased to discuss more if you have any plans or suggestions for attractive more submissions for our special issue.

Hope we could have an enjoyable cooperation.

Best regards,

We look forward to hearing from you.

Best regards,
Mejoe Wang
Section Managing Editor
Pathogens (http://www.mdpi.com/journal/pathogens/)

News:Pathogens receives its second Impact Factor, 3.018 (2019)
News:Join the Topic Board of /Pathogens/
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IMPACT FACTOR 3.018

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Diagnostics and Surveillance of Arboviral Diseases

Guest Editors:

Prof. Dr. Jose Mauro Peralta
Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil

peralta@micro.ufrj.br

Prof. Pedro Fernando da Costa Vasconcelos
Universidade do Estado do Pará, Belém, Pará, Brazil and Instituto Evandro Chagas, Ananindeua, Pará, Brazil

pedrofc.vasconcelos@gmail.com

Deadline for manuscript submissions:
30 April 2021

Message from the Guest Editors

Dear Colleagues

Arboviruses are a diverse group of viruses that are transmitted by bites of hematophagous insects to humans, many of which can cause diseases associated with significant human morbidity and mortality worldwide, while some are apparently restricted to certain geographic areas.

In this Special Issue, we invite the arboviral diseases community to submit research articles, reviews, or short communications highlighting critical advancements in our understanding of diagnostic approaches and surveillance of arboviruses. The development of new assays that can discriminate between different arboviral infections is of particular interest. Timely and accurate diagnosis is crucial for patient management, prevention of unnecessary therapies, rapid adoption of vector control measures, and collection of epidemiological data. Finally, considering the importance and global impact of arboviruses as public health threats and the emergence/re-emergence of such viruses we look forward to your submissions.

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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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High Visibility: Indexed in the Science Citation Index Expanded (SCIE) - Web of Science, BIOSIS Previews and Scopus. Ctations available in PubMed, full-text archived in PubMed Central.
CiteScore 2019 (Scopus): **3.1**, which equals rank 138/283 (Q2) in the 'Infectious Diseases' category, rank 26/45 (Q3) in 'General Immunology and Microbiology' and rank 61/115 (Q3) in 'Microbiology (medical).'

Contact Us

Pathogens
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
Fax: +41 61 302 89 18
www.mdpi.com

mdpi.com/journal/pathogens
pathogens@mdpi.com

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Diagnostics and Surveillance of Arboviral Diseases

Guest Editors

Prof. Dr. Jose Mauro Peralta, Prof. Pedro Fernando da Costa Vasconcelos

Deadline

30 April 2021

Special Issue

To: Alex Greninger[agrening@uw.edu]; amy.aegypti[amy.aegypti@gmail.com]; anneparedes[anneparedes@wustl.edu]; colomaj[colomaj@berkeley.edu]; dpark[dpark@broadinstitute.org]; dveasna[dveasna@pasteur-kh.org]; Emily Hagan[hagan@ecohealthalliance.org]; julie.dyall@nih.gov[julie.dyall@nih.gov]; lynnbob[lynnbob@uw.edu]; Vasilakis, Nikolaos[nivasila@utmb.edu]; samkariuki2[samkariuki2@gmail.com]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; sheahan[sheahan@email.unc.edu]; Weaver, Scott[sweaver@UTMB.EDU]; Sasha W Tilles[swtilles@uw.edu]; tcantaert[tcantaert@pasteur-kh.org]; Tony Moody, M.D.[tony.moody@duke.edu]; bbarnabas2001[bbarnabas2001@yahoo.com]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; colomaj[colomaj@berkeley.edu]; donkumfel[donkumfel@yahoo.co.uk]; gottlieb[gottlieb@uw.edu]; isaac.ngere[isaac.ngere@wsu.edu]; Judith N Wasserheit[jwasserh@uw.edu]; kathleen.victoir[kathleen.victoir@pasteur.fr]; leah.katzelnick[leah.katzelnick@gmail.com]; Hongying Li[li@ecohealthalliance.org]; lynnbob[lynnbob@uw.edu]; Raphaelle Marie Klitting[rklitting@scripps.edu]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; slopez[slopez@gorgas.gob.pa]; sujan[sujan@lji.org]; McLellan, Susan[sumclell@UTMB.EDU]; Tierra Smiley Evans[tsmevans@ucdavis.edu]; Van Vliet, Gretchen[gvanvliet@rti.org]; Linde, Amber (NIH/NIAID) [E][amber.linde@nih.gov]; Anavaj SAKUNTABHAI[anavaj.sakuntabhai@pasteur.fr]; Kristian Andersen[andersen@scripps.edu]; balthouse[balthouse@idmod.org]; Christopher M Barker[cmbarker@ucdavis.edu]; eric.lofgren[eric.lofgren@wsu.edu]; Golovko, Georgiy[gegolovk@UTMB.EDU]; Karthik Gangavarapu[gkarthik@scripps.edu]; gordonal[gordonal@umich.edu]; Emily Hagan[hagan@ecohealthalliance.org]; Hanlon, Sean[shanlon@rti.org]; leah.katzelnick[leah.katzelnick@gmail.com]; mauricio.nogueira[mauricio.nogueira@edu.famerp.br]; mauriciolnogueira[mauriciolnogueira@gmail.com]; mgale[mgale@uw.edu]; Edlefsen PhD, Paul T[pedlefse@fredhutch.org]; peterr7[peterr7@uw.edu]; rireton[rireton@uw.edu]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; shandley[shandley@wustl.edu]; Vandergrift, Nathan[nvandergrift@rti.org]; Alex Greninger[agrening@uw.edu]; Smither, Allison R[asmither@tulane.edu]; christian.drosten[christian.drosten@charite.de]; danielle.anderson[danielle.anderson@duke-nus.edu.sg]; desilva[desilva@med.unc.edu]; eric.laing[eric.laing@usuhs.edu]; Gregory Sempowski[greg.sempowski@duke.edu]; Waggoner, Jesse J.[jesse.waggoner@emoryhealthcare.org]; julie.dyall@nih.gov[julie.dyall@nih.gov]; Kathryn Hanley[khanley@nmsu.edu]; Lark L A Coffey[lcoffey@ucdavis.edu]; llmpoon[llmpoon@hku.hk]; lynnbob[lynnbob@uw.edu]; Njenga, M. Kariuki[mkariuki.njenga@wsu.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; njouom[njouom@pasteur-yaounde.org]; Shi, Pei yong[peshi@UTMB.EDU]; rfgarry[rfgarry@tulane.edu]; sadeuh[sadeuh@pasteur-yaounde.org]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Sasha W Tilles[swtilles@uw.edu]; Tineke CANTAERT[tineke.cantaert@pasteur.fr]; bhbird[bhbird@ucdavis.edu]; bronwyn[bronwyn@broadinstitute.org]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; eric.osoro[eric.osoro@wsu.edu]; gamou.fall[gamou.fall@pasteur.sn]; gathsaurie.malavige[gathsaurie.malavige@ndm.ox.ac.uk]; jboom[jboom@wustl.edu]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Dawa, Jeanette[jeanette.dawa@wsu.edu]; Waggoner, Jesse J.[jesse.waggoner@emoryhealthcare.org]; Judith N Wasserheit[jwasserh@uw.edu]; linfa.wang[linfa.wang@duke-nus.edu.sg]; MacDonald, Pia[pmacdonald@rti.org]; mauricio.nogueira[mauricio.nogueira@edu.famerp.br]; mauriciolnogueira[mauriciolnogueira@gmail.com]; neelikamalavige[neelikamalavige@gmail.com]; Kevin Olival[olival@ecohealthalliance.org]; pardis[pardis@broadinstitute.org]; petterr7@uw.edu[petterr7@uw.edu]; Cross, Robert W.[rwcross@UTMB.EDU]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Rossi, Shannan L.[slrossi@UTMB.EDU]; Wesley C. Van Voorhis[wesley@uw.edu]
Cc: Batsuli, Nefer[nbatsuli@rti.org]; Brambilla, Donald[dbrambilla@rti.org]; Hanlon, Sean[shanlon@rti.org]; MacDonald, Pia[pmacdonald@rti.org]; Van Vliet, Gretchen[gvanvliet@rti.org]; Vandergrift, Nathan[nvandergrift@rti.org]; Elizabeth Fallon[elizabeth.fallon@duke.edu]; Gregory Sempowski[greg.sempowski@duke.edu]; Heather Lynch, Ph.D.[heather.lynch@duke.edu]; Hilary Bouton-Verville[hilary.bouton-verville@duke.edu]; Isabel Wright[isabel.wright@duke.edu]; Tony Moody, M.D.[tony.moody@duke.edu]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; Challberg, Mark (NIH/NIAID) [E][mchallberg@niaid.nih.gov]; Dyall, Julie (NIH/NIAID) [E][dyallj@niaid.nih.gov]; Linde, Amber (NIH/NIAID) [E][amber.linde@nih.gov]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]
From: Macoubray, Aaron[amacoubray@rti.org]
Sent: Wed 9/2/2020 1:12:00 PM (UTC-05:00)
Subject: CREID Network Working Groups

Hello working group members,

I hope this finds you well. You have all been invited to the CREID Coordinating Center team in Microsoft Teams, as well as the CREID Working Groups channel within the team. This will be used as an information sharing and collaboration space for the CREID Network Working Groups. Please follow the link to access the team and channel, and let me know if you have any issues. Feel free to reach out to myself and Nefer Batsuli (nbatsuli@rti.org) with any questions or concerns.

Thank you,

Aaron
CREID CC Project Coordinator

Aaron Macoubray
RTI International
Public Health Analyst
Center for Applied Public Health Research
Biostatistics and Epidemiology Division
Phone: 301.770.8228
Cell: 503.577.2709
Email: amacoubray@rti.org

To: Linde, Amber (NIH/NIAID) [E][amber.linde@nih.gov]; Anavaj SAKUNTABHAI[anavaj.sakuntabhai@pasteur.fr]; Kristian Andersen[andersen@scripps.edu]; balthouse[balthouse@idmod.org]; Christopher M Barker[cmbarker@ucdavis.edu]; Lofgren, Eric[eric.lofgren@wsu.edu]; Golovko, Georgiy[gegolovk@UTMB.EDU]; gordonal[gordonal@umich.edu]; Emily Hagan[hagan@ecohealthalliance.org]; Hanlon, Sean[shanlon@rti.org]; mgale[mgale@uw.edu]; Handley, Scott[shandley@wustl.edu]; Vandergrift, Nathan[nvandergrift@rti.org]; Danielle Anderson[danielle.anderson@duke-nus.edu.sg]; desilva[desilva@med.unc.edu]; Gregory Sempowski[greg.sempowski@duke.edu]; julie.dyall@nih.gov[julie.dyall@nih.gov]; Lark L A Coffey[lcoffey@ucdavis.edu]; llmpoon[llmpoon@hku.hk]; Lynn K. Barrett[lynnbob@uw.edu]; Njenga, M. Kariuki[mkariuki.njenga@wsu.edu]; Eitzen, Melissa M.[mmeitzen@utmb.edu]; Shi, Pei yong[peshi@UTMB.EDU]; El-Duah, Philip[philip.el-duah@charite.de]; rfgarry[rfgarry@tulane.edu]; sadeuh[sadeuh@pasteur-yaounde.org]; Woodson, Sara (NIH/NIAID) [E][sara.woodson@nih.gov]; Alex Greninger[agrening@uw.edu]; amy.aegypti[amy.aegypti@gmail.com]; Paredes, Anne[anneparedes@wustl.edu]; colomaj[colomaj@berkeley.edu]; Daniel Park[dpark@broadinstitute.org]; Emily Hagan[hagan@ecohealthalliance.org]; Vasilakis, Nikolaos[nivasila@utmb.edu]; samkariuki2[samkariuki2@gmail.com]; Weaver, Scott[sweaver@UTMB.EDU]; tcantaert[tcantaert@pasteur-kh.org]; Tony Moody, M.D.[tony.moody@duke.edu]; Brian H Bird[bhbird@ucdavis.edu]; gamou.fall[gamou.fall@pasteur.sn]; Boon, Jacco[jboon@wustl.edu]; Patterson, Jean (NIH/NIAID) [E][jean.patterson@nih.gov]; Dawa, Jeanette[jeanette.dawa@wsu.edu]; Waggoner, Jesse J.[jesse.waggoner@emoryhealthcare.org]; MacDonald, Pia[pmacdonald@rti.org]; mauricio.nogueira[mauricio.nogueira@edu.famerp.br]; mauriciolnogueira[mauriciolnogueira@gmail.com]; Kevin Olival[olival@ecohealthalliance.org]; pardis[pardis@broadinstitute.org]; peterr7[peterr7@uw.edu]; Cross, Robert W.[rwcross@UTMB.EDU]
Cc: Karthik Gangavarapu[gkarthik@scripps.edu]; leah.katzelnick[leah.katzelnick@gmail.com]; mauricio.nogueira[mauricio.nogueira@edu.famerp.br]; mauriciolnogueira[mauriciolnogueira@gmail.com]; Edlefsen PhD, Paul T[pedlefse@fredhutch.org]; peterr7[peterr7@uw.edu]; rireton[rireton@uw.edu]; Heather Lynch, Ph.D.[heather.lynch@duke.edu]; eric.laing[eric.laing@usuhs.edu]; njouom[njouom@pasteur-yaounde.org]; Smither, Allison R[asmither@tulane.edu]; Waggoner, Jesse J.[jesse.waggoner@emoryhealthcare.org]; Kathryn Hanley[khanley@nmsu.edu]; Alex Greninger[agrening@uw.edu]; Sasha W Tilles[swtilles@uw.edu]; christian.drosten[christian.drosten@charite.de]; julie.dyall@nih.gov[julie.dyall@nih.gov]; sheahan[sheahan@email.unc.edu]; dveasna[dveasna@pasteur-kh.org]; Lynn K. Barrett[lynnbob@uw.edu]; Sasha W Tilles[swtilles@uw.edu]; Beaubien, Candice (NIH/NIAID) [E][candice.beaubien@nih.gov]; linfa.wang[linfa.wang@duke-nus.edu.sg]; bronwyn[bronwyn@broadinstitute.org]; neelikamalavige[neelikamalavige@gmail.com]; gathsaurie.malavige[gathsaurie.malavige@ndm.ox.ac.uk]; Rossi, Shannan L.[slrossi@UTMB.EDU]; Wesley C. Van Voorhis[wesley@uw.edu]; Judith N Wasserheit[jwasserh@uw.edu]; eric.osoro[eric.osoro@wsu.edu]; Macoubray, Aaron[amacoubray@rti.org]; Batsuli, Nefer[nbatsuli@rti.org]
From: Van Vliet, Gretchen[gvanvliet@rti.org]
Sent: Wed 9/9/2020 2:51:23 PM (UTC-05:00)
Subject: CREID Network Working Group materials

Dear CREID Network Working Group members,

We are looking forward to the NIAID-hosted CREID Network Kickoff meeting next week, September 16-18, 2020. The opportunity to officially move forward on establishing the CREID Network is exciting. My apologies for the long email!

We will be convening four of the CREID Working Groups for the first time next week on Days 2 and 3 of the Kickoff meeting. We will be convening the 5th Working Group, Capacity Building and Sustainability in December. At the Kickoff meeting, these Working Groups will meet:

- Data Capture and Harmonization
- Laboratory Assay Oversight and Quality
- Biorepository Oversight and Quality
- Outbreak Research Response

The Working Group facilitators from the Coordinating Center and DMID have crafted an agenda for the two days. These meetings will be an opportunity to get to know each other and define the purpose and goals of each Working Group.

Below is information we would like you to review ahead of the meeting to ensure a robust discussion.

Homework to prepare for the CREID Working Group meetings:

1. **Using Microsoft Teams**
   a. We will be collaborating and sharing materials via Microsoft Teams (until the CREID portal is established) and you have each been added to the CREID Network Working Groups Teams channel.
   b. Please make sure you can access the Teams site. If you have any issues, please contact Aaron Macoubray at amacoubray@rti.org to problem solve access issues.

2. **Please review the Working Group materials on the Working Group Teams channel:**
   a. In the Governance, Administration, and Membership folder:

      i. CREID Network Governance Guidelines
      ii. Membership lists for all Working Groups
      iii. NIAID Kickoff meeting agenda. *Please do not share this agenda as there are Zoom links for the closed meetings on Days 2 and 3.*

   b. In the WG specific folders

      i. Agenda for your Working Group
      ii. Draft charter for your Working Group

3. **We need a Research Center co-facilitator for each Working Group**
   a. Each Working Group is co-facilitated by DMID, the Coordinating Center, and a Research Center representative. *Please email me by September 15 if you are interested in self-nominating yourself to serve in this role.*
   b. We will have a voting process to select the Research Center facilitator following the first Working Group meeting on Day 2 of the Kickoff meeting.
   c. Role of Facilitators: The WG facilitators will be responsible for planning and leading meetings. During each meeting facilitators will guide the group through the agenda, catalyzing group discussion, and moving the group through the decision-making process. Facilitators will communicate with the CC and DMID about duplication of activities identified during the course of the WG and should communicate with other WG facilitator(s) to invite additional technical inputs as needed from other groups.

Please note that the primary representatives for the Research Centers on each Working Group will be unmuted during the meetings. All other secondary representatives, participants, and observers in the meetings will be muted. If others from your Research Center want to provide inputs during the meeting, please have them channel their inputs through you as the primary representative.

You will be receiving additional information about the Kickoff meeting from the DMID team in the next few days.

Have a good week and please let me know if you have any questions.

Gretchen
Project Director, CREID Coordinating Center

Gretchen Van Vliet, MPH
Senior Public Health Project Director
Center for Applied Public Health Research | Biostatistics and Epidemiology
RTI International
3040 Cornwallis Road |Research Triangle Park, NC 27709
Email: gvanvliet@rti.org | http://rti.org
Tel: +1.919.541.6238 | Fax: +1.919.541.6722

To: 'relman@stanford.edu'[relman@stanford.edu]; 'rbaric@email.unc.edu'[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'daszak@ecohealthalliance.org'[daszak@ecohealthalliance.org]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'dgriffi6@jhmi.edu'[dgriffi6@jhmi.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; 'Nancy Connell'[NancyConnell@jhu.edu]; Dave Franz (davidrfranz@gmail.com)[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; 'antoinette_baric@med.unc.edu'[antoinette_baric@med.unc.edu]; 'andre@ecohealthalliance.org'[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]
From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Mon 9/21/2020 8:00:55 PM (UTC-05:00)
Subject: Virtual U.S. China dialogue meeting October 13 and 14

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin

Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

To: Diane Griffin[dgriffi6@jhmi.edu]; Rusek, Benjamin[BRusek@nas.edu]; 'relman@stanford.edu'[relman@stanford.edu]; rbaric_email.unc[rbaric@email.unc.edu]; 'saif.2@osu.edu'[saif.2@osu.edu]; 'stanley-perlman@uiowa.edu'[stanley-perlman@uiowa.edu]; 'harvey.fineberg@moore.org'[harvey.fineberg@moore.org]; 'peggy@hbfam.net'[peggy@hbfam.net]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Dzau, Victor J.[VDzau@nas.edu]; Nancy Connell[NancyConnell@jhu.edu]; Dave Franz (davidrfranz@gmail.com)[davidrfranz@gmail.com]
Cc: 'fsharples_3@hotmail.com'[fsharples_3@hotmail.com]; Lowenthal, Micah[mlowenth@nas.edu]; antoinette_baric.med[antoinette_baric@med.unc.edu]; Alison Andre[andre@ecohealthalliance.org]; 'jennifer.ryan@moore.org'[jennifer.ryan@moore.org]; Bowman, Katherine[KBowman@nas.edu]; Kanarek, Morgan[MKanarek@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]
From: Peter Daszak[daszak@ecohealthalliance.org]
Sent: Wed 9/23/2020 11:45:12 PM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14

Happy to take part and look forward to the discussions. I know that the WHO team are planning their deeper dive into the animal reservoir question for COVID-19 origins, and it might be good to ask a couple of questions on animal infections that are not controversial, e.g.:

1. We have heard that there are policy measures under review to significantly reduce the wildlife trade, including closing down wildlife farms. Are there plans to test animals before they are killed, e.g. civets, raccoon dogs, bamboo rats, to see if they have had exposure to SARS-CoV-2?

2. We realize that the bat coronaviruses with the closest relationship to SARS-CoV-2 are not the parental strain, but more like fairly distant relatives. Are there plans to do more bat sampling, and try to identify viruses that are closer to SARS-CoV-2 than those nearest viruses (RaTG13 and RmYN02)?

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: +1-212-380-4474
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Diane Griffin <dgriffi6@jhmi.edu>
Sent: Tuesday, September 22, 2020 7:20 AM
To: Rusek, Benjamin <BRusek@nas.edu>; 'relman@stanford.edu' <relman@stanford.edu>; rbaric_email.unc <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; Peter Daszak <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; Nancy Connell <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; antoinette_baric.med

<antoinette_baric@med.unc.edu>; Alison Andre <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>
Subject: Re: Virtual U.S. China dialogue meeting October 13 and 14

Ben - I can participate.

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Monday, September 21, 2020 9:00 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; Diane Griffin <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; Nancy Connell <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
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Greetings,

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Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
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Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

From: Rusek, Benjamin
Sent: Thursday, June 4, 2020 1:25 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
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From: Diane Griffin[dgriffi6@jhmi.edu]
Sent: Tue 9/22/2020 6:19:51 AM (UTC-05:00)
Subject: Re: Virtual U.S. China dialogue meeting October 13 and 14

Ben - I can participate.

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

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Sent: Monday, September 21, 2020 9:00 PM
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From: Rusek, Benjamin[BRusek@nas.edu]
Sent: Fri 10/9/2020 4:42:45 PM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
October 2020 U.S.-China Bio Dialogue v3.docx

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

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To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year

3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu'

<saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

October Bio Dialogue Virtual Sessions

Session 1: Tuesday, October 13, 9-11 PM ET / 6-8 PM PT in U.S.
Wednesday, October 14, 9-11 AM in China

Session 1 Meeting Link: [HYPERLINK "https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password **552.136**

Welcome and Introduction — Diane Griffin and George Gao

Overview of current status of CoVID-19 vaccine development in China — George Gao
Overview of current status of CoVID-19 vaccine development in the U.S. — Nancy Connell

Topic 1: Human vaccine development and delivery
Moderator: Diane Griffin

- Vaccination programs in China: How are vaccine programs for particular subpopulations being implemented?
  - Pediatric populations
  - First responders
  - Military personnel
  - Elderly population

- Post-vaccination surveillance and monitoring strategies
  - Immunogenicity
  - Monitoring Immunity
  - Vaccine-associated adverse events

- Adapting current vaccine platforms to novel mass vaccination: strategies and issues

- Progress on other vaccines
  - Universal influenza vaccines
  - Enterovirus D68

Topic 2: Animal vaccine development and delivery
Moderator: Linda Saif

- Status of corona virus vaccination for animals
  - Vaccine types
  - Efficacy
  - Complications and other issues?

- African Swine Fever: vaccine progress in China

- New "swine flu" (G4) in China

- H5N1 avian influenza and domestic poultry

Session 2: Wednesday October 14, 9-11 PM ET / 6-8 PM PT in U.S.
Thursday, October 15, 9-11 AM in China

Session 2 Meeting Link: [HYPERLINK "https://nasem.zoom.us/j/98420889232?pwd=552.136
Password: 552.136

Topic 1: Immunity
Moderator: Diane Griffin

- Correlates of immunity – biomarkers predicting susceptibility or progression to severe disease
- Background immunity from circulating "common cold" coronaviruses
- How long will immunity last?

Topic 2: Testing and diagnostics
Moderator: Peggy Hamburg

- Chinese testing strategies for rapid, frequent population-level testing
- Antibody testing
- Importance of T-cell responses
- Long-term sequelae following COVID-19 infection—lung function, neurologic issues, other issues

NASEM Participants

Dr. Ralph Baric, PhD, is a Professor in the Department of Epidemiology at the University of North Carolina's School of Public Health.

Dr. Nancy Connell, PhD, is a Professor at the Johns Hopkins Center for Health Security in Baltimore, MD

Dr. Peter Daszak, PhD, is currently president of EcoHealth Alliance, a nonprofit non-governmental organization that supports various programs on global health.

Dr. Victor Dzau, is the current President of the U.S. National Academy of Medicine in Washington, D.C.

Dr. David R. Franz, DVM, PhD, is currently retired, but served in the U.S. Army Medical Research and Materiel Command for 23 of 27 years on active duty and as Commander of the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID).

Dr. Harvey Fineberg, MD, is currently president of the Gordon and Betty Moore Foundation, immediately prior to which he was President of the Institute of Medicine (now the National Academy of Medicine).

Dr. Diane Griffin, PhD, is University Distinguished Service Professor and Alfred and Jill Sommer Chair of the W. Harry Feinstone Department of Molecular Microbiology and Immunology at Johns Hopkins Bloomberg School of Public Health and the current vice-president of the U.S. National Academy of Sciences.

Dr. Margaret (Peggy) Hamburg, MD, is an American physician and public health administrator. She served as the 21st Commissioner of the U.S. Food and Drug Administration from May 2009 to April 2015 and is currently Foreign Secretary for the U.S. National Academy of Medicine.

Dr. James Le Duc, PhD, is the director of the Galveston National Laboratory, one of the largest active biocontainment facilities on a U.S. academic campus.

Dr. Stanley Perlman, MD, PhD, is Professor of Microbiology and Immunology and of Pediatrics at the University of Iowa Health Care.

Dr. David Relman is a microbiologist and the Thomas C. and Joan M. Merigan Professor in Medicine and in Microbiology & Immunology at the Stanford University School of Medicine.

Dr. Linda J. Saif, PhD,[HYPERLINK "https://en.wikipedia.org/wiki/Linda_Saif" \l "cite_note-:0-3"] is Distinguished University Professor, [HYPERLINK "http://vet.osu.edu/preventive-medicine" \o "Preventive Medicine"], [HYPERLINK "http://www.oardc.ohio-state.edu/fahrp/" \t "_blank"], Ohio Agricultural Research and Development Center of the Ohio State University.

Dr. Pei Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas.

To: Diane Griffin[dgriffi6@jhmi.edu]; Rusek, Benjamin[BRusek@nas.edu]; 'peggy@hbfam.net'[peggy@hbfam.net]; Shi, Pei yong[peshi@UTMB.EDU]; Nancy Connell[NancyConnell@jhu.edu]; 'Dave Franz (davidrfranz@gmail.com)'[davidrfranz@gmail.com]; Saif, Linda[saif.2@osu.edu]; Baric, Ralph S[rbaric@email.unc.edu]; "Harvey V. Fineberg" <harvey. fineberg@moore. org> (harvey.fineberg@moore.org)[harvey.fineberg@moore.org]; David A Relman[relman@stanford.edu]
Cc: Lowenthal, Micah[mlowenth@nas.edu]; Bowman, Katherine[KBowman@nas.edu]; 'Raymond JEANLOZ'[jeanloz@berkeley.edu]; Hare, Hope[HHare@nas.edu]; Sharples, Fran[FSharples@nas.edu]
From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: Wed 10/14/2020 12:28:50 PM (UTC-05:00)
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
COVID-19 Summary of Discussions between NASEM and CAS on vaccines 13Oct2020.docx

Attached please find my notes from last night's discussion. Please edit and correct as needed; I'm sure I missed some things.

Excellent discussions. These are very valuable.

Thanks, Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

From: Diane Griffin <dgriffi6@jhmi.edu>
Sent: Wednesday, October 14, 2020 6:53 AM
To: Rusek, Benjamin <BRusek@nas.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Nancy Connell <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: Lowenthal, Micah <mlowenth@nas.edu>; Bowman, Katherine <KBowman@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: Re: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

Ben - ok, thanks. I think that last night's session went well - clearly value in having these sessions relatively small and with people who now "know" each other.

See you tonight.

Diane

Diane E. Griffin, MD PhD
Vice President, National Academy of Sciences
University Distinguished Service Professor
W. Harry Feinstone Department of Molecular Microbiology and Immunology
Johns Hopkins Bloomberg School of Public Health
615 N. Wolfe St, Rm E5636
Baltimore, MD 21205
410-955-3459
dgriffi6@jhu.edu

From: Rusek, Benjamin <BRusek@nas.edu>
Sent: Tuesday, October 13, 2020 8:54 PM
To: Diane Griffin <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Nancy Connell <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: Lowenthal, Micah <mlowenth@nas.edu>; Bowman, Katherine <KBowman@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links

No major updates before we get started.

FYI Bu Zhigao from CAAS will not make it tonight and since Zhiming can't make the scheduled planning session next week we need to reschedule. I let CAS know that we would like at least Zhiming, George Gao, Zhengli Shi and maybe Mifang Liang as well as others who value and are interested in the dialogue and possible future topics to join the now to be scheduled planning call.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, October 12, 2020 12:36 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>; Block, Bruce <BBlock@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

I have attached what should be the final agenda for the U.S. China dialogue meeting sessions on Tuesday, October 13 and Wednesday October 14. It includes the Chinese participant list at the end. Links to join the Zooms are also below.

Looking forward to seeing/talking to you all on Tuesday and Wednesday evening.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Session 1: Tuesday, October 13, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/92754903815?pwd= **552.136**
Password: **552.136**

Session 2: Wednesday October 14, **9-11 PM ET / 6-8 PM PT in U.S.**
Meeting Link: https://nasem.zoom.us/j/98420889232?pwd= **552.136**
Password: **552.136**

From: Rusek, Benjamin
Sent: Friday, October 9, 2020 5:43 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; 'Dave Franz (davidrfranz@gmail.com)' <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; Cervenka, Nicole <NCervenka@nas.edu>; Sharples, Fran <FSharples@nas.edu>
Subject: RE: Virtual U.S. China dialogue meeting October 13 and 14 - agenda with zoom links
Importance: High

Greetings,

We are looking forward to the two virtual bio dialogue sessions set to take place on Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT) next week. Like in previous sessions we expect that the Chinese expert participants will lead the discussion on the majority of the topics and that the format will be more of a discussion among the participants instead of a series of formal presentations. I have attached an agenda that includes the Zoom connection links for both days along with the U.S. participant list. If I get the Chinese participant list before the session I will send that out to you all.

Feel free to respond to this email with any thoughts, points of emphasis or issues that you would like to discuss among the U.S. group before the sessions. Also let me know if you have any questions or concerns.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, September 21, 2020 9:01 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>; 'Nancy Connell' <NancyConnell@jhu.edu>; Dave Franz (davidrfranz@gmail.com) <davidrfranz@gmail.com>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>
Subject: Virtual U.S. China dialogue meeting October 13 and 14

Importance: High

Greetings,

I hope you all had a good summer and are staying safe and healthy. The Chinese Academy of Sciences has agreed to hold another (4th) virtual bio dialogue meeting with NASEM on **1) vaccine development and delivery** and **2) immunity, testing and diagnostics.** The agreed topics for the session are below. **We have reserved Tuesday, October 13 (9-11 PM ET / 6-8 PM PT) and Wednesday, October 14 (9-11 PM ET / 6-8 PM PT**) to discuss the topics on the agenda.

We hope you are able to participate. Please let me know if you are available and if so save the dates and times on your calendar. We will get back to you with more information and a detailed agenda for the sessions soon.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

***

Vaccine development and delivery

Human

1) **Current status of CoVID-19 vaccine development in China and the U.S.**
2) **Chinse vaccination of military personnel and other Chinese populations**
3) **Vaccination of pediatric populations**
4) **Active surveillance strategies for monitoring adverse events observed after vaccination (as well as immunogenicity)**
5) **Adapting current vaccine platforms to novel mass vax strategies and other mass vaccination strategic issues**
6) **Progress on a universal influenza vaccines**
7) **Vaccine for enterovirus D68**

Animal

1) **Status of corona virus vaccination for animals - kinds of vaccine, efficacy, complications, etc**
2) **ASF in China and ASF vaccine progress**
3) **New swine coronavirus**
4) **Vaccination strategy for H5N1 avian influenza and domestic poultry**

Immunity, testing and diagnostics

1) **Correlates of immunity including the possibility of background immunity from circulating "common cold" coronaviruses**
2) **Chinese diagnostic testing strategies for testing large populations quickly**
3) **Antibody and antibody testing topics, importance of T-cell responses**
4) **Long-term sequela following COVID-19 infection—lung function, neurologic issues, others**

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Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>; 'Nancy Connell' <NancyConnell@jhu.edu>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

I have attached the American version of the agenda for the 3rd U.S. China virtual dialogue meeting on immunity and related topics set to take place on **Tuesday night, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time).

As you can see we have incorporated George Gao's questions into the agenda, we hope that **Harvey Fineberg** can provide information on and lead the discussion of 1) serologic investigation in the U.S. 2) strategy in the U.S. for the second half of this year 3) vaccine availability in the U.S. and that **Ralph Baric** can do the same re progress in the development of vaccine in the U.S. (especially mRNA vaccine).

We have also listed delegation member names after the other Immunity questions. Like previously, folks are listed simply so someone is responsible for getting an answer from the Chinese to each question during the discussion. I will send a version to CAS without those names listed but will let them know who we have asked to answer George's questions.

Please let us know if you have any thoughts or comments on the agenda or this plan. I will send you the Zoom link later tonight or tomorrow morning.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Monday, June 1, 2020 10:03 AM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET
Importance: High

Greetings,

Good news, just heard back from CAS. They agreed to hold the 3rd dialogue meeting on the proposed immunity topics on **Tuesday, June 9 from 9:00-11:00 PM ET** (9-11 AM the next morning, Beijing time). Please hold that time on your calendar.

CAS let us know that George Gao wants to add the following questions to the discussion:

- Could any US participant introduce the progress in the development of vaccine in the US, especially mRNA vaccine?
- How is the overall situation of serologic investigation in the US?
- What is the COVID-19 prevention and control strategy in the US for the second half of this year? When do you expect COVID-19 vaccine to be available in the US ?

We will send out a new agenda and Zoom link for the meeting later in the week.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

From: Rusek, Benjamin
Sent: Friday, May 22, 2020 3:55 PM
To: 'relman@stanford.edu' <relman@stanford.edu>; 'rbaric@email.unc.edu' <rbaric@email.unc.edu>; 'saif.2@osu.edu' <saif.2@osu.edu>; 'stanley-perlman@uiowa.edu' <stanley-perlman@uiowa.edu>; 'daszak@ecohealthalliance.org' <daszak@ecohealthalliance.org>; 'harvey.fineberg@moore.org' <harvey.fineberg@moore.org>; 'dgriffi6@jhmi.edu' <dgriffi6@jhmi.edu>; 'peggy@hbfam.net' <peggy@hbfam.net>; 'jwleduc@UTMB.EDU' <jwleduc@UTMB.EDU>; 'peshi@UTMB.EDU' <peshi@UTMB.EDU>; Dzau, Victor J. <VDzau@nas.edu>
Cc: 'fsharples_3@hotmail.com' <fsharples_3@hotmail.com>; Lowenthal, Micah <mlowenth@nas.edu>; 'antoinette_baric@med.unc.edu' <antoinette_baric@med.unc.edu>; 'andre@ecohealthalliance.org' <andre@ecohealthalliance.org>; 'jennifer.ryan@moore.org' <jennifer.ryan@moore.org>; Bowman, Katherine <KBowman@nas.edu>; Kanarek, Morgan <MKanarek@nas.edu>; 'Raymond JEANLOZ' <jeanloz@berkeley.edu>; Hare, Hope <HHare@nas.edu>; 'davidrfranz@gmail.com' <davidrfranz@gmail.com>
Subject: RE: 3rd Virtual U.S. China dialogue meeting on COVID-19
Importance: High

Greetings,

Good news: Last night CAS leadership agreed to hold the 3rd virtual dialogue (Zoom meeting) on the list of Immunity topics we proposed. However they would like to push the dates for the 3rd meeting back to the first or second week of June (so no Zoom meeting on Tuesday night next week). Some of our Chinese counterparts are involved in China's National People's Congress taking place next week.

We are targeting **one night on June 1-4 or on June 8-11** (at 9-11 PM ET for the Americans, the following morning for the Chinese group.)

Please send your availability to participate on those nights (or maybe simply send the nights you can't participate) to Hope Hare [HHare@nas.edu] so we can propose a date or dates to CAS that works best for the American group.

Thanks again for your availability and willingness to participate in this initiative and I hope you have a good long weekend.

Kind regards,

Ben

Benjamin Rusek
The U.S. National Academy of Sciences
1-202-334-3975

Summary of Discussions between NASEM and CAS on COVID-19, 13Oct 2020

1. CAS (George Gao) provided an overview of the COVID-19 vaccine efforts underway in China. Key points were as follows:
    a. 7 different vaccine approaches are underway (list was shared)
    b. Range from classic inactivated vaccines to live, attenuated candidates
    c. Vaccine underdeveloped based on modified "cold adapted" influenza vaccine as a live, attenuated vaccine for COVID-19 following nasal administration.
    d. Several candidates are in Phase 3 clinical trials (Brazil, Argentina and UAE mentioned, but perhaps other locations as well)
2. Human monoclonal antibody candidates are being developed for clinical use
    a. Multiple candidates are under study
    b. Collaborations with Lilly to create a 2 monoclonal antibody cocktail was mentioned. This product is in clinical trials (now on hold) in the USA.
    c. Several questions were raised:
        i. Protective efficacy of candidates
        ii. Impact on/activity in lungs
        iii. Duration of maby protection
        iv. Possibility of antibody dependent enhancement
        v. Possible impact on vaccination
3. A general discussion of the value and challenges associated with the creation of a universal coronavirus vaccine similar to ongoing discussions about a possible universal vaccine for influenza.
    a. Comment (Stanley Perlman) about the possibility of including T cell epitopes as a component of a universal coronavirus vaccine given demonstrated cross-reactivity among recognized coronaviruses.
4. NAS (Nancy Connell) shared an overview of the USA "Warp Speed" vaccine development efforts underway.
    a. 4 vaccine platforms are being developed with 2 candidates supported in each platform technology (list shared)
    b. Most candidates will require a prime/boost administration
    c. mRNA candidates will require an ultralow temperature cold chain that will be demanding to implement
    d. Many are in Phase 3 clinical trials with the mRNA candidates most advanced
    e. Selection of technologies was based in part on ease of production
    f. Results of clinical studies may be available incrementally with the mRNA candidates farthest along; results known perhaps by Nov-Dec 2020; others at roughly 2 month intervals with the replicating live vaccine results available in late 2021.
    g. Vaccine production is underway concurrent with clinical trials, with approximately 100 M doses of mRNA vaccine available around the end of 2020. Manufacturing costs provided by USG (BARDA).
5. Discussion of challenges associated with USA vaccine development and roll-out strategy.
    a. Key questions: is the candidate safe, is it effective in preventing infection/disease, and what is the duration of protection (Harvey's comments)

b. How to manage multiple "successful" candidates with differing vaccination schedules and other requirements
c. How to detect adverse events
d. If EUA is granted early, those receiving placebo with receive the vaccine, leading to challenges in interpretation late onset adverse events (Ralph's comment)
e. For all candidate vaccines (USA and China), what is the strategy for select segments of the population—children, elderly, high risk occupations, others—still being addressed in China; Just released NASEM report on equitable distribution of vaccine discussed by Nancy and slide of 4 tiers of those to be vaccinated shared.

6. Review of vaccination efforts for animal diseases caused by coronaviruses (Linda Saif)
    a. Linda gave a comprehensive review of several vaccine development efforts, especially those associated with swine (list provided)
    b. Challenges encountered in producing protective vaccines for piglets
    c. Difficulties in generating mucosal immunity/IgA
7. Discussion of lessons learned from animal coronaviruses and how they might foretell problems with COVID-19 vaccination
    a. Relevance of past infection versus naïve populations on response to vaccines
    b. Mention of evidence of naturally occurring recombination of coronaviruses infecting swine in Europe.

To: george.r.painter@emory.edu[george.r.painter@emory.edu]; weller@uchc.edu[weller@uchc.edu]; msofia@arbutusbio.com[msofia@arbutusbio.com]; elizabeth.campbell@rockefeller.edu[elizabeth.campbell@rockefeller.edu]; gotte@ualberta.ca[gotte@ualberta.ca]; amesecar@purdue.edu[amesecar@purdue.edu]; celia.schiffer@umassmed.edu[celia.schiffer@umassmed.edu]; jen@1910genetics.com[jen@1910genetics.com]; charlotte.a.lanteri.mil@mail.mil[charlotte.a.lanteri.mil@mail.mil]; kumar.saikatendu@takeda.com[kumar.saikatendu@takeda.com]; dabaker@uw.edu[dabaker@uw.edu]; mweetall@ptcbio.com[mweetall@ptcbio.com]; lillian@evrysbio.com[lillian@evrysbio.com]; disney@scripps.edu[disney@scripps.edu]; cherrys@pennmedicine.upenn.edu[cherrys@pennmedicine.upenn.edu]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; Annaliesa.Anderson@pfizer.com[Annaliesa.Anderson@pfizer.com]; Shi, Pei yong[peshi@UTMB.EDU]; Whitley, Rich[rwhitley@peds.uab.edu]; Kara Carter[Kara.Carter@evotec.com]; tomas.cihlar@gilead.com[tomas.cihlar@gilead.com]; daria.hazuda@merck.com[daria.hazuda@merck.com]; Denison, Mark (NIH)[mark.denison@vanderbilt.edu]; Corbett, Kizzmekia (NIH/VRC) [E][kizzmekia.corbett@nih.gov]; hugh.smyth@austin.utexas.edu[hugh.smyth@austin.utexas.edu]; sheahan@email.unc.edu[sheahan@email.unc.edu]; O'Rear, Julian (FDA/CDER)[Jules.ORear@fda.hhs.gov]; cfletcher@unmc.edu[cfletcher@unmc.edu]; fgh@virginia.edu[fgh@virginia.edu]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; james.bradner@novartis.com[james.bradner@novartis.com]; Austin, Christopher (NIH/NCATS) [E][austinc@mail.nih.gov]; Fauci, Anthony (NIH/NIAID) [E][afauci@niaid.nih.gov]; Collins, Francis (NIH/OD) [E][collinsf@od.nih.gov]
Cc: Conley, Tony (NIH/NIAID) [E][conleyto@niaid.nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Brimacombe, Kyle (NIH/NCATS) [C][kyle.brimacombe@nih.gov]; Ford-Scheimer, Stephanie (NIH/NCATS) [C][stephanie.ford-scheimer@nih.gov]; Grossman, Abigail (NIH/NCATS) [C][abigail.grossman@nih.gov]; Anderson, James (NIH/OD) [E][james.anderson2@nih.gov]
From: Hall, Matthew (NIH/NCATS) [E][hallma@mail.nih.gov]
Sent: Tue 10/27/2020 11:38:49 AM (UTC-05:00)
Subject: Web site live: NIH SARS-CoV-2 Antiviral Therapeutics Summit
NIH antiviral summit poster[4][2][1].pdf
NIH-COVID-flyer-FINAL[2][4][1].png
NIH SARS-CoV-2 Antiviral Therapeutics Summit Agenda _27 Oct 2020.pdf

Colleagues,

Thank you for agreeing to participate in our NIH SARS-CoV-2 Antiviral Therapeutics Summit, to be held next Friday 6th November. We look forward to getting together with each panel group over the next two days, to discuss Q&A topics and enable the moderators to wrap up their introductory slides for each session (due at the end of the week).

We're excited to share that the **web site** for the summit is now live : https://www.nih.gov/antiviralcov2summit
Attached are two digital posters (PDF and JPG) and the agenda. Note that registration is not required, but a calendar invite can be downloaded from the summit web site.

Please forward and share information on the event with your colleagues. We recognize that the meeting has been organized at a rapid pace and are making an effort to ensure as many people are aware of the meeting as possible. The webcast will also be recorded and available for playback at videocast.nih.gov .

While I have your attention, please do pass along your **photo** and check your **affiliation** and **bio** on the web site 'Hosts & Presenters' section of the site (if you have not already). The organizing group will reach out again as we strive to fill out this page.

On behalf of my fellow organizers:

James Anderson, NIH OD
Anthony Conley, NIAID
Mindy Davis, NIAID
Kyle Brimacombe, NCATS
Stephanie Ford-Scheimer, NCATS
Abigail Grossman, NCATS

Matthew D. Hall
Acting Director, Early Translation Branch
Group Leader, Biology

National Center for Advancing Translational Sciences (NCATS)
National Institutes of Health
9800 Medical Center Drive
Rockville, MD 20850

Office: 301-480-9928
https://ncats.nih.gov/staff/hallma

@cispt2

NCATS Website: http://ncats.nih.gov

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NIH VIRTUAL SARS-COV-2 ANTIVIRAL THERAPEUTICS SUMMIT

An overview of the current state of direct anti-coronaviral targets and therapeutics, available tools, and challenges

FRIDAY NOVEMBER 6, 2020

Session Topics

Viral Replication Machinery

Proteases (Viral and Host)

Emerging Targets and Modalities

Preclinical Tools

Lessons from Other Viruses and Preparation for the Future

WWW.NIH.GOV/ANTIVIRALCOV2SUMMIT

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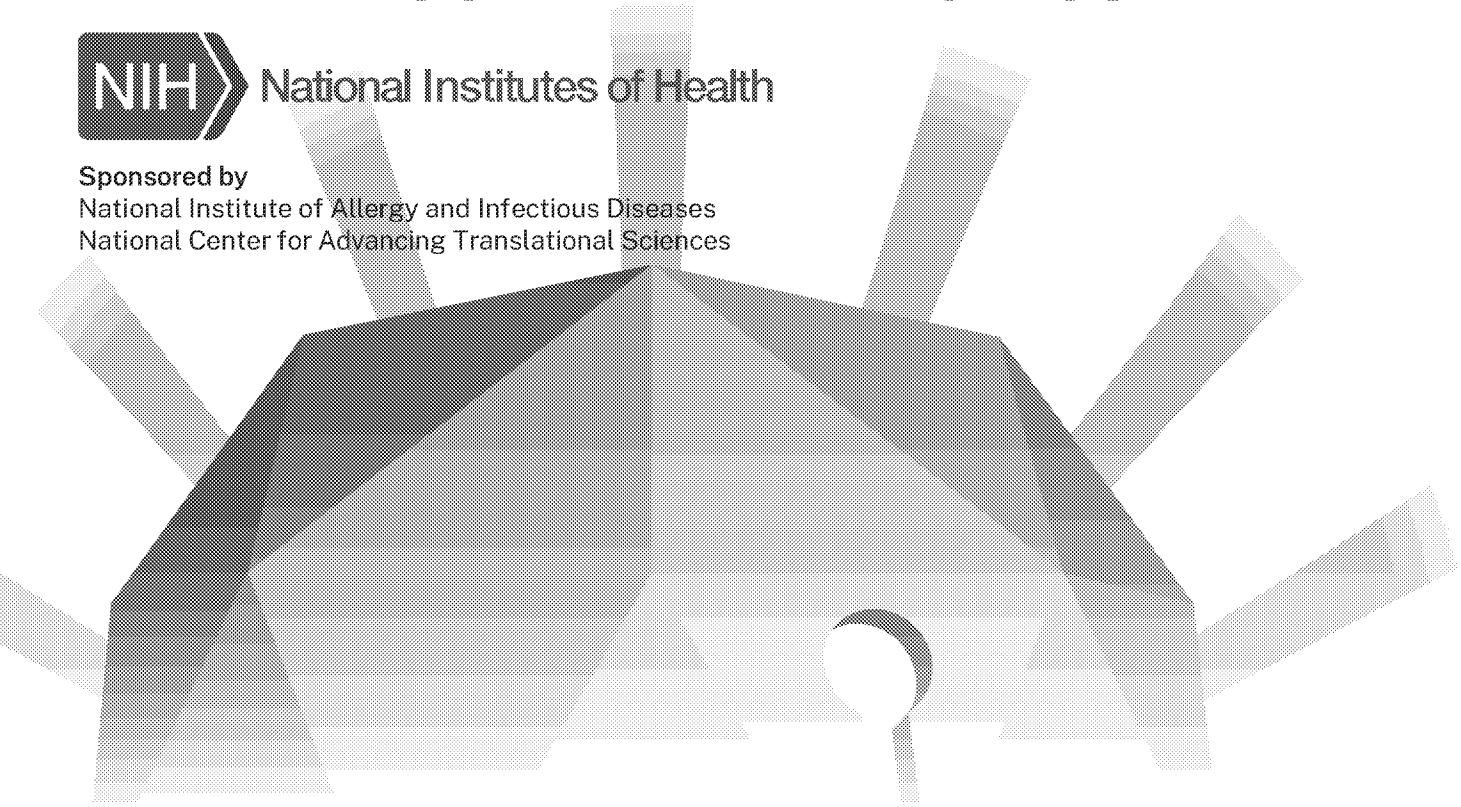
National Center for Advancing Translational Sciences



NIH VIRTUAL SARS-COV-2 ANTIVIRAL THERAPEUTICS SUMMIT

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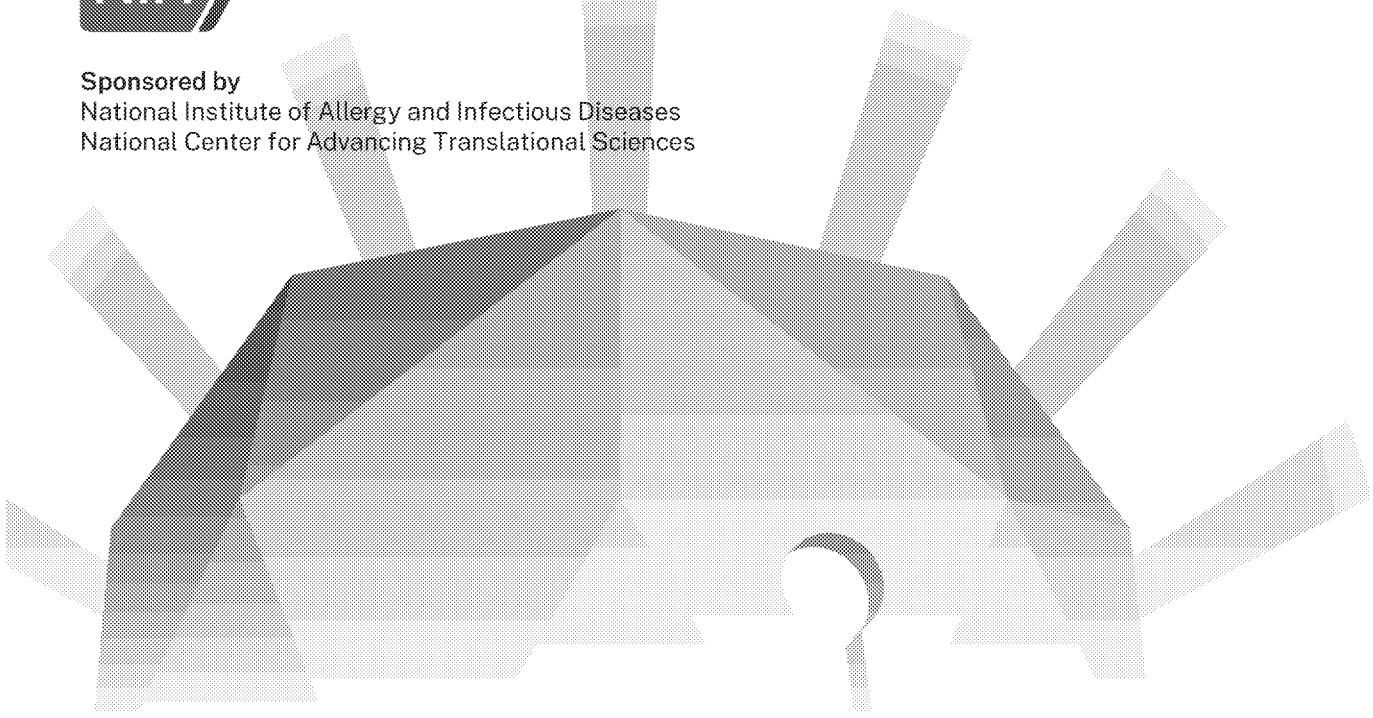

National Institutes of Health

NIH SARS-CoV-2 Antiviral Therapeutics Summit

Date: November 6, 2020 **Virtual Meeting**

Purpose: This summit will provide an overview of the current state of direct anti-coronaviral targets and therapeutics, available tools and challenges.

Agenda

11:00 AM – 11:20 AM **Introductory Comments**

- Dr. Francis Collins – Director, National Institutes of Health
- Dr. Anthony Fauci – Director, National Institute of Allergy and Infectious Diseases
- Dr. Christopher Austin – Director, National Center for Advancing Translational Sciences

11:20 AM – 11:40 AM **Overview of the Virus and Therapeutics Approaches**

- Dr. Mark Dennison, Vanderbilt University

11:40 AM – 12:15 PM **Viral Replication Machinery. Moderator: Dr. Tomas Cihlar, Gilead Sciences**

- Dr. Elizabeth Campbell, Rockefeller University
- Dr. Matthias Götte, University of Alberta
- Dr. George Painter, Emory University
- Dr. Michael Sofia, Arbutus Biopharma, Inc.
- Dr. Sandra Weller, University of Connecticut

12:15 PM – 12:25 PM **Highlight on Status of Vaccines and Neutralizing Antibodies to Prevent and Treat SARS-CoV-2 Infection**

- Dr. Kizzmekia Corbett, Vaccine Research Center, National Institute of Allergy and Infectious Diseases

12:25 PM – 1:00 PM **Proteases (Viral and Host). Moderator: Dr. Annaliesa Anderson, Pfizer**

- LTC Charlotte Lanteri, Walter Reed Army Institute of Research
- Dr. Andrew Mesecar, Purdue University
- Dr. Jen Nwankwo, 1910 Genetics
- Dr. Celia Schiffer, UMass Medical School

1:00 PM – 1:35 PM **Emerging Targets, Emerging Modalities. Moderator: Dr. Kara Carter, Evotec**

- Dr. David Baker, University of Washington
- Dr. Lillian Chiang, Evrys Bio
- Dr. Matthew Disney, Scripps Research
- Dr. Kumar Saikatendu, Takeda Pharmaceuticals
- Dr. Marla Weetall, PTC Therapeutics, Inc.

1:35 PM – 2:10 PM **Preclinical Tools. Moderator: Dr. Pei-Yong Shi, University of Texas Medical Branch**

- Dr. Sara Cherry, University of Pennsylvania
- Dr. Emmie de Wit, NIAID/Rocky Mountain Laboratories
- Dr. Jules O'Rear, Food and Drug Administration
- Dr. Timothy Sheahan, University of North Carolina
- Dr. Hugh Smyth, University of Texas at Austin

2:10 PM – 2:45 PM **Lessons from Other Viruses and Preparation for the Future. Moderator: Dr. Daria Hazuda, Merck**

- Dr. Jay Bradner, Novartis
- Dr. Courtney Fletcher, University of Nebraska Medical Center
- Dr. Frederick Hayden, University of Virginia
- Dr. Hilary Marston, National Institute of Allergy and Infectious Diseases

2:45 PM – 3:05 PM **Summary of Discussions and Perspectives on the Challenges Ahead**

- Dr. Richard Whitley, University of Alabama at Birmingham

3:05 PM – 3:25 PM **Closing Statement**

- Dr. Francis Collins, Director, National Institutes of Health

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina

Location: https://who.zoom.us/j/ **552.136**

Subject: [COVID-19] 36th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting " [COVID-19] 36th WHO TC - Assays"

Join Zoom Meeting
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Meeting ID: 948 0644 7981
Find your local number:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwho.zoom.us%2Fu%2FacoGi3wmrY&data=04%7C01%7Cpeshi%40utmb.edu%7Cf3fd5d9e80e245c59a4708d87f0cb08f%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637399039777254969%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=bxQSsD1Ju88%2BHTjfZvKTq8ZwgH%2F%2FV2dAj3ink5fzF6U%3D&reserved=0

From: GSELL, Pierre[gsellp@who.int]

Attendees: galter; (SPmig) Maria Baca Estrada; baihe; rbaric; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar; pbieniasz@mail.rockefeller.edu; karin.bok; Boyle, David; brooke.bozick@nih.gov; christian.brechot@pasteur.fr; Christine Bruce; zuz4@cdc.gov; Miles.Carroll; Cavaleri Marco; Monalisa Chatterji; Chu, May; Carolyn Clark; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak; de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael; mit666666@pitt.edu; katie.doores; William Dowling; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson; Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell; Luc.Gagnon; Mayra.Garcia; bhx1@cdc.gov; Volker.gerdts@usask.ca; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; Goldblatt, David; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ; Celine Gurry; ilj2@cdc.gov; B.L. Haagmans; Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND@mail.dstl.gov.uk; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; Cassandra Kelly; Jacqueline Kirchner; KNEZEVIC, Ivana; M.P.G. Koopmans; Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer@mssm.edu; philip.krause@fda.hhs.gov; Shelly Krebs; Greg Kulnis; Arun Kumar; pawinee.k@redcross.or.th; Teresa Lambe; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl; changguili; lyhchengdu; limhy0919@korea.kr; Little, James (OS/ASPR/BARDA); liub; MacGill, Tracy; Karen Makar; Mary.Matheson@phe.gov.uk; Giada Mattiuzzo; jmclellan; adrian.mcdermott; jmcelrat; gmedigeshi; jwm1@pitt.edu; (SPmig) Philip Minor; Kayvon Modjarrad; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela; Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o; n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim; Mark Page; gustavo.f.palacios.civ; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ; malik; PERKINS, Mark; (SPmig) Supaporn Phumiamorn; margaret.l.pitt.civ; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; Marc L Salit; erica; SATHIYAMOORTHY, Vaseeharan; Sharon Schendel; Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle; PScott; Shi, Pei yong; Shivji Ragini; Amy C. Shurtleff; Smith, Ashley (OS/ASPR/BARDA); Manki Song; Stemmy, Erik (NIH/NIAID) [E]; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue@usask.ca; georgia.tomaras; Julia Tree; john.c.trefry.civ; luk_vandenberghe; sylvie.van-der-werf; eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович; David Vaughn; linfa.wang; wangjz; wangyc; Weir, Jerry P.; alex@lji.org; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; (SPmig) David Wood; xumiaobj; solomon.yimer@cepi.net; tlying@fudan.edu.cn; Vidadi Yusibov; zlshi@wh.iov.cn; ydm9@cdc.gov; guy.gorochov@sorbonne-universite.fr; BRANGEL, Polina; gweiss@uci.edu; ZHOU, Tiequn; YOO, Si Hyung; Sutter Roland

Sent: Mon 11/9/2020 2:45:41 AM (UTC-06:00)

Subject: [COVID-19] 37th WHO TC - Assays

GSELL, Pierre is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting
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Meeting ID: 965 1507 1032
Passcode: **552.136**

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Passcode: **552.136**
Find your local number:
https://nam11.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwho.zoom.us%2Fu%2FaexBSd0VYs&data=04%7C01%7Cpeshi%40utmb.edu%7C84376630c17940796b0708d8848c76c8%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637405086121779806%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C1000&sdata=W6%2BcaNFvnuQK1zFOAdbc4LSEMP8KMaK95OAVunCfVoU%3D&reserved=0

To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]
From: William Dowling[william.dowling@cepi.net]
Sent: Wed 11/25/2020 6:26:10 AM (UTC-06:00)
Subject: COVID-19 assays review
State of the Art paper outline.docx

Dear colleagues,

Similar to what was done recently with the WHO COVID-19 models working group, we would like to publish a short review about the state-of-the-art regarding COVID-19 assays. Based on your expertise and the data you have generated and presented to the WHO assays group, we would like to ask you to contribute to this paper. As you can see in the attached outline, we have suggested subgroups for different topics. Please take this only as a suggestion and feel free to contribute to other parts of the review as you deem fit. Also, feel free to suggest additional authors as needed. Florian Krammer has graciously agreed to help coordinate and submit this to a high quality journal. We would like to have a draft by the end of the year if possible. Please confirm that you wish to participate in this endeavor.

Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

Introduction
This will include a discussion of assay use cases/purposes

ELISA and Spike proteins (Natalie Thornburg, Barney Graham, Jason McClellan, Marion Koopmans, Mary Matheson)

Multiplex assays (David Goldblatt)

Viral Neutralization (David Montefiori, Lin-fa Wang, Pei-Yong Shi, Sylvie van der Werf, William Lee, Miao Xu)

Antibody function (Galit Alter)

T-Cells (Alex Sette, Shane Crotty, Julie McElrath)

Duration of immunity (Florian Krammer, Katie Doors, Anita Iyer, Paul Bieniasz)

Performance evaluations (Jilian Sacks, Douglas Lowy)

Assay harmonization/ International Standards Mark Page

Correlates of Protection

Conclusions and Lessons Learned

To: Goldblatt, David[d.goldblatt@ucl.ac.uk]; William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
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From: Mark Page[Mark.Page@nibsc.org]
Sent: Wed 11/25/2020 6:47:34 AM (UTC-06:00)
Subject: RE: COVID-19 assays review

Hi Bill,

Yes, I am happy to contribute to this.

Regards

Mark

From: Goldblatt, David <d.goldblatt@ucl.ac.uk>
Sent: 25 November 2020 12:34
To: William Dowling <william.dowling@cepi.net>; Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; barney.graham@nih.gov; Jason McLellan <jmclellan@austin.utexas.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Mary.Matheson@phe.gov.uk; david.montefiori@duke.edu; linfa.wang@duke-nus.edu.sg; Shi, Pei yong <peshi@UTMB.EDU>; Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>; xumiaobj@126.com; Alter, Galit <GALTER@mgh.harvard.edu>; alex@lji.org; shane@lji.org; McElrath MD PhD, Julie <jmcelrat@fredhutch.org>; katie.doores@kcl.ac.uk; Paul Bieniasz <pbieniasz@rockefeller.edu>; Jilian Sacks <Jilian.Sacks@finddx.org>; Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>; Mark Page <Mark.Page@nibsc.org>; ASiver@mgh.harvard.edu; william.lee@health.ny.gov
Cc: GSELL, Pierre <gsellp@who.int>; Simon Funnell <Simon.Funnell@phe.gov.uk>; Cesar Munoz-fontela <munoz-fontela@bnitm.de>; RIVEROS BALTA, Alina Ximena <lauriex@who.int>; henaorestrepoa@who.int; KNEZEVIC, Ivana <knezevici@who.int>; florian.krammer@mssm.edu
Subject: Re: COVID-19 assays review

Thanks Bill
Happy to contribute
Regards
David

From: William Dowling <william.dowling@cepi.net>
Date: Wednesday, 25 November 2020 at 12:26
To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>, barney.graham@nih.gov <barney.graham@nih.gov>, Jason McLellan <jmclellan@austin.utexas.edu>, M.P.G. Koopmans <m.koopmans@erasmusmc.nl>, Mary.Matheson@phe.gov.uk <Mary.Matheson@phe.gov.uk>, Goldblatt, David <d.goldblatt@ucl.ac.uk>, david.montefiori@duke.edu <david.montefiori@duke.edu>, linfa.wang@duke-nus.edu.sg <linfa.wang@duke-nus.edu.sg>, Shi, Pei yong <peshi@UTMB.EDU>, Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>, xumiaobj@126.com <xumiaobj@126.com>, Alter, Galit <GALTER@mgh.harvard.edu>, alex@lji.org <alex@lji.org>, shane@lji.org <shane@lji.org>, McElrath MD PhD, Julie <jmcelrat@fredhutch.org>, katie.doores@kcl.ac.uk <katie.doores@kcl.ac.uk>, Paul Bieniasz <pbieniasz@rockefeller.edu>, Jilian Sacks <Jilian.Sacks@finddx.org>, Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>, Mark Page <mark.page@nibsc.org>, ASiver@mgh.harvard.edu <ASiver@mgh.harvard.edu>, william.lee@health.ny.gov <william.lee@health.ny.gov>
Cc: GSELL, Pierre <gsellp@who.int>, Simon Funnell <Simon.Funnell@phe.gov.uk>, Cesar Munoz-fontela <munoz-

fontela@bnitm.de>, RIVEROS BALTA, Alina Ximena <lauriex@who.int>, henaorestrepoa@who.int <henaorestrepoa@who.int>, KNEZEVIC, Ivana <knezevici@who.int>, florian.krammer@mssm.edu <florian.krammer@mssm.edu>
Subject: COVID-19 assays review

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Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Wed 11/25/2020 7:24:18 AM (UTC-06:00)
Subject: RE: COVID-19 assays review

Dear Bill,

Thanks and more than happy to participate.

Regards,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: William Dowling <william.dowling@cepi.net>
Sent: Wednesday, 25 November 2020 8:26 PM
To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; barney.graham@nih.gov; Jason McLellan <jmclellan@austin.utexas.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Mary.Matheson@phe.gov.uk; Goldblatt, David <d.goldblatt@ucl.ac.uk>; david.montefiori@duke.edu; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>; Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>; xumiaobj@126.com; Alter, Galit <GALTER@mgh.harvard.edu>; alex@lji.org; shane@lji.org; McElrath MD PhD, Julie <jmcelrat@fredhutch.org>; katie.doores@kcl.ac.uk; Paul Bieniasz <pbieniasz@rockefeller.edu>; Jilian Sacks <Jilian.Sacks@finddx.org>; Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>; Mark Page <mark.page@nibsc.org>; ASiver@mgh.harvard.edu; william.lee@health.ny.gov
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1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

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To: William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]
From: Goldblatt, David[d.goldblatt@ucl.ac.uk]
Sent: Wed 11/25/2020 6:34:02 AM (UTC-06:00)
Subject: Re: COVID-19 assays review

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From: William Dowling <william.dowling@cepi.net>
Date: Wednesday, 25 November 2020 at 12:26
To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>, barney.graham@nih.gov <barney.graham@nih.gov>, Jason McLellan <jmclellan@austin.utexas.edu>, M.P.G. Koopmans <m.koopmans@erasmusmc.nl>, Mary.Matheson@phe.gov.uk <Mary.Matheson@phe.gov.uk>, Goldblatt, David <d.goldblatt@ucl.ac.uk>, david.montefiori@duke.edu <david.montefiori@duke.edu>, linfa.wang@duke-nus.edu.sg <linfa.wang@duke-nus.edu.sg>, Shi, Pei yong <peshi@UTMB.EDU>, Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>, xumiaobj@126.com <xumiaobj@126.com>, Alter, Galit <GALTER@mgh.harvard.edu>, alex@lji.org <alex@lji.org>, shane@lji.org <shane@lji.org>, McElrath MD PhD, Julie <jmcelrat@fredhutch.org>, katie.doores@kcl.ac.uk <katie.doores@kcl.ac.uk>, Paul Bieniasz <pbieniasz@rockefeller.edu>, Jilian Sacks <Jilian.Sacks@finddx.org>, Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>, Mark Page <mark.page@nibsc.org>, ASiver@mgh.harvard.edu <ASiver@mgh.harvard.edu>, william.lee@health.ny.gov <william.lee@health.ny.gov>
Cc: GSELL, Pierre <gsellp@who.int>, Simon Funnell <Simon.Funnell@phe.gov.uk>, Cesar Munoz-fontela <munoz-fontela@bnitm.de>, RIVEROS BALTA, Alina Ximena <lauriex@who.int>, henaorestrepoa@who.int <henaorestrepoa@who.int>, KNEZEVIC, Ivana <knezevici@who.int>, florian.krammer@mssm.edu <florian.krammer@mssm.edu>
Subject: COVID-19 assays review

Dear colleagues,

Similar to what was done recently with the WHO COVID-19 models working group, we would like to publish a short review about the state-of-the-art regarding COVID-19 assays. Based on your expertise and the data you have generated and presented to the WHO assays group, we would like to ask you to contribute to this paper. As you can see in the attached outline, we have suggested subgroups for different topics. Please take this only as a suggestion and feel free to contribute to other parts of the review as you deem fit. Also, feel free to suggest additional authors as needed. Florian Krammer has graciously agreed to help coordinate and submit this to a high quality journal. We would like to have a draft by the end of the year if possible. Please confirm that you wish to participate in this endeavor.

Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; william.lee; ASiyer@mgh.harvard.edu; MAFUNGA, Neddy

Location: https://who-e.zoom.us/j/8348590949

Importance: Normal

Subject: WHO working group on COVID-19 assays

Dear All,

Please find below the agenda for our group call on Wednesday December 2, 2020 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Jilian Sacks, FIND – Assessment of serologic assays
2. Paul Bieniasz, Rockefeller – Coronavirus neutralizing antibodies before and after SARS-CoV-2 infection

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); GSELL, Pierre; Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Cassandra Kelly (Cassandra.Kelly@finddx.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk

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Agenda to follow.

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: jboyer@inovio.com; acope@iavi.org; adanalioser@gmail.com; akbulut@medicine.ankara.edu.tr; Alessandra.Vitelli@reithera.com; Stefania.Capone@reithera.com; annied@epivax.com; Anthony.Macaluso (Anthony.Macaluso@tonixpharma.com); boulayi@medicago.com; brian.zabel@lakepharma.com; C.M.Smales@kent.ac.uk; christoph.rademacher@mpikg.mpg.de; CKeech@Novavax.com; coleman (coleman@codagenix.com); rajeev.dhere@seruminstitute.com; CVHerst@flowpharma.com; cyrus.yang@sbc-biotech.com; d.watterson@uq.edu.au; dapengzhoulab@tongji.edu.cn; dguyongellin@osivax.com; diane.vanhoorick@etherna.be; dong.shen@rnaimmune.com; Thien Do (dothuanthien@vabiotech.com.vn); dsz@imbcams.com.cn; dulin@zhifeishengwu.com; dailp@biols.ac.cn; ercument.karasulu@ege.edu.tr; fguirakhoo (fguirakhoo@geovax.com); farshad@covaxx.com; fguirakhoo@unitedneuroscience.com; fred@imophoron.com; Gary Kobinger (Gary.Kobinger@crchudequebec.ulaval.ca); greanggrai.h@bionet-asia.com; guido.grandi@unitn.it; 秀樹 長谷川 (hasegawa@nih.go.jp); hendrikjan.thibaut@kuleuven.be; hironorinakagami@gmail.com; hlchen (hlchen@hku.hk); Holger.Martinius@neovii.com; hotez (hotez@bcm.edu); huyl@sinovac.com; james.hayward (james.hayward@adnas.com); James.Huleatt@sanofi.com; jarininger@lathambiopharm.com; jeff@stabilitech.com; jennifer@immunoprecise.com; yabdiche@immunoprecise.com; Ilse Roodink (iroodink@immunoprecise.com); JHendri1@its.jnj.com; jkalil@usp.br; jlh66@cam.ac.uk; jprice (jprice@greffex.com); jwolf (jwolf@heatbio.com); kandeil_a (kandeil_a@hotmail.com); Kapil Maithal (Kapil.Maithal@zyduscadila.com); khirullin@mail.ru; Kayvon Modjarrad (kmodjarrad@eidresearch.org); kovac@axon-neuroscience.eu; michelle.hoffmann@axon-neuroscience.eu; kozhemyakina@biocad.ru; lei.li@flinders.edu.au; lindy.durrant@nottingham.ac.uk; linjinzhong@fudan.edu.cn; luistataje@farvet.com; luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); maksyutov_ra@vector.nsc.ru; martin.reers@biologicale.com; Matthias.Schnell@jefferson.edu; mehmet.ozturk@ibg.edu.tr; mesteban (mesteban@cnb.csic.es); mgursel@metu.edu.tr; morishit@cgt.med.osaka-u.ac.jp; nakagami@gts.med.osaka-u.ac.jp; MStanford@imv-inc.com; Munir, Muhammad; nadirkocak@yahoo.com; naomi.van.vlies@intravacc.nl; nesrin.ozoren@boun.edu.tr; nhj1114@mogam.re.kr; Olaf-Oliver.Wolz@curevac.com; Hodgson, Paul; pdeshpande@indimmune.com; phil.yang@nantworks.com; prasadsd (prasadsd@bharatbiotech.com); qinjian_zhao (qinjian_zhao@xmu.edu.cn); Liang Qu (Jenny) (quliang@sinopharm.com); Ricardo.Gazzinelli@umassmed.edu; Webby, Richard; roland.tschismarov@themisbio.com; Christiane Gerke (christiane.gerke@pasteur.fr); Rolando.pajon@modernatx.com; Rong.Xu@sabin.org; roy.duncan@dal.ca; Senta.Walton@usz.ch; Shailesh.DEWASTHALY@valneva.com; somchaiya@gpo.or.th; songqiaoqiao@ystwt.com; steven.gong@cloverbiopharma.com; stucker (stucker@vaxart.com); sunL@antibodychina.com; tapia@mpi-magdeburg.mpg.de; tedross@uga.edu; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); THeiland@immunomix.com; Ugur.Sahin@biontech.de; vgarg (vgarg@altimmune.com); wdj@adaptvac.com; wdj@expres2ionbio.com; Xiao-Jian.Yao@umanitoba.ca; xuefeng.yu@cansinotech.com; zengming@biominhai.com; galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar

(Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; GILBERT Nick; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

Sent: Mon 12/21/2020 12:46:34 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays with Vaccine Developers

Agenda to follow.

Join Zoom Meeting
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213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Sun 11/24/2019 9:10:22 AM (UTC-06:00)
Subject: Email to Bob Tesh

Dear Pei Yong,

Hope this email finds you well!

I recently send an email to Bob (at rtesh@utmb.edu) with no reply so far. Can you confirm this is the correct email address? If he is around, can you ask him to check to see whether he has received my email?

I am not sure whether you are in the loop for Ping's submission to Scientific Reports. Both she and I have tried so many times with no reply at all from the editorial office. This $-making journals are cray! We have now written to the EiC and hope we can get some progress soon!

Cheers,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Sat 1/4/2020 6:42:41 PM (UTC-06:00)
Subject: Invitation as a guest speaker for the EID retreat 2020

Dear Pei Yong,

Happy 2020!

We are planning a BIG retreat for EID on 19-20 March 2020, first time to have a 2-day retreat.

We are going to invite all past PIs (Duane, Veronika, etc) and will officially farewell Mariano.

We thought it will be a good idea to give Mariano a surprise by inviting you as a guest speaker.

Duke-NUS will of course cover the return business class airfare and all associated costs.

Do let me know if you are available and able to do that.

Thanks in advance.

Cheers,

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

To: Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; Erdman,D (derdman05@gmail.com)[derdman05@gmail.com]; Holubar, Connie J.[cjholuba@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Tesh,R(Home)[rbtesh22@gmail.com][rbtesh22@gmail.com]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Fri 1/24/2020 5:44:37 PM (UTC-06:00)
Subject: Re: Munster 2020 reference from my EndNote library

https://www.mdpi.com/1999-4915/12/2/135#metrics

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Friday, January 24, 2020 5:44 PM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Subject: Re: Munster 2020 reference from my EndNote library

Hey all,

I wrote this commentary for Viruses on the new virus in case you are interested.

VDM

From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Friday, January 24, 2020 5:42 PM
To: Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Munster 2020 reference from my EndNote library

Bob Tesh sent this article over earlier. Some of you may have already received it, I apologize for any duplication.

Tom Ksiazek

Munster VJ, Koopmans M, van Doremalen N, van Riel D and de Wit E. 2020. A Novel Coronavirus Emerging in China — Key Questions for Impact Assessment. New England Journal of Medicine.

To: Shi, Pei yong[peshi@UTMB.EDU]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Fri 2/21/2020 4:38:41 AM (UTC-06:00)
Subject: EID director ad
EID Director advert-RAD_HR (17Feb2020) (002).pdf

FYI – it's officially out now.

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Director

Programme in Emerging Infectious Diseases

Duke-NUS Medical School (Duke-NUS), Singapore's only graduate-entry medical school was established as a landmark collaboration between two world-ranking institutions of higher education – Duke University and National University of Singapore. Duke-NUS provides innovative education and impactful research to enhance the practice of medicine in Singapore and beyond. Through its strategic partnership with Singapore Health Services (SingHealth) which includes Singapore General Hospital, the School is able to leverage its joint capabilities and infrastructure to develop outstanding clinical education programmes and cutting edge research collaborations that translate fundamental science into better health. Duke-NUS and its partners have created an academically-based Programme in Emerging Infectious Diseases (EID) designed to serve as a national and international resource of excellence in emerging infectious diseases. The mission of the Programme faculty is to conduct high-level basic and applied research, and to train graduate students, postdoctoral fellows and clinician-scientists in the disciplines relevant to emerging infectious diseases. Duke-NUS and its partners provide state-of-the-art research facilities, including a standalone ABSL3 unit.

We are seeking an individual with exceptional scientific credentials and leadership skills to head the EID Programme. The Programme Director will provide leadership, including engagement with the broader biomedical community in Singapore and with Duke University; strategic hiring and programme development; medical school and graduate education; faculty mentoring; budgetary and space planning. The School will provide the new Programme Director with the resources to support the highest level of research.

Interested candidates should send a CV and the names of three references to: **Chair, Search Committee on Emerging Infectious Diseases, Duke-NUS Medical School, Singapore by email to: hr@duke-nus.edu.sg**

Applications will be accepted until the position is filled. We anticipate to begin interviewing candidates in early April 2020.

More information on the Programme can be found at www.duke-nus.edu.sg.

To: Wang Linfa[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
From: Lawal, Adeola[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=132C1C41E99844A6A0FFDAD4C53D7E2E-LAWAL, ADEO]
Sent: Mon 3/30/2020 2:15:40 PM (UTC-05:00)
Subject: RE: MTA or collaboration agreement
Dr Shi - Standard MTA Duke NUS.docx

Hello,

Please see attached. Please complete in all respects, obtain necessary signatures and return to me for further processing.
Best,

Ade Lawal, JD
Associate Legal Officer
UTMB Office of Technology Transfer
409.772.0369

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, March 28, 2020 9:15 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Thanks Pei Yong.

Dear Ade,

Yih Shin will be our contact from Duke-NUS.

Dear Yih Shin,
With your guide, you can ask Xin Mei's help with paper work if needed.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Saturday, 28 March 2020 9:56 PM
To: Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: MTA or collaboration agreement

Hi Ade,

Please help the transfer of the following reagents to Dr. Linfa Wang?

Reagents

- mNeonGreen SARS-CoV-2 reporter virus
- Nano luciferase SARS-CoV-2 reporter virus
- RFP SARS-CoV-2 reporter virus
- Other recombinant SARS-CoV-2 Viruses

Recipients
Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Program in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Thanks!

Pei-Yong

MATERIAL TRANSFER AGREEMENT

This Material Transfer Agreement ("**Agreement**") is made between The University of Texas Medical Branch at Galveston, d/b/a UTMB Health ("**UTMB**"), a health institution of The University of Texas System ("System"), an agency of the State of Texas, located at 301 University Blvd., Galveston, TX 77555-0926, and Duke-NUS Medical School, ("**Recipient"),** located at 8 College Road, Singapore 169857 ("**Recipient**").

From the laboratory of Dr. Pei-Yong Shi, ("**Provider Scientist**"), UTMB agrees to provide Recipient with certain materials for the purpose stated herein under the following conditions:

Material and Research. The Materials covered by this Agreement are as follows:
Reagents

- mNeonGreen SARS-CoV-2 reporter virus
- Nano luciferase SARS-CoV-2 reporter virus
- RFP SARS-CoV-2 reporter virus
- Other recombinant SARS-CoV-2 Viruses

("**Material**"). The Material shall be used by Recipient in research ("**Research**"), as defined in **Attachment A**, and the Research will be conducted by Recipient under the supervision of Linfa Wang PhD FTSE, ("**Recipient Scientist**"). Materials shall be shipped separately. Recipient shall provide Provider with a FedEx account number for shipping of the materials requested.

1. **Use of Material.** This Material is made available for internal research use only in laboratory animals or in vitro experiments. The Material shall not be used in humans. The Material is considered proprietary to UTMB. UTMB shall be free, in its sole discretion, to distribute the Material to others and to use it for its own purposes. Except as provided for by this Agreement, Recipient shall not distribute, transfer, or release the Material to any person or entity other than laboratory personnel under Recipient Scientist's direct supervision, unless written permission is obtained from UTMB. Recipient agrees that all of its Recipient Scientist(s) involved in the Research will have read the terms and conditions of this Agreement and abide by the terms and conditions of this Agreement.
2. **Rights.** Subject to Section 6. Intellectual Property of this Agreement, Recipient agrees that nothing herein shall be deemed to grant to Recipient or Recipient Scientist any rights under any UTMB patents or any rights to use the Material for any products or processes for any purpose other than performing the Research. Recipient will not use Material for any commercial purposes. Recipient understands that UTMB shall have no obligation to grant a license to Recipient to use Material for commercial purposes, and may grant exclusive or non-exclusive commercial licenses to others, or sell or assign all or part of the rights in the Material to any third party(ies), subject to any pre-existing rights held by others and obligations to the Federal Government.
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7. **Liability.** In no event shall UTMB be liable for any use by Recipient Scientist or Recipient of the Material or any loss, claim, damage or liability, of whatsoever kind or nature, which may arise from or in connection with Recipient's breach of this Agreement or Recipient's use, handling or storage of the Material, unless such loss, claim, damage or liability results from the negligence or willful malfeasance of UTMB, System, their Regents, officers, agents and employees.
   a) **State Entities:** To the extent authorized by the Recipient's state law, Recipient agrees to indemnify and hold harmless UTMB, System, their Regents, officers, agents and employees, from any liability, loss or damage they may suffer as a result of claims, demands, costs or judgments against them arising out of the Recipient's activities to be carried out pursuant to this Agreement and the use by Recipient of the results obtained from Research, excluding claims, loss, or damage that arise from the negligence or willful malfeasance of any Regent, officer, agent or employee of UTMB or System.
   b) **Federal Entities**: Recipient assumes the liability for any claims, damages, injury, or expenses arising from the use, storage, handling, and disposal of the Material by the Recipient, but only to the extent provided under the Federal Tort Claims Act (28 U.S.C. Chapter 171).
   c) **All other entities**: Recipient shall indemnify and hold UTMB, System, their Regents, officers, agents, and employees harmless against any and all claims, demands, damages, liabilities and costs which directly or indirectly result from, or arise in connection with, any negligent act or omission of Recipient, its agents, or employees, pertaining to its activities and obligations under this Agreement.
8. **Compliance.** Recipient will use the Material in compliance with all laws, governmental regulations and guidelines applicable to the Material. Moreover, if the Material is used in the United States, then Recipient will comply with current United States NIH guidelines.
9. **Export Control.** Recipient further agrees that if the U.S. export laws are or become applicable, it will not export any Materials received under this Agreement to any countries for which the United States government requires an export license or other supporting documentation at the time of export or transfer, unless Recipient has obtained prior written authorization from the appropriate authority responsible for such matters.

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11. **Publicity.** Recipient may not use the name of UTMB, System or their Regents without express written consent, subject to Section 5. Publication of this Agreement.
12. **Term and Termination.** This Agreement shall be effective as of the date of the last signature and terminate one (1) year from that date. Upon termination, Recipient will immediately destroy all the Material then in its possession.

UNIVERSITY OF TEXAS MEDICAL BRANCH

_____
Carolee King, JD
Senior Vice President and General Counsel
Date: _____

Read and understood:

_____
Signature of Provider Scientist

RECIPIENT

_____
Name of Authorized Signatory
Title:

Date: _____

Read and understood:

_____
Signature of Recipient Scientist

Attachment A – Scope of Research

To: Lawal, Adeola[adlawal@UTMB.EDU]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Loh Jian Yun[jianyun.loh@duke-nus.edu.sg]
From: Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]
Sent: Mon 3/30/2020 6:57:22 PM (UTC-05:00)
Subject: RE: MTA or collaboration agreement

Dear Adeola,

Received with thanks and we will proceed with the review at NUS.

Thanks.

Regards,
Yih-Shin

From: Lawal, Adeola <adlawal@UTMB.EDU>
Sent: Tuesday, 31 March 2020 3:16 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Hello,

Please see attached. Please complete in all respects, obtain necessary signatures and return to me for further processing.
Best,

Ade Lawal, JD
Associate Legal Officer
UTMB Office of Technology Transfer
409.772.0369

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, March 28, 2020 9:15 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Thanks Pei Yong.

Dear Ade,

Yih Shin will be our contact from Duke-NUS.

Dear Yih Shin,
With your guide, you can ask Xin Mei's help with paper work if needed.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Saturday, 28 March 2020 9:56 PM
To: Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: MTA or collaboration agreement

Hi Ade,

Please help the transfer of the following reagents to Dr. Linfa Wang?

Reagents

- mNeonGreen SARS-CoV-2 reporter virus
- Nano luciferase SARS-CoV-2 reporter virus
- RFP SARS-CoV-2 reporter virus
- Other recombinant SARS-CoV-2 Viruses

Recipients
Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Program in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Thanks!

Pei-Yong

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

To: Wang Linfa[linfa.wang@duke-nus.edu.sg]; Lai Yih Shin[yihshin.lai@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]
Cc: Loh Jian Yun[jianyun.loh@duke-nus.edu.sg]
From: Lawal, Adeola[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=132C1C41E99844A6A0FFDAD4C53D7E2E-LAWAL, ADEO]
Sent: Tue 3/31/2020 10:12:19 AM (UTC-05:00)
Subject: RE: MTA or collaboration agreement

Always a pleasure.

Looking forward to getting this agreement in place.

Best,

Ade

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Monday, March 30, 2020 7:03 PM
To: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>; Lawal, Adeola <adlawal@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Loh Jian Yun <jianyun.loh@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Thank you both!

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Sent: Tuesday, 31 March 2020 7:57 AM
To: Lawal, Adeola <adlawal@UTMB.EDU>; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Loh Jian Yun <jianyun.loh@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

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Yih-Shin

From: Lawal, Adeola <adlawal@UTMB.EDU>
Sent: Tuesday, 31 March 2020 3:16 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Hello,

Please see attached. Please complete in all respects, obtain necessary signatures and return to me for further processing.
Best,

Ade Lawal, JD
Associate Legal Officer
UTMB Office of Technology Transfer
409.772.0369

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Saturday, March 28, 2020 9:15 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Lai Yih Shin <yihshin.lai@duke-nus.edu.sg>
Subject: RE: MTA or collaboration agreement

Thanks Pei Yong.

Dear Ade,

Yih Shin will be our contact from Duke-NUS.

Dear Yih Shin,
With your guide, you can ask Xin Mei's help with paper work if needed.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Saturday, 28 March 2020 9:56 PM
To: Lawal, Adeola <adlawal@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Subject: MTA or collaboration agreement

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Reagents

- mNeonGreen SARS-CoV-2 reporter virus
- Nano luciferase SARS-CoV-2 reporter virus
- RFP SARS-CoV-2 reporter virus
- Other recombinant SARS-CoV-2 Viruses

Recipients

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Program in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

Thanks!

Pei-Yong

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak (daszak@ecohealthalliance.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim

Sent: Sun 3/7/2021 10:51:05 AM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Agenda to follow.

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- +1 267 831 0333 US (Philadelphia)
- +1 301 715 8592 US (Washington D.C)
- +1 312 626 6799 US (Chicago)

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Find your local number: https://who.zoom.us/u/acLh9DwRd3

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115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)

149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

To: Whitley, Rich[rwhitley@peds.uab.edu]; Denison, Mark[mark.denison@vumc.org]; Tomas Cihlar[Tomas.Cihlar@gilead.com]; Elizabeth Campbell[elizabeth.campbell0@gmail.com]; Matthias Gotte[gotte@ualberta.ca]; Painter, George R.[george.r.painter@emory.edu]; Michael Sofia[msofia@arbutusbio.com]; Weller,Sandra K.[weller@uchc.edu]; Anderson, Annaliesa S[Annaliesa.Anderson@pfizer.com]; Lanteri, Charlotte A LTC USARMY FUTURES COMMAND (USA)[charlotte.a.lanteri.mil@mail.mil]; Andrew Mesecar[amesecar@purdue.edu]; Jen Nwankwo[jen@1910genetics.com]; Schiffer, Celia[Celia.Schiffer@umassmed.edu]; Kara Carter[Kara.Carter@evotec.com]; David Baker[dabaker@uw.edu]; Lillian Chiang[lillian@evrysbio.com]; Matthew Disney[disney@scripps.edu]; Singh Saikatendu, Kumar[kumar.saikatendu@takeda.com]; Weetall, Marla[mweetall@ptcbio.com]; Shi, Pei yong[peshi@UTMB.EDU]; Cherry, Sara[cherrys@pennmedicine.upenn.edu]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; O'Rear, Julian (FDA/CDER)[Jules.ORear@fda.hhs.gov]; Sheahan, Timothy Patrick[sheahan@email.unc.edu]; Smyth, Hugh D[hugh.smyth@austin.utexas.edu]; Hazuda, Daria J[daria_hazuda@merck.com]; Bradner, James[james.bradner@novartis.com]; Fletcher, Courtney V[cfletcher@unmc.edu]; Hayden, Frederick G (fgh)[fgh@virginia.edu]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]
Cc: Anderson, James (NIH/OD) [E][james.anderson2@nih.gov]; Davis, Mindy (NIH/NIAID) [E][mindy.davis@nih.gov]; Conley, Tony (NIH/NIAID) [E][conleyto@niaid.nih.gov]; Brimacombe, Kyle (NIH/NCATS) [E][kyle.brimacombe@nih.gov]; Grossman, Abigail (NIH/NCATS) [C][abigail.grossman@nih.gov]; Ford-Scheimer, Stephanie (NIH/NCATS) [C][stephanie.ford-scheimer@nih.gov]; Austin, Christopher (NIH/NCATS) [E][austinc@mail.nih.gov]; Fauci, Anthony (NIH/NIAID) [E][afauci@niaid.nih.gov]; Collins, Francis (NIH/OD) [E][collinsf@od.nih.gov]
From: Hall, Matthew (NIH/NCATS) [E][hallma@mail.nih.gov]
Sent: Wed 1/20/2021 11:09:35 AM (UTC-06:00)
Subject: SARS-CoV-2 Antiviral summit report available
2020_NIH_Antiviral_Summit_Report_508.pdf

Colleagues,

The SARS-CoV-2 Antiviral Summit report was completed just prior to the holiday break, was reviewed and cleared by NIH Director Dr. Collins, along with NIAID (Dr.Fauci's office) and NCATS (Dr. Austin) leadership, and underwent final formatting to ensure it is accessible ('508 compliant').

The Summit report has now been posted at the following link, and is also attached to this email:
https://www.nih.gov/research-training/medical-research-initiatives/activ/events
At the link, you can also access the agenda for the meeting, and a link to the recording of the meeting. Note that the equivalent information on the previous neutralizing antibody summit

Please circulate this report among your colleagues, and consider citing this report when publishing.

On behalf of my fellow organizers (Mindy Davis, Tony Conley, Jim Anderson, Abigail Grossman, Kyle Brimacombe, and Stephanie Ford-Scheimer), thank you again for your participation and contributions to create a very successful Summit and report. This report has already been helpful in planning to meet challenges in developing antiviral drugs. We aim to create an amended version of the report for publication at some point in the very near future.

Any questions, please let me know.

Matt

Matthew D. Hall
Director, Early Translation Branch

National Center for Advancing Translational Sciences (NCATS)
National Institutes of Health
9800 Medical Center Drive
Rockville, MD 20850

Office: 301-480-9928
https://ncats.nih.gov/staff/hallma

@cispt2

NCATS Website: http://ncats.nih.gov

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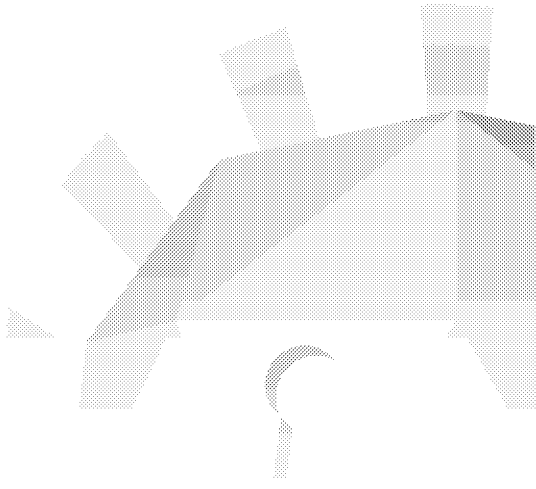
SARS-COV-2 ANTIVIRAL THERAPEUTICS SUMMIT REPORT

Summit sponsored by the National Institute of Allergy and Infectious Diseases and the National Center for Advancing Translational Sciences

NOVEMBER 6, 2020



NIH National Institutes of Health

Summit Report Authors
Annaliesa Anderson, Pfizer
James M. Anderson, Office of the Director, NIH
Kara Carter, Evotec*
Tomas Cihlar, Gilead Sciences
Anthony J. Conley, National Institute of Allergy and Infectious Diseases, NIH
Mindy I. Davis, National Institute of Allergy and Infectious Diseases, NIH
Mark Denison, Vanderbilt University
Matthew D. Hall, National Center for Advancing Translational Sciences, NIH
Daria Hazuda, Merck & Co.
Stephanie Moore, University of Alabama at Birmingham
George Painter, Emory University
Pei-Yong Shi, University of Texas Medical Branch
Richard Whitley, University of Alabama at Birmingham

**Current affiliation: Dewpoint Therapeutics*

Summit Hosts

Dr. Francis Collins, Director, National Institutes of Health (NIH)
Dr. Anthony Fauci, Director, National Institute of Allergy and Infectious Diseases (NIAID)
Dr. Christopher Austin, Director, National Center for Advancing Translational Sciences (NCATS)

Summit Organizers

James M. Anderson, Office of the Director, NIH
Kyle R. Brimacombe, NCATS, NIH
Anthony J. Conley, NIAID, NIH
Mindy I. Davis, NIAID, NIH
Stephanie Ford-Scheimer, NCATS, NIH
Abigail Grossman, NCATS, NIH
Matthew D. Hall, NCATS, NIH

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INTRODUCTION

NIH SARS-COV-2 ANTIVIRAL THERAPEUTICS SUMMIT

Presenters:
Dr. Francis Collins (NIH)
Dr. Anthony Fauci (NIAID)
Dr. Christopher Austin (NCATS)

The NIH Virtual SARS-CoV-2 Antiviral Summit was held on November 6, 2020. The virtual Summit was organized to provide an overview on the status and remaining challenges in developing antiviral therapeutics for COVID-19, including combinations of antivirals, and streamed live to allow broad public access while maintaining social distancing. Scientific experts from the public and private sectors were brought together to discuss SARS-CoV-2 targets for drug development, and the preclinical tools needed to evaluate and develop effective small molecule antivirals. The goal of the Summit was to review the current state of the science, identify unmet research needs, share insights and lessons learned from treating other infectious diseases, identify opportunities for public-private partnerships, and assist the research community in designing and developing antiviral therapeutics.

The Summit was jointly organized by NIAID, NCATS, and the NIH Office of the Director (NIH OD), and hosted by the respective Directors: Dr. Francis Collins (NIH), Dr. Anthony Fauci (NIAID), and Dr. Christopher Austin (NCATS). The meeting moderators and panelists were from academia, industry (pharma/biotech), NIH Institutes and Centers, and Federal agencies working in the COVID-19 therapeutics space.

The Summit itself was comprised of introductory remarks, an overview of the virus and therapeutic opportunities, followed by five scientific panels. In each panel, the session moderator provided an overview of the topic (slides are included in the Appendix) and facilitated discussion with panelists. An update on vaccines and neutralizing antibodies was provided, and a final summary session was held to identify key points from the Summit. The sessions were:

- Viral Replication Machinery
- Proteases (Viral and Host)
- Emerging Targets, Emerging Modalities
- Preclinical Tools
- Lessons from Other Viruses and Preparation for the Future

This Summit report is structured to reflect the meeting itself, providing an overview of the virus and therapeutics approaches, individual panel summaries, and a summary of the discussions and perspectives on the challenges ahead. The report was written utilizing the meeting transcript and recorded notes, and it was prepared by the Summit organizers with contributions and input from session moderators and panelists.

OVERVIEW OF THE VIRUS AND THERAPEUTICS APPROACHES

Speaker:
Dr. Mark Denison, Vanderbilt University

Coronaviruses are enveloped positive-sense single-stranded RNA viruses enclosed by capsid comprised of multiple proteins, most notably the spike proteins that are responsible for the virus's crown-like appearance. Cellular entry of coronaviruses, such as SARS-CoV-2 (Severe Acute Respiratory Syndrome-Coronavirus-2), can occur in a number of ways, primarily via the spike (S) proteins of SARS-CoV-2 binding to the host ACE2 (Angiotensin-converting enzyme 2) receptor[1]. Two-thirds of the SARS-CoV-2 genome is dedicated to the synthesis of two replicase polyproteins called polyprotein 1a and polyprotein 1ab. Within the polyprotein are two proteases, the papain-like protease (PL^{pro}) and $3CL^{pro}$ (also known as nsp5 or M^{pro}, short for main protease). In general, any inactivation of these proteases leads to a loss of RNA synthesis, and it is well established that disruption of viral RNA replication or viral protease functions are vulnerable to intervention[2,3]. The next step after the formation of replicase proteins is the modification of host cell membranes, probably occurring in parallel to replication processes. A multiprotein complex formed by coronaviruses termed the replication transcription complex (RTC) is responsible for RNA replication and proof-reading. Nonstructural proteins nsp7 through nsp16 form the core of the RTC and represent a prime target for antiviral drug development, as the function of the core replicase is highly conserved. A detailed outline of the viral replication process, and druggable targets, is displayed in Figure 1.

Importantly in the context of antiviral drugs, when the SARS-CoV-2 epidemic (now a pandemic) emerged, there were no approved treatments or vaccines for treating any betacoronavirus infection. The endemic common cold betacoronaviruses OC42-CoV and HKU1-CoV generally cause mild symptoms, and have not stimulated significant therapeutic or vaccine development investigation. The SARS (caused by SARS-CoV-1) and MERS (Middle East Respiratory Syndrome, caused by MERS-CoV) epidemics were resolved using public health measures, though the translational science response to the SARS-CoV-2 pandemic has benefited from the intensive research efforts that took place to understand the SARS and MERS viruses[4,5].

From a therapeutic perspective, there are multiple windows of opportunity for preventing and managing COVID-19, which include the prophylactic pre-infection stage, early post-infection pre- or asymptomatic stage (antiviral window), and the symptomatic stages during which antiviral efficacy wanes and treatment strategy shifts towards immunomodulatory and anticoagulant therapies. As antiviral drugs are developed, some principles for SARS-CoV-2 antiviral development to be considered include:

- Antivirals should be broadly active for coronaviruses in both in vitro and in vivo models.
- Bioavailability of antivirals should be sought for multiple routes of administration: IV, oral, inhalational, intranasal, etc.

- Antivirals should have limited or no toxicity, especially for outpatient use, have a high barrier to resistance, and a large therapeutic window.
- Combinations of antivirals should be a priority in order to maximize potency and prevent resistance emergence. Combinations of antivirals and immunomodulatory therapies will be needed for treatment in later stages of illness.
- Vulnerable populations should be considered when designing new therapeutics as well as designing clinical trials.

Antiviral drug development for SARS-CoV-2 should take place with the recognition that unlike SARS and MERS (that sporadically re-emerges), the pandemic may continue for a long time, and the virus itself will likely be with us forever (endemic). There is also the high likelihood for another novel coronavirus(-es) to emerge from animal reservoirs. Given these realities, irrespective of vaccine effectiveness, there will be a need for antivirals. Teams working together across industry, academia, and government can drive fundamental discovery for this virus, and create the "playbook" for responding to the next zoonotic coronavirus. In the context of future pandemics, antivirals with broad-spectrum activity against betacoronaviruses would be positioned to enable rapid pre-clinical testing and clinical trials if and when a new zoonotic coronavirus appears (and for sporadic MERS outbreaks)[6].

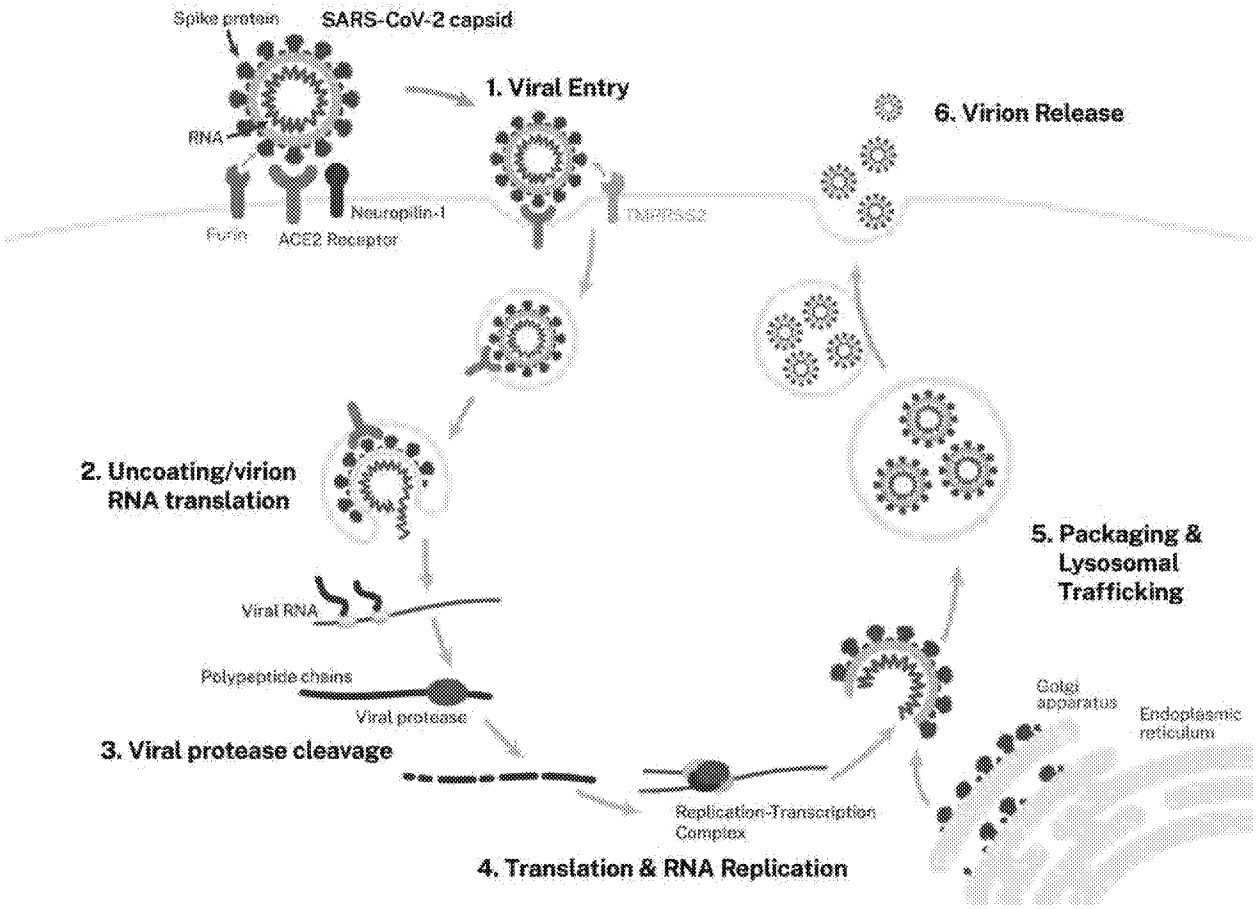

Figure 1. Scheme showing the SARS-CoV-2 viral replication cycle and highlighting "druggable" events. The SARS-CoV-2 virion is composed of a capsid protein coat, with an internal core of the viral genetic material (RNA). **1. Viral entry.** The SARS-CoV-2 virion in the extracellular space presents Spike (S) protein on the capsid surface. The S protein contains a number of protease cleavage sites, as well as the receptor binding domain (RBD). Engagement of spike protein at the extracellular surface involves engagement of multiple host cell proteins including (but may not be limited to) cleavage of S by the protease furin (gene FURIN), binding of the S RBD to ACE2 (ACE2), engagement of a liberated S terminal peptide to neuropilin-1 (Nrp-1, NRP1), and cleavage of S by the serine protease TMPRSS2 (TMPRSS2). **2.** Following endocytosis, the virion is uncoated, and the viral RNA translated into polypeptide chains. **3.** Two **viral proteases** cleave the viral polypeptide chains to produce up to 29 mature protein products. These proteases are the main protease (M^{pro}) and the papain-like protease (PL^{pro}). **4. Viral RNA replication** follows, with the formation of a replication-transcription complex, incorporating the RNA-dependent RNA polymerase (RdRp). **5.** The arising viral RNA (genetic material) is then packaged into capsid formed by viral protein including envelope (E), membrane (M), nucleocapsid (N) and aforementioned spike. Mature packaged virion is then trafficked via lysosomes, and **6. virion is released** via exocytosis. For other viruses, the time from viral entry to emergence of first progeny (the "eclipse time") can be as little as 15 minute or as long as 7-8 hours[7]. Schematic prepared by Kyle R. Brimacombe (NCATS).

SESSION 1

VIRAL REPLICATION MACHINERY

Moderator:
Dr. Tomas Cihlar, Gilead Sciences

Panelists:
Dr. Elizabeth Campbell, Rockefeller University
Dr. Matthias Götte, University of Alberta
Dr. George Painter, Emory University
Dr. Michael Sofia, Arbutus Biopharma, Inc.
Dr. Sandra Weller, University of Connecticut

Summary of Current Status

Since the emergence of SARS-CoV-2 at the beginning of 2020, considerable progress over a very short period of time has been made in the development of antivirals for the treatment of COVID-19, in part because of ongoing studies for inhibitors of MERS-CoV. The identified agents include small molecule antivirals and biologics targeting both viral and host functions critical for SARS-CoV-2 infection and replication. Multiple potent neutralizing antibodies targeting independent epitopes on viral spike protein alongside a battery of direct acting small molecule antivirals interfering with various steps of viral replication have been quickly identified and brought to clinical testing. Across these efforts viral RNA synthesis stands out as one of the most critical functions for selective targeting by antiviral therapies[8].

SARS-CoV-2 and other coronaviruses contain a ~30kb positive-sense non-segmented single strand RNA genome. Their RNA synthesis is a complex process consisting of two independent parts:

1. Viral genomic RNA replication through synthesis of a full-length negative (-) strand copy of the viral RNA genome that serves as a template for subsequent amplification of the genomic positive strand (+) RNA.
2. RNA transcription progressing via synthesis of subgenomic (sg) (-)RNA intermediates that are subsequently transcribed into mRNA. Some of the (-)sgRNA species are made through discontinuous processes that include template shifting. Once synthesized, the viral mRNAs are 5′-capped and 3′-polyadenylated to enable efficient translation of viral proteins.

All steps of the coronavirus RNA synthesis are carried out by the viral RTC encoded by approximately one third of the viral genome[9,10]. The RTC is an assembly of at least nine viral nonstructural proteins (nsp) known as nsp7 through nsp16, as well as some less characterized host factors. Core catalytic function of the RNA synthesis is performed by RNA-dependent RNA polymerase (RdRp; nsp12) and two of its co-factors (nsp7 and 8). Coronaviruses also encode for RNA proofreading 3′-5′ exonuclease function, carried out by nsp14, that increases the fidelity of replication and maintains genetic stability of the large coronavirus genome. The 5′-capping of RNA is performed by two methyl-transferases (nps14 and nsp16). Table 1 summarizes the viral RTC proteins and their functions.

Table 1. Virally encoded components of coronavirus RTC

Coronavirus protein	Function in RTC
Nsp7	RdRp cofactor
Nsp8	RdRp cofactor
Nsp9	RNA binding protein, capping regulator
Nsp10	Cofactor of Nsp14 and Nsp16
Nsp12	RNA-dependent RNA polymerase, capping
Nsp13	Zn-binding RNA helicase/RNA 5'-phosphatase
Nsp14	3'-5' exonuclease; N7-methyltransferase
Nsp15	Uridylate-specific endoribonuclease
Nsp16	2'-O-methyltransferase

Viral nucleic acid synthesis has been successfully targeted by a wide range of small molecule direct-acting antivirals, many of which have been developed into commercial drug products and are widely used in clinical practice[11]. Examples include inhibitors of HIV reverse transcriptase (a DNA polymerase), hepatitis C virus (HCV), hepatitis B virus (HBV), and herpesvirus DNA polymerases. While some of these enzymes can be targeted effectively by non-nucleoside allosteric inhibitors (e.g., non-nucleoside reverse transcriptase inhibitors for HIV), nucleoside and nucleotide analogs mimicking the natural nucleic acid building blocks remain the most abundant class of viral replication inhibitors[12].

Potent and selective antiviral inhibitors of coronaviruses including SARS-CoV-2 have been identified among nucleoside and nucleotide analogs with known broad-spectrum antiviral activity, several of which quickly progressed into clinical testing for the treatment of COVID-19 (Figure 2). Table 2 lists a summary of profiles of these agents. Each candidate is a pro-drug that requires intracellular activation to a triphosphate form that is incorporated into viral RNA, resulting in effects including delayed RNA termination, RNA mutagenesis, and/or second RNA strand synthesis stalling.

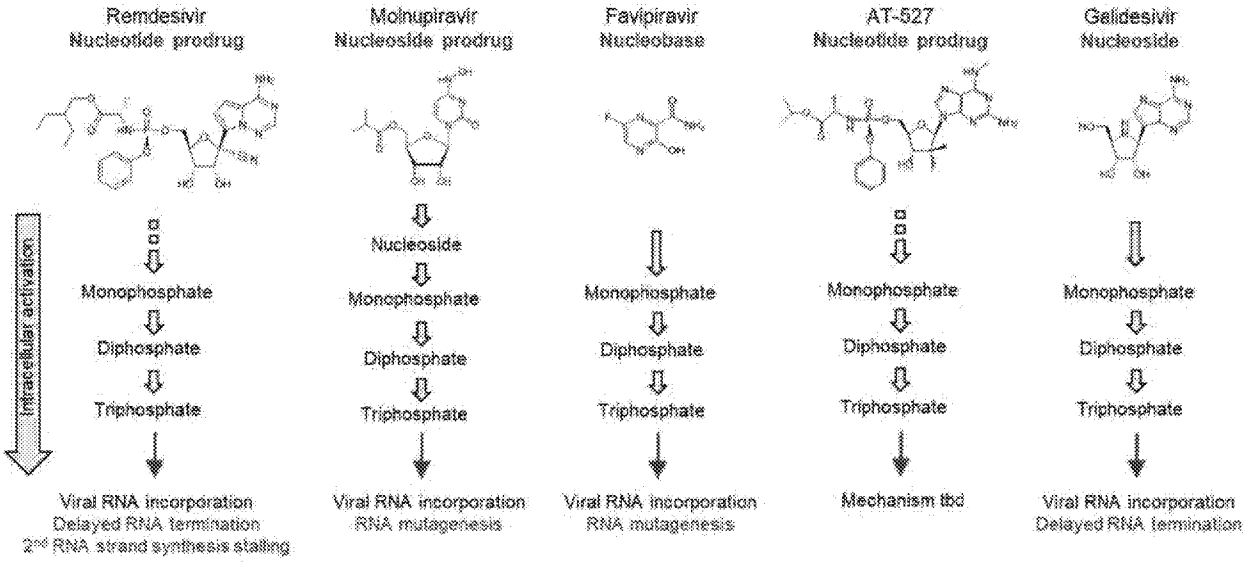

Figure 2. Structures of nucleoside analogs for the treatment of COVID-19, and their metabolic activation.

Table 2. Nucleoside analogs for the treatment of COVID-19. Status as of November 2020.

Nucleoside drug	**Form**	**Mechanism of action**	**In vitro activity** EC50 [μM]	**Animal model efficacy**	**Clinical dosing**	**Development status** (Target population)
Remdesivir (GS-5734)	Nucleoside monophosphate prodrug	Delayed RNA chain termination	0.01 - 1.5	NHP, mouse	IV QD 200/100 mg	Approved in US & 50+ countries (Hospitalized); Phase 3 (Outpatient)
Molnupiravir (EIDD-2801; MK-4482)	Nucleoside prodrug	Viral RNA mutagenesis	0.05 - 0.3	Mouse	Oral BID 200-800 mg	Phase 2/3 (Outpatient and Hospitalized)
Favipiravir (T-705)	Nucleobase	Viral RNA mutagenesis	60 - 250	Hamster	Oral BID 1800/800 mg	Approved in Russia; under review in Japan
AT-527	Nucleoside monophosphate prodrug	tbd	0.5 (EC_{90})	tbd	Oral BID 550 mg	Phase 2 (Hospitalized)
Galidesivir (BCX-4430)	Nucleoside	Delayed RNA chain termination	58 - 68*	tbd	IV	Phase1b

* In vitro activity against SARS- and MERS-CoVs. TBD = to be disclosed.

Remdesivir is a phosphoramidate prodrug that liberates an adenosine nucleotide analog within cells (the core nucleoside being GS-441524)[13]. Remdesivir was developed by Gilead Sciences with support from several U.S. Government organizations. Remdesivir was shown to be active against Ebola virus, and its safety profile was demonstrated in Ebola clinical trials. In several randomized clinical trials, remdesivir has demonstrated efficacy in hospitalized COVID-19 patients by reducing disease progression and accelerating time to recovery. In October 2020, remdesivir was approved by FDA as the first treatment for COVID-19[14,15].

Molnupiravir (EIDD-2801) is an orally bioavailable prodrug of N6-hydroxycytidine. It was developed at Emory (University) Institute for Drug Discovery (EIDD) as part of a program against Venezuelan equine encephalitis virus, and a Phase I trial was planned against influenza in 2019. As SARS-CoV-2 emerged, molnupiravir showed potent anti-SARS-CoV-2 activity both in vitro and in animal models[16]. It is currently in Phase 2-3 testing both in out-patient settings and in hospitalized COVID-19 patients.

Favipiravir, a guanine base analog, is a drug product approved in Japan (2014) for the treatment of influenza infections due to novel strains not responsive to other available agents[17]. It is also under regulatory review for the treatment of COVID-19 in Japan and has recently been approved for the same indication in Russia. It is active against SARS-CoV-2 in models, and is being tested in several advanced clinical studies around the world[18]. While it can be administered orally, it is substantially less potent than molnupiravir and remdesivir in vitro, which is reflected in a much higher dose required for favipiravir.

AT-527 is a prodrug of a guanosine nucleotide analog, developed by Atea Pharmaceuticals[19]. AT-527 was developed against the HCV RdRp, and safety was demonstrated in an HCV Phase 1-2 clinical trials in healthy and HCV-infected subjects. AT-527 was recently found to be active in vitro against SARS-CoV-2, and is currently being tested in Phase 2 in patients hospitalized with moderate COVID-19 disease[20].

Galidesivir is an adenine nucleoside analog developed by BioCryst for HCV, but it has broad-spectrum activity against RNA viruses and has been in development for treating deadly filoviruses (e.g., Ebola, Marburg)[21]. It has shown relatively weak activity in vitro against SARS- and MERS-CoVs and is slated for testing in a small proof-of-concept Phase 2 study in Brazil. It is the least characterized molecule among the SARS-CoV-2 nucleoside inhibitors.

It is worth noting that all the drug candidates described above existed before the COVID-19 pandemic, and novel chemical matter developed specifically for the SARS-CoV-2 replication

machinery has not yet been disclosed. While diverse in structures as well as formulations administered (see Figure 1 and Table 2), all SARS-CoV-2 nucleoside inhibitors require intracellular activation to their nucleoside triphosphate (NTP) metabolites, which then interact with the active site of coronavirus RdRp and are incorporated into viral RNA. The metabolic pathways leading to the respective NTP metabolites are cell-type dependent and differ for each molecule, as do their molecular mechanisms of viral RNA synthesis inhibition. Once incorporated into viral RNA, the metabolites of remdesivir and galidesivir cause delayed RNA chain termination, in the case of remdesivir template-dependent inhibition has also been shown, while those of molnupiravir and favipiravir act as specific viral RNA mutagens due to their capability of promiscuous base-pairing[22]. The mechanism of action for AT-527 is less well characterized and structural as well as biochemical data suggest that it might not interact very effectively with SARS-CoV-2 RdRp.

Challenges and Opportunities

Nucleoside and nucleotide analogs represent the most extensively explored class of antivirals with well understood advantages and limitations that both are related primarily to their function as mimetics of natural nucleotide molecules. Because the active sites of viral RNA polymerases to which the active NTP metabolites bind are often highly conserved within as well as across multiple viral families, many nucleosides exhibit broad-spectrum antiviral activity. Remdesivir, favipiravir, and molnupiravir are good examples of broad-spectrum antivirals with pan-coronavirus activity that may be leveraged as a part of future pandemic preparedness not only for the treatment of COVID-19, but likely also for other existing and newly emerging coronaviruses. The similarity of antiviral nucleoside analogs with natural substrates can also represent a significant liability, mainly because of their potential for off-target effects, such as impairment of mitochondrial functions through the inhibition of (host) mitochondrial RNA polymerase. Some nucleoside analogs might require prodrug strategies using established principles of medicinal chemistry to optimize oral delivery (bioavailability). In the case of SARS-CoV-2, the primary target tissue is the lung, and effective distribution into target cells irrespective of administration route is required.

Besides the inhibition of nsp12 (RdRp) by nucleoside analogs, the highly dynamic and multi-functional coronavirus RTC offers variety of other opportunities to interfere with viral RNA synthesis, including the other critical catalytic enzymatic functions present in RTC, such as the nsp13 helicase, nsp14 and nsp16 methyltransferases, or nsp14 exonuclease. In addition, the concerted function of this multiprotein complex relies on a multitude of specific protein-protein interactions, many of which have been mapped across the spectrum of coronaviruses including SARS-CoV-2. These efforts can be greatly facilitated by structural information generated by X-ray crystallography and cryo-electron microscopy studies conducted with many of the RTC proteins

and their complexes, including the nsp15 endonuclease, nsp14/10 and nsp16/10 methyltransferases, and particularly the multiprotein RdRp complex of nsp12/nsp7/nsp8 together with a dimer of nsp13 helicase. This wealth of structural information can facilitate the identification of critical interfaces and conserved pockets that might be amenable to targeting with small molecule inhibitors.

These alternative RTC targets offer the opportunity for non-nucleoside drug-like molecules, with the potential for candidates with desirable pharmacokinetic properties, like oral bioavailability, low protein binding, and adequate delivery to the respiratory tract. Unfortunately, the current state of the field underscores a complete absence of any validated small molecule inhibitors targeting some of these critical replicative functions, which in turn hinders advancement towards optimization of any new class of RTC inhibitors and their rapid progression into clinical testing. Therefore, the drug discovery process will rely on de novo high throughput screening approaches of suitable small molecule libraries (either pooled or arrayed). To that end, a number of recombinant RTC proteins have been cloned, expressed, and functionally characterized. Several options for functional biochemical assays exist depending on the desired format and preferred mode of read-out particularly for the catalytic complex of nsp12/nsp7/nsp8 RdRp. Similarly, functional assays have been established for coronavirus exonuclease as well as methyltransferases.

To effectively target some of the critical protein-protein interfaces, the field can employ a wide array of screening techniques for small molecule ligand binding, some of which are quite suitable for large compound libraries. Options include high-throughput affinity selection mass spectrometry (ASMS) DNA-encoded libraries (DELs), or surface plasmon resonance (SPR) assays. Alternatively, computational docking algorithms for putative binding sites can be employed for screening of vast virtual small molecule libraries. The major advantage of these approaches is speed and the number of potential candidate molecules identified, but these techniques need to be always coupled with relevant functional testing assays to triage the hits and validate their functional relevance. Newly-developed cell-based replicon assays for SARS-CoV-2 should be valuable to characterize activity of candidate compounds and certify cell-based activity and activation of candidate pro-drugs[23,24].

As will be discussed elsewhere, work remains to identify optimal target combinations with RdRp/RTC inhibitors (both small molecule antivirals and other modalities/approaches), and the patient populations most likely to benefit depending on individual drug product profiles, to maximize clinical effectiveness in the treatment and/or prevention of COVID-19.

SESSION 2

PROTEASES (VIRAL AND HOST)

Moderator:
Dr. Annaliesa Anderson, Pfizer

Panelists:
LTC Charlotte Lanteri, Walter Reed Army Institute of Research
Dr. Andrew Mesecar, Purdue University
Dr. Jennifer Nwankwo, 1910 Genetics
Dr. Celia Schiffer, University of Massachusetts Medical School

The SARS-CoV-2 Infection Cycle Requires Host and Viral Proteases

SARS-CoV-2 uses both host and viral proteases in its replication cycle (see Figure 1 in Overview). The generalizability of host proteases makes them a good target for many distinct coronaviruses that tend to use similar host factors. The spike proteins of SARS-CoV and SARS-CoV-2 have commonalities, such as sequence similarities and multi-basic proteolytic cleavage sites at both the S1 and S2 residue site as well as the S2 prime residue sites where host proteases (such as furin and TMPRSS2) cleave to facilitate viral entry. Host proteases do not mutate as easily as the viral proteases.

Host proteases TMPRSS2 and furin have a role in cleaving spike protein between S1 and S2 to reveal the fusion peptide and helical repeat domains that are necessary for viral entry[25,26]. Currently two compounds are being investigated that potentially inhibit the host proteases and could be used as COVID-19 treatments: camostat and nafamostat. Both are repurposed drugs that are approved in Japan for the treatment of several conditions including pancreatitis[27]. Since these compounds have existing human safety data, late-stage clinical studies for COVID-19 treatment are underway.

Drug discovery efforts to identify new host and viral proteases are actively being pursued. These include two efforts being led by the panelists in this session. The group at 1910 Genetics (founder Dr. Jen Nwankwo) is using machine learning design to screen millions of compounds to identify a suitable chemical substrate for host TMPRSS2 inhibitors. A second AI approach to identify viral protease inhibitors, led by LTC Lanteri at Walter Reed Army Institute of Research (WRAIR), combines X-ray crystallographic data with high performance machine learning.

Viral Protease Inhibitors (PIs) Have Been Used to Treat HIV and HCV Successfully

The first viral protease inhibitors were identified in the search for HIV cures[28]. The HIV protease inhibitors are some of the first examples of structural based design, a move away from the traditional high throughput screening approaches that had been previously deployed for drug discovery efforts. A similar approach was also used for HCV and was so successful it was able to provide a cure for what was previously a chronic disease.

Structural design was first applied to coronaviruses in 2003 during the SARS epidemic caused by SARS-CoV-1 with the discovery of the first protease inhibitors specifically designed for coronaviruses. Both the public health measures that led to control of SARS-CoV-1 and the resulting lack of patients for clinical studies meant that that these drugs were never developed; it is not yet known if this approach will work for SARS-CoV-2, though there is promising in vivo data of these compounds against coronaviruses with similar proteases.

Two SARS-CoV-2 Cysteine Proteases can be Targeted for Potential COVID-19 Treatment

There are two SARS-CoV-2 encoded cysteine proteases that are potential antiviral targets: a papain-like protease and a 3C-like protease. These proteases are responsible for cleaving the polypeptide that is translated after the viral RNA enters the host cell. The single polypeptide makes up the machinery that the virus needs for replication. If it is not cleaved into the 16 individual non-structural proteins, the virus cannot replicate. The papain-like protease is a multifunctional enzyme that is also associated with pore formation and immune modulation[29]. The 3C-like protease, which is also known as the main protease, functions as a dimer and has a single role that is to cleave the polypeptide at 11 sites[30].

HCV and HIV Drugs Have Limited Utility for COVID-19 Treatment, Current Potential Antiviral Inhibitor Candidates

Early in the pandemic, steps were taken to investigate whether existing HIV and HCV protease inhibitors could be redeployed to treat COVID-19 patients. There are considerable differences in the structure of the different proteases, so this approach led to little success, although some inhibition had been observed. Clinical studies are still in progress with the HIV drug ritonavir-boosted lopinavir, but an early controlled trial in COVID-19 patients in China failed to find evidence of antiviral effects or clinical benefits, and subsequent trials have confirmed the lack of therapeutic efficacy in hospitalized COVID-19 patients. Also, it is unclear what is its mechanism of action. Lopinavir and isotretinoin are examples of drugs repurposed for potential antiviral therapy. A Phase 1 study of PF-07304814 (termed PF-'814) is ongoing. This drug was specifically designed to inhibit coronavirus proteases. Several preclinical protease inhibitors are also under investigation and extensive screening for additional protease inhibitors is ongoing.

Example of 3-CL PI Development: Pivoting to a Pro-Drug Candidate PF-007304814 to Enable Clinical Dosing of Therapeutic Concentrations of Active Drug Candidate PF-0835231

In January 2020, as the potential force of the COVID-19 pandemic became apparent, Pfizer restarted its coronavirus PI development program that had been conducted in response to the SARS epidemic more than 15 years earlier. After comparing sequences of the two coronaviruses, a high degree of similarity was observed between the 3CL proteases, suggesting that Pfizer's lead compound PF-0835231 (termed PF-'231) could be developed and then potentially be deployed against SARS-CoV-2.

The following 8 months (to October 2020) saw the usual long development program dramatically compressed with the help of many coronavirus experts in the field to generate data for evidence that the candidate drug was highly potent and specific for the inhibition of coronavirus 3CL proteases including that from SARS-CoV-2. When it was recognized that the compound's potential pharmacokinetic exposure was suboptimal, teams of chemists quickly developed the phosphate

prodrug PF-'814[31]. This prodrug increased the exposure of the drug to allow for effective dosing in clinical studies, the first of which was initiated in September 2020 (NCT04535167).

PF-0835231 SARS-CoV-2 Protease Inhibitor has Additive Activity with Remdesivir In Vitro Due to Differentiated Mechanism of Action and Has the Potential to be Broadly Cross Reactive Across Coronaviruses

Remdesivir and Pfizer's PF-'814 have distinct antiviral mechanisms of action. Since antiviral treatment has benefitted from combination therapy, the antiviral activity of combinations was explored in vitro. The PF-'231 starting point showed potent single agent EC_{90} in a SARS-CoV-2 antiviral assay, indicating potential clinical efficacy for viral protease inhibitors. Combining PF-'231 with remdesivir increased the observed in vitro potency. These in vitro data suggest that a combination may result in control over the virus with reduced amounts of each compound.

Collectively these in vitro data suggest Pfizer's prodrug has the potential to be effective as a single or a combination agent against SARS-CoV-2. In addition, it appears the compound has the potential to be a pan-coronavirus drug that can be deployed in the event of potential future coronaviruses that emerge as a result of additional species crossover events. The data generated suggests that this potential first-in-class protease inhibitor may provide the best opportunity to show meaningful antiviral activity to help treat COVID-19 patients. Two clinical studies are ongoing: one is a Phase 1 single ascending dose (SAD) study in healthy volunteers (NCT04627532), and a second is a Phase 1b in patients (NCT04535167). A pivotal Phase 2/3 study is planned to start in early 2021, with a projected approval in the second half of 2021.

PL^{pro} Has Other Functions in Addition to Protease Activity that PL^{pro} Inhibitors May Also Prevent

Coronavirus PL protease inhibitor development is not as advanced as the $3CL^{pro}$ inhibitors. Inhibitors targeted to this protease may provide a unique opportunity to not only inhibit viral replication via inhibition of cleaving the nsp3, but also inhibit nsp3 from antagonizing the NF-κB and IRF3 host innate pathways via deubiquitination and deISGylation as well as removing ISG15 from proteins in the Jak/Stat pathway. The dysregulation of these pathways may contribute to excessive cytokine release from infected cells. In addition, Nsp3 has recently been shown to be part of a molecular pore in double-membrane vesicles (DMVs). The DMVs form after viral infection as a result of nsp3, nsp4 and nsp6 embedding in the rough endoplasmic reticulum and reshaping it.

Challenges and Opportunities

The challenges and opportunities for the discovery and development of SARS-CoV-2 protease

inhibitor treatments were discussed by the panel, with a focus on how advanced screening methodologies are being used to accelerate screening and the importance of structural analysis to identify potential resistance challenges and facilitate compound discovery. Current research into protease inhibitors has been enhanced by consortia and collaborations. For example, work conducted by the Center for Structural Genomics enables the acceleration of drug design and validation programs.

With each new mechanistic insight come new targets, including host factors. These targets provide an opportunity for rational drug design accelerated by artificial intelligence (AI) that can be deployed at all stages of the early drug discovery process, from novel hit discovery to identification and optimization. For example, a 1910 Genetics AI platform allows the rapid screening of a billion-chemical library in less than 6 hours to identify hit compounds. Hit compounds are synthesized to ensure that they are not cytotoxic and then confirmed as actively inhibiting viral entry into Vero E6 cells engineered to overexpress TMPRSS2.

With the arrival of the COVID-19 pandemic, WRAIR scientists initiated a discovery program in small molecules therapeutics directed at SARS-CoV-2, with the goal of developing a small molecule therapeutic that can treat or prevent SARS-CoV-2 and other circulating coronaviruses in anticipation of the next emerging virus. LTC Charlotte Lanteri explained that this involved a significant pivot for the WRAIR Experimental Therapeutics (ET) Branch, the Department of Defense's (DoD's) sole drug development group, into a new therapeutic area of developing antivirals. The WRAIR ET team leveraged their inherent drug discovery and development capabilities and expertise for developing malaria and antibacterial drugs to address COVID-19.

WRAIR partnered with the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID) scientists who established a high throughput in vitro SARS-CoV-2 Vero cell-based test system at their biosafety level-3 (BSL-3) labs. As part of this DoD COVID-19 Small Molecule Therapeutics effort, collaborators at the Southwest Research Institute in San Antonio, TX, in conjunction with the DoD's High Performance Computing Modernization Center, applied a proprietary AI/machine learning algorithm to screen >41 million compounds against two SARS-CoV-2 targets: the main protease and Spike protein Receptor Domain. The virtual screens were built based on published crystal and cryo-electron structures, as well as X-ray structures of the virus produced by the WRAIR Emerging Infectious Diseases Branch. The DoD group screened a library of >41 million compound structures in a matter of weeks. Compound structures came from a diversity of sources, some of them were existing drugs that may be repurposed for SARS CoV-2 and other coronaviruses. Others were novel chemical matter from a large repository of compounds that had already been analyzed for drug like properties. In contrast to traditional in silico

method introduces the ligand to the target with no pre-conceived notions of binding pose. Their ultimate goal is to develop a pan-coronavirus drug; as such, virtual screen hits were also screened against an analogous target (RBD) from SARS-CoV-1 and MERS to select compounds with the greatest overlap in predicted binding. From this large scale initial screen, they rapidly down-selected approximately 800 compounds within a few weeks, dramatically shortening the traditional years-long discovery phase. To date, testing of in silico hits resulted in a 9% hit rate in USAMRIID's SARS2 antiviral Vero cell screen. This outcome is orders of magnitude better than more traditional high throughput put methods. The combination of AI and then high-throughput screening using an invitro assay has been key for accelerating the discovery of potential new coronavirus treatments. The molecules are currently being studied from a medicinal chemistry perspective including determination of their metabolic properties, safety evaluation and pharmacokinetics in mouse models.

PL^{pro} Has Other Functions in Addition to Protease Activity that PL^{pro} Inhibitors May Also Prevent

Dr. Mesecar of Purdue University described working on PL^{pro} and M^{pro} after the SARS-CoV-1 pandemic in 2003-2004 with a collaborative team[32–35]. At that time, the papain-like protease was an overlooked protease with no established structure. Cleavage of ubiquitin off host cell proteins was also identified as another potential role for the PL^{pro}. Dr. Mesecar and his group confirmed that PL^{pro} was capable of utilizing ubiquitin substrates. He evaluated interferon-stimulated gene 15 (ISG15) and determined it is also capable of hydrolyzing 7-amino-4-methylcoumarin (AMC) of ISG15 causing its removal from ubiquitin in host cells. Understanding the complete role of PL^{pro} antagonism of an aspect of host innate immune response will be important to the successful use of PIs of this protease.

Dr. Mesecar and colleagues elucidated the structure of PL^{pro} and found that it was indeed a ubiquitin-specific protease (USP). They then conducted a high-throughput screen of 50,000 compounds, identifying two potential compound templates for anti-viral drug development. These non-covalent inhibitors had the ability to target only a certain subclass of coronaviral papain-like proteases selectively, making it possible to target papain-like proteases selectively. To date these compounds have shown efficacy in a non-SARS-CoV-2 coronavirus animal model.

Design of protease inhibitors to pre-emptively avoid Drug Resistance:

Viral proteases are key drug targets and have been one of the most successful structure-based drug designs. However, drug resistance can come from mutations in the active site, or remote changes that alter the flexibility of the protease[36–38]. The necessity of the protease to cut a series of cleavage sites is a key evolutionary constraint. Dr. Celia Schiffer's laboratory at University of

Massachusetts Medical School, for example, have focused on this evolutionary constraint of substrate recognition and processing and how to combine that evolutionary constraint to preemptively avoid drug resistance. Inhibitors that fit within the substrate envelope are less likely to produce resistant strains because the mutation impacting these inhibitors will simultaneously impact the recognition and processing of the majority of the substrates. Dr Schiffer's team has previously demonstrated this approach with HIV and HCV proteases[39,40]. Similar to other viruses, SARS-CoV-2 has already evolved during the current pandemic. As the SARS-CoV-2 viral proteases both recognize multiple substrates, the substrate envelope approach is being pursued as a way to pre-emptively avoid resistance. Combining protein crystallography, medicinal chemistry, and computational methods to SARS-CoV-2 $3CL^{pro}$ and PL^{pro} with a collaborative team at University of Massachusetts Medical School, the aim is not only to have inhibitors that retain effectiveness during the current pandemic but are potent against any future coronaviral outbreaks.

SESSION 3

EMERGING TARGETS, EMERGING MODALITIES

Moderator:
Dr. Kara Carter, Evotec*
**Current affiliation: Dewpoint Therapeutics*

Panelists:
Dr. David Baker, University of Washington
Dr. Lillian Chiang, Evrys Bio, LLC
Dr. Matthew Disney, Scripps Research Institute
Dr. Kumar Saikatendu, Takeda Pharmaceuticals
Dr. Marla Weetall, PTC Therapeutics, Inc

As discussed above, small molecule inhibitors of essential viral enzymes, such as polymerases and proteases, are well validated approaches for antivirals. However, as with all complex viral diseases, multiple therapeutics to address different aspects of the SARS-CoV-2 viral life cycle and in different COVID-19 patient populations are needed to have the ability to effectively treat patients. Several new modalities have arisen for therapeutics in general over the last several years including RNAi, CRISPR/Cas9 and other targeted nucleases, bifunctional molecules, and others. Dr. Matt Disney of Scripps Research Institute described how sections of viral genomes in general, and SARS-CoV-2 in particular, form constrained secondary structures that are specifically targetable by small molecules. Such regions of the SARS-CoV-2 genome include the 5' untranslated region and the frame shift motif. Small molecule screens have been conducted and identified binders to these elements[41]. These binders have been used as the basis of a chimeric compound that can target a host ribonuclease to the viral genome and ultimately lead to its degradation. Such a mechanism has demonstrated potent antiviral activity. In addition, Dr. David Baker of the University of Washington described his work generating mini-proteins that specifically bind to the receptor binding domain of the viral spike protein with potent nanomolar antiviral activity[42]. These mini-proteins were computationally designed and are able to be produced in large quantities that could lead to minimal cost of goods. In vivo, these mini-proteins delivered either intranasally to hamsters or as Fc-fusions by injection to mice, had protective effects when the animals were challenged with virus.

Both of these newer modalities have potential significant advantages. First, drug discovery can begin as soon as a new genome is sequenced (a parallel with vaccine development). For mini-proteins, computational methods lead to the synthesis of small numbers of molecules for testing. For RNA binders, analysis and comparison to sequences of related viruses can accurately predict genome sequences/structures to start screening for small molecule binders. The mini-proteins, as mentioned above, can be developed with different formulations for different routes of administration and have good potential for low cost. Additionally, at least in the case of the mini-protein generated against SARS-CoV-2 spike, the molecule is thermostable and can be stored at room temperature. The RNA targeting small molecules may have a lower incidence of mutation given there are only three options of nucleotides to be incorporated into the RNA for such mutations, and to maintain functional structure of the RNA, even substitution by those three options may not be tolerated by the virus. Both of these modalities, though, lead to molecules that will likely have activity limited to viruses with close sequence homology in the viral target.

Complementing the advances in new modalities is the identification of novel targets for antivirals beyond the traditional viral enzymes such as polymerases and proteases. Both systems biology studies[43,44] and compound repurposing screens[32,45–49] have identified a number of potential

host cell targets to be explored for validation and ultimately drug discovery and development. One example is dihydroorotate dehydrogenase (DHODH), an essential host enzyme in de novo pyrimidine biosynthesis. Studies to identify pathways and/or targets can vary in their methodology, including use of different cell types and tagging or knock-out of proteins, which can lead to conflicting results. The public visibility and combination of large data sets may allow identification of potential targets. These targets become actionable as they are verified with the use of probe molecules to test the therapeutic hypothesis, and demonstration of activity in multiple orthogonal assay systems.

Drug discovery focused on host cell targets is anticipated to present multiple opportunities that will require verification. As opposed to direct acting antivirals that may have a less risky developmental path, drugging host proteins or processes presents less potential for resistance emergence and should be effective irrespective of the viral load. Additionally, such molecules tend to be more refractory to drug block release, meaning that after removal of the drug, the changes that the drug induced in the host cell are maintained by extending the antiviral effect. Particularly compelling cellular targets are those engaged in stress activated signal transduction and the dysregulated metabolism induced upon viral infection[50,51]. For example, Evrys Bio, LLC is developing inhibitors of host SIRT2, which have demonstrated potent and durable antiviral activity across a number of viruses[52,53].

As host genes are nominated as druggable candidates, rigorous validation of the target and modality, translating active molecules to drugs and ultimately to medicines requires focus on physical properties, pharmacokinetics, formulation, and other key pillars of drug development. These new modalities and targets do not replace small molecule drug discovery against traditional, validated targets like polymerases and proteases. Rather, they are expected to complement those efforts and increase the diversity of agents that can be used to treat COVID-19 patients. In some cases, these approaches may provide more rapid discovery and development of drugs in a pandemic setting. Additionally, the breadth of activity and potency, even in the face of high viral load, of drugs targeting cellular proteins can complement more traditional antivirals. These new modalities and targets should certainly be explored as part of the SARS-CoV-2 response.

SESSION 4

PRECLINICAL TOOLS

Moderator:
Dr. Pei-Yong Shi, University of Texas Medical Branch

Panelists:
Dr. Sara Cherry, University of Pennsylvania
Dr. Emmie de Wit, NIAID/Rocky Mountain Laboratories, NIH
Dr. Jules O'Rear, US Food and Drug Administration
Dr. Timothy Sheahan, University of North Carolina
Dr. Hugh Smyth, University of Texas at Austin

Biologically and clinically relevant models are required for the evaluation of antiviral drug candidates in order to obtain the most meaningful and informative preclinical data. Both in vitro (cell-based) and in vivo (animal) models of SARS-CoV-2 infection have been developed to evaluate antiviral activity and therapeutic efficacy of candidate drugs. Various in vitro systems have been used to identify potential COVID-19 therapeutics in the screening of drug libraries comprised of approved drugs with the hope of repurposing in addition to the screening of compound libraries to identify new antiviral compounds to then be optimized into a more drug-like form through medicinal chemistry. Animal models of SARS-CoV-2 infection that recapitulate viral tropism and COVID-19 disease pathology are required to ensure that pre-clinical candidates are active at the target site (e.g. lung) and to assess antiviral combinations. As SARS-CoV-2 is a respiratory virus, formulation of oral or intranasal delivery of therapeutics will be most impactful as dosing would not require assistance from a medical professional. Preclinical animal models are essential to determine if therapeutic candidates have antiviral activity, optimal pharmacokinetic profiles, and mitigate SARS-CoV-2 pathogenesis.

In vitro Models

For cell-based antiviral testing, both wild-type virus and those engineered to express reporter genes like luciferase or fluorescent proteins have been used to screen compounds for antiviral activity[54]. Antiviral activity and potency have been determined by multiple techniques including through the measurement of reporter gene products, direct measure of infectious virus by classical virological techniques, measurement of viral cytopathic effect in cell monolayers, and immunostaining-based measurement of viral proteins via high-content imaging which can also monitor cytotoxicity[45]. To most efficiently triage compounds, early removal of toxic compounds is preferable. Compared with wild-type virus, reporter virus assays typically have a higher dynamic range and potentially higher throughput capacity. High-throughput assay formats also allow the screening and assessment of antiviral combinations in cell culture, which require a large number of experimental conditions to be evaluated[55].

The target cell type employed is also critical to accurately predict antiviral activity of candidates in humans. A number of seemingly simple considerations, including the species of origin of a given cell line (e.g., human versus other animal-derived cell lines), and the tissue of origin (e.g., respiratory epithelial versus kidney or colon) significantly impact the relevance of antiviral candidate potency. For example, the FDA-approved RdRp inhibitor remdesivir IC_{50} values differed by 1,000-fold when remdesivir was tested in Vero cells (African green monkey kidney epithelial cell line, weak activity) compared with primary human airway culture (potent activity)[56]. This is likely due to differences in cellular enzymes that transport and/or metabolize the prodrug into its pharmacologically active triphosphate form. Conversely, chloroquine and its derivatives

showed anti-SARS-CoV-2 activity in Vero cells, but not on primary human airway cultures or animals[57]. These results underline the importance of selecting the right cell types for antiviral testing, and primary or multicellular airway models should be considered to confirm antiviral activity.

Reverse Genetic Systems

Reverse genetic systems have been developed for SARS-CoV-2, leading to the generation of both fluorescent and luminescent reporter viruses that can increase the throughput of screening assays with authentic virus particles at BSL-3[58,59]. In addition, reverse genetics enables the phenotypic confirmation of drug resistance mutations derived through passage in cell culture or those that naturally arise in humans and drug target deconvolution in mechanism of action studies with newly discovered drug candidates. Functional genomics screening approaches such as CRISPRi can enable the identification of human (host) genes that play a cooperative role in mediation the viral replication cycle and may be druggable.

In vivo Models

Several animal models have been developed for SARS-CoV-2, including mouse, hamster, ferret, and non-human primates. A detailed list of SARS-CoV-2 animal models is maintained by the NIH ACTIV Preclincal Working Group at the NCATS OpenData Portal[60,61]. For both small animal and non-human primate models, information on background, primary references, and viral model endpoints are provided.

The establishment of any animal model relies on that species being susceptible to infection by SARS-CoV-2[62], and a secondary consideration is the species being amenable to maintenance in a vivarium setting. Although mice are typically used widely to study viral pathogenesis and antiviral efficacy due to their size, ease of use, available genetic models, and experimental tools, due to differences in the murine ortholog of the human receptor, angiotensin converting enzyme 2 (ACE2), SARS-CoV-2 spike cannot bind mouse ACE2 and cannot infect standard laboratory mice. To circumvent this issue, approaches have been taken to enable SARS-CoV-2 infection in mice. First, transgenic mice have been made that express human ACE2[54]. Second, viral vectors have been used to deliver and overexpress human ACE2 in the mouse lung[63]. Lastly, SARS-CoV-2 has been genetically adapted to utilize mouse ACE2 for entry resulting in a virus with high titer replication in the lungs of standard laboratory mice (i.e. BALB/c), loss of pulmonary function, severe end stage lung disease like ARDS and death[64]. In general, any of these mouse models can be useful for antiviral testing. In addition, because the mouse-adapted infection model recapitulates multiple aspects of the human disease, this model may be more useful to study viral pathogenesis and genetically dissect host immune responses driving disease.

Hamster models have been developed to study viral replication, pathogenesis, and transmission[65,66]. Unlike mice, wild-type SARS-CoV-2 robustly infects hamster respiratory tract, causing weight loss and lung pathology. The hamster model also recapitulates age-dependent disease severity. The kinetics of viral replication in young hamsters is faster than that in aged hamsters, whereas the immune response in aged animals lasts longer, leading to somewhat more severe disease. Moreover, hamsters can transmit the virus allowing for the study of SARS-CoV-2 transmission. Ferret models have also been established to study viral transmission. Compared with other animal models, the viral replication level and disease severity are milder in ferrets.

Several non-human primate models of SARS-CoV-2 have been reported, including rhesus macaque, cynomolgus macaque, and African green monkey[67–69]. In the rhesus macaque model, the infected animals develop mild to moderate clinical signs of disease, develop pulmonary infiltrates on radiographs, and virus shedding in nose and throat swabs is similar to that observed in COVID-19 patients. Although no non-human primate models have been established that recapitulate severe COVID-19, these models have been used successfully to show the efficacy of several direct-acting antivirals and antibody treatments.

In summary, antiviral models have been developed to support in vitro and in vivo drug discovery. However, limitations remain, in large part due to the biosafety considerations, to enable more efficient therapeutic development.

Challenges and opportunities

Data reproducibility and assay comparisons

One challenge to SARS-CoV-2 drug discovery and development is that different research teams have reported different activity, or lack of activity, for the same compound. One "side effect" of so many research groups converging on SARS-CoV-2 research has been the use of differing models and assays (described above). The adoption of common reference assays and criteria would set standards for the field. This would include recommendations on appropriate cell lines and reagents and making sure these are readily available to qualified investigators. For example, HIV repositories exist for small molecules, viruses and cell lines promoting standardization which has been beneficial to drug development (though this was implemented over a longer timeline, see for a general example the Biodefense and Emerging Infections Research Resources Repository, BEI Resources). Importantly, the reliance on a single assay model for demonstrating activity is not adequate, and orthogonal assays are essential. In addition, testing against standardized positive and negative controls in assays is also important.

Combination antiviral therapy

Combination antiviral therapy is expected to be critical to effectively treating infections and minimizing the development of resistant strains. Screening approaches can be used to identify potent synergism of antiviral candidates, and functional/genetic approaches can be used to predict drugged target combinations that should be effective. Moreover, any new therapeutic, especially other RdRp inhibitors, must be tested for antagonism against approved therapies, such as remdesivir, to ensure that unwanted impedance of antiviral activity does not occur in combination. Also initial clinical studies of potential drug-drug interactions with respect to human pharmacokinetics and tolerability are necessary.

In vivo models

Before the SARS-CoV and MERS-CoV outbreaks, very few models of coronavirus pathogenesis existed, but researchers responding to the SARS-CoV-2 pandemic rapidly took advantage of previous approaches and models developed for other emerging coronaviruses (e.g., human ACE2 transgenic mice). However, the numbers of researchers able to engage in research with an authentic emerging coronavirus is limited by the need to perform this work in a BSL-3 laboratory of which there are only a handful in the United States. Another major gap is that it remains difficult to study long-term effects of either treatment or disease in animal models. From an antiviral candidate perspective, "direct-acting" compounds against viral proteins can be applied to many animal models, but host-target antiviral candidates (for example, host proteases described earlier) rely on an understanding of the species homolog of the human gene. Current animal models are not adequate for studying extrapulmonary manifestations of disease. Studying comorbidities is also difficult in animal models, which is a major weakness given the pathology of COVID-19 in humans, and the anticipation that newly developed antivirals will be effective in reducing mortality in patients with such complicating comorbidities.

To date, the FDA has not been requiring animal model data for some clinical trials using agents with known activity during viral infections, and well-defined safety based on prior in-human use. However, antiviral activity information remains essential in instances when other data, on topics such as the mechanism of action or toxicity, are lacking. Mechanism of action and resistance data is of vital importance. In this context, the designation of a standard accepted in vivo model with gold standard positive and negative controls for assessing and comparing antiviral activity of a new therapeutic has not been designated.

SESSION 5

LESSONS FROM OTHER VIRUSES AND PREPARATION FOR THE FUTURE

Moderator:
Dr. Daria Hazuda, Merck & Co.

Panelists:
Dr. Jay Bradner, Novartis
Dr. Courtney Fletcher, University of Nebraska Medical Center
Dr. Frederick Hayden, University of Virginia
Dr. Hilary Marston, NIAID

There is a long history of antiviral drug discovery and development dating back to the 1960s. While these earliest efforts were largely empiric, the tremendous effort against HIV in the 1980s and 1990s was pivotal in the shifting emphasis to more target-based drug discovery and some of the earliest successes in structure-based and rational drug design. The success of antiretroviral therapy for HIV illustrated the critical importance of combination therapy and adherence in treating chronic infections and highlighted the value of fixed dose combinations, convenience, and tolerability. These fundamental lessons were subsequently relearnt in the discovery and development of direct acting antiviral drugs for HCV.

HCV drug discovery also emphasized a target-based approach for the development of protease and polymerase inhibitors, but in the end, empiricism was also critical to this amazing success story. The HCV NS5a inhibitors, which became pivotal to most successful combination therapies, were discovered from agnostic cell-based screens that were only made possible by the development of replicon assays. The development of replicons for multiple diverse HCV genotypes was fundamental to achieving the breadth of activity needed to address both spectrum and resistance, also illustrating the critical value of having the right in vitro models to drive the drug discovery process.

Throughout the 1980s, 1990s, and 2000s, advances were also made in therapeutics for HBV, influenza, and various herpesviruses. Today there are more than 90 approved antiviral agents to treat a variety of both acute and chronic viral infections. While there are successful antiviral drugs across multiple distinct target classes, the largest number and broadest class of approved antiviral drugs are those which target viral polymerases. Polymerase inhibitors have been approved to treat infections across both RNA and DNA viruses as well as retroviruses and comprise a myriad of mechanisms, including substrate mimetics such as nucleoside and pyrophosphate analogs but also non-nucleoside or allosteric inhibitors. It is worth noting even nucleosides can exhibit distinct mechanisms of action, including chain termination, inhibition of translocation, and error catastrophe with unique implications for pharmacology and resistance.

In general, enzyme targets dominate the list of approved antiviral agents, but after polymerase, other enzyme targets are generally unique to different virus families making it challenging to find drugs that work broadly. The challenge of finding approaches that are effective across a virus or virus family is particularly true for viral entry targets, which can often vary even for a specific virus in cases where multiple receptors or modes of entry are observed. The best clinical illustration of this challenge is the development of CCR5 inhibitors for HIV, where having a diagnostic to differentiate CCR5 vs CXCR4 tropism was critical and became an impediment for the use of such

agents in the real world. CCR5 inhibitors are also one of the only examples of a successful antiviral development against a host target, another challenge for antiviral development generally.

Despite a tremendous track record of success, there are lessons from notable disappointments in antiviral drug development. There is always the potential for failure due to toxicity or pharmacology that plague drug development more generally, but in the case of antivirals, in some cases poor efficacy can be attributed to a drug's inability to address either inherent diversity or easily acquired resistance. One such example is the first generation HCV protease inhibitors that were obsolete by the time they launched, being replaced by agents with improved resistance profiles and spectrum. While in many cases, learnings from the initial clinical disappointments resulted in improved agents, an earlier understanding of diversity and resistance could have avoided many of these early mistakes. Therefore, understanding the impact of genetic diversity and resistance is important even at the earliest stages of target and lead selection.

While it is certainly preferable to develop agents which have a high barrier to the development of resistance, as seen in HIV and HCV, even agents with a low barrier to resistance development can work when combined if there is adequate pharmacologic coverage. The importance of combinations appears to be more important in treating chronic infections, where there is ongoing replication and a larger more diverse population as compared to prevention where dual and even monotherapy is highly effective. But even in chronic infection, monotherapy can sometimes work, as is the case in HBV, likely a consequence of both the biology of the virus and the specific agents.

It is important to note that resistance and antiviral efficacy are intrinsically linked to pharmacology. The following characteristics have been found to decrease the probability of the development of resistance: high bioavailability, high plasma and/or organ/tissue/site-of-action distribution, long elimination half-life, low intra- and interpatient variability, low probability as a victim or perpetrator of drug-drug interactions, and convenient dosing regimens (which promote high adherence and are forgivable of missed doses). To maximize the potential for broad impact and global use, oral agents with low cost of goods that are easy to formulate and also suitable for pediatric formulations are critical. For chronic therapy and prevention, drugs which are amenable to long-acting formulations are highly desirable. In addition, understanding where the agent needs to be delivered to treat or prevent infection is key. In respiratory infection for example, intranasal administration may not be sufficient to treat or prevent lower respiratory tract disease but may be useful for prophylaxis.

For both acute and chronic infections, timing is key. As has been shown in HIV, early treatment and prophylaxis lead to profound patient, public health, and economic benefit. The same has been

observed in the setting of preemptive therapy or post exposure prophylaxis. How soon post-exposure prophylaxis needs to be administered may vary between different viral infections and antiviral mode of action, but in all preclinical models and clinical studies of respiratory viral infections, sooner is better. In a pandemic setting, this is especially critical. For influenza, insufficient and delayed use of neuraminidase inhibitor treatment resulted in these drugs having a diminished impact on patient mortality during the 2009 pandemic despite their known effectiveness. The exceptions included countries like Japan that had high levels of antiviral coverage, including children and pregnant women.

A number of potential SARS-CoV-2 inhibitors are being considered for topical administration (e.g. intranasal, inhaled) to the respiratory tract. One issue for topically delivered respiratory virus antivirals is whether intranasal administration is sufficient, which in turn, depends on the principal site(s) of initial acquisition. Intranasal interferons (IFNs) protect against rhinovirus and likely common respiratory coronavirus illness. However, neither intranasal IFN nor intranasal zanamivir prevent natural influenza illness. In contrast, inhaled zanamivir is highly effective for prevention of influenza illness (75-80% in household contacts). It remains to be determined whether antivirals administered intranasally (i.e. protecting only the nose) might prevent some SARS-CoV-2 infections. Inhaled investigational agents like IFN-beta, which has shown some efficacy in hospitalized COVID-19 patients, and when available, inhaled remdesivir may prove effective in prevention and early treatment.

It is well established that antiviral drugs are highly effective in both treating and preventing infections, if they have the right pharmacologic properties, can be easily accessed, and administered to at risk populations. Having the appropriate in vitro tools and in vivo models to develop antivirals are key. Investing in the basic biology to develop these tools, assays, and models, understand the implications of resistance and overcoming the barriers which impede rapid access to the use of such drugs once developed, are critical for limiting future pandemics and outbreaks and requires a collaborative effort which crosses public, private, and governmental boundaries.

Preclinical Pharmacokinetics and Formulation

As with any preclinical drug development program, it is essential to understand the physicochemical properties of the drug compound and the resulting pharmacokinetic profile in order to improve chances of success in demonstrating in vivo efficacy. For example, Remdesivir is given intravenously due to poor oral bioavailability. Moreover, remdesivir required solubility enhancement using cyclodextrins due to its limited solubility[70] Preclinical formulation development should take into account drug solubility, stability, and absorption. In the case of

alternative routes of administration may also be considered. Notably, intranasal and pulmonary administration appears a promising strategy for SARS-CoV-2 antiviral delivery where ACE2 receptor distribution is implicated in initial infection and subsequent pathology[71].

SUMMARY OF DISCUSSIONS AND PERSPECTIVES ON THE CHALLENGES AHEAD

Speakers:
Dr. George Painter, Emory University
Dr. Richard Whitley, University of Alabama at Birmingham

Overview of the Virus and Therapeutic Approaches

An overarching goal for the coronavirus antiviral program is the discovery of broadly active compounds that act at multiple sites in the virus replication cycle, and that target diverse coronaviruses (CoV) both in vitro and in animal models. The ability to administer drug by multiple routes (IV, oral, inhalation, and nasal) is highly desirable. A toxicity profile that supports prophylactic as well as therapeutic use is key. As the current pandemic emerged, the problems associated with clinical development in the absence of a clear understanding of the virologic and immunologic course of disease became apparent. Important considerations moving forward include determining acute viral burden, establishing the effective therapeutic window, and identifying potent combination therapies designed to improve efficacy and prevent resistance. Even with the availability of effective vaccines, antiviral drugs will be required to protect highly vulnerable populations with diminished immune function or who cannot take vaccines due to allergic reactions.

Targeting Viral Replication Machinery of SARS-CoV-2

Therapeutics against SARS-CoV-2 consist of many subtypes: antibodies, early inhibitors of entry, fusion inhibitors, RNA polymerase inhibitors, protease inhibitors, and virus release inhibitors, among others. These can be either host or viral targeted therapeutics. One of the most successful methods to mitigate SARS-CoV-2 replication is by direct acting antivirals; currently, those that target the replication machinery are of high interest. To date, progress has been made in the development of nucleoside analogs, as these are the only class of antivirals that have been approved clinically for COVID-19 (e.g., remdesivir)[14]. There are pros and cons of developing nucleosides. Those nucleosides in which the sugar is ribose, called "ribonucleosides," have had the advantage in that they had been jump started from other viral indications. Advantages include: 1. they mimic natural substances; 2. in vitro work has suggested a high threshold of viral resistance; 3. the development pathway is well understood; and 4. tests are in place to detect off target toxicities. The fact that ribonucleosides tend to be broadly active make this family of therapeutics desirable for interrogation (both for now, and off-the-shelf for future pandemics)[72–74].

It has proven difficult to establish structure-activity relationships for nucleoside/nucleotide analogs, consequently nucleoside discovery generally is a trial and error process. The current approach is to simply introduce modification on the base or ribosugar, and then test each derivative for activity. In addition, nucleosides require multistep metabolic activation for conversion to the 5'-triphosphate derivative in order to be inhibitory. This effort can be a challenge as metabolic activation varies between different cell types, which makes selection of assay types and cell types a challenge for downstream evaluation. Further, the delivery of nucleosides to the target tissue of interest can be a challenge. However, there is a wealth of historical data that

informs the selection of those nucleosides that provide a starting place for synthetic efforts. Nevertheless, chemistry can be challenging working through the many variations of modifications that are possible on base versus ribosugar. Nucleosides, because they mimic natural factors, also can act through different mechanisms, targeting aspects of the replication machinery of either host or virus (selectivity). While tools have improved the design of antiviral nucleosides, these compounds must be tested in whole cell screens and must be evaluated for the potential off-target effects (mitochondrial or host cell compartment interactions). Lastly, the design of alternative delivery options, e.g. such as oral delivery - can be challenging. Tactics to make all the information surrounding the work in nucleoside therapeutics more widely known across disciplines including the assays to determine antiviral effect must be made more generally available.

Proteases (Viral and Hosts)

An obvious target is viral and host proteases, as these proteins are important for viral entry and processing. Of benefit is that libraries of HIV and HCV protease inhibitors provide a logical starting point for synthesis. Repurposing protease inhibitors provides an invaluable and rich resource especially for combination therapies. Proteases have been demonstrated to be broadly druggable, and new pre-clinical candidates will emerge. Currently, success has been extremely limited in contrast to that which has been achieved with HIV and HCV infections

Emerging Targets and Emerging Modalities

Nucleosides are of interest because they function as directly interacting with replication processes within either the virus or host. However, there are numerous proteins that are part of the replication machinery, providing opportunities for other target strategies. Efforts to selectively target downstream proteins are now becoming well advanced. In addition, through the application of AI computational oversight to identify properties of likely drug candidates would be expected to be a major step forward, including helicase, endoribonuclease, exonucleases, and methyltransferase.

Knowledge of the lifecycle of SARS-CoV-2 virus indicates that there are numerous other targets of the viral or host genome or proteome that are largely unexplored and could be suitable for drug discovery. The fact that these targets are unexplored makes this route of therapeutic discovery and development more contingent on unknown factors. These unknown risks and benefits must be recognized, but it should not be a factor that impedes progress.

Preclinical Tools

When choosing the preclinical tools to test compounds in vitro and in vivo, the choice of cell type is crucial for cell assays. Orthogonal assays as well as AI are necessary tools to complement discovery efforts[75]. In vivo models can be problematic but are ultimately helpful for therapeutic development. In vivo models can help determine if a drug is capable of engaging a target tissue. In particular, animal models provide a critical true tool for the assessment of drug distribution, e.g. site of viral replication is essential. Further, the half-life, oral bioavailability, metabolism, distribution, microsomal stability, etc. can all be evaluated in animal systems[76]. However, animal models may fail to determine if metabolic differences can drastically alter the way a drug is metabolized. Further, it should be emphasized that a drop in viral burden is not a validated endpoint for efficacy. Each animal model has its own set of peculiarities and other models could be considered. Especially for SARS-CoV-2 (and other respiratory viruses), the air-liquid interface human airway cell model may provide insight into tissue site needs better than an animal model[77].

Clinical Trials and Lessons from Other Viruses and Preparation for the Future

When considering lessons from previous antiviral drug development, clinical trial design and execution should be carefully reviewed. Decrease in viral burden is not a traditionally validated endpoint with the exception of HIV, HCV, and cytomegalovirus (CMV) after hematopoietic stem cell transplantation (HSCT). However, for SARS-CoV-2 antiviral candidates, the lack of antiviral efficacy in early clinical studies of prevention or treatment of mild illnesses should raise concerns about advancing such candidates further. For agents demonstrating antiviral efficacy, what should antiviral clinical trial endpoints be? For SARS-CoV-2 the answer is dependent on the indication (e.g., pre-exposure or post-exposure prophylaxis, treatment) and target population (e.g., early treatment in outpatients to ameliorate illness, prevent disease progression, and/or reduce transmission; treatment in seriously or critically ill hospitalized patients). The logistical issues are many, such as defining diverse patient populations or, often forgotten, the staffing and supply needs to accommodate the appropriate trial. Standardization of platforms for each stage of development, including the clinical trials, would be a helpful step for all. This has been achieved in the pandemic response in part through creation of large pragmatic, adaptive trials in hospitalized COVID-19 patients like RECOVERY in the UK, WHO's Solidarity Trial, and ACTT and ACTIV in the US. These platforms have provided key outcomes data on therapeutics that helped (i.e., dexamethasone, baricitinib), those that did not (hydroxychloroquine, lopinavir-ritonavir, azithromycin) and those with inconsistent results (e.g., remdesivir). Availability of databases and algorithms for AI to provide computational oversite for in vitro and in vivo models and clinical trial design as well as openly sharing negative data among all research groups is useful to avoid rabbit holes that are a waste of time and money. Standardized endpoints would also enable "basket antiviral trials" that test multiple antivirals (or combinations) with a single placebo arm.

Ultimately, for the development of any drug, the most important factor is to guarantee that the lead is safe for human administration[78]. As emphasized, the early stages of the drug discovery and development process should include considerations regarding what the final product insert will recommend as the indication. Considerations would include: will a compound be used for prophylaxis? What formulation options are required according to the route of delivery? Drug delivery to the site of viral replication/disease must be included in the development pathway and crucial treatment paradigm. Establishing these goals at the outset ensures the appropriate design, particularly outpatient or inpatient, with or without multiorgan involvement. In the medicinal chemistry field these are referred to as "target product profiles." The breadth of knowledge critical for drug discovery and development is vast. A translational science approach with a combination of skill sets from virologic and immunologic backgrounds as well as chemistry, toxicology, and other fields are important factors of success.

Forming Partnerships

Forming product development partnerships (PDPs) around direct acting antivirals is a powerful means of rapidly discovering and developing antiviral therapeutics. PDPs are synergistic initiatives between academic innovators at the cutting edge of their discipline and biotechnology/pharma-based drug developers, who can rapidly move clinical development candidates forward through preclinical and into clinical development[79]. Formation of these partnerships is absolutely necessary to maximize the possibility of success in a time and cost-efficient manner. Working with regulators during a pandemic is also important. Defining the resources that are needed and are already available is key. Both NCATS and NIAID have preclinical development resources that are readily accessible.

RESOURCES

National Institutes of Health Accelerating COVID-19 Therapeutic Interventions and Vaccines (NIH ACTIV)

- In response to the emergence and rapid spread of the SARS-CoV-2 virus and of the Coronavirus Disease 2019 (COVID-19), NIH ACTIV brought together senior members of the National Institutes of Health (NIH), the biopharmaceutical industry, the U.S. Food and Drug Administration (FDA), the European Medicines Agency (EMA), and academic researchers to establish a new biomedical research PPP to coordinate respond to COVID-19 and to plan for future pandemics.

- ACTIV working groups have been evaluating potential new therapeutics for preclinical and clinical development. Sponsors are encouraged to submitted agents to the therapeutic agent survey portal for expert review, guidance, and potential support for further efforts (e.g., inclusion in one of the ACTIV managed master protocols). (https://redcap.ncats.nih.gov/redcap/surveys/index.php?s=DAE87WPTE7)

- Description of the ACTIV clinical trial master protocols and additional resources to guide preclinical and clinical research on SARS-CoV2 can be found at the following link (https://fnih.org/what-we-do/programs/activ-partnership)

National Institute of Allergy and Infectious Diseases (NIAID)

- NIAID has a comprehensive suite of preclinical services available to the infectious disease research community to facilitate research in various stages in the product development pathway (www.niaid.nih.gov/research/microbiology-and-infectious-diseases-resources), including assays for testing candidate products against the SARS-CoV-2 in vitro and in animal models. Note that the purpose of these resources is not to assist researchers in developing a product from start to finish, but rather to lower the financial risk to product developers by providing limited, but critical, information to fill specific gaps in the product development pipeline.

- NIAID has many research resources available that may be of interest to you (https://www.niaid.nih.gov/research/resources), including SARS-CoV-2 reagents available from the BEI Resources Repository (https://www.beiresources.org/).

National Institute of Allergy and Infectious Diseases (NIAID, continued)

- In addition to grants and contracts, NIAID also offers a range of basic, preclinical, and clinical resources for the scientific community to advance product development. Information on these services can be found at (https://www.niaid.nih.gov/research/resources). You do not need NIH funding to utilize these resources.

- The National Biocontainment Laboratories (NBLs) and Regional Biocontainment Laboratories (RBLs) provide BSL-4/3/2 and BSL-3/2 biocontainment facilities, respectively, for research on biodefense and emerging infectious disease agents. Investigators in academia, not-for-profit organizations, industry, and government studying biodefense and emerging infectious diseases may request the use of biocontainment laboratories. Please contact the NBLs and RBLs directly for further information.

National Center for Advancing Translational Sciences (NCATS)

- NCATS aims to address scientific and operational challenges that slow the development of new interventions to improve human health. Experts in NCATS's Division of Preclinical Innovation actively seek collaborators on various research projects, including SARS-CoV-2-related targets:
  - NCATS's early stage collaborative programs include 3-D Tissue model development, assay development (Assay Development and Screening Technology), high-throughput screening and hit-to-lead medicinal chemistry (Early Translation Branch), and informatics, as well as many others (https://ncats.nih.gov/about/center/org/dpi/collaborate).

  - NCATS staff can also provide expertise that enables and accelerates Investigational New Drug (IND) applications. Investigators or companies who have identified promising small molecules, biologics or gene therapies can form joint project teams with NCATS' Therapeutic Development Branch staff — including Bridging Interventional Development Gaps (BrIDGs) and Therapeutics for Rare and Neglected Diseases (TRND) scientists — to develop IND-ready therapies for consideration by the Food and Drug Administration for clinical testing.

National Center for Advancing Translational Sciences (NCATS, continued)

- The NCATS COVID-19 OpenData Portal: NCATS has been generating a collection of datasets by screening a panel of SARS-CoV-2-related assays against ~10,000 annotated small molecules (including all approved drugs). These complete datasets, as well as the assay protocols used to generate them, are being made immediately available to the scientific community on the OpenData Portal as the screens are completed (https://opendata.ncats.nih.gov/covid19).

- In coordination with NCATS, and with support from the Foundation for the National Institutes of Health (FNIH), the National Institutes of Health (NIH) Accelerating COVID-19 Therapeutic Interventions and Vaccines (ACTIV) Preclinical Working Group has been collecting and maintaining up-to-date summaries of COVID-19-related animal models, in both small animals and non-human primates (https://opendata.ncats.nih.gov/covid19/animal).

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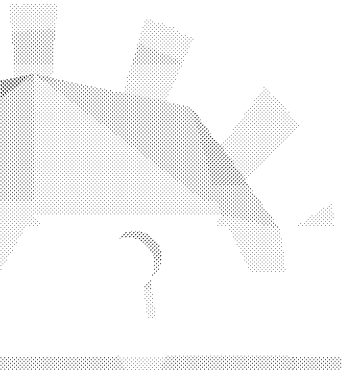

National Institutes of Health

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); viviana.simon; pintol; kemptj; Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Camille Escadafal; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA)

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Vasan, Vasan (H&B, Geelong ACDP); a.luttick; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; Kelvin, Alyson; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); tlying (tlying@fudan.edu.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); baihe (baihe@nmpa.gov.cn); zlshi (zlshi@wh.iov.cn); Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); rawcraig@yahoo.com; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; diane.descamps@aphp.fr; IRAHETA SIGUENZA, Raul Emilio; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); christian.drosten (christian.drosten@charite.de); Barbara.Schnierle (Barbara.Schnierle@pei.de); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; epstein@ecohealthalliance.org; Peter Daszak; christian.brechot (christian.brechot@pasteur.fr); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); Boyle, David; de los Santos, Tala; Leader, Troy; COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver; PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; malik (malik@hku.hk); shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); Daniel Cohen (dancohen@tauex.tau.ac.il); Youngmee Jee (jeey62@gmail.com); alankhoo.imr; Celine Gurry (Celine.gurry@cepi.net); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); ramadany; linfa.wang (linfa.wang@duke-nus.edu.sg); engeong.ooi; alex.sigal@ahri.org; pennym@nicd.ac.za; leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); qiang.pan-hammarstrom@ki.se; Jilian Sacks (Jilian.sacks@finddx.org); SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; KAZI, Fatema; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); pilailuk.o (pilailuk.o@dmsc.mail.go.th); pawinee.k@redcross.or.th; B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Javier Castillo-Olivares Pallardo; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); r.tedder@imperial.ac.uk; katie.doores (katie.doores@kcl.ac.uk); Liz Miller (Liz.Miller@lshtm.ac.uk); Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; jma; GILBERT Nick; Goldblatt, David; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); t.desilva; Turtle, Lance; susie.dunachie; paul.klenerman; ellie.barnes; William James; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk); Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Griffiths, Anthony; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Chu, May; eric.vangieson@darpa.mil; john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); Sarah Mudrak, Ph.D.; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; McElrath MD PhD, Julie; Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Vidadi Yusibov (vyusibov@indianabiosciences.org); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; daniela@lji.org; Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Lee, William T (HEALTH); tcs38@psu.edu; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Marc L Salit (msalit@stanford.edu); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu);

wilsonp@uchicago.edu; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); rbaric (rbaric@email.unc.edu); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); Theodora Hatziioannou; jakim; Donis, Ruben (OS/ASPR/BARDA); renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; viviana.simon; pintol; kemptj; Cassels, Fred; Sabourin, Carol (OS/ASPR/BARDA); Yusibov, Vidadi (OS/ASPR/BARDA); Iturriza-Gomara, Miren; david.montefiori@duke.edu; sujan@lji.org; Camille Escadafal

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela

Sent: Sun 1/24/2021 4:00:33 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Please note this meeting will be 1.5hrs instead of the usual one hour to allow for an additional presentation and discussion on the new variant.

Agenda to follow.

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Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute; alain.townsend (alain.townsend@imm.ox.ac.uk)

Sent: Sun 2/7/2021 1:27:14 PM (UTC-06:00)

Subject: WHO Working Group on COVID-19 Assays

Dear All,

Please find below the agenda and call-in information for this week's WHO working group on COVID-19 assays group call.

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays group call Wednesday February 10 2:30PM CET (Geneva Time)

1. Alain Townsend (University of Oxford)- *A haemagglutination test for rapid detection of antibodies to SARS-CoV-2*
2. David Montefiori (Duke) - *SARS-CoV-2 variant B.1.1.7 is susceptible to neutralizing antibodies elicited by ancestral Spike vaccines*

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; GILBERT Nick; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

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Meeting ID: 361 256 8290

From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: Alter, Galit; Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); dbarouch (dbarouch@bidmc.harvard.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk); fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); Daniel Cohen (dancohen@tauex.tau.ac.il); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); GILBERT Nick; Goldblatt, David; guy.gorochov@sorbonne-universite.fr; Graham, Barney (NIH/VRC) [E]; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; Hyde, Terri (CDC/DDPHSIS/CGH/GID); IRAHETA SIGUENZA, Raul Emilio; REIRELAND (REIRELAND@mail.dstl.gov.uk); ASiyer@mgh.harvard.edu; Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); Krause, Philip; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); Lee, William T (HEALTH); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); jma; MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); McElrath MD PhD, Julie; gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Liz Miller (Liz.Miller@lshtm.ac.uk); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; pennym@nicd.ac.za; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); qiang.pan-hammarstrom@ki.se; Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Perlman, Stanley; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Jilian Sacks (Jilian.sacks@finddx.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; Shi, Pei yong; Shivji Ragini (Ragini.Shivji@ema.europa.eu); sujan@lji.org; Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; alex.sigal@ahri.org; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; tomwhite42450@gmail.com; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org);

zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; diane.descamps@aphp.fr; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); SALAMI, Kolawole; tcs38@psu.edu; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); BUDA Mihaela; Kelvin, Alyson; STRÖHER, Ute

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak (daszak@ecohealthalliance.org); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; Kemp, Troy (NIH/NCI) [C]; Pinto, Ligia (NIH/NCI) [C]

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); florian.krammer (florian.krammer@mssm.edu); Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: alex.sigal@ahri.org; rawcraig@yahoo.com; Karl.Erlandson (Karl.Erlandson@hhs.gov); Jayashankar, Lakshmi (OS/ASPR/BARDA); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); Little, James (OS/ASPR/BARDA); Smith, Ashley (OS/ASPR/BARDA); Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Griffiths, Anthony; Javier Castillo-Olivares Pallardo; SGalloway@cdc.gov; lny1@cdc.gov; Wentworth, David E. (CDC/OID/NCIRD); mbo2@cdc.gov; sot1@cdc.gov; Angeliki Melidou (angeliki.melidou@ecdc.europa.eu); liyl (liyl@cde.org.cn); liub (liub@cde.org.cn); zuz4 (zuz4@cdc.gov); Coughlin, Melissa (CDC/DDID/NCIRD/DVD); Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); bhx1 (bhx1@cdc.gov); ilj2 (ilj2@cdc.gov); Helfand, Rita (CDC/DDID/NCEZID/OD); Hyde, Terri (CDC/DDPHSIS/CGH/GID); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); valentina.bernasconi@cepi.net; Carolyn Clark (carolyn.clark@cepi.net); William Dowling (william.dowling@cepi.net); elwyn.griffiths@cepi.net; Celine Gurry (Celine.gurry@cepi.net); johan.holst@cepi.net; Arun Kumar (arun.kumar@cepi.net); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); solomon.yimer@cepi.net; christian.drosten (christian.drosten@charite.de); Chu, May; Vasan, Vasan (H&B, Geelong ACDP); eric.vangieson@darpa.mil; REIRELAND (REIRELAND@mail.dstl.gov.uk); MSLEVER (MSLEVER@dstl.gov.uk); MNELSON (MNELSON@dstl.gov.uk); JLPRIOR (JLPRIOR@dstl.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); georgia.tomaras (georgia.tomaras@duke.edu); david.montefiori@duke.edu; Sarah Mudrak, Ph.D.; linfa.wang (linfa.wang@duke-nus.edu.sg); Eeva Broberg (Eeva.Broberg@ecdc.europa.eu); epstein@ecohealthalliance.org; Peter Daszak; Emmanuelle Charton (emmanuelle.charton@edqm.eu); Mihaela BUDA; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Shivji Ragini (Ragini.Shivji@ema.europa.eu); B.L. Haagmans (b.haagmans@erasmusmc.nl); M.P.G. Koopmans (m.koopmans@erasmusmc.nl); n.okba@erasmusmc.nl; Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); Krause, Philip; MacGill, Tracy; Myers, Todd; Peden, Keith; Weir, Jerry P.; Jilian Sacks (Jilian.sacks@finddx.org); McElrath MD PhD, Julie; tlying (tlying@fudan.edu.cn); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); Karen Makar (Karen.Makar@gatesfoundation.org); David Vaughn (David.Vaughn@gatesfoundation.org); cheryl (cheryl@gisaid.org); christian.brechot (christian.brechot@pasteur.fr); dbarouch (dbarouch@bidmc.harvard.edu); Vandenberghe, Luk; ASiyer@mgh.harvard.edu; Maria Baca Estrada (maria.baca-estrada@canada.ca); jason.fernandes@canada.ca; mireille.plamondon@canada.ca; malik (malik@hku.hk); r.tedder@imperial.ac.uk; Vidadi Yusibov (vyusibov@indianabiosciences.org); guy.gorochov@sorbonne-universite.fr; Sylvie VAN DER WERF; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); Jae Ouk Kim (jokim@ivi.int); Manki Song (mksong@ivi.int); qiang.pan-hammarstrom@ki.se; katie.doores (katie.doores@kcl.ac.uk); leejooyeon (leejooyeon@korea.kr); limhy0919 (limhy0919@korea.kr); shane@lji.org; erica (erica@lji.org); Sharon Schendel (schendel@lji.org); alex@lji.org; sujan@lji.org; daniela@lji.org; Liz Miller (Liz.Miller@lshtm.ac.uk); Krammer, Florian; Olinger, Gene; Luc.Gagnon (Luc.Gagnon@nexelis.com); Greg Kulnis (Greg.Kulnis@nexelis.com); brooke.bozick@nih.gov; Degrace, Marciela (NIH/NIAID) [E]; Florence, Clint (NIH/NIAID) [E]; Lathey, Janet (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Wolfraim, Larry (NIH/NIAID) [E]; Crozier, Ian (NIH) [C]; Hensley, Lisa (NIH/NIAID) [E]; Holbrook, Michael (NIH/NIAID) [C]; johnsonreed@niaid.nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; karin.bok (karin.bok@nih.gov); kizzmekia.corbett@nih.gov; Graham, Barney (NIH/VRC) [E]; adrian.mcdermott (adrian.mcdermott@nih.gov); kaitlyn.dambach@nih.gov; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); Philip Minor (Philip.Minor2@gmail.com); Clare.Morris@nibsc.org; Mark Page (Mark.Page@nibsc.org); Nicola Rose (Nicola.Rose@nibsc.org); pennym@nicd.ac.za; changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); xumiaobj (xumiaobj@126.com); pilailuk.o (pilailuk.o@dmsc.mail.go.th); baihe (baihe@nmpa.gov.cn); Lee, William T (HEALTH); Boyle, David; de los Santos, Tala; Leader, Troy; Barbara.Schnierle (Barbara.Schnierle@pei.de); tcs38@psu.edu; Christine Bruce (Christine.bruce@phe.gov.uk); Miles.Carroll (Miles.Carroll@phe.gov.uk); Simon Funnell (simon.funnell@phe.gov.uk); Julia Tree (Julia.Tree@phe.gov.uk); Mary.Matheson@phe.gov.uk; Alter, Galit; tomwhite42450@gmail.com; pbieniasz@mail.rockefeller.edu; Daniel Cohen (dancohen@tauex.tau.ac.il); Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); jma; Marc L Salit (msalit@stanford.edu); pawinee.k@redcross.or.th; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); gmedigeshi (gmedigeshi@thsti.res.in); gweiss@uci.edu; arimoin (arimoin@g.ucla.edu); jmclellan (jmclellan@austin.utexas.edu); wilsonp@uchicago.edu; GILBERT Nick; diane.descamps@aphp.fr; Goldblatt, David; Perlman, Stanley; Frieman, Matthew; mit666666 (mit666666@pitt.edu); jwm1 (jwm1@pitt.edu); Kelvin, Alyson; rbaric (rbaric@email.unc.edu); Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); ydm9@cdc.gov; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); Shi, Pei yong; Falzarano, Darryl; Volker.gerdts (Volker.gerdts@usask.ca); Hodgson, Paul; scott.napper (scott.napper@usask.ca); tracey.thue (tracey.thue@usask.ca); Lisa@amicitiam.com; PNorris@vitalant.org; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Shelly Krebs (skrebs@hivresearch.org); Kayvon Modjarrad (kmodjarrad@eidresearch.org); sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); PScott (PScott@eidresearch.org); COSTA, Alejandro Javier; HENAO RESTREPO, Ana Maria; MORGAN, Oliver;

PERKINS, Mark; RIVEROS BALTA, Ximena; SATHIYAMOORTHY, Vaseeharan; YOO, Si Hyung; SUBISSI, Lorenzo; David Wood (dj56wood@gmail.com); ZHOU, Tiequn; SALAMI, Kolawole; STRÖHER, Ute; SANDS, Anita; BRANGEL, Polina; IRAHETA SIGUENZA, Raul Emilio; KNEZEVIC, Ivana; SWAMINATHAN, Soumya; zlshi (zlshi@wh.iov.cn); Youngmee Jee (jeey62@gmail.com); ramadany; Theodora Hatziioannou; Manuel Antonio Franco Cortes (mafranco@javeriana.edu.co); KAZI, Fatema; jakim; Donis, Ruben (OS/ASPR/BARDA); alankhoo.imr; a.luttick; renuka.kumar; melanie.ott; arjun.rustagi; sastanley; Pillai, Satish; joe; raul.andino; charles.chiu; GSimmons; Chris Miller (cjmiller@ucdavis.edu); MaryKate.Morris; amy.kistler; cblish; bertozzi; tdcarroll; douglas_fox; Wadford, Debra@CDPH; Carl.Hanson; t.desilva; Lance.Turtle; susie.dunachie; paul.klenerman; ellie.barnes; william.james; Meera.Chand; Victoria.Hall; KurtW; Aodhan.Breathnach; alain.townsend (alain.townsend@imm.ox.ac.uk); viviana.simon; pintol; kemptj; Jacqueline.Fryer; Kevin Bewley (Kevin.bewley@phe.gov.uk)

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From: SCHWARTZ, Lauren[schwartzl@who.int]

Attendees: SCHWARTZ, Lauren; galter@partners.org; maria.baca-estrada@canada.ca; baihe@nmpa.gov.cn; rbaric@email.unc.edu; cheryl@gisaid.org; valentina.bernasconi@cepi.net; shinjini.bhatnagar@thsti.res.in; pbieniasz@mail.rockefeller.edu; karin.bok@nih.gov; dboyle@path.org; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot@pasteur.fr; Christine.bruce@phe.gov.uk; zuz4@cdc.gov; Miles.Carroll@phe.gov.uk; fjc37@cam.ac.uk; Marco.Cavaleri@ema.europa.eu; MONALISA.CHATTERJI@gatesfoundation.org; MAY.CHU@CUANSCHUTZ.EDU; carolyn.clark@cepi.net; kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; htq4@cdc.gov; shane@lji.org; ian.crozier@nih.gov; lad7@cdc.gov; Lisa@amicitiam.com; daszak@ecohealthalliance.org; tdelossantos@path.org; emmie.dewit@nih.gov; marciela.degrace@nih.gov; rafael.delgado@salud.madrid.org; mit666666@pitt.edu; katie.doores@kcl.ac.uk; william.dowling@cepi.net; christian.drosten@charite.de; epstein@ecohealthalliance.org; Karl.Erlandson@hhs.gov; darryl.falzarano@usask.ca; jason.fernandes@canada.ca; clint.florence@nih.gov; MFrieman@som.umaryland.edu; Simon.Funnell@phe.gov.uk; Luc.Gagnon@nexelis.com; Mayra.Garcia@fda.hhs.gov; bhx1@cdc.gov; Volker.gerdts@usask.ca; d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; ahgriff@bu.edu; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ@mail.mil; celine.gurry@cepi.net; ilj2@cdc.gov; b.haagmans@erasmusmc.nl; rzh7@cdc.gov; HENAO RESTREPO, Ana Maria; lisa.hensley@nih.gov; paul.hodgson@usask.ca; Michael.holbrook@nih.gov; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND@mail.dstl.gov.uk; Lakshmi.Jayashankar@hhs.gov; djernigan@cdc.gov; johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline.Kirchner@gatesfoundation.org; KNEZEVIC, Ivana; m.koopmans@erasmusmc.nl; Gerald.Kovacs@hhs.gov; florian.krammer@mssm.edu; Philip.Krause@fda.hhs.gov; skrebs@hivresearch.org; Greg.Kulnis@nexelis.com; arun.kumar@cepi.net; pawinee.k@redcross.or.th; teresa.lambe@ndm.ox.ac.uk; janet.lathey@nih.gov; bleader@path.org; leejooyeon@korea.kr; MSLEVER@dstl.gov.uk; liyl@cde.org.cn; changguili@aliyun.com; lyhchengdu@163.com; limhy0919@korea.kr; James.Little@hhs.gov; liub@cde.org.cn; Tracy.MacGill@fda.hhs.gov; Karen.Makar@gatesfoundation.org; Mary.Matheson@phe.gov.uk; Giada.Mattiuzzo@nibsc.org; jmclellan@austin.utexas.edu; adrian.mcdermott@nih.gov; jmcelrat@fredhutch.org; gmedigeshi@thsti.res.in; jwm1@pitt.edu; philip.minor2@gmail.com; kmodjarrad@eidresearch.org; david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; sarah.mudrak@duke.edu; munoz-fontela@bnitm.de; vincent.munster@nih.gov; Todd.Myers@fda.hhs.gov; aysegul.nalca.civ@mail.mil; scott.napper@usask.ca; MNELSON@dstl.gov.uk; PNorris@vitalant.org; pilailuk.o@dmsc.mail.go.th; n.okba@erasmusmc.nl; golinger@MRIGLOBAL.ORG; jokim@ivi.int; Mark.Page@nibsc.org; gustavo.f.palacios.civ@mail.mil; map1@cdc.gov; xdv3@cdc.gov; Keith.Peden@fda.hhs.gov; sheila.a.peel2.civ@mail.mil; malik@hku.hk; PERKINS, Mark; supaporn.p@dmsc.mail.go.th; margaret.l.pitt.civ@mail.mil; mireille.plamondon@canada.ca; JLPRIOR@dstl.gov.uk; arimoin@g.ucla.edu; RIVEROS BALTA, Ximena; Nicola.Rose@nibsc.org; msalit@stanford.edu; erica@lji.org; SATHIYAMOORTHY, Vaseeharan; schendel@lji.org; connie.schmaljohn@nih.gov; Barbara.Schnierle@pei.de; PScott@eidresearch.org; alex@lji.org; peshi@UTMB.EDU; Ragini.Shivji@ema.europa.eu; amy.c.shurtleff@cepi.net; YOO, Si Hyung; Ashley.Smith1@hhs.gov; mksong@ivi.int; erik.stemmy@nih.gov; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; nax3@cdc.gov; tracey.thue@usask.ca; georgia.tomaras@duke.edu; Julia.Tree@phe.gov.uk; john.c.trefry.civ@mail.mil; luk_vandenberghe@meei.harvard.edu; sylvie.van-der-werf@pasteur.fr; eric.vangieson@darpa.mil; Vasan.Vasan@csiro.au; y.m.vasiliev@spbniivs.ru; David.Vaughn@gatesfoundation.org; linfa.wang@duke-nus.edu.sg; wangjz@nifdc.org.cn; wangyc@nifdc.org.cn; Jerry.Weir@fda.hhs.gov; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; larry.wolfraim@nih.gov; dj56wood@gmail.com; xumiaobj@126.com; solomon.yimer@cepi.net; tlying@fudan.edu.cn; vyusibov@indianabiosciences.org; zlshi@wh.iov.cn; ZHOU, Tiequn; william.lee@health.ny.gov; ASiyer@mgh.harvard.edu; Nick.Gilbert@ed.ac.uk; Jilian.Sacks@finddx.org; jma@sgul.ac.uk; sujan@lji.org; dbarouch@bidmc.harvard.edu; qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz.Miller@lshtm.ac.uk; emmanuelle.charton@edqm.eu; stanley-perlman@uiowa.edu; Javier Castillo-Olivares Pallardo; Carolyn Clark; Griffiths, Anthony; Alter, Galit; BUDA Mihaela; PAVLIN, Boris; Brys, April (OS/ASPR/BARDA); Malkevich, Nina (OS/ASPR/BARDA) (CTR); Yates, Jennifer L (HEALTH)

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Start Time: Wed 1/6/2021 7:30:00 AM (UTC-06:00)

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Required Attendees: SCHWARTZ, Lauren; galter (galter@partners.org); Maria Baca Estrada (maria.baca-estrada@canada.ca); baihe (baihe@nmpa.gov.cn); rbaric (rbaric@email.unc.edu); cheryl (cheryl@gisaid.org); valentina.bernasconi@cepi.net; shinjini.bhatnagar (shinjini.bhatnagar@thsti.res.in); pbieniasz@mail.rockefeller.edu; karin.bok (karin.bok@nih.gov); Boyle, David; brooke.bozick@nih.gov; BRANGEL, Polina; christian.brechot (christian.brechot@pasteur.fr); Christine Bruce (Christine.bruce@phe.gov.uk); zuz4 (zuz4@cdc.gov); Miles.Carroll (Miles.Carroll@phe.gov.uk);

fjc37@cam.ac.uk; Cavaleri Marco (Marco.Cavaleri@ema.europa.eu); Monalisa Chatterji (MONALISA.CHATTERJI@gatesfoundation.org); Chu, May; Carolyn Clark (carolyn.clark@cepi.net); kizzmekia.corbett@nih.gov; COSTA, Alejandro Javier; Coughlin, Melissa (CDC/DDID/NCIRD/DVD); shane@lji.org; ian.crozier@nih.gov; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP); Lisa@amicitiam.com; Peter Daszak (daszak@ecohealthalliance.org); de los Santos, Tala; De wit, Emmie (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; Delgado Vazquez.Rafael (rafael.delgado@salud.madrid.org); mit666666 (mit666666@pitt.edu); katie.doores (katie.doores@kcl.ac.uk); William Dowling (william.dowling@cepi.net); christian.drosten (christian.drosten@charite.de); epstein@ecohealthalliance.org; Karl.Erlandson (Karl.Erlandson@hhs.gov); Falzarano, Darryl; jason.fernandes@canada.ca; Florence, Clint (NIH/NIAID) [E]; Frieman, Matthew; Simon Funnell (simon.funnell@phe.gov.uk); Luc.Gagnon (Luc.Gagnon@nexelis.com); Mayra.Garcia (Mayra.Garcia@fda.hhs.gov); bhx1 (bhx1@cdc.gov); Volker.gerdts (Volker.gerdts@usask.ca); d.goldblatt@ucl.ac.uk; guy.gorochov@sorbonne-universite.fr; barney.graham@nih.gov; Griffiths, Anthony; elwyn.griffiths@cepi.net; gregory.d.gromowski.civ (gregory.d.gromowski.civ@mail.mil); Celine Gurry (Celine.gurry@cepi.net); ilj2 (ilj2@cdc.gov); B.L. Haagmans (b.haagmans@erasmusmc.nl); Helfand, Rita (CDC/DDID/NCEZID/OD); HENAO RESTREPO, Ana Maria; Hensley, Lisa (NIH/NIAID) [E]; Hodgson, Paul; Holbrook, Michael (NIH/NIAID) [C]; johan.holst@cepi.net; rawcraig@yahoo.com; tkh4@cdc.gov; REIRELAND (REIRELAND@mail.dstl.gov.uk); Jayashankar, Lakshmi (OS/ASPR/BARDA); Jernigan, Daniel B. (CDC/DDID/NCIRD/ID); johnsonreed@niaid.nih.gov; ydm9@cdc.gov; Jacqueline Kirchner (Jacqueline.Kirchner@gatesfoundation.org); KNEZEVIC, Ivana; M.P.G. Koopmans (m.koopmans@erasmusmc.nl); Kovacs, Gerald (OS/ASPR/BARDA) (CTR); florian.krammer (florian.krammer@mssm.edu); philip.krause@fda.hhs.gov; Shelly Krebs (skrebs@hivresearch.org); Greg Kulnis (Greg.Kulnis@nexelis.com); Arun Kumar (arun.kumar@cepi.net); pawinee.k@redcross.or.th; Teresa Lambe (teresa.lambe@ndm.ox.ac.uk); Lathey, Janet (NIH/NIAID) [E]; Leader, Troy; leejooyeon (leejooyeon@korea.kr); MSLEVER (MSLEVER@dstl.gov.uk); liyl (liyl@cde.org.cn); changguili (changguili@aliyun.com); lyhchengdu (lyhchengdu@163.com); limhy0919 (limhy0919@korea.kr); Little, James (OS/ASPR/BARDA); liub (liub@cde.org.cn); MacGill, Tracy; Karen Makar (Karen.Makar@gatesfoundation.org); Mary.Matheson@phe.gov.uk; Giada Mattiuzzo (Giada.Mattiuzzo@nibsc.org); jmclellan (jmclellan@austin.utexas.edu); adrian.mcdermott (adrian.mcdermott@nih.gov); jmcelrat (jmcelrat@fredhutch.org); gmedigeshi (gmedigeshi@thsti.res.in); jwm1 (jwm1@pitt.edu); Philip Minor (Philip.Minor2@gmail.com); Kayvon Modjarrad (kmodjarrad@eidresearch.org); david.montefiori@duke.edu; kaitlyn.dambach@nih.gov; MORGAN, Oliver; Clare.Morris@nibsc.org; Sarah Mudrak, Ph.D.; Cesar Munoz-Fontela (munoz-fontela@bnitm.de); Munster, Vincent (NIH/NIAID) [E]; Myers, Todd; aysegul.nalca.civ (aysegul.nalca.civ@mail.mil); scott.napper (scott.napper@usask.ca); MNELSON (MNELSON@dstl.gov.uk); PNorris@vitalant.org; pilailuk.o (pilailuk.o@dmsc.mail.go.th); n.okba@erasmusmc.nl; Olinger, Gene; Jae Ouk Kim (jokim@ivi.int); Mark Page (Mark.Page@nibsc.org); gustavo.f.palacios.civ (gustavo.f.palacios.civ@mail.mil); Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); Panayampalli, Subbian Satheshkumar (CDC/DDID/NCEZID/DHCPP); Peden, Keith; sheila.a.peel2.civ (sheila.a.peel2.civ@mail.mil); malik (malik@hku.hk); PERKINS, Mark; Supaporn Phumiamorn (supaporn.p@dmsc.mail.go.th); margaret.l.pitt.civ (margaret.l.pitt.civ@mail.mil); mireille.plamondon@canada.ca; JLPRIOR (JLPRIOR@dstl.gov.uk); arimoin (arimoin@g.ucla.edu); RIVEROS BALTA, Ximena; Nicola Rose (Nicola.Rose@nibsc.org); Marc L Salit (msalit@stanford.edu); erica (erica@lji.org); SATHIYAMOORTHY, Vaseeharan; Sharon Schendel (schendel@lji.org); Schmaljohn, Connie (NIH/NIAID) [E]; Barbara.Schnierle (Barbara.Schnierle@pei.de); PScott (PScott@eidresearch.org); alex@lji.org; peshi@UTMB.EDU; Shivji Ragini (Ragini.Shivji@ema.europa.eu); Amy C. Shurtleff (amy.c.shurtleff@cepi.net); YOO, Si Hyung; Smith, Ashley (OS/ASPR/BARDA); Manki Song (mksong@ivi.int); Stemmy, Erik (NIH/NIAID) [E]; SUBISSI, Lorenzo; SWAMINATHAN, Soumya; r.tedder@imperial.ac.uk; Thornburg, Natalie (CDC/DDID/NCIRD/DVD); tracey.thue (tracey.thue@usask.ca); georgia.tomaras (georgia.tomaras@duke.edu); Julia Tree (Julia.Tree@phe.gov.uk); john.c.trefry.civ (john.c.trefry.civ@mail.mil); luk_vandenberghe (luk_vandenberghe@meei.harvard.edu); sylvie.van-der-werf (sylvie.van-der-werf@pasteur.fr); eric.vangieson@darpa.mil; Vasan, Vasan (H&B, Geelong ACDP); Васильев Юрий Михайлович (y.m.vasiliev@spbniivs.ru); David Vaughn (David.Vaughn@gatesfoundation.org); linfa.wang (linfa.wang@duke-nus.edu.sg); wangjz (wangjz@nifdc.org.cn); wangyc (wangyc@nifdc.org.cn); Weir, Jerry P.; gweiss@uci.edu; daniela@lji.org; wilsonp@uchicago.edu; Wolfraim, Larry (NIH/NIAID) [E]; David Wood (dj56wood@gmail.com); xumiaobj (xumiaobj@126.com); solomon.yimer@cepi.net; tlying (tlying@fudan.edu.cn); Vidadi Yusibov (vyusibov@indianabiosciences.org); zlshi (zlshi@wh.iov.cn); ZHOU, Tiequn; Lee, William T (HEALTH); ASiyer@mgh.harvard.edu; GILBERT Nick; Jilian Sacks (Jilian.sacks@finddx.org); jma@sgul.ac.uk; sujan@lji.org; dbarouch (dbarouch@bidmc.harvard.edu); qiang.pan-hammarstrom@ki.se; tomwhite42450@gmail.com; Liz Miller (Liz.Miller@lshtm.ac.uk); Emmanuelle Charton (emmanuelle.charton@edqm.eu); Perlman, Stanley

Agenda to follow.

Join Zoom Meeting

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- +1 267 831 0333 US (Philadelphia)
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115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
149.137.40.110 (Singapore)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)
Meeting ID: 361 256 8290

Dear All,

Please find below the agenda for our group call on Wednesday January 6, 2021 at 2:30PM CET (Geneva time).

Best,
Lauren - Bill, Simon and César

Agenda for WHO working group on COVID-19 assays

1. Kevin McCarthy and Paul Duprex (University of Pittsburgh)- *Natural deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape*
2. Discussion on the UK variant

To: Shi, Pei yong[peshi@UTMB.EDU]
From: 钟有权[2019203010049@whu.edu.cn]
Sent: Tue 5/26/2020 4:56:22 AM (UTC-05:00)
Subject: Dengue NS2A Protein Orchestrates Virus Assembly

尊敬的老师：

您好！我是武汉大学的钟有权，最近在阅读您发表的文章"Dengue NS2A Protein Orchestrates Virus Assembly"发现，文末提供的补充材料链接是原文PDF的链接，并不是补充材料的链接。所以我想问问您方便提供补充材料的链接吗？

冒昧致信，恳请海涵，感谢老师能在百忙之中阅读我的邮件。

敬颂

时安

学生：钟有权

To: Ong Xin Mei[xinmei_ong@duke-nus.edu.sg]; Plante, Kenneth S.[ksplante@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Plante, Jessica A.[japlante@UTMB.EDU]
Cc: Kong Pui San[puisan.kong@duke-nus.edu.sg]
From: Blakeman, David S.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=626EE7FACBBC4914A070FEC442B29F1C-BLAKEMAN, D]
Sent: Tue 6/30/2020 12:10:44 PM (UTC-05:00)
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hello Xin Mei,

I just wanted to point out that these materials have to be shipped with a CITES permit due to the fact that the virus is grown on Vero cells. I already have the permit on my end, but you might also have to apply for this permit to be able to receive.

Can you please check with your customs office to verify?

The package will be picked up at my office location:

David Blakeman
1302 Mechanic Street
Galveston TX, 77555
552.117

Thanks,
David

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Tuesday, June 30, 2020 11:00 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>; Plante, Jessica A. <japlante@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Dear Dr Plante,

Kindly find attached fully executed MTA for the transfer.

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Plante, Kenneth S." <ksplante@UTMB.EDU>
Date: Tuesday, 30 June 2020 at 11:45 PM
To: "Shi, Pei yong" <peshi@UTMB.EDU>, Wang Linfa <linfa.wang@duke-nus.edu.sg>, Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Jessica A." <japlante@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

- External Email -

Ok then, that is a little easier. We are likely 10 or so days from a production lot of virus being ready as we have to amplify up our cells.

Thanks

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
Department of Microbiology and Immunology
University of Texas Medical Branch
301 University Blvd. Rte. 0609
Galveston, TX 77555
O-(409) 747-2432
C-(978) 726-1697
F-(409) 747-2429
https://www.utmb.edu/wrceva/

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, June 30, 2020 10:41 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hi Ken,
The MTA for this request has already been executed. Sorry I should have mentioned to you earlier.

Hi Xin Mei,
Could you email Ken the fully executed MTA? Thanks!

Cheers,

- Pei-Yong

From: Plante, Kenneth S. <ksplante@UTMB.EDU>
Sent: Tuesday, June 30, 2020 10:37 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

I can start the MTA process and wait until I have Nano-luc ready to go before I ship.

Let me know.

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
Department of Microbiology and Immunology

University of Texas Medical Branch
301 University Blvd. Rte. 0609
Galveston, TX 77555
O-(409) 747-2432
C-(978) 726-1697
F-(409) 747-2429
https://www.utmb.edu/wrceva/

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Tuesday, June 30, 2020 2:10 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Dear Ken and Pei-Yong,

0.5 ml is sufficient.

For Nano luciferase reporter, any chance to send us a small aliquot as well? I know that you are in the process of setting up a formal depository, but for us to get two import shipments, there is a lot more effort involved. So it will be greatly appreciated if we can have both shipped at your earliest convenience.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Plante, Kenneth S. <ksplante@UTMB.EDU>
Sent: Tuesday, 30 June 2020 2:32 AM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Hello,

A couple of things,

we can send you the SARS-CoV-2mNG, but we will only be able to send you (2) 0.5ml aliquots. This should be more then enough for you to grow massive working stocks. We use 100ul these stocks to infect a t-850 rolling bottle and produce 220ml of virus.

We are in the process of depositing the Nano luciferase reporter currently.

The RFP is still in development and will be unavailable for some time.

Do you want me to start that process now?

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
Department of Microbiology and Immunology
University of Texas Medical Branch
301 University Blvd. Rte. 0609
Galveston, TX 77555
O-(409) 747-2432
C-(978) 726-1697
F-(409) 747-2429
https://www.utmb.edu/wrceva/

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Monday, June 29, 2020 7:55 AM
To: Blakeman, David S. <dsblakem@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Dear David and Dr Plante,

May we also get your assistance to confirm the details and insert the institution's letterhead for the declaration letter attached?

We will be submitting this to apply for import permit from relevant authorities.

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Shi, Pei yong" <peshi@UTMB.EDU>
Date: Monday, 29 June 2020 at 8:06 PM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Kenneth S." <ksplante@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>, Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hi David,
We are shipping the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility through Ken's World Reference Centre. The Singapore receiver is arranging courier for the shipment. Could you help them with the question?

Hi Xin Mei,
Dr. Ken Plante (cc'd) from the World Reference will lead the shipment arrangement from UTMB side.

Thanks!

- Pei-Yong

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Monday, June 29, 2020 3:53 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Transfer of SARS-CoV-2 reporter virus

Dear Prof Shi,

This is Xin Mei from Prof Wang Linfa's lab at Duke-NUS Medical School.

We are currently arranging for the transfer of the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility. May we confirm that the following is the full address for pick up by the courier company and if there is a contact person we can liaise with for the transfer?

Pick up address for courier company:
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

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Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

To: Shi, Pei yong[peshi@UTMB.EDU]
Cc: Ong Xin Mei[xinmei_ong@duke-nus.edu.sg]; Kong Pui San[puisan.kong@duke-nus.edu.sg]
From: Wang Linfa[linfa.wang@duke-nus.edu.sg]
Sent: Mon 6/29/2020 7:10:11 AM (UTC-05:00)
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Thanks a lot!

Sent from my iPhone

On 29 Jun 2020, at 8:08 PM, Shi, Pei yong <peshi@utmb.edu> wrote:

Hi Linfa,
No worries. I will arrange from our side.
I will catch up with you when things become clear from my side.
Best,

- Pei-Yong

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Monday, June 29, 2020 4:54 AM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Thanks Xin Mei.

Dear Pei-Yong,
Sorry it took much longer than I wanted, but that is the "norm" we all face.
It will be appreciated if you (or your lab manager) can assist us to speed up the shipment.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Monday, 29 June 2020 4:53 PM

To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Transfer of SARS-CoV-2 reporter virus

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Pick up address for courier company:
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

To: Blakeman, David S.[dsblakem@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Plante, Jessica A.[japlante@UTMB.EDU]
Cc: Kong Pui San[puisan.kong@duke-nus.edu.sg]
From: Ong Xin Mei[xinmei_ong@duke-nus.edu.sg]
Sent: Wed 7/1/2020 1:54:05 AM (UTC-05:00)
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Dear David,

Noted that a CITES permit may be required, we will verify with the customs on our end. Thanks for highlighting that to us!

Best regards,
Xin Mei

From: "Blakeman, David S." <dsblakem@UTMB.EDU>
Date: Wednesday, 1 July 2020 at 1:10 AM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Plante, Kenneth S." <ksplante@UTMB.EDU>, "Shi, Pei yong" <peshi@UTMB.EDU>, Wang Linfa <linfa.wang@duke-nus.edu.sg>, "Plante, Jessica A." <japlante@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hello Xin Mei,

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Can you please check with your customs office to verify?

The package will be picked up at my office location:

David Blakeman
1302 Mechanic Street
Galveston TX, 77555
409 682 2874

Thanks,
David

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Tuesday, June 30, 2020 11:00 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>; Plante, Jessica A. <japlante@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Dear Dr Plante,

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Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Plante, Kenneth S." <ksplante@UTMB.EDU>
Date: Tuesday, 30 June 2020 at 11:45 PM
To: "Shi, Pei yong" <peshi@UTMB.EDU>, Wang Linfa <linfa.wang@duke-nus.edu.sg>, Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Jessica A." <japlante@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

Ok then, that is a little easier. We are likely 10 or so days from a production lot of virus being ready as we have to amplify up our cells.

Thanks

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
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Galveston, TX 77555
O-(409) 747-2432
C-(978) 726-1697
F-(409) 747-2429
https://www.utmb.edu/wrceva/

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, June 30, 2020 10:41 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Wang Linfa <linfa.wang@duke-nus.edu.sg>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hi Ken,
The MTA for this request has already been executed. Sorry I should have mentioned to you earlier.

Hi Xin Mei,
Could you email Ken the fully executed MTA? Thanks!

Cheers,

- Pei-Yong

From: Plante, Kenneth S. <ksplante@UTMB.EDU>
Sent: Tuesday, June 30, 2020 10:37 AM
To: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: Re: Transfer of SARS-CoV-2 reporter virus

I can start the MTA process and wait until I have Nano-luc ready to go before I ship.

Let me know.

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
Department of Microbiology and Immunology
University of Texas Medical Branch
301 University Blvd. Rte. 0609
Galveston, TX 77555
O-(409) 747-2432
C-(978) 726-1697
F-(409) 747-2429
https://www.utmb.edu/wrceva/

From: Wang Linfa <linfa.wang@duke-nus.edu.sg>
Sent: Tuesday, June 30, 2020 2:10 AM
To: Plante, Kenneth S. <ksplante@UTMB.EDU>; Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Dear Ken and Pei-Yong,

0.5 ml is sufficient.

For Nano luciferase reporter, any chance to send us a small aliquot as well? I know that you are in the process of setting up a formal depository, but for us to get two import shipments, there is a lot more effort involved. So it will be greatly appreciated if we can have both shipped at your earliest convenience.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Plante, Kenneth S. <ksplante@UTMB.EDU>
Sent: Tuesday, 30 June 2020 2:32 AM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>; Blakeman, David S. <dsblakem@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>
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Dear David and Dr Plante,

May we also get your assistance to confirm the details and insert the institution's letterhead for the declaration letter attached?

We will be submitting this to apply for import permit from relevant authorities.

Thank you.

Best regards,

Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Shi, Pei yong" <peshi@UTMB.EDU>
Date: Monday, 29 June 2020 at 8:06 PM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Kenneth S." <ksplante@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>, Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hi David,
We are shipping the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility through Ken's World Reference Centre. The Singapore receiver is arranging courier for the shipment. Could you help them with the question?

Hi Xin Mei,
Dr. Ken Plante (cc'd) from the World Reference will lead the shipment arrangement from UTMB side.

Thanks!

- Pei-Yong

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Monday, June 29, 2020 3:53 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Transfer of SARS-CoV-2 reporter virus

Dear Prof Shi,

This is Xin Mei from Prof Wang Linfa's lab at Duke-NUS Medical School.

We are currently arranging for the transfer of the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility. May we confirm that the following is the full address for pick up by the courier company and if there is a contact person we can liaise with for the transfer?

Pick up address for courier company:
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

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To: Mark.Mulligan@nyulangone.org[Mark.Mulligan@nyulangone.org]; klyke@som.umaryland.edu[klyke@som.umaryland.edu]; nicholas.kitchin@pfizer.com[nicholas.kitchin@pfizer.com]; judith.absalon@pfizer.com[judith.absalon@pfizer.com]; alejandra.gurtman@pfizer.com[alejandra.gurtman@pfizer.com]; stephen.p.lockhart@pfizer.com[stephen.p.lockhart@pfizer.com]; kneuzil@som.umaryland.edu[kneuzil@som.umaryland.edu]; vanessa.raabe@nyulangone.org[vanessa.raabe@nyulangone.org]; ruth.bailey@pfizer.com[ruth.bailey@pfizer.com]; kena.swanson@pfizer.com[kena.swanson@pfizer.com]; ping.li4@pfizer.com[ping.li4@pfizer.com]; kenneth.koury@pfizer.com[kenneth.koury@pfizer.com]; warren.kalina@pfizer.com[warren.kalina@pfizer.com]; david.cooper1@pfizer.com[david.cooper1@pfizer.com]; Fontes-Garfias, Camila R.[crfontes@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; oezlem.tuereci@biontech.de[oezlem.tuereci@biontech.de]; kristin.tompkins@pfizer.com[kristin.tompkins@pfizer.com]; edward.walsh@rochesterregional.org[edward.walsh@rochesterregional.org]; ann.falsey@rochesterregional.org[ann.falsey@rochesterregional.org]; philip.dormitzer@pfizer.com[philip.dormitzer@pfizer.com]; bill.gruber@pfizer.com[bill.gruber@pfizer.com]; sahin@uni-mainz.de[sahin@uni-mainz.de]; kathrin.jansen@pfizer.com[kathrin.jansen@pfizer.com]; jay.slater@fda.hhs.gov[jay.slater@fda.hhs.gov]; jane.woo@fda.hhs.gov[jane.woo@fda.hhs.gov]; maureen.hess@fda.hhs.gov[maureen.hess@fda.hhs.gov]; Richard.Forshee@fda.hhs.gov[Richard.Forshee@fda.hhs.gov]; Mark.Walderhaug@fda.hhs.gov[Mark.Walderhaug@fda.hhs.gov]; CBER OCOD Consumer Account[cberocod@fda.hhs.gov]; Destefano, Frank (CDC/OID/NCEZID)[fxd1@cdc.gov]; isq8@cdc.gov[isq8@cdc.gov]; nar5@cdc.gov[nar5@cdc.gov]; hjn0@cdc.gov[hjn0@cdc.gov]; Secretary@HHS.gov[Secretary@HHS.gov]; CommissionerFDA@fda.hhs.gov[CommissionerFDA@fda.hhs.gov]; olx1@cdc.gov[olx1@cdc.gov]; directorsincoming@cdc.gov[directorsincoming@cdc.gov]; francis.collins@nih.gov[francis.collins@nih.gov]; mrolfes1@cdc.gov[mrolfes1@cdc.gov]; xzd2@cdc.gov[xzd2@cdc.gov]; acy9@cdc.gov[acy9@cdc.gov]; dbj0@cdc.gov[dbj0@cdc.gov]; jmk9@cdc.gov[jmk9@cdc.gov]; tft9@cdc.gov[tft9@cdc.gov]; gll9@cdc.gov[gll9@cdc.gov]; sharplessne@nih.hhs.gov[sharplessne@nih.hhs.gov]; tnc4@cdc.gov[tnc4@cdc.gov]; kok4@cdc.gov[kok4@cdc.gov]; rxl3@cdc.gov[rxl3@cdc.gov]; gbq7@cdc.gov[gbq7@cdc.gov]; fwf7@cdc.gov[fwf7@cdc.gov]; megan.mcseveney@fda.hhs.gov[megan.mcseveney@fda.hhs.gov]; afauci@niaid.nih.gov[afauci@niaid.nih.gov]; rburke@cdc.gov[rburke@cdc.gov]; hfw3@cdc.gov[hfw3@cdc.gov]; qay0@cdc.gov[qay0@cdc.gov]; hgj0@cdc.gov[hgj0@cdc.gov]; crb5@cdc.gov[crb5@cdc.gov]; jchung@cdc.gov[jchung@cdc.gov]; Konstantin.Chumakov@fda.hhs.gov[Konstantin.Chumakov@fda.hhs.gov]; aul3@cdc.gov[aul3@cdc.gov]; empoweredpatient@cnn.com[empoweredpatient@cnn.com]; munro.peter@abc.net.au[munro.peter@abc.net.au]; beth.mole@arstechnica.com[beth.mole@arstechnica.com]; news@axios.com[news@axios.com]; newswatch@bbc.co.uk[newswatch@bbc.co.uk]; edith.bracho.sanchez@gmail.com[edith.bracho.sanchez@gmail.com]; cnn@cnn.com[cnn@cnn.com]; 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truthometer@politifact.com[truthometer@politifact.com]; skirkey@postmedia.com[skirkey@postmedia.com]; newsroom@prairiemountainmedia.com[newsroom@prairiemountainmedia.com]; smc@sciencemediacentre.org[smc@sciencemediacentre.org]; news@spectrumnews.org[news@spectrumnews.org]; feedback@thetimes.co.uk[feedback@thetimes.co.uk]; cgoodman@sunsentinel.com[cgoodman@sunsentinel.com]; letters@theatlantic.com[letters@theatlantic.com]; info@thebureauinvestigates.com[info@thebureauinvestigates.com]; editor@thehill.com[editor@thehill.com]; letters@time.com[letters@time.com]; press@verywell.com[press@verywell.com]; lena.sun@washpost.com[lena.sun@washpost.com]; mike.agogliati@wfsb.com[mike.agogliati@wfsb.com]; submit@wired.com[submit@wired.com]; fox2newsdesk@foxtv.com[fox2newsdesk@foxtv.com]; betsy.mckay@wsj.com[betsy.mckay@wsj.com]; jodonnel@usatoday.com[jodonnel@usatoday.com]; investigate@ap.org[investigate@ap.org]; editor@bayareanewsgroup.com[editor@bayareanewsgroup.com]; michele.berman@prodigy.net[michele.berman@prodigy.net]; 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From: vinu arumugham[vaccine.safety@aol.com]
Sent: Fri 7/3/2020 1:06:56 AM (UTC-05:00)

Subject: BNT162b1 vaccine development is fundamentally flawed, the trials are invalid and the safety claims are laughable

BNT162b1 vaccine development is fundamentally flawed, the trials are invalid and the safety claims are laughable

Lack of Design for Safety

Vaccines must be designed not developed using trial and error as is the case for BNT162b1. Among the first steps during design is publishing design FMEA (Failure Modes and Effects Analysis). This team has **utterly failed** since there is no FMEA published before going into trial. Without FMEA, a proper trial cannot be designed. All failure modes need to be identified. Only then we can test in the trial if the design has successfully avoided the failure modes.

U.S. Consumer Product Safety Commission (CPSC) says:
"**Design** is the dominant influence on product safety. **Product safety starts in the mind of the product designers.** If all the elements of manufacturing were ranked in order of their potential effect on consumer product safety, **the design function would lead the list**. Additionally, **design importantly affects subsequent decisions** and practices related to materials, production, **testing**, processes, labeling, packaging and distribution."
Vaccine safety: Learning from the Boeing 737 MAX disasters
https://doi.org/10.5281/zenodo.2648251

Lack of testing for de novo IgE synthesis directed against vaccine antigens

The vaccination can result in IgE mediated sensitization to the RBD antigen. The Moderna mRNA vaccine failed by doing exactly that. Causing IgE mediated sensitization directed against the vaccine antigen. 3 of 45 recipients therefore predictably suffered severe allergic reaction following the second dose. A textbook case of sensitization followed by elicitation - a type 1 hypersensitivity reaction. You cannot escape by talking about vaccine antigen dose. Vaccine-induced protection is usually short term. IgE is long-term persistent. So recipients can develop severe COVID-19 due to the allergic reaction since vaccine-induced protection has waned. Exactly same failure as the Dengvaxia disaster. You cannot control the RBD antigen dose during a SARS-CoV-2 infection.

www.statnews.com/2020/05/26/moderna-vaccine-candidate-trial-participant-severe-reaction/

Lack of autoimmune serology

You have not performed autoimmune serology to check for vaccine-induced de novo autoimmune disorders.

You excluded individuals with autoimmune disease (AD)? How did you do that? Obesity is AD. Heart disease is AD. Type 2 diabetes is AD. How did you detect subclinical AD?

Vaccines and Biologics injury table based on mechanistic evidence – Feb 2020 Covering over 125 conditions
https://doi.org/10.5281/zenodo.2582634

The insanity of completely relying on testing

You are insanely relying on testing alone to check for safety problems. You follow-up for 2 months, you MAY catch problems that show up in two months. You test for 2 years, you MAY catch problem for that duration. How do you catch say vaccine-induced type 1 diabetes that shows up after 15 years? Run a trial for 15 years? You should stop this insanity.

The Biontech/Pfizer vaccine development process is fundamentally flawed, the trials are invalid and the safety claims are laughable.
You need to go back to the drawing board. Per CPSC, your vaccine is **UNSAFE BY DEFINITION** because you lacked a design process.
Obviously, having learned **NOTHING** from the Pandemrix induced narcolepsy disaster, you are proceeding at warp speed to create the next humongous disaster.

Pandemrix and Arepanrix vaccine safety analysis and scrutiny fell short

www.bmj.com/content/363/bmj.k4152/rr-14
Pharmacovigilance is no substitute for good vaccine design

www.bmj.com/content/362/bmj.k3948/rr-11

Vinu

To: Plante, Kenneth S.[ksplante@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Wang Linfa[linfa.wang@duke-nus.edu.sg]; Blakeman, David S.[dsblakem@UTMB.EDU]; Plante, Jessica A.[japlante@UTMB.EDU]
Cc: Kong Pui San[puisan.kong@duke-nus.edu.sg]
From: Ong Xin Mei[xinmei_ong@duke-nus.edu.sg]
Sent: Tue 6/30/2020 10:59:53 AM (UTC-05:00)
Subject: Re: Transfer of SARS-CoV-2 reporter virus
Signed MTA.pdf

Dear Dr Plante,

Kindly find attached fully executed MTA for the transfer.

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Plante, Kenneth S." <ksplante@UTMB.EDU>
Date: Tuesday, 30 June 2020 at 11:45 PM
To: "Shi, Pei yong" <peshi@UTMB.EDU>, Wang Linfa <linfa.wang@duke-nus.edu.sg>, Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Jessica A." <japlante@UTMB.EDU>
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Ok then, that is a little easier. We are likely 10 or so days from a production lot of virus being ready as we have to amplify up our cells.

Thanks

Ken

Kenneth Plante PhD.
Associate Director, Curator
World Reference Center for Emerging Viruses and Arboviruses
Department of Microbiology and Immunology
University of Texas Medical Branch
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can have both shipped at your earliest convenience.

Thanks

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

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We will be submitting this to apply for import permit from relevant authorities.

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

From: "Shi, Pei yong" <peshi@UTMB.EDU>
Date: Monday, 29 June 2020 at 8:06 PM
To: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>, "Blakeman, David S." <dsblakem@UTMB.EDU>, "Plante, Kenneth S." <ksplante@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>, Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: RE: Transfer of SARS-CoV-2 reporter virus

Hi David,
We are shipping the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility through Ken's World Reference Centre. The Singapore receiver is arranging courier for the shipment. Could you help them with the question?

Hi Xin Mei,
Dr. Ken Plante (cc'd) from the World Reference will lead the shipment arrangement from UTMB side.

Thanks!

- Pei-Yong

From: Ong Xin Mei <xinmei_ong@duke-nus.edu.sg>
Sent: Monday, June 29, 2020 3:53 AM
To: Shi, Pei yong <peshi@UTMB.EDU>
Cc: Wang Linfa <linfa.wang@duke-nus.edu.sg>; Kong Pui San <puisan.kong@duke-nus.edu.sg>
Subject: Transfer of SARS-CoV-2 reporter virus

Dear Prof Shi,

This is Xin Mei from Prof Wang Linfa's lab at Duke-NUS Medical School.

We are currently arranging for the transfer of the SARS-CoV-2 reporter viruses from UTMB to Duke-NUS BSL3 facility. May we confirm that the following is the full address for pick up by the courier company and if there is a contact person we can liaise with for the transfer?

Pick up address for courier company:
Department of Biochemistry & Molecular Biology
University of Texas Medical Branch
Galveston, Texas 77555

Thank you.

Best regards,
Xin Mei

--
Xin Mei ONG (Ms)
Research Assistant
Programme in Emerging Infectious Diseases
Duke-NUS Medical School
8 College Road, Singapore 169857
Phone: +65 9845 7836
E-mail: xinmei_ong@duke-nus.edu.sg

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P.Y. SHI

MATERIAL TRANSFER AGREEMENT

This Material Transfer Agreement **("Agreement")** is made between The University of Texas Medical Branch at Galveston, d/b/a UTMB Health ("UTMB"), a health institution of The University of Texas System ("System"), an agency of the State of Texas, located at 301 University Blvd., Galveston, TX 77555-0926, and National University of Singapore, a public company limited by guarantee incorporated in Singapore, located at 21 Lower Kent Ridge Road, Singapore 119077, acting through Duke-NUS Medical School (**"Recipient"**).

From the laboratory of Dr. Pei-Yong Shi, **("Provider Scientist")**, UTMB agrees to provide Recipient with certain materials for the purpose stated herein under the following conditions:

Material and Research. The Materials covered by this Agreement includes reagents (mNeonGreen SARS-CoV-2 reporter virus, Nano luciferase SARS-CoV-2 reporter virus, RFP SARS-CoV-2 reporter virus, and other recombinant SARS-CoV-2 Viruses) **("Material")**. The Material shall be used by Recipient in the scope of research **("Research")**, as defined in **Attachment A,** and the Research will be conducted by Recipient under the supervision of Prof WANG Linfa **("Recipient Scientist")**. Recipient shall provide Provider Scientist with a FedEx account number for shipping of the materials requested.

1. **Use of Material.** This Material is made available solely for use in the Research. The Recipient shall not use the Materials or any substance that is replicated or derived therefrom for any commercial purpose, or in the conduct of research that is subject to legal or commercial obligations to another institution, corporation or business entity, unless UTMB provides its prior written consent. The Material shall be used only in laboratory animals or in vitro experiments. The Material shall not be used in humans. The Material is considered proprietary to UTMB. UTMB shall be free, in its sole discretion, to distribute the Material to others and to use it for its own purposes. Except as provided for by this Agreement, Recipient shall not distribute, transfer, or release the Material to any person or entity other than laboratory personnel under Recipient Scientist's direct supervision, unless written permission is obtained from UTMB. Recipient agrees that all of its Recipient Scientist(s) involved in the Research will have read the terms and conditions of this Agreement and shall abide by the terms and conditions of this Agreement.
2. **Rights.** Subject to Section 5. Intellectual Property of this Agreement, Recipient agrees that nothing herein shall be deemed to grant to Recipient or Recipient Scientist any rights under any UTMB patents or any rights to use the Material for any products or processes for any purpose other than performing the Research. Recipient will not use Material for any commercial purposes. Recipient understands that UTMB shall have no obligation to grant a license to Recipient to use Material for commercial purposes, and may grant exclusive or non-exclusive commercial licenses to others, or sell or assign all or part of the rights in the Material to any third party(ies), subject to any pre-existing rights held by others and obligations to the Federal Government.
3. **Confidentiality**. All Material and information relating to the Material that is disclosed by UTMB to Recipient shall be considered to be confidential, subject to Section 4. Publication of this Agreement. Recipient will use reasonable efforts to prevent the disclosure of UTMB's confidential information to third parties for a period of three (3) years from receipt, provided that the Recipient party's obligation shall not apply to information that:
   a) is already in the Recipient's possession at the time of disclosure;
   b) is or later becomes part of the public domain through no fault of the Recipient;
   c) is received from a third party having no obligations of confidentiality to UTMB;
   d) is independently developed by the Recipient; or
   e) is required by law or regulation to be disclosed.

In the event that information is required to be disclosed pursuant to subsection (e), Recipient shall notify the UTMB, in order to allow UTMB to assert whatever exclusions or exemptions may be available to it under such law or regulation.

4. **Publication.** Recipient will inform UTMB of results of Research, in confidence, related to the Material by providing UTMB with a draft manuscript describing such results. If Recipient's Scientist desires to publish or present such Research results, then, not less than forty-five (45) days prior to submission to a third-party, Recipient will provide UTMB with a copy of any manuscript or abstract disclosing such Research results for the purpose of protecting the Material and intellectual property of UTMB that might be disclosed by such publication. In any such publication or presentation of Research results, Recipient agrees to acknowledge UTMB scientist as provider of the Material.
5. **Intellectual Property.** If the Research involving the Material results in an invention, Recipient Scientist will promptly disclose the invention to Recipient's Patent Administrator and will notify the Patent Administrator of UTMB's role as a supplier of the Material used. Recipient, in cooperation with Recipient Scientist, will promptly supply UTMB with a copy of the disclosure, in confidence for UTMB's research and evaluation purposes only. Inventorship of any invention will be determined based on U.S. patent law. Ownership shall follow inventorship. Recipient recognizes the property rights of UTMB in the Material.
6. **Warranty.** The Material is experimental in nature and it is provided "AS IS" WITHOUT WARRANTY OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE OR SAFETY OR ANY OTHER WARRANTY, EXPRESS OR IMPLIED. UTMB MAKES NO REPRESENTATION OR WARRANTY THAT THE USE OF THE MATERIAL WILL NOT INFRINGE ANY PATENT OR OTHER PROPRIETARY RIGHT.
7. **Liability.** In no event shall UTMB be liable for any use by Recipient Scientist or Recipient of the Material or any loss, claim, damage or liability, of whatsoever kind or nature, which may arise from or in connection with Recipient's breach of this Agreement or Recipient's use, handling or storage of the Material, unless such loss, claim, damage or liability results from the negligence or willful malfeasance of UTMB, System, their Regents, officers, agents and employees.
   a) **State Entities:** To the extent authorized by the Recipient's state law, Recipient agrees to indemnify and hold harmless UTMB, System, their Regents, officers, agents and employees, from any liability, loss or damage they may suffer as a result of claims, demands, costs or judgments against them arising out of the Recipient's activities to be carried out pursuant to this Agreement and the use by Recipient of the results obtained from Research, excluding claims, loss, or damage that arise from the negligence or willful malfeasance of any Regent, officer, agent or employee of UTMB or System.
   b) **Federal Entities**: Recipient assumes the liability for any claims, damages, injury, or expenses arising from the use, storage, handling, and disposal of the Material by the Recipient, but only to the extent provided under the Federal Tort Claims Act (28 U.S.C. Chapter 171).
   c) **All other entities**: Recipient shall indemnify and hold UTMB, System, their Regents, officers, agents, and employees harmless against any and all claims, demands, damages, liabilities and costs which directly or indirectly result from, or arise in connection with, any negligent act or omission of Recipient, its agents, or employees, pertaining to its activities and obligations under this Agreement.
8. **Compliance.** Recipient will use the Material in compliance with all laws, governmental regulations and guidelines applicable to the Material. Moreover, if the Material is used in the United States, then Recipient will comply with current United States NIH guidelines.
9. **Export Control.** Recipient further agrees that if the U.S. export laws are or become applicable, it will not export any Materials received under this Agreement to any countries for which the United States government requires an export license or other supporting documentation at the time of export or transfer, unless Recipient has obtained prior written authorization from the appropriate authority responsible for such matters.

10. **Assignment.** This Agreement is not assignable, whether by operation of law or otherwise, without the prior written consent of UTMB.
11. **Publicity.** Recipient may not use the name of UTMB, System or their Regents without express written consent, subject to Section 4. Publication of this Agreement.
12. **Term and Termination.** This Agreement shall be effective as of the date of the last signature and terminate one (1) year from that date. Upon termination, Recipient will immediately destroy all the Material then in its possession.

UNIVERSITY OF TEXAS MEDICAL BRANCH

Carolee King, JD
Senior Vice President and General Counsel
Date: 05 / 12 / 2020

Read and understood:

Signature of Provider Scientist

NATIONAL UNIVERSITY OF SINGAPORE

Dr. Subbu Venkatraman
Director, Industry Liaison Office
Date: 11 May 2020

Read and understood:

Signature of Recipient Scientist

Attachment A – Scope of Research

The reporter viruses being transferred will allow Prof Wang Linfa to better quantify and localize the virus in the following key applications:

1. For improved virus neutralization test
2. For pathogenesis studies in future animal infection studies
3. For screening of potential antiviral agents

To: Mary Matheson[Mary.Matheson@phe.gov.uk]; William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]
From: M.P.G. Koopmans[m.koopmans@erasmusmc.nl]
Sent: Fri 11/27/2020 12:35:13 PM (UTC-06:00)
Subject: Re: COVID-19 assays review

Same here

Professor M.P.G. Koopmans, DVM PhD

Head department of Viroscience

Erasmus MC
Universitair Medisch Centrum Rotterdam

P.O. box 2040, 3000 CA Rotterdam, The Netherlands

Office address: room Ee-1722, Dr. Molewaterplein 40, 3015 GD Rotterdam, The Netherlands

E-mail: m.koopmans@erasmusmc.nl | Phone +31 10 704 40 66

From: Mary Matheson <Mary.Matheson@phe.gov.uk>
Sent: 27 November 2020 15:21
To: William Dowling <william.dowling@cepi.net>; Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; barney.graham@nih.gov <barney.graham@nih.gov>; Jason McLellan <jmclellan@austin.utexas.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Goldblatt, David <d.goldblatt@ucl.ac.uk>; david.montefiori@duke.edu <david.montefiori@duke.edu>; linfa.wang@duke-nus.edu.sg <linfa.wang@duke-nus.edu.sg>; Shi, Pei yong <peshi@UTMB.EDU>; Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>; xumiaobj@126.com <xumiaobj@126.com>; Alter, Galit <GALTER@mgh.harvard.edu>; alex@lji.org <alex@lji.org>; shane@lji.org <shane@lji.org>; McElrath MD PhD, Julie <jmcelrat@fredhutch.org>; katie.doores@kcl.ac.uk <katie.doores@kcl.ac.uk>; Paul Bieniasz <pbieniasz@rockefeller.edu>; Jilian Sacks <Jilian.Sacks@finddx.org>; Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>; Mark Page <mark.page@nibsc.org>; ASiver@mgh.harvard.edu <ASiver@mgh.harvard.edu>; william.lee@health.ny.gov <william.lee@health.ny.gov>
Cc: GSELL, Pierre <gsellp@who.int>; Simon Funnell <Simon.Funnell@phe.gov.uk>; Cesar Munoz-fontela <munoz-fontela@bnitm.de>; RIVEROS BALTA, Alina Ximena <lauriex@who.int>; henaorestrepoa@who.int <henaorestrepoa@who.int>; KNEZEVIC, Ivana <knezevici@who.int>; florian.krammer@mssm.edu <florian.krammer@mssm.edu>
Subject: RE: COVID-19 assays review

Hi Bill,

I am also happy to contribute.

Best Regards

Mary

Mary Matheson PhD
Project Manager, Scientific Leader
Immunoassay Group, Research
Public Health England
Porton Down, Salisbury, SP4 0JG

mary.matheson@phe.gov.uk
Tel: 01980 612713/612317

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Public Health England

From: William Dowling <william.dowling@cepi.net>
Sent: 25 November 2020 12:26
To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; barney.graham@nih.gov; Jason McLellan <jmclellan@austin.utexas.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Mary Matheson <Mary.Matheson@phe.gov.uk>; Goldblatt, David <d.goldblatt@ucl.ac.uk>; david.montefiori@duke.edu; linfa.wang@duke-nus.edu.sg; Shi, Pei yong <peshi@UTMB.EDU>; Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>; xumiaobj@126.com; Alter, Galit <GALTER@mgh.harvard.edu>; alex@lji.org; shane@lji.org; McElrath MD PhD, Julie <jmcelrat@fredhutch.org>; katie.doores@kcl.ac.uk; Paul Bieniasz <pbieniasz@rockefeller.edu>; Jilian Sacks <Jilian.Sacks@finddx.org>; Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>; Mark Page <mark.page@nibsc.org>; ASiver@mgh.harvard.edu; william.lee@health.ny.gov
Cc: GSELL, Pierre <gsellp@who.int>; Simon Funnell <Simon.Funnell@phe.gov.uk>; Cesar Munoz-fontela <munoz-fontela@bnitm.de>; RIVEROS BALTA, Alina Ximena <lauriex@who.int>; henaorestrepoa@who.int; KNEZEVIC, Ivana <knezevici@who.int>; florian.krammer@mssm.edu
Subject: COVID-19 assays review

Dear colleagues,

Similar to what was done recently with the WHO COVID-19 models working group, we would like to publish a short review about the state-of-the-art regarding COVID-19 assays. Based on your expertise and the data you have generated and presented to the WHO assays group, we would like to ask you to contribute to this paper. As you can see in the attached outline, we have suggested subgroups for different topics. Please take this only as a suggestion and feel free to contribute to other parts of the review as you deem fit. Also, feel free to suggest additional authors as needed. Florian Krammer has graciously agreed to help coordinate and submit this to a high quality journal. We would like to have a draft by the end of the year if possible. Please confirm that you wish to participate in this endeavor.

Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
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From: Mary Matheson[Mary.Matheson@phe.gov.uk]
Sent: Fri 11/27/2020 8:21:35 AM (UTC-06:00)
Subject: RE: COVID-19 assays review

Hi Bill,

I am also happy to contribute.

Best Regards

Mary

Mary Matheson PhD
Project Manager, Scientific Leader
Immunoassay Group, Research
Public Health England
Porton Down, Salisbury, SP4 0JG

mary.matheson@phe.gov.uk
Tel: 01980 612713/612317

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Public Health England

From: William Dowling <william.dowling@cepi.net>
Sent: 25 November 2020 12:26
To: Thornburg, Natalie (CDC/DDID/NCIRD/DVD) <nax3@cdc.gov>; barney.graham@nih.gov; Jason McLellan <jmclellan@austin.utexas.edu>; M.P.G. Koopmans <m.koopmans@erasmusmc.nl>; Mary Matheson <Mary.Matheson@phe.gov.uk>; Goldblatt, David <d.goldblatt@ucl.ac.uk>; david.montefiori@duke.edu; linfa.wang@duke-nus.edu.sg; Shi, Pei yong <peshi@UTMB.EDU>; Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>; xumiaobj@126.com; Alter, Galit <GALTER@mgh.harvard.edu>; alex@lji.org; shane@lji.org; McElrath MD PhD, Julie <jmcelrat@fredhutch.org>; katie.doores@kcl.ac.uk; Paul Bieniasz <pbieniasz@rockefeller.edu>; Jilian Sacks <Jilian.Sacks@finddx.org>; Lowy, Douglas (NIH/NCI) [E] <lowyd@mail.nih.gov>; Mark Page <mark.page@nibsc.org>; ASiver@mgh.harvard.edu; william.lee@health.ny.gov

Cc: GSELL, Pierre <gsellp@who.int>; Simon Funnell <Simon.Funnell@phe.gov.uk>; Cesar Munoz-fontela <munoz-fontela@bnitm.de>; RIVEROS BALTA, Alina Ximena <lauriex@who.int>; henaorestrepoa@who.int; KNEZEVIC, Ivana <knezevici@who.int>; florian.krammer@mssm.edu
Subject: COVID-19 assays review

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Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; David Montefiori, Ph.D.[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]; xumiaobj@126.com[xumiaobj@126.com]; galter[galter@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; Roessner, Ashley G[aroessne@fredhutch.org]
From: McElrath MD PhD, Julie[jmcelrat@fredhutch.org]
Sent: Wed 11/25/2020 10:03:15 AM (UTC-06:00)
Subject: Re: COVID-19 assays review

Thanks, Bill. I'm happy to participate.

Best,
Julie

Julie McElrath, M.D., Ph.D.
Director, Vaccine and Infectious Disease Division
Senior Vice President
Joel D. Meyers Endowed Chair

FRED HUTCH
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Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N.
Mail Stop E5-110
Seattle, WA 98109
Tel: 206-667-6704

From: William Dowling <william.dowling@cepi.net>
Date: Wednesday, November 25, 2020 at 4:27 AM
To: "Thornburg, Natalie (CDC/DDID/NCIRD/DVD)" <nax3@cdc.gov>, "barney.graham@nih.gov" <barney.graham@nih.gov>, Jason McLellan <jmclellan@austin.utexas.edu>, "M.P.G. Koopmans" <m.koopmans@erasmusmc.nl>, "Mary.Matheson@phe.gov.uk" <Mary.Matheson@phe.gov.uk>, "Goldblatt, David" <d.goldblatt@ucl.ac.uk>, David Montefiori <david.montefiori@duke.edu>, "linfa.wang@duke-nus.edu.sg" <linfa.wang@duke-nus.edu.sg>, "Shi, Pei yong" <peshi@UTMB.EDU>, Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>, "xumiaobj@126.com" <xumiaobj@126.com>, galter <galter@mgh.harvard.edu>, "alex@lji.org" <alex@lji.org>, Shane Crotty <shane@lji.org>, "McElrath MD PhD, Julie" <jmcelrat@fredhutch.org>, "katie.doores@kcl.ac.uk" <katie.doores@kcl.ac.uk>, Paul Bieniasz <pbieniasz@rockefeller.edu>, Jilian Sacks <Jilian.Sacks@finddx.org>, "Lowy, Douglas (NIH/NCI) [E]" <lowyd@mail.nih.gov>, Mark Page <mark.page@nibsc.org>, "ASiver@mgh.harvard.edu" <ASiver@mgh.harvard.edu>, "william.lee@health.ny.gov" <william.lee@health.ny.gov>
Cc: "GSELL, Pierre" <gsellp@who.int>, Simon Funnell <Simon.Funnell@phe.gov.uk>, Cesar Munoz-fontela <munoz-fontela@bnitm.de>, "RIVEROS BALTA, Alina Ximena" <lauriex@who.int>, "henaorestrepoa@who.int" <henaorestrepoa@who.int>, "KNEZEVIC, Ivana" <knezevici@who.int>, "florian.krammer@mssm.edu" <florian.krammer@mssm.edu>
Subject: COVID-19 assays review

Dear colleagues,

Similar to what was done recently with the WHO COVID-19 models working group, we would like to publish a short review

about the state-of-the-art regarding COVID-19 assays. Based on your expertise and the data you have generated and presented to the WHO assays group, we would like to ask you to contribute to this paper. As you can see in the attached outline, we have suggested subgroups for different topics. Please take this only as a suggestion and feel free to contribute to other parts of the review as you deem fit. Also, feel free to suggest additional authors as needed. Florian Krammer has graciously agreed to help coordinate and submit this to a high quality journal. We would like to have a draft by the end of the year if possible. Please confirm that you wish to participate in this endeavor.

Thank you all in advance for your support.

Best regards
Bill Dowling ,
Co-Chair WHO COVID-19 assays working group

William Dowling, PhD

Non-Clinical Vaccine Development Leader

CEPI New vaccines for a safer world

(+1) 202 800-3148 (o)
(+1) 202 897-8180 (m)

William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: William Dowling[william.dowling@cepi.net]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; barney.graham@nih.gov[barney.graham@nih.gov]; Jason McLellan[jmclellan@austin.utexas.edu]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Mary.Matheson@phe.gov.uk[Mary.Matheson@phe.gov.uk]; Goldblatt, David[d.goldblatt@ucl.ac.uk]; david.montefiori@duke.edu[david.montefiori@duke.edu]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; Shi, Pei yong[peshi@UTMB.EDU]; xumiaobj@126.com[xumiaobj@126.com]; Alter, Galit[GALTER@mgh.harvard.edu]; alex@lji.org[alex@lji.org]; shane@lji.org[shane@lji.org]; McElrath MD PhD, Julie[jmcelrat@fredhutch.org]; katie.doores@kcl.ac.uk[katie.doores@kcl.ac.uk]; Paul Bieniasz[pbieniasz@rockefeller.edu]; Jilian Sacks[Jilian.Sacks@finddx.org]; Lowy, Douglas (NIH/NCI) [E][lowyd@mail.nih.gov]; Mark Page[mark.page@nibsc.org]; ASiver@mgh.harvard.edu[ASiver@mgh.harvard.edu]; william.lee@health.ny.gov[william.lee@health.ny.gov]
Cc: GSELL, Pierre[gsellp@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; henaorestrepoa@who.int[henaorestrepoa@who.int]; KNEZEVIC, Ivana[knezevici@who.int]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]
From: Sylvie VAN DER WERF[sylvie.van-der-werf@pasteur.fr]
Sent: Thur 11/26/2020 7:21:28 AM (UTC-06:00)
Subject: Re: COVID-19 assays review

Happy to contribute as well.
Thank you
Best regards,
Sylvie

De : William Dowling <william.dowling@cepi.net>
Date : mercredi 25 novembre 2020 à 13:26
À : "Thornburg, Natalie (CDC/DDID/NCIRD/DVD)" <nax3@cdc.gov>, "barney.graham@nih.gov" <barney.graham@nih.gov>, Jason McLellan <jmclellan@austin.utexas.edu>, "M.P.G. Koopmans" <m.koopmans@erasmusmc.nl>, "Mary.Matheson@phe.gov.uk" <Mary.Matheson@phe.gov.uk>, "Goldblatt, David" <d.goldblatt@ucl.ac.uk>, "david.montefiori@duke.edu" <david.montefiori@duke.edu>, "linfa.wang@duke-nus.edu.sg" <linfa.wang@duke-nus.edu.sg>, "Shi, Pei yong" <peshi@UTMB.EDU>, Sylvie VAN DER WERF <sylvie.van-der-werf@pasteur.fr>, "xumiaobj@126.com" <xumiaobj@126.com>, "Alter, Galit" <GALTER@mgh.harvard.edu>, "alex@lji.org" <alex@lji.org>, "shane@lji.org" <shane@lji.org>, "McElrath MD PhD, Julie" <jmcelrat@fredhutch.org>, "katie.doores@kcl.ac.uk" <katie.doores@kcl.ac.uk>, Paul Bieniasz <pbieniasz@rockefeller.edu>, Jilian Sacks <Jilian.Sacks@finddx.org>, "Lowy, Douglas (NIH/NCI) [E]" <lowyd@mail.nih.gov>, Mark Page <mark.page@nibsc.org>, "ASiver@mgh.harvard.edu" <ASiver@mgh.harvard.edu>, "william.lee@health.ny.gov" <william.lee@health.ny.gov>
Cc : "GSELL, Pierre" <gsellp@who.int>, Simon Funnell <Simon.Funnell@phe.gov.uk>, Cesar Munoz-fontela <munoz-fontela@bnitm.de>, "RIVEROS BALTA, Alina Ximena" <lauriex@who.int>, "henaorestrepoa@who.int" <henaorestrepoa@who.int>, "KNEZEVIC, Ivana" <knezevici@who.int>, "florian.krammer@mssm.edu" <florian.krammer@mssm.edu>
Objet : COVID-19 assays review

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Co-Chair WHO COVID-19 assays working group

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William.dowling@cepi.net

1901 Pennsylvania Ave, NW, Suite 1003, Washington, DC 20006 USA

www.cepi.net

To: carmen.zorrilla@upr.edu[carmen.zorrilla@upr.edu]; afauci@niaid.nih.gov[afauci@niaid.nih.gov]; Gregory.Ebel@colostate.edu[Gregory.Ebel@colostate.edu]; akp7@cdc.gov[akp7@cdc.gov]; shw2@cdc.gov[shw2@cdc.gov]; mxf2@cdc.gov[mxf2@cdc.gov]; jlr6@cdc.gov[jlr6@cdc.gov]; mark.challberg@niaid.nih.gov[mark.challberg@niaid.nih.gov]; desilva@med.unc.edu[desilva@med.unc.edu]; Vasilakis, Nikolaos[nivasila@utmb.edu]; ckq2@cdc.gov[ckq2@cdc.gov]; Shi, Pei yong[peshi@UTMB.EDU]; acostero@niaid.nih.gov[acostero@niaid.nih.gov]; lounibos@ufl.edu[lounibos@ufl.edu]; Carol.Blair@colostate.edu[Carol.Blair@colostate.edu]; gdimopo1@jhu.edu[gdimopo1@jhu.edu]; jrey@ufl.edu[jrey@ufl.edu]; barney.graham@niaid.nih.gov[barney.graham@niaid.nih.gov]; steve.whitehead@niaid.nih.gov[steve.whitehead@niaid.nih.gov]; theresa.finn@fda.hhs.gov[theresa.finn@fda.hhs.gov]; jaketu@vt.edu[jaketu@vt.edu]; cbb0@cdc.gov[cbb0@cdc.gov]; wsleal@ucdavis.edu[wsleal@ucdavis.edu]; sallie.permar@duke.edu[sallie.permar@duke.edu]; mrh7@cdc.gov[mrh7@cdc.gov]; laura.kramer@health.ny.gov[laura.kramer@health.ny.gov]; dominiquejk@nih.gov[dominiquejk@nih.gov]; rosawi@mail.nih.gov[rosawi@mail.nih.gov]; Lu, Tami (NIH/NIAID) [C][tami.lu@nih.gov]; ccassetti@niaid.nih.gov[ccassetti@niaid.nih.gov]; halsteads@erols.com[halsteads@erols.com]; tsharp@cdc.gov[tsharp@cdc.gov]; kdk6@cdc.gov[kdk6@cdc.gov]; gwr5@cdc.gov[gwr5@cdc.gov]
From: Jorge Fraga Nodarse[jorgefragan@gmail.com]
Sent: Wed 4/29/2020 11:30:55 AM (UTC-05:00)
Subject: INVITATION TO TELECONFERENCE CUBA-USA COVID-19

Dears Proffesors

Our Minister of Cuban Health organize THE VIDEO CONFERENCE BETWEEN EXPERTS FROM CUBA AND THE UNITED STATES with the objetive to discuss the experience about the management of Covid19. The video-conference will be do next Tuesday, May 5, 2020, TIME: 16:30 hrs (Cuban time).

You coming to the meeting that we organized in 2016 **Exploring Opportunities for Arbovirus Research Collaboration**
and this is the reason that you receive this invitation email.

THIS IS THE PREMILINARY PROGRAM:
Meeting objectives:
- Update globally situation of COVID-19, Americas region and fundamentally in Cuba and the United States.
- To make known to the United States experts how Cuba has faced the COVID-19 pandemic and the available scientific resources.
- Share what both countries have done to obtain understanding and rigor from the American scientific community about what they do in Cuba.
- Arouse interest in the people of the United States in what we do to confront the pandemic.

Introduction: Brief update on the situation of the new coronavirus (COVID-19) in the world, from its surgery and behavior up to now, emphasizing morbidity and mortality. General overview.

Presentation of the Plans to confront the pandemic in Cuba and in the United States. Offer brief information on how Cuba organized its confrontation, management and control plan for Covid-19.
-Epidemiology. Minister of Cuban Health

Brief exposition of the diagnostic models used. Experiences and results.
- Institute of Tropical Medicine Pedro Kouri

Presentation of the clinical management of the disease, in pediatric and adult ages, according to the established protocol.
- Institute of Tropical Medicine Pedro Kouri.

- Minister of Cuban Health

Presentation of the innovative Cuban biotechnology products incorporated into the treatment models used in the different stages of treatment.
- Center for Molecular Immunology (CIM).
- Center for Genetic Engineering and Biotechnology (CIGB)
- Director of Science and Innovation of BioCubaFarma

Exchange of questions and answers between the participants.

If you are agre to participate only tell me in order to send you later on more detail about the video-conference.

Also if you kwon others proffesors that are involve in Covid managemnet we appreciate that you help us to comunicate and invite him.

Best wishes

Jorge Fraga, PhD
Head of Science and Technology Department
Institute of Tropical Medicine Pedro Kouri

To: Brasher, Tina C.[tcbrashe@UTMB.EDU]; Beasley, David W.[dwbeasle@UTMB.EDU]; Bente, Dennis A.[dabente@UTMB.EDU]; Boldogh, Istvan[sboldogh@UTMB.EDU]; Brasel, Trevor[trbrasel@UTMB.EDU]; Comer, Jason E.[jscomer@UTMB.EDU]; Cong, Yingzi[yicong@UTMB.EDU]; Cross, Robert W.[rwcross@UTMB.EDU]; Eaves-Pyles, Tonyia D.[tdeavesp@UTMB.EDU]; Endsley, Mark A.[maendsle@utmb.edu]; Gagnon, Matthieu[magagnon@UTMB.EDU]; Garg, Nisha[nigarg@utmb.edu]; Geisbert, Thomas W.[twgeisbe@UTMB.EDU]; Hosakote madaiah, Yashoda[yahosako@utmb.edu]; Hu, Haitao[haihu@UTMB.EDU]; Huda, Ruksana[rhuda@UTMB.EDU]; Lawrence, William S.[wslawren@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Lee, Sunhee[sunhlee@UTMB.EDU]; Liang, Yuejin[yu2liang@UTMB.EDU]; Makino, Shinji[shmakino@UTMB.EDU]; Mire, Chad[chmire@UTMB.EDU]; Rajsbaum, Ricardo[rirajsba@UTMB.EDU]; Sha, Jian[jisha@UTMB.EDU]; Terasaki, Kaori[katerasa@UTMB.EDU]; Torres, Alfredo G.[altorres@utmb.edu]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Wang, Tian[ti1wang@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Yao, Suxia[suyao@UTMB.EDU]
Cc: Rubio, Marcela L.[mlrubio@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Sun 1/31/2021 3:41:43 PM (UTC-06:00)
Subject: Re: M&I Depart.Review - 2014-2020 Publications

From: Brasher, Tina C. <tcbrashe@UTMB.EDU>
Sent: Monday, January 11, 2021 10:38 AM
To: Beasley, David W. <dwbeasle@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; Boldogh, Istvan <sboldogh@UTMB.EDU>; Brasel, Trevor <trbrasel@UTMB.EDU>; Comer, Jason E. <jscomer@UTMB.EDU>; Cong, Yingzi <yicong@UTMB.EDU>; Cross, Robert W. <rwcross@UTMB.EDU>; Eaves-Pyles, Tonyia D. <tdeavesp@UTMB.EDU>; Endsley, Mark A. <maendsle@utmb.edu>; Gagnon, Matthieu <magagnon@UTMB.EDU>; Garg, Nisha <nigarg@utmb.edu>; Geisbert, Thomas W. <twgeisbe@UTMB.EDU>; Hosakote madaiah, Yashoda <yahosako@utmb.edu>; Hu, Haitao <haihu@UTMB.EDU>; Huda, Ruksana <rhuda@UTMB.EDU>; Lawrence, William S. <wslawren@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Lee, Sunhee <sunhlee@UTMB.EDU>; Liang, Yuejin <yu2liang@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Rajsbaum, Ricardo <rirajsba@UTMB.EDU>; Sha, Jian <jisha@UTMB.EDU>; Terasaki, Kaori <katerasa@UTMB.EDU>; Torres, Alfredo G. <altorres@utmb.edu>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Wang, Tian <ti1wang@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Yao, Suxia <suyao@UTMB.EDU>
Cc: Rubio, Marcela L. <mlrubio@UTMB.EDU>
Subject: RE: M&I Depart.Review - 2014-2020 Publications

Please include
Grad student author =underline and postdoc=asterisk (includes accepted manuscripts).

From: Brasher, Tina C.
Sent: Monday, January 11, 2021 10:07 AM
To: Beasley, David W. <dwbeasle@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; Boldogh, Istvan <sboldogh@UTMB.EDU>; Brasel, Trevor <trbrasel@UTMB.EDU>; Comer, Jason E. <jscomer@UTMB.EDU>; Cong, Yingzi <yicong@UTMB.EDU>; Cross, Robert W. <rwcross@UTMB.EDU>; Eaves-Pyles, Tonyia D. <tdeavesp@UTMB.EDU>; Endsley, Mark A. <maendsle@utmb.edu>; Gagnon, Matthieu <magagnon@UTMB.EDU>; Garg, Nisha <nigarg@utmb.edu>; Geisbert, Thomas W. <twgeisbe@UTMB.EDU>; Hosakote madaiah, Yashoda <yahosako@utmb.edu>; Hu, Haitao <haihu@UTMB.EDU>; Huda, Ruksana <rhuda@UTMB.EDU>; Lawrence, William S. <wslawren@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Lee, Sunhee <sunhlee@UTMB.EDU>; Liang, Yuejin <yu2liang@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Rajsbaum, Ricardo <rirajsba@UTMB.EDU>; Sha, Jian <jisha@UTMB.EDU>; Terasaki, Kaori <katerasa@UTMB.EDU>; Torres, Alfredo G. <altorres@utmb.edu>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Wang, Tian <ti1wang@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Yao, Suxia <suyao@UTMB.EDU>
Cc: Rubio, Marcela L. <mlrubio@UTMB.EDU>
Subject: M&I Depart.Review - 2014-2020 Publications
Importance: High

Good Morning,
Re: 2014-2020 Micro & Immun Departmental Review
Please send me your publication from 2014-2020 by January 15, 2021.
I have provide below format, citation format, and guidelines.

Please let me know if you have any questions.

NLM Style - Citation Format - ARTICLES

JOURNAL ARTICLES

Sample Article Citations:

Benny BV, Nagpal AS, Singh P, Smuck M. Vascular causes of radiculopathy: a literature review. Spine J. 2011 Jan;11(1):73-85.

Brantingham JW, Bonnefin D, Perle SM, Cassa TK, Globe G, Pribicevic M, Hicks M, Korporaal C. Manipulative therapy for lower extremity conditions: update of a literature review. J Manipulative Physiol Ther. 2012 Feb;35(2):127-66.

Daniels CJ, Morrell AP. Chiropractic management of pediatric plantar fasciitis: a case report. J Chiropr Med. 2012 Mar;11(1):58-63.

Brief Guidelines:

- List all authors, last name first, then first initial and middle initial (if available), separate each author by a comma.
- List full article title, capitalize only first word and any proper nouns.
- Abbreviate journal title according to NLM Catalog of Journals.
- Put year first, followed by month and date, if listed. End with semicolon.
- Put volume and issue (optionally, issue may be omitted if pagination continues for each issue). Do not add space after semicolon. End with colon.
- Indicate page number range. Do not repeat numbers or put a space after colon. i.e. if date range is 1235 through 1237, record as 1235-7.

Thank you
Tina

Tina Brasher
Sr. Adminastrative Assistant
Department of Microbiology & Immunology
tcbrashe@utmb.edu
Ph.409-772-8141
Mail Rt. 1070

To: Menachery, Vineet[vimenach@UTMB.EDU]; vineet.menachery@gmail.com[vineet.menachery@gmail.com]
From: Richard Green[greener@uw.edu]
Sent: Sat 4/4/2020 1:56:56 PM (UTC-05:00)
Subject: first draft: gene mania network
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vineet_genemania_network.pdf
vineet_genemania_network.png
vineet_genemania_network.svg

How is this ? This is based off the genes you sent me

Visual Legend for H sapiens (1)

Node Shape Mapping

Node Shape	node type
	attribute

Node Fill Color Mapping

Node Fill Color	node type
	attribute
	query
	result

Edge Stroke Color (Unselected) Mapping

Edge Stroke Color (Unselected)	data type
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	Genetic Interactions
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	Physical Interactions
	Predicted
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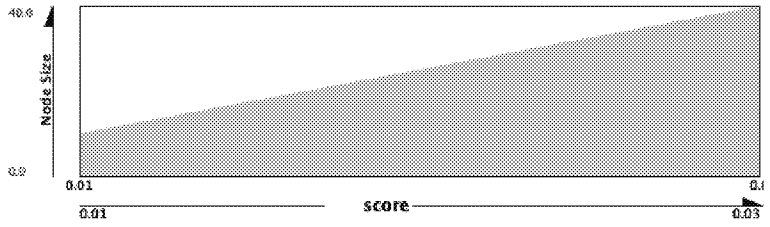
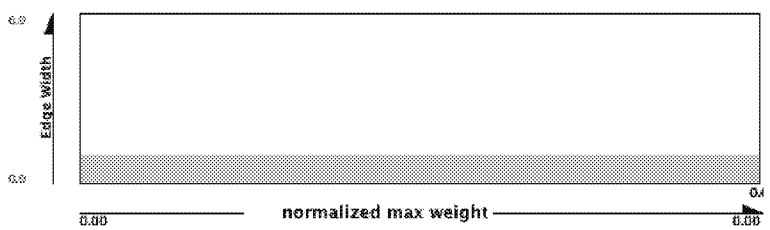
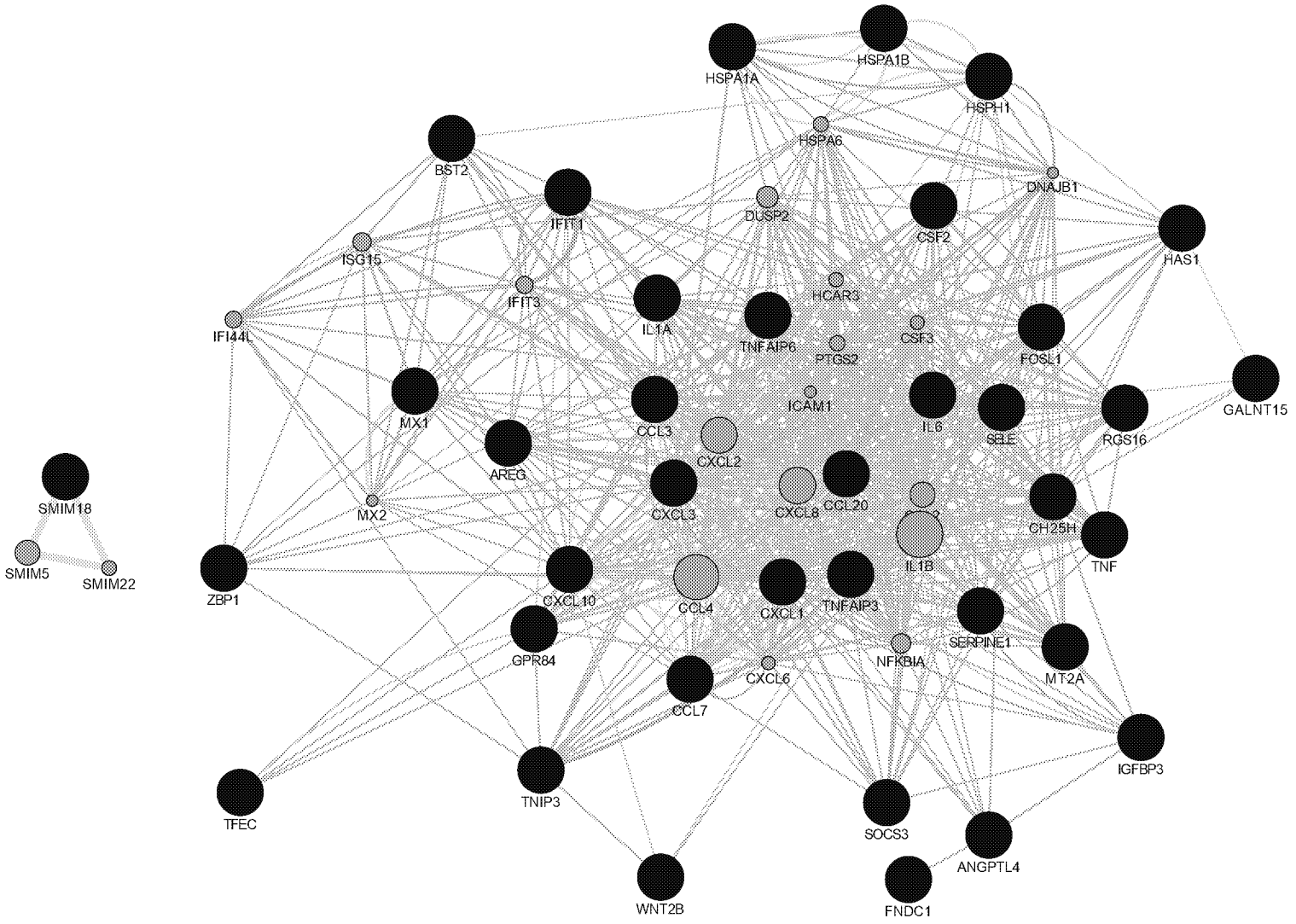


Edge Width Mapping

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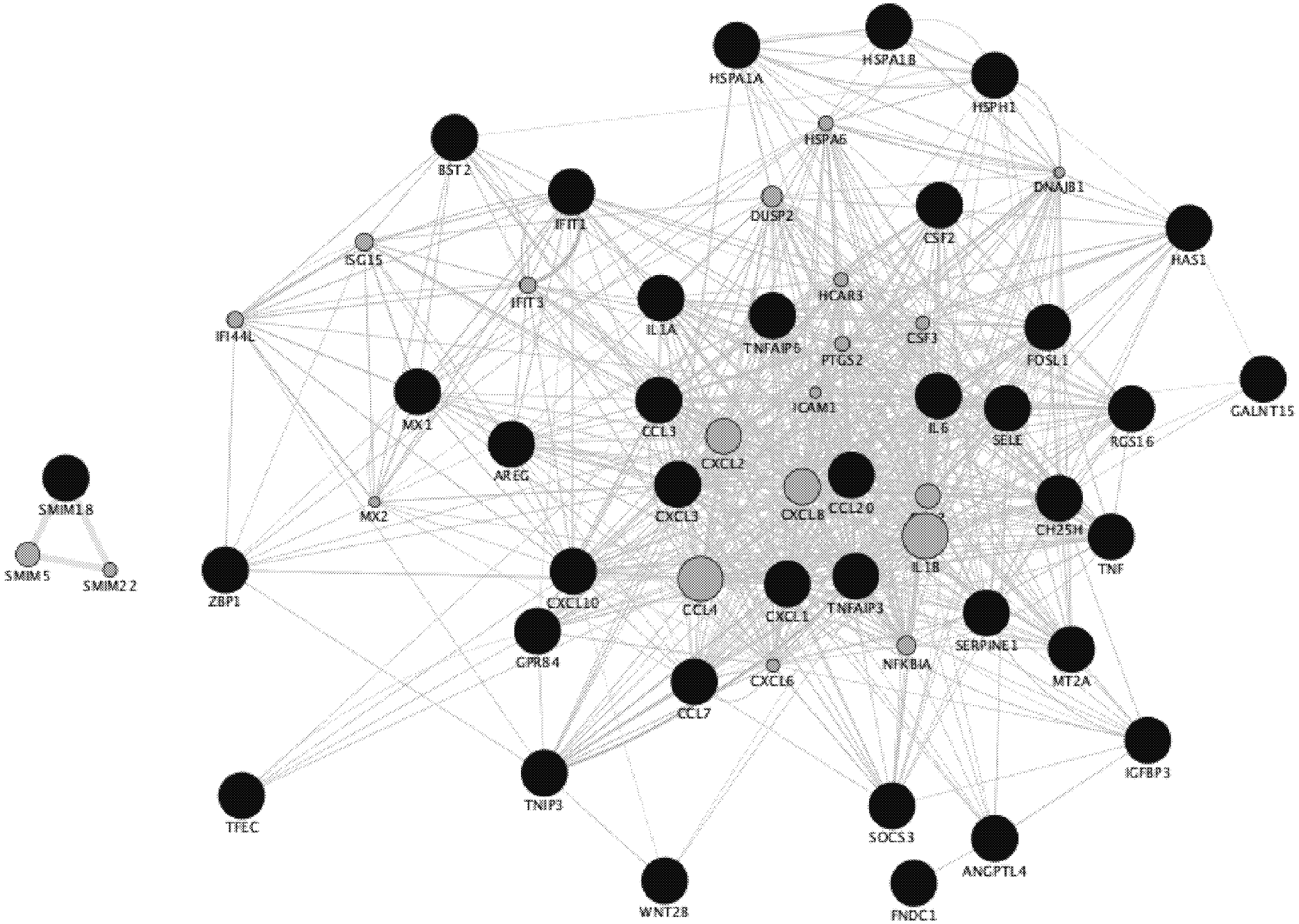
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2020 11:53:48 AM PDT</desc>

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<path d="M -36.26039123535156 -80.86711120605469 C -29.9877986907959 -62.38701248168945
-9.286752700805664 -48.97639465332031 9.976688385009766 -50.91365432739258"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -35.12821578979492 -81.3012924194336 C -22.65814781188965 -52.22682571411133
-28.376911163330078 -10.769472122192383 -47.901432037353516 11.296296119689941"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -43.133243560791016 -80.15443420410156 C -47.36841583251953 -
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18.28120231628418"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -47.38452911376953 -81.2967758178711 C -64.62871551513672 -
41.009368896484375 -110.68448638916016 1.4409993886947632 -150.25296020507812
13.518777847290039"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -37.49573516845703 -80.50405883789062 C -24.526884078979492 -
28.51177406311035 -33.228328704833984 50.36553955078125 -56.93095397949219
95.67335510253906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -26.48073959350586 -100.46400451660156 C 1.8350398540496826 -
109.77888488769531 38.43472671508789 -99.84811401367188 55.26695251464844 -
78.28300476074219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -55.6230583190918 -89.61266326904297 C -73.66841125488281 -82.08745574951172
-90.51630401611328 -89.6701431274414 -93.2538833618164 -106.549072265625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -56.66206741333008 -97.82527160644531 C -74.93679809570312 -
100.46394348144531 -87.21996307373047 -89.8718032836914 -84.09728240966797 -
74.16706848144531"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0010716915130615" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -31.91238021850586 -108.03984069824219 L 177.7084197998047 -386.918701171875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.408555507659912" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -28.345277786254883 -104.27833557128906 C 10.95938491821289 -130.6817169189453 78.33863067626953 -144.12985229492188 122.15047454833984 -134.31556701660156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2373113632202148" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -26.412050247192383 -90.95323181152344 C 39.53782272338867 -70.30886840820312 127.42973327636719 -11.929037094116211 169.9000244140625 39.44176483154297"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1473108530044556" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -25.779598236083984 -97.1585922241211 C -6.361916542053223 -99.11136627197266 14.423771858215332 -85.83232879638672 20.646535873413086 -67.49903106689453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2392818927764893" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -28.726993560791016 -86.38204193115234 C -0.3628493547439575 -65.5194320678711 19.436641693115234 -22.24385643005371 15.496407508850098 10.276657104492188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2503060102462769" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -38.227115631103516 -80.3402328491211 C -34.62623977661133 -62.23051452636719 -44.554351806640625 -49.404685974121094 -60.40217971801758 -51.692935943603516"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.048893690109253" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -32.562015533447266 -82.7006607055664 L 178.52151489257812 230.32200622558594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2228606939315796" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -25.73628807067871 -96.64143371582031 L 286.3017272949219 -117.54033660888672"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.418170690536499" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -34.80717468261719 -81.44329071044922 L 93.89099884033203 200.86517333984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.250359058380127" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -48.57340621948242 -81.86640167236328 L -184.55120849609375 173.56906127929688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3192473649978638" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -30.630651473999023 -106.96383666992188 L 128.98973083496094 -277.56341552734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

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<g stroke-linejoin="round" stroke-width="1.3017483949661255" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -56.28984069824219 -91.56788635253906 L -446.3174743652344
13.119802474975586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2900171279907227" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -25.77614402770996 -97.12384796142578 L 180.7261962890625 -
117.42313385009766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.101193904876709" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -43.105403900146484 -80.15108489990234 L -63.8320198059082
93.53571319580078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6549274921417236" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -30.57164764404297 -84.29488372802734 L 57.6633415222168
9.030637741088867"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7122814655303955" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -26.197736740112305 -91.70333099365234 L 269.5197448730469 -
15.176557540893555"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8936185836791992" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -47.67404556274414 -109.77903747558594 L -86.15352630615234 -
194.854736328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g stroke-linejoin="round" stroke-width="1.8333454132080078" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -43.73452377319336 -80.23922729492188 L -57.72101593017578 6.649575233459473"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5918054580688477" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -27.309633255004883 -88.71253967285156 L 112.64018249511719 -19.60956382751465"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3693418502807617" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -49.48512649536133 -108.81117248535156 L -160.20106506347656 -286.6564636230469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4042210578918457" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -56.660926818847656 -97.83316040039062 L -282.1260986328125 -130.5057830810547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.387043833732605" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -56.81108856201172 -95.0250244140625 L -201.95916748046875 -89.64277648925781"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.723410725593567" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -54.86091995239258 -103.16319274902344 L -78.97618103027344 -116.57193756103516"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5721251964569092" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -35.08742904663086 -81.31885528564453 L 5.154841423034668
11.773320198059082"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.234889030456543" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -52.84306716918945 -85.2098617553711 L -154.4956817626953
6.00069522857666"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.58940589427948" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -28.175601959228516 -87.18297576904297 L 12.415909767150879 -
61.0692253112793"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7009187936782837" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -25.96866798400879 -98.47264862060547 L 122.01019287109375 -
126.25348663330078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.57789945602417" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -35.39473342895508 -110.01333618164062 L -7.048645973205566 -
179.6438751220703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3888605833053589" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -27.98912239074707 -87.48014831542969 L 238.04888916015625
75.30875396728516"/>
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.335344910621643" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -26.374181747436523 -91.07597351074219 L 48.43740463256836 -68.333984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2862582206726074" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -28.346521377563477 -86.92304229736328 L 166.04336547851562
43.701175689697266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2493270635604858" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -25.960371017456055 -92.77513885498047 L 224.9586944580078 -
46.424930572509766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.0906119346618652" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -51.9696044921875 -84.31190490722656 L -66.43357849121094 -
69.06214141845703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -2.0068368911743164 94.34942626953125 C -28.835655212402344
46.959102630615234 -47.03179931640625 -31.146108627319336 -42.6490592956543 -
80.10344696044922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">
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<path d="M 122.05406951904297 -44.200801849365234 C 75.1463851928711 -42.03604507446289 7.719137668609619 -61.03188705444336 -28.54890251159668 -86.62920379638672"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2359697818756104" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 55.08213424682617 -223.72813415527344 L -31.910099029541016 -108.03812408447266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1342501640319824" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.4803695678711 -47.76437759399414 L -26.325851440429688 -91.23812103271484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4018762111663818" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.11297607421875 -188.96664428710938 L -27.731727600097656 -103.28662872314453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3925710916519165" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -202.08407592773438 -219.6669921875 L -53.58179473876953 -105.10591888427734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3382657766342163" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -340.134765625 -257.2646789550781 L -54.9478874206543 -103.00462341308594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.283665657043457" stroke-linecap="round"

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.6912078857422 -317.2380676269531 L -29.028568267822266 -
105.21774291992188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3186719417572021" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.183013916015625 -130.4949493408203 L -27.207046508789062 -
102.2789077758789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2797996997833252" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -0.33133652806282043 93.71104431152344 L -37.97343444824219 -
80.39286804199219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3120125532150269" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 43.7860221862793 -355.59661865234375 L -36.42396545410156 -
110.39063262939453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4385713338851929" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.51428985595703 -170.17404174804688 L -28.984182357788086 -
105.1610107421875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5784235000610352" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 109.11075592041016 76.34858703613281 L -31.018455505371094 -
83.88858032226562"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.562148928642273" stroke-linecap="round"
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<path d="M -1.8053970336914062 -290.4817810058594 L -38.17391586303711 -
110.85232543945312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2508947849273682" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 9.357722282409668 -180.24000549316406 L 58.70735549926758 -
80.44476318359375"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.673810601234436" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -8.44264030456543 -180.27455139160156 L -185.01434326171875
173.33021545410156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 19.1021785736084 -190.8416290283203 L 182.0203857421875 -
126.70584106445312"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.517844319343567" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 17.175132751464844 -209.19874572753906 L 125.97127532958984 -
281.1366882324219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1747992038726807" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -17.458843231201172 -189.3497772216797 L -203.99429321289062 -
97.71964263916016"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0861968994140625" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -14.346047401428223 -184.75791931152344 L -436.7300109863281
196.96263122558594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0886222124099731" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 17.364957809448242 -187.4293670654297 L 227.7532958984375 -
53.53035354614258"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4492677450180054" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -15.573838233947754 -186.25643920898438 L -80.38969421386719 -
138.20242309570312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2983918190002441" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 13.845270156860352 -183.27822875976562 L 241.7555389404297
70.85803985595703"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5431276559829712" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -19.265289306640625 -201.2722625732422 L -74.63803100585938 -
209.97296142578125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2910853624343872" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 19.851943969726562 -193.1474151611328 L 286.8973693847656 -
123.8971939086914"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5875102281570435" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -3.694133758544922 -178.61080932617188 L -62.015445709228516
93.83787536621094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8021776676177979" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 20.06275749206543 -202.2904815673828 L 335.615478515625 -
268.7650146484375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1673119068145752" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 123.09336853027344 -189.00143432617188 C 89.666259765625 -170.29954528808594
42.13508224487305 -169.3022918701172 16.92951202392578 -186.77398681640625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0827879905700684" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 109.59564208984375 75.95542907714844 C 60.39181900024414 10.42726993560791
12.687712669372559 -103.42082214355469 3.0455431938171387 -178.33140563964844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.123059630393982" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 123.2901611328125 -49.771141052246094 C 75.32640075683594 -74.91565704345703
23.30215835571289 -132.9021453857422 7.090771198272705 -179.28759765625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1190699338912964" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">
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<path d="M 15.930807113647461 -64.93861389160156 C -7.391151428222656 -
94.52124786376953 -17.15729522705078 -145.6826934814453 -5.882485389709473 -
179.21090698242188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.194170594215393" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 114.37474060058594 -22.485517501831055 C 69.2518081665039 -55.16301727294922
20.648740768432617 -125.1874771118164 5.816753387451172 -178.8895263671875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1055569648742676" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 59.45106887817383 7.528059005737305 C 25.429092407226562 -38.115943908691406
-1.159970998764038 -121.2568588256836 0.06273499876260757 -178.17236328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.109079360961914" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 121.67147827148438 -129.51129150390625 C 84.11802673339844 -
128.69912719726562 35.27500534057617 -152.3030242919922 12.577546119689941 -
182.2320556640625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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<g stroke-linejoin="round" stroke-width="1.0171024799346924" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -333.8608093261719 -41.71558380126953 L -17.62262535095215 -
189.6913299560547"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0161666870117188" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -200.58541870117188 -223.3053741455078 L -19.353229522705078 -
200.6487274169922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5742229223251343" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 0.9185059666633606 93.57655334472656 L 0.521510660648346 -
178.1677703857422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5039032697677612" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 65.31138610839844 4.5140252113342285 L 6.584475040435791 -
179.1182098388672"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4352878332138062" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 34.36138916015625 -137.30142211914062 L 10.217098236083984 -
180.69125366210938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.513227105140686" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.268211364746094 -225.8614959716797 L 18.202131271362305 -
207.46084594726562"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5437966585159302" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -55.674076080322266 7.093035697937012 L -4.786337852478027 -
178.87692260742188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.393817663192749" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 111.47268676757812 74.89299011230469 L 8.022714614868164 -
179.63958740234375"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 125.82495880126953 -52.96548843383789 L 13.560550689697266 -
183.02772521972656"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.290047526359558" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 214.78041076660156 -189.03741455078125 L 20.474163055419922 -
197.31637573242188"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.4432979822158813" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 11.98876667022705 10.161835670471191 L 1.5942970514297485 -
178.19813537597656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -153.7411346435547 -293.1478271484375 L -16.537561416625977 -
208.65509033203125"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.9000440835952759" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.31415557861328 -192.31385803222656 L 20.469242095947266 -
197.2078094482422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.4725638628005981" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.569679260253906 -176.87557983398438 L 19.054433822631836 -
190.7214813232422"/>
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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.444960594177246" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 0.08488159626722336 -290.29656982421875 L 0.4038495421409607 -
218.1675567626953"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4171777963638306" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 23.03297233581543 -68.10690307617188 L 3.9075560569763184 -
178.46151733398438"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.512637972831726" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

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181.73760986328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.563808560371399" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.65930938720703 -138.64602661132812 L 18.499786376953125 -
189.4654541015625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1121431589126587" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 54.11753463745117 -170.74098205566406 C -14.115897178649902 -
127.996337890625 -128.7629852294922 -91.61638641357422 -201.95391845703125 -
89.48408508300781"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2252429723739624" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">
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<path d="M 53.196170806884766 -175.5902862548828 L -200.65402221679688 -222.8641357421875"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1539143323898315" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 64.88497161865234 -169.76226806640625 C 101.91905975341797 -135.88339233398438 131.45408630371094 -73.6467514038086 130.85330200195312 -30.752824783325195"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1890820264816284" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 60.8174934387207 -167.62060546875 C 68.91239929199219 -109.94326782226562 52.52085876464844 -28.85075569152832 24.205963134765625 13.504591941833496"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.192613124847412" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 66.5125732421875 -175.78045654296875 C 95.9723129272461 -182.14208984375 126.43704223632812 -169.98977661132812 134.5574493408203 -148.63748168945312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1974973678588867" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 53.948726654052734 -177.6679229736328 L -153.32498168945312 -293.8557434082031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0941096544265747" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 64.73941802978516 -169.6080780029297 C 92.73436737060547 -142.34503173828125 122.1716079711914 -91.18325805664062 130.48931884765625 -55.335044860839844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

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<g stroke-linejoin="round" stroke-width="1.135688304901123" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 61.163536071777344 -167.67832946777344 C 67.87345886230469 -
132.99368286132812 56.781375885009766 -86.67585754394531 36.38867950439453 -
64.22455596923828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4213260412216187" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.77818298339844 -179.90431213378906 L 131.15635681152344 -
275.80303955078125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1655703783035278" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 61.873966217041016 -167.85597229003906 L 183.81285095214844
227.7912139892578"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6959587335586548" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.68535232543945 -169.9631805419922 L -154.10475158691406
6.449643611907959"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4652931690216064" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 56.36729431152344 -168.52963256835938 L -50.7562141418457
9.199931144714355"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6110520362854004" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.373558044433594 -172.37606811523438 L -202.80580139160156 -
94.70464324951172"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.438720941543579" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 66.2002944946289 -171.8760986328125 L 182.00039672851562 -126.6548843383789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4572597742080688" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 61.288787841796875 -167.7037811279297 L 112.88214874267578 74.46011352539062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3386662006378174" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.95094680786133 -168.9147491455078 L 243.10205078125 69.7524185180664"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2310874462127686" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 60.34000778198242 -167.5707244873047 L 66.1990737915039 -82.46977996826172"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2427024841308594" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.08051681518555 -168.3594970703125 L 173.20022583007812 37.22591018676758"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5397493839263916" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 56.94622039794922 -180.4757080078125 L 4.059621334075928 -291.206298828125"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2413785457611084" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.20888137817383 -168.4300537109375 L 127.5967025756836 -
54.21092987060547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3694790601730347" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 58.041236877441406 -167.80648803710938 L 30.011266708374023 -
67.7522964477539"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3819512128829956" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 62.56797409057617 -168.1120147705078 L 122.6390151977539 -
29.11367416381836"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4569069147109985" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 60.26852035522461 -167.56617736816406 L 70.2403564453125
3.597428798675537"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3452883958816528" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 58.35865783691406 -167.72576904296875 L 17.55133056640625
10.635211944580078"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4775102138519287" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 65.84272766113281 -171.1062774658203 L 124.08982849121094 -
139.4857177734375"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2907546758651733" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 65.39356994628906 -170.3893280029297 L 272.6275329589844 -
21.819053649902344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3675647974014282" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 66.49974822998047 -172.85498046875 L 286.7453918457031 -123.2696304321289"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3463306427001953" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 57.147666931152344 -168.1256561279297 L -58.17543029785156
95.0760726928711"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3825962543487549" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.381195068359375 -172.35105895996094 L -77.33867645263672 -
132.167724609375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2302775382995605" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 66.31637573242188 -176.49667358398438 L 336.2142639160156 -
266.55718994140625"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5162187814712524" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.71171951293945 -169.93215942382812 L -64.99758911132812 -
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67.55034637451172"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.209887981414795" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 65.4062728881836 -170.4071044921875 L 228.33416748046875 -
54.392696380615234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2498937845230103" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.929542541503906 -169.68951416015625 L -185.1895294189453
56.5062141418457"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2869583368301392" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 57.60857391357422 -180.75013732910156 L -23.275156021118164 -
409.4239807128906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1343905925750732" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 241.08016967773438 -316.7989196777344 C 196.6707000732422 -272.5498962402344
118.1280517578125 -210.3712921142578 65.65026092529297 -177.91912841796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.426096796989441" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 39.42622375488281 -137.3098907470703 L 56.590763092041016 -
168.40066528320312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.424942135810852" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 2.1803133487701416 93.70986938476562 L 58.444366455078125 -
167.7067413330078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2565460205078125" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.69900512695312 -317.2281799316406 L 65.20271301269531 -
178.5577392578125"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3470724821090698" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.50224304199219 -190.47679138183594 L 66.45095825195312 -
176.0408172607422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3367100954055786" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 59.02626037597656 -222.44920349121094 L 59.753875732421875 -
181.13783264160156"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2685586214065552" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 46.37904357910156 -355.28173828125 L 59.368324279785156 -
181.1200714111328"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.0750627517700195" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 119.6151123046875 -27.485605239868164 C 78.3160171508789 -90.5411148071289 -
9.53258991241455 -169.54656982421875 -76.60023498535156 -203.94924926757812"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.01755952835083" stroke-linecap="round"
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201.48941040039062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0011506080627441" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 21.623844146728516 -67.79597473144531 C 8.411035537719727 -
116.92377471923828 -35.89384078979492 -177.29644775390625 -77.3338623046875 -
202.64210510253906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0007120370864868" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 64.71406555175781 4.715480804443359 C 40.71696090698242 -62.897926330566406
-23.61026954650879 -154.71058654785156 -78.96482849121094 -200.3538360595703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.42693293094635" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 52.57149124145508 -228.17262268066406 L -74.50028228759766 -
215.12094116210938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.3086767196655273" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 52.924190521240234 -76.13386535644531 L -79.74701690673828 -
199.4606170654297"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3165642023086548" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.33442687988281 -192.59844970703125 L -74.48430633544922 -
211.19602966308594"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4541771411895752" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 109.79070281982422 75.81330871582031 L -82.85201263427734 -
196.74513244628906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.50320303440094" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -6.8264007568359375 -293.31939697265625 L -79.6500244140625 -
226.5892333984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5487455129623413" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 16.24869728088379 -65.18276977539062 L -82.41480255126953 -
197.06309509277344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.711553692817688" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -63.531227111816406 6.591440677642822 L -91.61286926269531 -
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</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5229476690292358" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 115.70240783691406 -24.128629684448242 L -79.52482604980469 -
199.70362854003906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5739375352859497" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 59.927330017089844 7.183830261230469 L -82.91938018798828 -
196.69772338867188"/>
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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.4898971319198608" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 5.006110668182373 11.838332176208496 L -86.31095123291016 -
194.7843475341797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6811524629592896" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.80242919921875 -136.587158203125 L -75.53123474121094 -
206.4340362548828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.54774010181427" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 271.2061767578125 -19.523698806762695 L -76.71985626220703 -
203.71971130371094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5842082500457764" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -95.9811782836914 -146.2854766845703 L -94.8702621459961 -
193.08309936523438"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2766414880752563" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.44557571411133 -135.4632110595703 L -77.33597564697266 -
202.63865661621094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.429832935333252" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M -0.8098409175872803 93.83549499511719 L -88.562255859375 -
193.94708251953125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5049421787261963" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 214.81922912597656 -189.69415283203125 L -74.45256042480469 -
211.56935119628906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7201486825942993" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -157.87680053710938 -288.34661865234375 L -107.28981018066406 -
228.3660125732422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.192928433418274" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 150.62144470214844 -147.8270721435547 C 168.03955078125 -182.6128387451172
168.38385009765625 -239.1814727783203 151.3904266357422 -274.1766662597656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.133542776107788" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 143.8883514404297 -110.0675048828125 C 153.7108154296875 -22.186054229736328
137.99789428710938 116.71900177001953 108.79254913330078 200.1856231689453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.237229585647583" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 150.64308166503906 -112.07123565673828 C 158.072021484375 -97.27961730957031
173.90513610839844 -94.44292449951172 186.00733947753906 -105.73529815673828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1850589513778687" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 153.256103515625 -113.64379119873047 C 179.73849487304688 -76.39725494384766
194.51345825195312 -9.764266967773438 186.25689697265625 35.18515396118164"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3556379079818726" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 125.82503509521484 -117.73561096191406 C 80.41604614257812 -
82.74215698242188 -2.868821859359741 -54.44069290161133 -60.196922302246094 -
54.52252960205078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.631496787071228" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 141.7885284423828 -149.94334411621094 L 142.5323944091797 -
272.1680603027344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5227099657058716" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 157.1805419921875 -117.32137298583984 L 273.3681945800781 -
22.78830337524414"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5348175764083862" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.63629913330078 -121.28919982910156 L -151.3511962890625
10.703052520751953"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5838623046875" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 139.4187469482422 -110.07048797607422 L 104.43521118164062
199.19009399414062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.631725788116455" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 161.3533477783203 -126.4166488647461 L 180.9437255859375 -122.90679168701172"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.326359510421753" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 150.97659301757812 -112.24266815185547 L 245.79873657226562 68.04649353027344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.254652976989746" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 126.87481689453125 -116.4827880859375 L 82.36477661132812 -75.97795104980469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2701139450073242" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 145.99636840820312 -110.4179916381836 L 178.31405639648438 35.33030700683594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3803246021270752" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 161.6217498779297 -128.6019744873047 L 286.30206298828125 -120.21859741210938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3337002992630005" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 128.67648315429688 -114.73678588867188 L -53.21154022216797 98.18785858154297"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5959525108337402" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 121.66915130615234 -129.63697814941406 L -76.45817565917969 -
126.59785461425781"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6586722135543823" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 158.2863006591797 -141.06993103027344 L 338.5664367675781 -
261.76153564453125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6557995080947876" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.73028564453125 -123.5088119506836 L -61.26038360595703 -
60.98599624633789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3626253604888916" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 156.93215942382812 -117.02207946777344 L 229.36061096191406 -
55.71360778808594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4765067100524902" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 124.41338348388672 -119.82842254638672 L -182.4940185546875
60.10467529296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2946281433105469" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 131.6944122314453 -147.28012084960938 L -19.97200584411621 -
410.94281005859375"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.0512969493865967" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 124.54766845703125 -187.25711059570312 C 108.75252532958984 -
168.1556854248047 108.39879608154297 -146.48153686523438 123.7575912475586 -
138.84654235839844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1054619550704956" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 227.30401611328125 -169.6287078857422 C 217.4322509765625 -145.0662078857422
188.02317810058594 -126.66734313964844 161.61703491210938 -128.53367614746094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3943077325820923" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 134.0151824951172 -189.2677764892578 C 156.21017456054688 -
178.23446655273438 165.3421173095703 -158.57481384277344 154.41195678710938 -
145.3567352294922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3193867206573486" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 32.783287048339844 -66.68661499023438 C 48.63358688354492 -98.60620880126953
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</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.374514102935791" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 19.099712371826172 11.055482864379883 C 34.062984466552734 -
36.44689178466797 81.17880249023438 -95.10536193847656 124.3358383178711 -
119.96186828613281"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.2471709251403809" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 41.13680648803711 -135.79454040527344 C 68.31655883789062 -155.4180145263672
106.35508728027344 -158.41941833496094 126.09822845458984 -142.4983673095703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1099073886871338" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 126.35763549804688 -53.3968391418457 C 110.4302978515625 -74.38005828857422
110.53987884521484 -102.76141357421875 126.6023941040039 -116.78837585449219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0970542430877686" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 121.04908752441406 -28.341466903686523 C 107.3761978149414 -
53.589054107666016 110.96308898925781 -92.12631225585938 129.0606231689453 -
114.4168472290039"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3823095560073853" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -200.7854461669922 -222.2865447998047 L 122.35652923583984 -
135.15077209472656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4045648574829102" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 217.80703735351562 -177.57850646972656 L 158.62205505371094 -
140.55125427246094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.533625841140747" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 42.123470306396484 -132.59744262695312 L 121.67390441894531 -
130.47671508789062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6899563074111938" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.040859222412109 94.45530700683594 L 131.21054077148438 -112.89479064941406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5911883115768433" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 115.68634033203125 74.34309387207031 L 139.1436004638672 -110.10354614257812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.453294277191162" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 242.24371337890625 -315.9299621582031 L 151.1803436279297 -147.53611755371094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5245261192321777" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 129.76718139648438 -185.9751739501953 L 137.51199340820312 -149.50738525390625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6634161472320557" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.0059814453125 -223.93458557128906 L 128.83087158203125 -145.28121948242188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4565812349319458" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 48.44649887084961 -355.77227783203125 L 134.0355682373047 -148.43057250976562"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6480392217636108" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.014745712280273 -292.46099853515625 L 128.85079956054688 -
145.29786682128906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.627487063407898" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 134.0655059814453 -55.560916900634766 L 139.63356018066406 -
110.04736328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3821650743484497" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 38.9100227355957 -61.29814147949219 L 125.03634643554688 -
118.83392333984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6363780498504639" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -45.37107467651367 14.006000518798828 L 125.81737518310547 -
117.74555206298828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.609488606452942" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 132.42669677734375 -30.668712615966797 L 139.8133087158203 -
110.02981567382812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4919151067733765" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 79.72743225097656 5.378050327301025 L 133.3429412841797 -
111.75820922851562"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4637744426727295" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 25.61528968811035 14.538620948791504 L 129.1422882080078 -
114.35089874267578"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2391468286514282" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 38.481300354003906 -127.75740814208984 C 52.892662048339844 -
82.33688354492188 46.562984466552734 -19.050174713134766 24.343570709228516
13.597411155700684"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3263880014419556" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 34.557106018066406 -128.06837463378906 C 15.78316593170166 -
90.68379211425781 -26.662860870361328 -58.41331481933594 -60.248748779296875 -
55.9902458190918"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0849086046218872" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 39.3677978515625 -128.1316680908203 C 68.17868041992188 -74.33800506591797
101.12519073486328 16.35854721069336 112.95589447021484 74.44475555419922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0934005975723267" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 41.67437744140625 -130.6134490966797 C 73.70793151855469 -116.36351776123047
112.2093505859375 -82.17520141601562 127.6697006225586 -54.251712799072266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.299364686012268" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 39.522098541259766 -128.2176971435547 C 52.32244873046875 -
106.14519500732422 51.24864196777344 -77.17559051513672 37.12368392944336 -
63.51227569580078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1077134609222412" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 41.63600158691406 -130.52920532226562 C 82.40921783447266 -
111.51885986328125 120.66677856445312 -66.71121978759766 127.08665466308594 -
30.44854164123535"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1094493865966797" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 40.18922424316406 -128.67718505859375 C 69.4729995727539 -92.51992797851562
85.6307601928711 -33.04364013671875 76.2785873413086 4.1668171882629395"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2195477485656738" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.106361389160156 -128.6114501953125 L 170.37338256835938
39.06235122680664"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3555822372436523" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 39.78901672363281 -137.0899200439453 L 131.5988311767578 -
275.5009460449219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1315454244613647" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.28678894042969 -135.5752716064453 L 123.29855346679688 -
188.660888671875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1708468198776245" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.59294128417969 -129.0404815673828 L 240.97535705566406
71.5964584350586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5006333589553833" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 42.108028411865234 -132.31192016601562 L 180.6964874267578 -
121.00590515136719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2695518732070923" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 36.18158721923828 -127.5626220703125 L 27.92090606689453 -
68.18844604492188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4778250455856323" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.08307647705078 -128.5934600830078 L 118.39209747314453 -
26.61734390258789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4414799213409424" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.59904479980469 -130.4516143798828 L 270.8968200683594 -
18.914432525634766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2250615358352661" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 36.10189437866211 -127.5743408203125 L 1.8387478590011597
93.64672088623047"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4887171983718872" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 34.16157531738281 -128.28897094726562 L -50.59492492675781
9.298213005065918"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.22565758228302" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.93153381347656 -134.1463165283203 L 215.5042266845703 -
182.78907775878906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5893869400024414" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.696868896484375 -129.6365966796875 L -153.28416442871094
7.488738536834717"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4889284372329712" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 31.68366050720215 -132.48446655273438 L -76.4791488647461 -
127.25663757324219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4367440938949585" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.634132385253906 -135.74978637695312 L -254.0408172607422 -
338.169189453125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3378331661224365" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 38.67461395263672 -127.82292938232422 L 111.78356170654297
74.7737808227539"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4117224216461182" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 38.02747344970703 -127.63558959960938 L 67.09249877929688
4.033732891082764"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.545468807220459" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 38.06795883178711 -137.82862854003906 L 57.49022674560547 -
222.6092071533203"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2389309406280518" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.752593994140625 -129.20713806152344 L 124.91032409667969 -
52.07768249511719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.251886010169983" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 36.14577102661133 -127.56773376464844 L 15.98393726348877
10.341818809509277"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3816436529159546" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 42.11842346191406 -132.4682159423828 L 286.283447265625 -
119.90460205078125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2949963808059692" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M 38.992427825927734 -127.94952392578125 L 59.56731033325195 -
80.84492492675781"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2991827726364136" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 37.85459899902344 -127.60047912597656 L 98.53793334960938
199.3990936279297"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2365880012512207" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.556976318359375 -129.8358917236328 L -63.56377029418945 -
65.6568832397461"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2181917428970337" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.936134338378906 -129.33590698242188 L -184.56594848632812
57.19990921020508"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1180176734924316" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 240.91134643554688 -316.9768981933594 L 40.77835464477539 -
136.2378692626953"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -79.1054916381836 -116.34293365478516 C -62.653038024902344 -
106.90958404541016 -58.05290603637695 -86.61219024658203 -68.830810546875 -
71.00743865966797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

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<g stroke-linejoin="round" stroke-width="1.3797427415847778" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -92.03520202636719 -106.7857666015625 L -84.6175308227539 -
74.05641174316406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.511451005935669" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -80.02288818359375 -137.6910400390625 L 126.22117614746094 -
280.76776123046875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5538033246994019" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -105.7612075805664 -108.58771514892578 L -190.44204711914062
52.51659393310547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3208953142166138" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -86.48397827148438 -108.9543685913086 L 92.2153091430664
201.72662353515625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4374003410339355" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -77.43283081054688 -132.4656982421875 L 336.1629638671875 -
266.713134765625"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.3166037797927856" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -77.02947235107422 -121.535400390625 L 225.19960021972656 -
47.54766082763672"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -3.0071661472320557 95.06114196777344 C -48.01142883300781 43.91889572143555 -89.02151489257812 -46.267967224121094 -94.60575103759766 -106.3768539428711"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 122.04566955566406 -44.96843719482422 C 57.31863021850586 -46.5377197265625 -33.429237365722656 -77.46320343017578 -80.64537048339844 -114.04244232177734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

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<path d="M 9.905532836914062 -53.01284408569336 C -26.51338768005371 -54.195472717285156 -69.7094497680664 -79.21790313720703 -86.57556915283203 -108.90200805664062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -56.127777099609375 6.974733352661133 C -47.049957275390625 -29.637685775756836 -59.315818786621094 -82.47203063964844 -83.52433776855469 -111.0340805053711"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -3.8208606243133545 19.45452880859375 C -42.82649612426758 -5.171138286590576 -82.39690399169922 -61.674072265625 -92.20384216308594 -106.74830627441406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -169.22833251953125 -0.6418316960334778 C -168.92874145507812 -

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39.70682144165039 -143.4754638671875 -90.5425033569336 -112.37683868408203 -
114.1865005493164"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -68.70646667480469 93.55226135253906 L -93.95123291015625 -
106.44854736328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

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fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 48.932125091552734 -69.76447296142578 L -77.8151626586914 -
119.04364013671875"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.372036099433899" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M -73.42285919189453 11.024653434753418 C -97.81230926513672 -
17.75086784362793 -110.27943420410156 -70.5380859375 -101.26895904541016 -
106.87889099121094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.505415678024292" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -1.4311102628707886 94.06336975097656 L -88.53611755371094 -
107.92596435546875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2503563165664673" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -281.93121337890625 -132.6850128173828 L -116.44395446777344 -
126.98015594482422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.433917760848999" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.5549545288086 -190.28494262695312 L -77.25855255126953 -
131.90045166015625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3258382081985474" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 286.2604064941406 -119.24500274658203 L -76.45921325683594 -
125.9229507446289"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4196078777313232" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 12.177972793579102 -60.68756866455078 L -79.33546447753906 -
115.95218658447266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4557733535766602" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -160.42745971679688 1.4740259647369385 L -105.41007232666016 -
108.40754699707031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.476802945137024" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -340.1249084472656 -257.2829284667969 L -114.07172393798828 -
135.7610626220703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.514112114906311" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 108.67156219482422 76.76146697998047 L -82.24198913574219 -
112.22103118896484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5819677114486694" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 56.48394012451172 10.244237899780273 L -81.53620147705078 -112.97176361083984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.4442150592803955" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 180.63568115234375 -119.8448715209961 L -76.46123504638672 -125.8259506225586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.332658052444458" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 237.9823455810547 75.41827392578125 L -79.32965087890625 -115.9618148803711"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.5895705223083496" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.59245681762695 -225.31224060058594 L -79.7630844116211 -137.30711364746094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.418114423751831" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -4.4891037940979 -291.4732666015625 L -86.72689819335938 -143.76531982421875"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.395485758781433" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.67337036132812 -48.36079788208008 L -77.61201477050781 -119.58956146240234"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7650095224380493" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -65.26342010498047 6.915255546569824 L -91.89585876464844 -
106.81787109375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6132787466049194" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 112.74859619140625 -19.825820922851562 L -78.6312255859375 -
117.2200698852539"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5010733604431152" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.6179530620574951 13.749314308166504 L -84.9830093383789 -
109.90896606445312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7789509296417236" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 269.7325744628906 -15.936784744262695 L -77.30648040771484 -
120.52027130126953"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1929291486740112" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 132.9567413330078 -196.27755737304688 C 156.27301025390625 -
218.48561096191406 165.1307373046875 -253.68504333496094 152.7410430908203 -
274.8976745605469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2454962730407715" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 124.60730743408203 -187.2084197998047 C 81.2753677368164 -133.4556884765625
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-1.795096516609192 -76.4743423461914 -60.935760498046875 -59.937015533447266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1057730913162231" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 128.92166137695312 -185.85595703125 C 134.10107421875 -112.94273376464844 128.3432159423828 3.5775561332702637 116.0611343383789 74.3993911743164"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1196316480636597" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 130.41714477539062 -186.15072631835938 C 142.6336212158203 -149.07708740234375 145.01519775390625 -90.47410583496094 135.73654174804688 -55.2573127746582"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1114414930343628" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 126.75218200683594 -186.08816528320312 C 113.4251937866211 -140.46011352539062 74.11068725585938 -84.56903076171875 38.940773010253906 -61.25193786621094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1451727151870728" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 131.0428924560547 -186.3953857421875 C 152.29647827148438 -139.70065307617188 155.60684204101562 -69.29682159423828 138.436767578125 -29.144027709960938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1822943687438965" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 125.85491180419922 -186.4278564453125 L 76.08527374267578 -80.6150131225586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3779706954956055" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.02407836914062 -194.90599060058594 L 64.5497055053711 -
225.84243774414062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2890498638153076" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 134.1963348388672 -189.6671600341797 L 287.7612609863281 -
126.48649597167969"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5242555141448975" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 129.34933471679688 -198.1334228515625 L 139.8522491455078 -
272.36492919921875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.453128457069397" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.65809631347656 -188.1617889404297 L -184.1219940185547
57.736175537109375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3814669847488403" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 132.83689880371094 -187.63482666015625 L 186.5362091064453 -
133.56976318359375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1264749765396118" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 128.67140197753906 -185.84326171875 L 132.62486267089844 -
55.6124382019043"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.1410237550735474" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 128.0896453857422 -185.85302734375 L 103.46393585205078
199.10415649414062"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3805440664291382" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 128.17279052734375 -185.8482666015625 L 115.05110931396484
74.28675842285156"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.404244065284729" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 124.43306732177734 -187.354248046875 L -48.035037994384766
11.179158210754395"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3722788095474243" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 128.55517578125 -185.84083557128906 L 130.3426971435547 -
30.75345802307129"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3486539125442505" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 125.63663482666016 -186.53582763671875 L 22.310014724731445
12.383057594299316"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3712912797927856" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 125.7840347290039 -197.57301330566406 L 48.820281982421875 -
355.9400634765625"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4709670543670654" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.74895477294922 -195.9840087890625 L 7.186633110046387 -
293.63079833984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4791430234909058" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 124.82113647460938 -187.04360961914062 L 35.131385803222656 -
65.25397491455078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6608085632324219" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 134.6569061279297 -191.7948455810547 L 214.7752685546875 -
188.9065704345703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5873769521713257" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 126.9029541015625 -186.0461883544922 L 76.52266693115234
4.229799270629883"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6580313444137573" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 125.16368865966797 -186.80870056152344 L -55.4512939453125
96.5299072265625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.615015983581543" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M 134.3018341064453 -194.09275817871094 L 336.3486022949219 -266.16796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.706371545791626" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.32565307617188 -188.619384765625 L -63.49504089355469 -65.55325317382812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4660634994506836" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 3.314371347427368 94.07589721679688 L 126.0080795288086 -186.3583526611328"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4981168508529663" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 241.26678466796875 -316.6210632324219 L 132.6291046142578 -196.5969696044922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.177124500274658" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -340.021484375 -44.443382263183594 C -349.6639099121094 -75.67279052734375 -340.34112548828125 -110.97929382324219 -319.19842529296875 -123.30266571044922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0282422304153442" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -334.0344543457031 -37.02872848510742 L -83.63983917236328 103.60107421875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2977521419525146" stroke-linecap="round"

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -333.6626281738281 -37.853763580322266 L -188.26913452148438
12.779973983764648"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.270365834236145" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -343.177734375 -37.41619873046875 L -447.4297180175781 10.02119255065918"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.07468843460083" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -333.3854064941406 -39.83094787597656 L 47.6047248840332 -
61.38722610473633"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1751741170883179" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -333.4593811035156 -38.62668228149414 L 162.9638671875 51.291419982910156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4945446252822876" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -333.3858642578125 -39.838748931884766 L -100.16322326660156 -
53.390872955322266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.586056113243103" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -335.54705810546875 -43.73122787475586 L -212.31582641601562 -
218.12814331054688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7832057476043701" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -335.7571105957031 -43.87202072143555 L -181.49380493164062 -
286.7525939941406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4260015487670898" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -337.4071044921875 -44.55227279663086 L -274.66937255859375 -
330.1708679199219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.041759967803955" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -341.6270446777344 -43.61466979980469 L -452.8052062988281 -
188.8085174560547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6689016819000244" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -338.7091979980469 -44.66778564453125 L -346.8941955566406 -
253.05401611328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.091118335723877" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -336.6439514160156 -44.32119369506836 L -309.1851501464844 -
114.74053955078125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 10.068586349487305 -50.17474365234375 C -19.63355255126953 -
45.76953887939453 -49.24448776245117 -20.17630958557129 -56.06928634643555
6.98933219909668"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 13.18005084991455 -42.843162536621094 C -5.213903903961182 -28.7004337310791 -10.394966125488281 -3.359941005706787 1.6078240871429443 13.756412506103516"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 13.830255508422852 -42.05182647705078 C -25.839778900146484 -7.248580455780029 -98.9131851196289 20.37455940246582 -149.38377380371094 19.64618492126465"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 24.047531127929688 -36.748321533203125 C 18.915035247802734 11.071866035461426 -14.447892189025879 72.76383972167969 -50.47065353393555 101.0445556640625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 36.28303527832031 -40.67778015136719 C 47.15635681152344 -28.488822937011725 8.87782287597656 -29.609373092651367 62.46365737915039 -43.180599212646484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 13.283248901367188 -62.287025451660156 C -8.663381576538086 -79.53507995605469 -43.26657485961914 -81.32775115966797 -64.0051498413086 -66.29106140136719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2851067781448364" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 21.878267288208008 -37.13528823852539 C 14.561963081359863 -

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8.013240814208984 -13.829830169677734 18.92605972290039 -41.53657913208008
23.035324096679688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0946259498596191" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 41.0252685546875 -56.64977264404297 C 102.33123779296875 -73.29661560058594
183.40933227539062 -125.24957275390625 222.11827087402344 -172.68994140625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2634154558181763" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 37.12102508544922 -63.51502227783203 C 71.23878479003906 -96.53365325927734
135.4967041015625 -121.88997650146484 180.6450958251953 -120.14994812011719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2573961019515991" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 41.13313674926758 -56.22989273071289 C 69.75251007080078 -63.166107177734375
104.92549896240234 -50.319923400878906 119.69420623779297 -27.53714370727539"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0976227521896362" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 40.88840103149414 -47.87300109863281 C 64.07138061523438 -40.794776916503906
79.4516830444336 -17.599445343017578 75.24126434326172 3.935225009918213"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.290561556816101" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 34.832984924316406 -39.528995513916016 C 48.15461349487305 -
20.53193473815918 45.518898010253906 5.198142051696777 28.94594383239746
17.94074058532715"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.1176420450210571" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 29.784656524658203 -67.81397247314453 C 33.95728302001953 -83.60601806640625
44.91484832763672 -87.9164810180664 54.259063720703125 -77.441650390625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.335387945175171" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 12.91346549987793 -43.200164794921875 C -9.684767723083496 -
26.815109252929688 -44.3314323425293 -26.364076614379883 -64.4720230102539 -
42.192752838134766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3850681781768799" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.53386306762695 -58.156837463378906 L 181.94960021972656 -
112.23599243164062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.274308443069458" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.15314483642578 -56.146339416503906 L 286.7944641113281 -
114.27149963378906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2358030080795288" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 15.132049560546875 -40.732418060302734 L -180.55862426757812
176.36776733398438"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4279794692993164" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.68321990966797 -66.7358627319336 L 133.8853759765625 -
274.19244384765625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3629348278045654" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 11.82433032989502 -44.926307678222656 L -182.18057250976562 60.65935516357422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1923431158065796" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.377742767333984 -49.982704162597656 L 269.13580322265625 -13.342567443847656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1343250274658203" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 18.059261322021484 -38.6434211730957 L -56.50700378417969 95.90168762207031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2917755842208862" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 15.97616958618164 -64.9742431640625 L -158.4460906982422 -287.8840637207031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2862809896469116" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 10.358746528625488 -56.29476547241211 L -282.5020751953125 -128.58132934570312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3160662651062012" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 10.06555461883545 -54.802154541015625 L -202.1580047607422 -85.9934310913086"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6397793292999268" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 13.996889114379883 -41.86489486694336 L -46.370662689208984
12.809442520141602"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4704663753509521" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 39.02482986450195 -61.12380599975586 L 217.9868621826172 -
177.2963409423828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4246244430541992" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 39.30509567260742 -44.321556091308594 L 237.979248046875
75.42340850830078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3274356126785278" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 10.873140335083008 -47.02446365356445 L -150.61390686035156
12.446006774902344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.319750428199768" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 38.81162643432617 -43.55375289916992 L 166.1374053955078 43.5625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4771841764450073" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.45502853393555 -46.63859939575195 L 111.9920654296875 -
18.15353775024414"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5652782917022705" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 33.891754150390625 -38.91752624511719 L 61.108978271484375
6.416519641876221"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7616932392120361" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 23.34134292602539 -36.84021759033203 L 16.11669921875 10.36168384552002"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4225876331329346" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.14326095581055 -56.18785858154297 L 48.122718811035156 -
57.859249114990234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5946284532546997" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 9.900158882141113 -52.80555725097656 L -60.20065689086914 -
54.16367721557617"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2951382398605347" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.56327438354492 -51.796932220458984 L 224.64559936523438 -
43.678001403808594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -0.42167118191719055 93.73130798339844 C -10.094266891479492
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52.134639739990234 -2.101335287094116 -7.295979022979736 17.431041717529297 -
39.01069641113281"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 123.98069763183594 -50.912723541259766 C 100.59890747070312 -
67.08743286132812 62.969017028808594 -70.94627380371094 39.93199157714844 -
59.531681060791016"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0849990844726562" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 107.78581237792969 77.81732177734375 C 72.39961242675781 52.78306198120117
37.13313293457031 1.3772716522216797 29.015933990478516 -37.00072479248047"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0987483263015747" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 123.17705535888672 -39.85855484008789 C 97.70167541503906 -27.23578453063965
59.90934371948242 -28.86017608642578 38.76552200317383 -43.48673629760742"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3027455806732178" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -201.97872924804688 -219.80691528320312 L 12.972332954406738 -
61.87792205810547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2775827646255493" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -340.18951416015625 -257.1651306152344 L 11.912715911865234 -
60.231319427490234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.3958107233047485" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 110.02277374267578 75.65503692626953 L 34.44245529174805 -39.263729095458984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2373732328414917" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.0073515176773071 -290.346435546875 L 24.099756240844727 -68.25463104248047"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4600220918655396" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.886440634727478 93.65430450439453 L 23.18659782409668 -36.86468505859375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3836420774459839" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 241.45806884765625 -316.4565124511719 L 35.76219177246094 -64.76443481445312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6769545078277588" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 57.73503494262695 -222.5581512451172 L 28.667098999023438 -68.06640625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3696147203445435" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 45.441429138183594 -355.27728271484375 L 26.766679763793945 -68.30613708496094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3466075658798218" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.0711898803711 -45.4952507019043 L 41.53712844848633 -
51.35011291503906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 124.68568420410156 -37.58302307128906 C 83.11457824707031 -1.789562463760376
8.788132667541504 26.736003875732422 -41.32707977294922 26.130611419677734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 122.05253601074219 -44.23513412475586 C 83.27511596679688 -
42.567928314208984 38.764774322509766 -17.14159393310547 22.635908126831055
12.55617618560791"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 123.18708038330078 -39.838375091552734 C 49.673274993896484 -
3.223867416381836 -72.36878204345703 23.67738914489746 -149.4014892578125
20.247262954711914"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 126.83871459960938 -35.66598892211914 C 88.95652770996094 20.302640914916992
10.890019416809082 83.8334732055664 -47.527713775634766 106.23409271240234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 123.96110534667969 -38.52353286743164 C 105.06681823730469 -
25.54129409790039 83.6090316772461 -28.16999053955078 76.03380584716797 -
44.394893646240234"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 122.92475891113281 -49.002685546875 C 70.62379455566406 -71.41561889648438 -
11.796333312988281 -76.65290069580078 -61.16575241088867 -60.70048904418945"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3321369886398315" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 139.27137756347656 -53.60456848144531 L 223.1888427734375 -
171.8748321533203"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.119614839553833" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 142.67483520507812 -39.73906326293945 C 158.68646240234375 -
31.55954360961914 161.7332763671875 -21.50257110595703 149.4801025390625 -
17.276187896728516"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0846514701843262" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 132.76458740234375 -33.79205322265625 C 132.28012084960938 -
6.173774719238281 113.69679260253906 18.425277709960938 91.25757598876953
21.15146827697754"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1067920923233032" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 127.74744415283203 -35.11349105834961 C 109.22355651855469 -
1.005811095237732 66.83605194091797 27.82071876525879 33.07231140136719
29.272363662719727"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.1310598850250244" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 122.42625427246094 -47.57265853881836 L 86.86946105957031 -
57.25979995727539"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.107912421226501 5" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 122.5711441040039 -41.34832763671875 C 68.426513671875 -23.85293197631836 -
14.125429153442383 -26.23696517944336 -61.813777923583984 -46.6732177734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.083847999572754" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 140.25608825683594 -36.59131622314453 L 306.6844787597656
148.36114501953125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3206536769866943" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.27950286865234 -42.44170379638672 L -149.8160858154297
15.211877822875977"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2941664457321167" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 133.3833770751953 -55.609092712402344 L 141.87091064453125 -
272.18304443359375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.11981201171875" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 137.82945251464844 -34.938926696777344 L 173.712646484375
36.96087646484375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1549383401870728" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.1261215209961 -46.05261993408203 L -202.09873962402344 -
86.4300537109375"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0531147718429565" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 134.664306640625 -55.482933044433594 L 186.59474182128906 -
383.15252685546875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.424015760421753" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 140.41549682617188 -36.73764419555664 L 241.43838500976562
71.14868927001953"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.469983458518982" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 125.64791107177734 -36.598541259765625 L 84.79627990722656
8.709782600402832"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5990382432937622" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 140.57037353515625 -52.52228546142578 L 341.2319641113281 -
258.5599060058594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.500387191772461" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 140.2846221923828 -52.790748596191406 L 187.199951171875 -
104.55990600585938"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3481143712997437" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.70183563232422 -40.967960357666016 L -42.50339889526367
19.222137451171875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4678308963775635" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 132.19189453125 -33.81715774536133 L 131.9735107421875 -
30.705703735351562"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5673073530197144" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.69855499267578 -38.924217224121094 L 30.055849075317383
19.53965950012207"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.403151035308838" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 143.61129760742188 -42.343746185302734 L 269.355224609375 -
14.49116325378418"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4578269720077515" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 142.9892120361328 -48.99813461303711 L 287.8703308105469 -
111.00733184814453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8720712661743164" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 124.4083251953125 -37.91845703125 L -50.53750991821289 100.95986938476562"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.316949725151062" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 131.69149780273438 -33.8638801574707 L 104.50446319580078
199.19805908203125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.38347327709198" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.05409240722656 -45.20756149291992 L -60.21821212768555 -
53.628108978271484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3204562664031982" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 143.86795043945312 -44.51708984375 L 224.62889099121094 -
43.134334564208984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3464139699935913" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.64054107666016 -41.14070129394531 L -180.8434600830078
63.69008255004883"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 3.8946352005004883 94.36846923828125 C 29.822538375854492 49.25117111206055
83.60009765625 -10.214903831481934 124.01016998291016 -38.452728271484375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.079728364944458" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">
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<path d="M 113.0938491821289 74.41785430908203 C 107.07064056396484 42.0818977355957
113.7503890991211 -6.894375801086426 128.01348876953125 -34.97371292114258"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3071123361587524" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 115.8227310180664 74.36157989501953 L 131.40158081054688 -
33.901641845703125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4811592102050781" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 242.74462890625 -315.6939392089844 L 137.05397033691406 -
54.81886672973633"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4885760545730 59" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 47.659690856933594 -355.5030822753906 L 130.0676727294922 -
55.22831726074219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3524508476257324" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.948429107666016 95.13909149169922 L 125.58715057373047 -
36.653743743896484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2943538427352905" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 61.29281997680664 -222.9086151123047 L 128.8841552734375 -
54.829402923583984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

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<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 50.516571044921875 -52.07261657714844 C 20.32015609741211 -33.58180236816406
-30.10748863220215 -30.863359451293945 -62.11672592163086 -46.00080490112305"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3359947204589844" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.21870803833008 -48.59004211425781 L -179.59519958496094
177.29644775390625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.297023892402649" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 47.601783752441406 -61.4404182434082 L -60.22589874267578 -
55.62767028808594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2632155418395996" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 81.57416534423828 -48.23550796508789 L 168.6422576904297
40.57455062866211"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1894689798355103" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 87.44981384277344 -60.30256271362305 L 224.74893188476562 -
45.006404876708984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 0.7002103328704834 93.58087158203125 C -1.2017536163330078 43.71641159057617
22.200458526611328 -20.05228614807129 52.97051239013672 -48.85049819946289"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -51.582855224609375 8.728798866271973 C -33.758567810058594 -24.39961051940918 10.709211349487305 -55.14643096923828 47.73870849609375 -59.946144104003906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 10.929594039916992 10.248562812805176 C 8.12511157989502 -15.552760124206543 25.23541259765625 -44.649391174316406 49.146522521972656 -54.74058532714844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -153.358642578125 7.388383388519287 C -103.98942565917969 -29.49034309387207 -14.02682876586914 -60.57501220703125 47.57844924926758 -62.04116439819336"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -60.23710632324219 94.30498504638672 C -44.17490005493164 42.898990631103516 5.52495002746582 -22.45562744140625 50.7706184387207 -51.66864013671875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0107821226119995" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 182.23927307128906 -111.5202407836914 L 85.96378326416016 -70.3764877319336"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.096927523612976" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 108.63751220703125 76.79606628417969 C 77.9372329711914 46.756324768066406 58.04249954223633 -6.79010009765625 64.20137786865234 -42.803218841552734"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2042222023010254" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 110.6507568359375 -8.995141983032227 C 90.23233032226562 -7.191691875457764
71.90313720703125 -22.251279830932617 69.71134185791016 -42.63167190551758"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1228195428848267" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 57.15739440917969 9.526246070861816 C 41.89794921875 -5.509504795074463
40.766326904296875 -30.93791961669922 54.62984848022461 -47.26970672607422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2211596965789795" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 59.24549102783203 -222.4568328857422 L 66.53289031982422 -
82.48995971679688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.270021677017212" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 2.5961203575134277 -290.65289306640625 L 62.09434509277344 -
81.7520523071289"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5318344831466675" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 112.0442123413086 74.68453979492188 L 73.73957061767578 -
43.49148178100586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4107857942581177" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M -44.764007568359375 14.839496612548828 L 51.10050582885742 -
51.17399597167969"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5513893365859985" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -150.47833251953125 12.825922012329102 L 48.66941833496094 -55.9853515625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0616801977157593" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 218.77500915527344 -176.16909790039062 L 83.56006622314453 -
74.53395080566406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.270304560661316" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 70.514404296875 3.5833489894866943 L 68.46195220947266 -42.53678512573242"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4318677186965942" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 23.228811264038086 12.891379356384277 L 57.43474578857422 -
45.276939392089844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3023194074630737" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 3.1924474239349365 94.02416229248047 L 59.96564865112305 -
44.02021408081055"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3200311660766602" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M 46.36475372314453 -355.2806701660156 L 66.12775421142578 -
82.4647445678711"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.334639072418213" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 115.12010192871094 -23.45131492614746 L 83.02587890625 -49.82048034667969"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3173366785049438" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -54.095523834228516 97.47512817382812 L 55.466434478759766 -
46.597328186035156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3622366189956665" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.47739791870117 -357.977783203125 L -449.5836486816406
6.371608257293701"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.346261978149414" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -457.5733947753906 -187.2960968017578 L -464.85028076171875 -
1.6801438331604004"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.022726058959961" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -350.3489990234375 -253.6856231689453 L -457.82879638671875 -
0.10968593508005142"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.024470567703247" stroke-linecap="round"

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -316.5904846191406 -119.78150939941406 L -450.9626159667969
4.711946487426758"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2168141603469849" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -6.903128147125244 29.637502670288086 L -445.6398620605469
18.7984561920166"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.451192021369934" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -99.84891510009766 -50.83644104003906 L -445.98175048828125
14.589865684509277"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.325315237045288" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -210.8217010498047 180.48463439941406 L -448.7613525390625
29.04328727722168"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2657966613769531" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -80.30886840820312 25.529695510864258 L -445.63726806640625
18.67945671081543"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="6" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#dad4a2">

<path d="M -566.6243896484375 12.294883728027344 L -592.6647338867188 -
41.95014572143555"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="6" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#dad4a2">

<path d="M -628.9318237304688 -4.648495197296143 L -610.2503662109375 -
42.084716796875"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="6" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#dad4a2">

<path d="M -570.2291870117188 16.990659713745117 L -623.1384887695312
7.020166397094727"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1581807136535645" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 191.7774658203125 72.6485595703125 C 211.0004119873047 110.0944595336914
259.7358093261719 148.5284881591797 300.63104248046875 158.49334716796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2439837455749512" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 180.35406494140625 34.98754119873047 L 144.9436798095703 -
272.2991638183594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.192793846130371" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 198.34776306152344 67.24073791503906 L 304.3583679199219
150.84349060058594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1332095861434937" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 173.84378051757812 72.81608581542969 L 110.98700714111328
201.10333251953125"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0366612672805786" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 191.96047973632812 37.15870666503906 L 345.86907958984375 -
255.19036865234375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2712408304214478" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 164.17935180664062 47.170318603515625 L -61.732627868652344 -
46.86534118652344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0032633543014526" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -340.30108642578125 -256.97198486328125 L 165.4657440185547
44.613006591796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.001777172088623" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 90.31585693359375 17.057802200317383 C 116.57122802734375 8.026032447814941
152.20083618164062 18.048852920532227 169.89683532714844 39.44439697265625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0722999572753906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 236.76156616210938 -168.2862091064453 C 242.86553955078125 -
107.53032684326172 223.1056671142578 -15.38516902923584 192.62664794921875
37.525753021240234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.203173279762268" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 243.8071746826172 -315.3949279785156 L 185.90335083007812
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35.12348937988281"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0251359939575195" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -46.733299255371094 108.81499481201172 L 163.17506408691406
59.43587112426758"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0161924362182617" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.88146209716797 33.01737976074219 L 162.85293579101562
51.970130920410156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1708565950393677" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 230.56875610351562 -168.630615234375 L 186.837158203125
35.300636291503906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0491271018981934" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 90.65630340576172 28.979482650756836 L 163.39089965820312
49.440147399902344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5692723989486694" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 294.66217041015625 -102.58084869384766 L 194.23846435546875
38.56005096435547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2764829397201538" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.710563659667969 98.11023712158203 L 163.22198486328125 59.6309814453125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3035706281661987" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 47.976593017578125 -355.5984802246094 L 176.40878295898438
35.85272216796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3517205715179443" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.310868263244629 -291.3309631347656 L 173.4847412109375
37.076438903808594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.312543511390686" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 143.006103515625 4.9111857414245605 L 170.21072387695312
39.190086364746094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0031932592391968" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 148.7167205810547 -19.1697998046875 L 400.2422180175781 -
135.82797241210938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2133002281188965" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 118.24203491210938 4.991401195526123 C 99.8715591430664 28.449438095092773
61.49855041503906 41.804012298583984 32.53351974487305 34.819679260253906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.1149413585662842" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 126.95682525634766 8.915544509887695 C 123.69849395751953 26.63842010498047
107.2746810913086 36.164222717285156 90.2732162475586 30.1920223236084"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0326210260391235" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 135.04672241210938 8.738485336303711 L 185.2299346923828
227.41078186035156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.017464518547058" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 146.38226318359375 1.4956544637680054 L 239.29945373535156
73.49712371826172"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2249575853347778" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 111.04722595214844 -15.083333969116211 L -202.41946411132812 -
84.5731201171875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3248605728149414" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 113.59330749511719 -0.18674466013908386 L -176.96939086914062
180.65538024902344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3244807720184326" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 131.43099975585938 -30.73638153076172 L 141.7963104248047 -
272.18609619140625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2675645351409912" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 113.65840148925781 -0.08287836611270905 L -49.28707504272461 102.722900390625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4516180753707886" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 110.67322540283203 -8.757034301757812 L -149.48171997070312 17.35982894897461"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6204023361206055" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 140.700439453125 -28.001205444335938 L 224.63504028320312 -170.9396209716797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5012301206588745" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 113.27256774902344 -0.7204292416572571 L 88.70419311523438 13.529218673706055"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4337729215621948" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 111.68439483642578 -4.18110466003418 L 31.979570388793945 23.55777359008789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4631803035736084" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 141.4131622314453 -27.5623779296875 L 189.79029846191406 -102.5721206665039"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4870579242706299" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 150.57305908203125 -10.680395126342773 L 268.882080078125 -
10.240039279174805"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4445961713790894" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 147.60597229003906 -21.237361907958984 L 289.2242431640625 -
108.39427185058594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3426792621612549" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 143.5865936279297 -25.941997528076172 L 342.17254638671875 -
257.70050048828125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3728328943252563" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 110.99147033691406 -14.82370662689209 L -60.61518096923828 -
50.48215866088867"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2840687036514282" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 149.82798767089844 -16.16341209411621 L 225.3711700439453 -
37.38332748413086"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3234617710113525" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 111.1483383178711 -5.992977619171143 L -180.32257080078125
65.45816802978516"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.089935064315796" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 110.37637329101562 75.43486785888672 C 95.35140228271484 49.912052154541016
97.54878234863281 17.096406936645508 115.28436279296875 2.139075517654419"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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<g stroke-linejoin="round" stroke-width="1.3817509412765503" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -201.6795654296875 -220.2459716796875 L 113.65531921386719 -
21.42180633544922"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4665820598602295" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 116.03917694091797 74.39561462402344 L 127.20813751220703
8.960090637207031"/>

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</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 5.46347713470459 95.67321014404297 L 115.3395004272461 2.204171657562256"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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<g stroke-linejoin="round" stroke-width="1.36329185962677" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 47.456146240234375 -355.45062255859375 L 125.88493347167969 -
30.197526931762695"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2475606203079224" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 242.8936309814453 -315.6363220214844 L 137.48707580566406 -
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29.5217342376709"/>

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</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 60.9044189453125 -222.76686096191406 L 124.32951354980469 -
29.755216598510742"/>

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</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

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28.980382919311523"/>

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</g> <!-- transform -->

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<path d="M -41.673519134521484 22.228960037231445 L 110.93009948730469 -
6.993303298950195"/>

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218.65205957242523)">

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fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 122.9654312133789 81.78424072265625 C 176.86622619628906 76.13184356689453
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.028760552406311" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 113.86741638183594 91.00617218017578 L 104.00383758544922
199.14602661132812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0660974979400635" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 120.0054702758789 76.2276611328125 C 154.7683868408203 34.64900588989258
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</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0854007005691528" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 106.29681396484375 81.74139404296875 C 81.13156127929688 78.9715347290039
63.74689483642578 61.703582763671875 67.46707153320312 43.17234802246094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0967564582824707" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 106.32073211669922 83.77155303955078 C 72.71979522705078 88.27326202392578
35.13652420043945 72.18855285644531 22.376148223876953 47.845340728759766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2150964736938477" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 118.11351776123047 90.28216552734375 L 181.3890838623047
228.7141876220703"/>

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6076831817626953" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 106.65351104736328 80.07818603515625 L -42.27219009399414
31.89566421508789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2508708238601685" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 107.7755126953125 77.83190155029297 L -63.84511947631836 -
43.035037994384766"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5892720222473145" stroke-linecap="round"
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<path d="M 107.18370819091797 78.80701446533203 L 30.85460090637207 39.3209228515625"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5306659936904907" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 122.02694702148438 78.71749877929688 L 271.230224609375 -
0.7629055976867676"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4138128757476807" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 109.05436706542969 76.39835357666016 L -257.07806396484375 -
334.76873779296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4268507957458496" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 123.00911712646484 82.8427505493164 L 235.1133575439453 85.30787658691406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4588261842727661" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 112.22203826904297 74.62907409667969 L 2.719151735305786 -
290.6888427734375"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8839435577392578" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 109.6800765991211 75.89285278320312 L 83.21111297607422 39.70612335205078"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.395185112953186" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 107.16071319580078 78.85179138183594 L -204.12673950195312 -
79.81903839111328"/>

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0747040510177612" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 243.0871124267578 -315.56951904296875 L 117.20218658447266
74.68090057373047"/>

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1147516965866089" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.818270683288574 98.6578598022461 L 106.3373031616211 83.88895416259766"/>

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</g> <!-- transform -->

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 60.0366096496582 -222.54782104492188 L 113.15289306640625
74.40707397460938"/>

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<path d="M 91.02533721923828 27.43475914001465 C 143.62928771972656 37.81300735473633
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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.679837465286255" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 57.657997131347656 38.091453552246094 C 3.774397373199463 95.04176330566406
-100.35736846923828 160.8361053466797 -174.9268035888672 185.04722595214844"/>

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2561023235321045" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#9bd8de">

<path d="M 88.93095397949219 13.93078899383545 C 135.9200897216797 -11.893717765808105
216.65621948242188 -24.41538429260254 269.2601623535156 -14.037135124206543"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0008950233459473" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 85.5479507446289 37.703460693359375 C 135.58306884765625 87.72266387939453
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</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-linecap="round" fill="none" stroke-opacity="1"
stroke="#90e190">

<path d="M 76.75048828125 4.291562080383301 L 184.37843322753906 -383.63397216796875"/>

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</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0009511709213257" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 60.769718170166016 40.50232696533203 L -80.76121520996094
265.9482116699219"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.5366097688674927" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.49576187133789 34.246559143066406 L -177.04147338867188
180.54043579101562"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2286304235458374" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 88.84124755859375 33.35782241821289 L 302.62481689453125
153.43392944335938"/>

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</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0525599718093872" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0346651077270508" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

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<path d="M 51.529232025146484 25.802059173583984 L 32.96510696411133 27.89297103881836"/>

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<path d="M 90.34766387939453 29.976139068603516 L 236.16441345214844 79.33499908447266"/>

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<path d="M 91.16727447509766 20.498348236083984 L 269.11822509765625 -7.10072135925293"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.4569870233535767" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 84.81595611572266 8.727544784545898 L 187.21788024902344 -104.54368591308594"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 90.08016204833984 16.409215927124023 L 225.94937133789062 -
35.63759231567383"/>

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<g stroke-linejoin="round" stroke-width="1.313572645187378" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

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81.74212646484375"/>

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 53.624908447265625 14.402827262878418 L -62.41824722290039 -
45.39033126831055"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.0008617639541626" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -202.41009521484375 -219.27301025390625 L 56.44037628173828
10.293198585510254"/>

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<g stroke-linejoin="round" stroke-width="1.545107364654541" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.977650165557861 95.16602325439453 L 57.80137252807617 38.22578048706055"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.5592511892318726" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 59.22910690307617 -222.4560089111328 L 70.4150619506836 3.588017225265503"/>

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -41.32868576049805 25.551462173461914 L 51.40667724609375
23.916194915771484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3970606327056885" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 242.37281799316406 -315.862548828125 L 80.40068054199219
5.7015509605407715"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3343756198883057" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 46.32307052612305 -355.2778015136719 L 70.0823974609375
3.6072587966918945"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5285499095916748" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 2.0527889728546143 -290.5156555175781 L 67.09130859375 4.033996105194092"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6469391584396362" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 91.09422302246094 202.421630859375 L -69.1039810180664 -37.90935516357422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.286649227142334" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 111.74394989013672 201.49441528320312 L 235.0691680908203 -
25.2230167388916"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1462565660476685" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 21.621387481689453 48.220916748046875 L 93.65653228759766
200.97389221191406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1275213956832886" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 300.6885681152344 168.1931610107422 L 121.56107330322266
214.09837341308594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.292657494544983" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -48.247379302978516 40.79294967651367 L 89.28878784179688 203.7783203125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.061149001121521" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 228.57130432128906 -169.16836547851562 L 108.37812042236328
200.04568481445312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1991885900497437" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.776778697967529 104.07630157470703 L 89.259521484375 203.80307006835938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2194170951843262" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -49.26116943359375 124.02555084228516 L 85.24644470214844 208.4326171875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3695015907287598" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 195.0443572998047 -100.17561340332031 L 107.77305603027344 199.8592529296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2927156686782837" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 172.1936798095703 256.56884765625 L 138.3964385986328 275.2237243652344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1930313110351562" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 25.723506927490234 45.636741638183594 L 177.07070922851562 231.3987579345703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1938339471817017" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -258.1651306152344 -333.86749267578125 L 177.4900360107422 231.0663604736328"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3841981887817383" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 200.03390502929688 -99.38861083984375 L 190.29981994628906 226.91294860839844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5013171434402466" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 303.23150634765625 174.0317840576172 L 206.53443908691406 236.10044860839844"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3731422424316406" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 313.185791015625 144.4475860595703 L 251.502685546875 -24.01136016845703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1488463878631592" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 29.087039947509766 42.13642501831055 C 96.23253631591797 92.52816009521484
217.688232421875 145.1888885498047 300.3659362792969 159.75746154785156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1847411394119263" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 31.44023323059082 38.08740997314453 L 301.7130432128906
155.27223205566406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0946033000946045" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.767594814300537 100.69779205322266 L 300.4493408203125
159.3135986328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.457440972328186" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 267.9573059082031 101.07429504394531 L 307.2137145996094
147.9014434814453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -5.672084331512451 37.056427001953125 C -47.0001220703125 52.30973434448242
-112.31820678710938 48.453102111816406 -151.56411743164062 28.44240379333496"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 10.04096508026123 49.897552490234375 C 5.827038288116455 77.20843505859375 -
19.53567886352539 103.84123229980469 -46.60824966430664 109.38357543945312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 7.7951250076293945 10.845288276672363 C -0.19252340495586395 -
18.244855880737305 -30.76472282409668 -45.99698257446289 -60.48979568481445 -
51.14081954956055"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.414596438407898" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -6.616337776184082 26.721195220947266 C -36.34141159057617
21.577356338500977 -66.91361236572266 -6.174771308898926 -74.90126037597656 -
35.264915466308594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2043540477752686" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 28.729293823242188 17.664031982421875 L 184.9917449951172 -
106.91229248046875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1642159223556519" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 30.91992950439453 21.069385528564453 L 288.4278564453125 -
109.81478118896484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.096369743347168" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -0.7018049955368042 44.614715576171875 L -52.409297943115234
98.91155242919922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1635103225708008" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -4.751532554626465 21.095293045043945 L -204.10313415527344 -
79.8655014038086"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3588594198226929" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.88063049316406 27.239845275878906 L 269.0920715332031 -
7.274340629577637"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.599694013595581" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.1288344860076904 14.102975845336914 L -258.4165954589844 -
333.67669677734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5259475708007812" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.58271789550781 34.61073684692383 L 235.6165771484375 81.26828002929688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.836424708366394" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -2.694026231765747 42.41315460205078 L -178.16448974609375
178.94171142578125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.2293260097503662" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -6.874457836151123 28.9526309967041 L -149.41647338867188 20.536405563354492"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2699167728424072" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 20.644481658935547 11.612773895263672 L 182.17164611816406 -384.3872985839844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.755910038948059" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -1.7178596258163452 16.688817977905273 L -65.38827514648438 -41.10844039916992"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4314837455749512" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 32.16698455810547 24.1232852935791 L 225.54974365234375 -36.783782958984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -2.795464515686035 94.88339233398438 C -19.14032554626465 74.47261047363281 -19.668296813964844 50.151512145996094 -3.9747202396392822 40.560691833496094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -46.782188415527344 12.368950843811035 C -32.86073684692383 -1.0461052656173706 -11.750380516052246 -0.0028881642501801252 0.36910951137542725 14.699041366577148"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3833421468734741" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 57.80300521850586 -222.54574584960938 L 16.57571029663086 10.437413215637207"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4038851261138916" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 0.4120791256427765 -290.30377197265625 L 12.300047874450684 10.147089958190918"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5495495796203613" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -41.35759735107422 27.010622024536133 L -6.8764567375183105 28.98698616027832"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.1190004348754883" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.955342173576355 93.66596221923828 L 9.638083457946777 49.831172943115234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -4.919665336608887 98.39939880371094 C -35.24021911621094 92.52542114257812 -60.12627410888672 68.79048156738281 -60.50422668457031 45.38592529296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -4.461157321929932 96.99549102783203 L -151.28651428222656 27.87605857849121"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -3.782353401184082 95.88671112060547 C -24.186298370361328 80.09319305419922
-47.80192565917969 80.09436798095703 -56.52933120727539 95.88932800292969"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -3.7939586639404297 95.9017562866211 C -43.135963439941406 65.64958953857422
-76.8597640991211 7.230828762054443 -79.11817932128906 -34.580192565917797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.084944248199463" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -1.953068733215332 104.74486541748047 C -14.431739807128906
127.32891082763672 -36.11600875854492 136.6825408935547 -50.3862419128418
125.63677978515625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.600975871086206" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -4.46167516708374 102.06763458251953 L -175.85235595703125
182.70863342285156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.494831919670105" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.962916612625122 93.66729736328125 L 57.805179595947266 -
222.5453643798828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.38326895236969" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 5.771084308624268 96.06718444824219 L 289.9903259277344 -
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107.24093627929688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6065552234649658" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -4.965839862823486 98.67132568359375 L -179.9574432373047
73.11066436767578"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4442622661590576" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -2.899413585662842 94.96858215332031 L -48.29397964477539
40.83214569091797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0947924852371216" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -4.905307292938232 100.736572265625 L -46.61515426635742
109.34999084472656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1742472648620605" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -3.6207146644592285 95.68695068359375 L -206.67262268066406 -
75.98883819580078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4124115705490112" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -3.7937228679656982 95.90145111083984 L -286.0655212402344 -
121.18158721923828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5058544874191284" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 4.9409708976745605 95.13227844238281 L 187.1512451171875 -
104.60419464111328"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.31950843334198" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.069979667663574 96.52864837646484 L 227.35552978515625 -
32.70573043823242"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5790661573410034" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 1.5045299530029297 93.6045913696289 L 45.22605514526367 -
355.2947998046875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.476701021194458" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -1.847320556640625 94.26231384277344 L -70.87948608398438 -
36.854026794433594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0014584064483643" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 252.4561004638672 65.92423248291016 L 192.37777709960938 -
383.0826416015625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2142410278320312" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 253.48289489746094 65.8137435913086 L 246.25160217285156 -
22.858131408691406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.300187110900879" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -283.3075866699219 -126.05265045166016 L 236.4967803955078
78.4261474609375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0580228567123413" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -201.7907257080078 -220.07489013671875 L 238.4880828857422
74.6227798461914"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5485557317733765" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 244.7511749267578 -315.3297424316406 L 254.5922088623047
65.75423431396484"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3140195608139038" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -41.66633224487305 29.52361297607422 L 235.4580535888672
82.02478790283203"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4376473426818848" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 236.24368286132812 -168.24098205566406 L 253.6271209716797
65.80250549316406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5373505353927612" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 205.76394653320312 -100.04981231689453 L 249.97483825683594
66.41766357421875"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4657247066497803" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 5.18669319152832 -291.8443603515625 L 244.06980895996094
69.06983184814453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0002272129058838" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 169.85772705078125 -400.6087341308594 L -250.5109100341797 -
352.0024108886719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.121830940246582" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -207.5733642578125 -231.69493103027344 C -205.25320434570312 -
272.0560302734375 -225.93490600585938 -319.9041442871094 -253.7672576904297 -
338.56671142578125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4993914365768433" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -451.6138000488281 -199.36294555664062 L -285.7716369628906 -
336.9359436035156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4420630931854248" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -211.32972717285156 -230.92579650878906 L -261.47540283203125 -
331.7961120605469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5278375148773193" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -341.9404296875 -267.1692199707031 L -283.4803771972656 -
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334.59417724609375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4205752611160278" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -188.92343139648438 -312.03094482421875 L -252.22610473632812 -
341.30938720703125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4666459560394287" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -299.03387451171875 -153.1648406982422 L -273.2640075683594 -
329.9143981933594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.165173053741455" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -342.9023742675781 -254.29837036132812 L -180.09178161621094
2.4669277667999268"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4093835353851318" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -342.47784423828125 -254.5869598388672 L -233.71104431152344 -
105.0748062133789"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4443306922912598" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -339.215087890625 -261.97857666015625 L -9.217656135559082 -
298.58721923828125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.9830936193466187" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -339.3901672363281 -262.9772033691406 L -190.21377563476562 -
298.9470520019531"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.9607689380645752" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -344.5214538574219 -253.51039123535156 L -308.6037902832031 -
152.22396850585938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.004086971282959" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -452.0894470214844 -199.88348388671875 C -429.1534118652344 -
222.9498291015625 -385.64007568359375 -249.29701232910156 -354.89971923828125 -
258.7315673828125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.0908873081207275" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -450.9764099121094 -198.4658966064453 L -354.0967102050781 -
256.935302734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6370435953140259" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -215.22799682617188 -226.14578247070312 L -339.4339904785156 -
259.03277587890625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0076968669891357" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -152.12098693847656 -296.41180419921875 L 287.60699462890625 -
126.10021209716797"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0109584331512451" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -172.31649780273438 -283.6949768066406 L -198.20193481445312 50.279781341552734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4341381788253784" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -175.407470703125 -284.17999267578125 L -217.3089599609375 -108.35681915283203"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2335160970687866" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -170.68496704101562 -283.6353454589844 L -169.4677276611328 -0.642234742641449"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.882897138595581" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -182.9756317138672 -287.79071044921875 L -289.7146911621094 -149.21853637695312"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0598653554916382" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -212.41172790527344 -230.26812744140625 C -239.69883728027344 -267.6185607910156 -229.99221801757812 -299.9029235839844 -190.7313995361328 -302.3772277832031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="3.9080352783203125" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M -201.09698486328125 -227.0938262939453 C -174.6278076171875 -238.06134033203125 -158.39505004882812 -263.7785339355469 -164.84010314941406 -284.5347900390625"/>

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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2569379806518555" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -451.2825622558594 -198.93226623535156 C -383.33251953125 -247.3132781982422
-266.64520263671875 -293.2236633300781 -190.6540985107422 -301.4759521484375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3383703231811523" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -210.21890258789062 -231.37103271484375 C -218.71531677246094 -
258.7336730957031 -209.32618713378906 -287.6598205566406 -189.24769592285156 -
295.9793395996094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7331936359405518" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 52.851593017578125 -230.7986602783203 L -151.75430297851562 -
297.4411926269531"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.320408582687378" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -66.98878479003906 7.403992176055908 L -164.44081115722656 -
284.6633605957031"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4541460275650024" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 215.52658081054688 -193.66213989257812 L -151.53529357910156 -
298.1590576171875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6275441646575928" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M -450.39788818359375 -197.27809143066406 L -189.4644775390625 -
296.5250244140625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.6377334594726562" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -204.82904052734375 -231.00021362304688 L -179.2617950439453 -
285.5269775390625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3959373235702515" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -208.7683868408203 -216.7972869873047 L -219.89569091796875 -
108.79634857177734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4384709596633911" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -203.5052947998047 -218.26206970214844 L -92.22967529296875 -
70.52645111083984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4571322202682495" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -204.2115936279297 -217.7904815673828 L -70.70494842529297
9.094640731811523"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4287464618682861" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -206.8318634033203 -216.8501434326172 L -172.51353454589844 -
0.39568832516670227"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6494477987289429" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -213.3744659423828 -219.03541564941406 L -287.5450744628906 -147.28021240234375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.128208041191101" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M -450.12188720703125 -196.38595581054688 C -386.21307373046875 -211.79737854003906 -281.1589660644531 -224.26629638671875 -215.47698974609375 -224.2360382080078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1666356325149536" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 39.96296691894531 -358.78350830078125 L -201.43255615234375 -227.7974853515625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7480993270874023" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -449.9678649902344 -195.5266876220703 L -215.42494201660156 -223.3520050048828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.082260012626648" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#a0b3dc">

<path d="M 230.7418212890625 -207.77777099609375 C 224.0638427734375 -240.319580078125 193.11587524414062 -275.2569885253906 161.6175994873047 -285.8126525878906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0218696594238281" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 221.50076293945312 -203.15707397460938 L 155.91563415527344 -277.1966552734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5229393243789673" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.998924255371094 -232.67047119140625 L 126.70348358154297 -280.1021423339844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.427256703376777" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -50.3142204284668 9.474442481994629 L 131.87631225585938 -275.3201599121094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5207350254058838" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 194.26817321777344 -138.34083557128906 L 149.01620483398438 -273.2065734863281"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4108115434646606" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 292.5272521972656 -133.41964721679688 L 156.38389587402344 -277.6248779296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1388338804244995" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -57.04517364501953 95.61406707763672 L 133.49740600585938 -274.386962890625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0201311111450195" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 55.7820930480957 -223.2704315185547 C 2.7927284240722656 -129.3068389892578 -104.52717590332031 -3.382896423339844 -183.9236297607422 57.98857498168945"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.401011347770691" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.9601936340332 -224.92698669433594 L 184.80111694335938 -
131.60421752929688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4432604312896729" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.74293518066406 -224.0018310546875 L -186.66355895996094
55.09343338012695"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2221221923828125" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 65.12610626220703 -227.38845825195312 L 215.27586364746094 -
192.6892852783203"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1320867538452148" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.936378479003906 -223.84107971191406 L -67.7198257446289 -
70.18190002441406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.463506817817688" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 64.74015808105469 -226.2342529296875 L 287.98126220703125 -
127.00066375732422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5900527238845825" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 54.59748840332031 -224.13157653808594 L -155.84158325195312
4.638031482696533"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2745575904846191" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 58.2928352355957 -235.16958618164062 L 46.534149169921875 -
355.29510498046875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6298340559005737" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 56.20166015625 -223.05389404296875 L -52.52642822265625 8.253631591796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7333695888519287" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.534576416015625 -224.4307098388672 L 274.38787841796875 -
23.94718360900879"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2943464517593384" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 63.41850280761719 -224.31178283691406 L 230.4960174560547 -
56.946266174316406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3118053674697876" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.13699340820312 -318.1181335449219 L 64.63324737548828 -
231.64212036132812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 50.718170166015625 -366.67034912109375 C 81.72400665283203 -
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396.6336975097656 135.20977783203125 -414.75946044921875 170.18199157714844 -
407.15533447265625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 39.15567398071289 -362.310302734375 C 7.39073371887207 -363.8077087402344 -
21.93342399597168 -384.5351867675781 -26.341663360595703 -408.6064147949219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 52.29536437988281 -364.023193359375 C 82.08809661865234 -373.44732666015625
104.23922729492188 -400.37384033203125 101.77130126953125 -424.1652526855469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.10514497756958" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 49.569847106933594 -367.62103271484375 L 88.7383041381836 -
427.3351135253906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.533715844154358" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 42.55314254760742 -356.1419677734375 L -189.86572265625 52.83171463012695"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.201425313949585" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 50.831050872802734 -357.4361267089844 L 220.0449981689453 -
201.72860717773438"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.445924162864685" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 49.4978141784668 -356.3191223144531 L 189.87489318847656 -
136.24156188964844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2240467071533203" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.25444412231445 -358.2965087890625 L -285.2066955566406 -
144.35986328125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.519864797592163" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 52.34573745727539 -360.1302795410156 L 335.967529296875 -
278.4241943359375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2914903163909912" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 41.89332580566406 -356.5697937011719 L 5.561161041259766 -
307.1236267089844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5137025117874146" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 52.35200881958008 -363.8345642089844 L 170.48829650878906 -
397.43463134765625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.404750943183899" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 43.32490539550781 -355.7663269042969 L -72.60860443115234 -
73.05561065673828"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2033272981643677" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 49.43581771850586 -356.2800598144531 L 234.05482482910156 -
59.7699089050293"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5195174217224l2" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 40.81147003173828 -366.4230651855469 L -14.887055397033691 -
415.1158142089844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1289358139038086" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 239.63609313964844 -320.7019348144531 C 185.98291015625 -324.72509765625
102.07696533203125 -342.21142578125 52.2269287109375 -359.75872802734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.7758046388626099" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 239.72848510742188 -321.3539733886719 L 52.465553283691406 -
360.6124267578125"/>

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</g> <!-- transform -->

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<g stroke-linejoin="round" stroke-width="1.255281686782837" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -8.119194984436035 -295.1206970214844 L -284.3989562988281 -
143.0196075439453"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2938299179077148" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 8.461419105529785 -295.6184387207031 L 216.69485473632812 -
196.7632293701172"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4858908653259277" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.625640869140625 -293.01873779296875 L 274.7547302246094 -
24.3230037689209"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.452501654624939" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 6.9748311042785645 -293.38671875 L 185.7535858154297 -132.7469940185547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5060940980911255" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -1.6689189672470093 -290.4552001953125 L -57.236270904541016
6.733893871307373"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5743263959884644" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 8.068283081054688 -294.87823486328125 L 289.0334167480469 -
129.04283142089844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4425113201141357" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -6.71466064453125 -293.1995849609375 L -207.43968200683594 -
102.67058563232422"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.497731328010559" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 9.335545539855957 -298.91534423828125 L 335.2423400878906 -
274.38861083984375"/>
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```
</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.635905146598816" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -2.8558712005615234 -290.75909423828125 L -73.97346496582031 -
73.55815124511719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6457616090774536" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -2.071432113647461 -308.6895446777344 L -25.404651641845703 -
408.80126953125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1004291772842407" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 239.6399383544922 -319.9061279296875 L 9.328582763671875 -
300.4009704589844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1488231420516968" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -453.1314697265625 -188.5725555419922 L -205.2228546142578
174.7035369873047"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4155278205871582" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -449.9643249511719 -193.821044921875 L 180.75991821289062 -
121.65328979492188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.005953788757324" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">
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<path d="M -450.4305419921875 -191.95497131347656 L -320.52423095703125 -
140.71286010742188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6378391981124878" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -451.37139892578125 -190.2628936767578 L -185.4326934814453
7.425878524780273"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -11.752300262451172 -419.96978759765625 C 16.671855926513672 -
406.9867248535156 59.55942153930664 -412.2063293457031 84.03975677490234 -
431.62811279296875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2.076713085174560 5" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -10.09090518951416 -430.69549560546875 L 79.85421752929688 -
441.6422424316406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 171.82321166992188 -411.822998046875 C 123.58500671386719 -435.8503723144531
41.964698791503906 -445.2780456542969 -10.48084545135498 -432.8802795410156"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.027406096458435" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 239.6522216796875 -320.8760070800781 C 158.49423217773438 -329.8238830566406
44.97712326049805 -372.5667724609375 -13.895325660705566 -416.344970703125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.504294514656067" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 170.2617950439453 -398.304931640625 C 117.81625366210938 -385.90716552734375 36.19594192504883 -395.3348388671875 -12.042269706726074 -419.3622131347656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6594713926315308" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 239.96884155273438 -322.1575927734375 L -11.33135986328125 -420.9611511230469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8206154108047485" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 169.85745239257812 -405.2008361816406 L -10.076507568359375 -425.984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.77378249168396" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -77.5316390991211 -74.37268829345703 L -32.60968017578125 -408.4576110839844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3402103185653687" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 233.02297973632812 -59.0821533203125 L -18.341419219970703 -411.9890441894531"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.8039894104003906" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 180.80613708496094 -420.8070373535156 C 170.05941772460938 -442.3759460449219 142.42422485351562 -455.0096740722656 119.08120727539062 -449.0252380371094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.914284110069275" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 171.53599548339844 -411.221435546875 L 117.89710235595703 -435.7430419921875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7955063581466675" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.819580078125 -323.5747375488281 L 114.9178237915039 -431.0718688964844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3614888191223145" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -88.59741973876953 -36.40083694458008 L -185.54876708984375 173.07318115234375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3314378261566162" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -60.20999526977539 -53.827518463134766 L 224.63905334472656 -43.5155143737793"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -77.2734146118164 15.443315505981445 C -95.0140380859375 4.174503803253174 -100.86616516113281 -19.446929931640625 -90.34451293945312 -37.31663513183594"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.474826455116272" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -153.9823455810547 6.595924377441406 L -95.59626007080078 -41.78942108154297"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -76.24932861328125 96.10179138183594 C -96.5799789428711 61.110015869140625
-101.50228118896484 2.040532350540161 -87.24358367919922 -35.83359146118164"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3963831663131714" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 181.1427764892578 -114.88105010986328 L -60.70941925048828 -
59.04974365234375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.184688687324524" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 269.0249938964844 -12.553927421569824 L -60.3399772644043 -
52.16310119628906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1509301662445068" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -67.86272430419922 93.4638900756836 L -78.53604888916016 -
34.62015914916992"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4571311473846436" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -65.38396453857422 6.943887233734131 L -75.51325988769531 -
35.10722351074219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5504502058029175" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -283.0747375488281 -126.67475128173828 L -99.04151153564453 -
61.25039291381836"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.536805272102356" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.75241088867188 -317.1617736816406 L -64.71813201904297 -
67.21629333496094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6969987154006958" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 286.5284423828125 -115.59300231933594 L -60.46833801269531 -
57.83492660522461"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4779260158538818" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -202.50804138183594 -84.1913070678711 L -99.63430786132812 -
59.261436462402344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -77.18763732910156 36.48081588745117 C -99.45416259765625 50.88065719604492
-133.8497314453125 48.94404220581055 -154.01226806640625 32.15526580810547"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2948811054229736" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -48.58792495727539 41.07378005981445 C -34.779685974121094
58.209693908691406 -36.23509216308594 84.35781860351562 -51.83866500854492
99.47725677490234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0976121425628662" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#a0b3dc">
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<path d="M -62.01592254638672 45.3516845703125 L -64.97381591796875
93.43254852294922"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.402769684791565" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -73.04488372802734 41.07792663574219 L -181.4055938720703 175.64599609375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3596503734588623" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -79.39000701904297 31.8201961517334 L -180.69369506835938
64.14092254638672"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5274806022644043" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -80.27704620361328 24.723398208618164 L -149.41786193847656
20.559789657592773"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3030272722244263" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -45.03152084350586 14.460739135742188 L 218.56446838378906 -
176.4544219970703"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3735591173171997" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -43.779449462890625 16.42709732055664 L 183.14784240722656 -
109.66556549072266"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2566602230072021" stroke-linecap="round"

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fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -78.446533203125 34.217323303222656 L -433.48260498046875 201.833984375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7624560594558716" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -41.42848205566406 23.89560317993164 L 268.9874267578125 -
8.114431381225586"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4497368335723877" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -44.986122131347656 14.523683547973633 L 338.9415588378906 -
261.2206726074219"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2671356201171875" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -41.80059814453125 21.618379592895508 L 225.11325073242188 -
38.404022216796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1634373664855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -78.40252685546875 97.54728698730469 L -209.74478149414062 -
73.05413818359375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.847011685371399" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -83.28172302246094 123.80050659179688 L -176.8694305419922
180.81771850585938"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">
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<g stroke-linejoin="round" stroke-width="1.1233983039855957" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M -149.8581085205078 23.69687271118164 C -117.26753234863281 30.94041633605957
-82.55648803710938 62.57577133178711 -72.32881927490234 94.35641479492188"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4535115957260132" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -154.59983825683594 32.829647064208984 L -80.98373413085938
99.92274475097656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5170525312423706" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 220.63462829589844 -174.02943420410156 L -52.07421875 99.23820495605469"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0049540996551514" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -163.70635986328125 38.53544998168945 L -97.07039642333984
263.7091064453125"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6184818744659424" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -178.11717224121094 1.3661552667617798 L -213.2099609375 -
70.91024017333984"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2463555335998535" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -185.94398498535156 30.568758010864258 L -435.0060729980469
199.16128540039062"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,

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218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6427857875823975" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -288.8111267089844 -118.26861572265625 L -182.4899139404297
4.252133846282959"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.7030528783798218" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 268.9233093261719 -8.880119323730469 L -149.42308044433594
18.07175064086914"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0067930221557617" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M -437.3309020996094 196.3262939453125 C -386.3988952636719 146.07859802246094
-288.7329406738281 91.7220230102539 -219.1879425048828 74.91749572753906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4832813739776611" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 182.55458068847656 -110.81993865966797 L -181.6717529296875
61.66020202636719"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2639193534851074" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -194.90652465820312 171.246337890625 L -198.79019165039062
90.19705963134766"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.323468804359436" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -434.0926513671875 200.64625549316406 L -217.22315979003906
79.94619750976562"/>

</g> <!-- drawing style -->
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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.271994709968567" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 225.2429656982422 -37.862518310546875 L -180.36444091796875
65.29054260253906"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3199877738952637" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -179.0375518798828 204.55160522460938 L -106.3067855834961
269.55877685546875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.277574062347412" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 184.91505432128906 -107.00909423828125 L -178.23406982421875
178.85279846191406"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4552987813949585" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -284.44012451171875 -123.65412139892578 L -239.4246368408203 -
98.62161254882812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2673348188400269" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M -202.04238891601562 -86.9347152709961 L 224.72291564941406 -
44.758907318115234"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1874525547027588" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 215.21875 -183.93743896484375 L -202.4019012451172 -93.15026092529297"/>
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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1109884977340698" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 223.37738037109375 -171.74267578125 L -80.01016235351562 266.443603515625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0922809839248657" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#dad4a2">

<path d="M 364.0046691894531 -254.9369659423828 L 409.5670166015625 -
162.19374084472656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.365645408630371" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 346.5240783691406 -254.86074829101562 L 253.287841796875 -
60.818931579589844"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.002215027809143" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 205.4510955810547 -390.5487365722656 L 339.460205078125 -
285.2449645996094"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4149572849273682" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 249.21697998046875 -318.35650634765625 L 336.806396484375 -
280.7739562988281"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0021097660064697" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 220.50115966796875 -121.64856719970703 L 398.5148620605469 -
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141.97412109375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.6392109394073486" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 220.63003540039062 -119.28450012207031 L 286.2572326660156 -
118.97206115722656"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.571367621421814" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 213.20050048828125 -103.82371520996094 L 276.3116760253906 -
25.721948623657227"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3466006517410278" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 210.59249877929688 -102.0374526977539 L 234.6637420654297 -
60.13421630859375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.128332257270813" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 243.55282592773438 -315.4437255859375 L 204.9073944091797 -
138.91702270507812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.460114598274231" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 225.87454223632812 -170.2693328857422 L 209.51800537109375 -
137.29641723632812"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.5278871059417725" stroke-linecap="round"
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fill="none" stroke-opacity="1" stroke="#eaa2a2">

<path d="M 245.08224487304688 -325.3068542480469 C 248.06588745117188 -
357.5905456542969 231.82215881347656 -389.64190673828125 208.80087280273438 -
396.89556884765625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0017186403274536" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#90e190">

<path d="M 239.8532257080078 -321.8306579589844 C 208.93060302734375 -
331.57391357421875 185.66354370117188 -358.9562683105469 187.8848114013672 -
382.9908447265625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.013323187828064" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 230.65667724609375 -207.76010131835938 L 193.83096313476562 -
383.3319091796875"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.686769723892212" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 241.85401916503906 -324.4919128417969 L 200.7976837158203 -
386.25054931640625"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4677157402038574" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 244.25006103515625 -315.3419189453125 L 236.25045776367188 -
208.13058471679688"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.2681065797805786" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 244.62217712402344 -315.32806396484375 L 244.6256866455078 -
62.791954040527344"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0377498865127563" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 249.12220764160156 -174.2650909423828 L 291.8970947265625 -132.79779052734375"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.0556682348251343" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 236.11599731445312 -168.23190307617188 L 243.2722625732422 -62.746089935302734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4011832475662231" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 240.57957458496094 -169.05075073242188 L 283.06463623046875 -29.301233291625977"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.4343931674957275" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 293.6683044433594 -103.33580017089844 L 257.2146911621094 -58.333003997802734"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.409857988357544" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 292.0384216308594 -29.9152889251709 L 303.10052490234375 -99.12751007080078"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.1204508543014526" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 261.8976135253906 -52.876136779785156 L 401.1141052246094 -134.15879821777344"/>

</g> <!-- drawing style -->

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</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="1.3572708368301392" stroke-linecap="round"
fill="none" stroke-opacity="1" stroke="#d0b7d5">

<path d="M 272.7836608886719 -22.033784866333008 L 260.7242431640625 -
30.924116134643555"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -26.701505661010742 -95.60161590576172 C -26.701505661010742 -
87.5602670246118 -33.22029966777811 -81.04146575927734 -41.26163959503174 -
81.04146575927734 C -49.30297952228537 -81.04146575927734 -55.821773529052734 -
87.5602670246118 -55.821773529052734 -95.60161590576172 C -55.821773529052734 -
103.64296478691163 -49.30297952228537 -110.1617660522461 -41.26163959503174 -
110.1617660522461 C -33.22029966777811 -110.1617660522461 -26.701505661010742 -
103.64296478691163 -26.701505661010742 -95.60161590576172 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -26.701505661010742 -95.60161590576172 C -26.701505661010742 -
87.5602670246118 -33.22029966777811 -81.04146575927734 -41.26163959503174 -
81.04146575927734 C -49.30297952228537 -81.04146575927734 -55.821773529052734 -
87.5602670246118 -55.821773529052734 -95.60161590576172 C -55.821773529052734 -
103.64296478691163 -49.30297952228537 -110.1617660522461 -41.26163959503174 -
110.1617660522461 C -33.22029966777811 -110.1617660522461 -26.701505661010742 -
103.64296478691163 -26.701505661010742 -95.60161590576172 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
291.46839522830595, 187.0940279930552)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 19.492292404174805 -198.16775512695312 C 19.492292404174805 -
187.67434488016806 10.985702650959876 -179.16775512695312 0.4922924041748047 -
179.16775512695312 C -10.001117842610268 -179.16775512695312 -18.507707595825195 -
187.67434488016806 -18.507707595825195 -198.16775512695312 C -18.507707595825195 -
208.66116537373819 -10.001117842610268 -217.16775512695312 0.4922924041748047 -
217.16775512695312 C 10.985702650959876 -217.16775512695312 19.492292404174805 -
208.66116537373819 19.492292404174805 -198.16775512695312 z"/>

</g> <!-- drawing style -->
```

```
</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 19.492292404174805 -198.16775512695312 C 19.492292404174805 -
187.67434488016806 10.985702650959876 -179.16775512695312 0.4922924041748047 -
179.16775512695312 C -10.001117842610268 -179.16775512695312 -18.507707595825195 -
187.67434488016806 -18.507707595825195 -198.16775512695312 C -18.507707595825195 -
208.66116537373819 -10.001117842610268 -217.16775512695312 0.4922924041748047 -
217.16775512695312 C 10.985702650959876 -217.16775512695312 19.492292404174805 -
208.66116537373819 19.492292404174805 -198.16775512695312 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
308.24518029125176, 141.8474336648882)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">TNFAIP6</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 65.66560363769531 -174.34678649902344 C 65.66560363769531 -171.1478985523526
63.072384899801094 -168.5546875 59.87348747253418 -168.5546875 C 56.674590045267266 -
168.5546875 54.08137130737305 -171.1478985523526 54.08137130737305 -174.34678649902344
C 54.08137130737305 -177.5456744456943 56.674590045267266 -180.13888549804688
59.87348747253418 -180.13888549804688 C 63.072384899801094 -180.13888549804688
65.66560363769531 -177.5456744456943 65.66560363769531 -174.34678649902344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 65.66560363769531 -174.34678649902344 C 65.66560363769531 -171.1478985523526
63.072384899801094 -168.5546875 59.87348747253418 -168.5546875 C 56.674590045267266 -
168.5546875 54.08137130737305 -171.1478985523526 54.08137130737305 -174.34678649902344
C 54.08137130737305 -177.5456744456943 56.674590045267266 -180.13888549804688
59.87348747253418 -180.13888549804688 C 63.072384899801094 -180.13888549804688
65.66560363769531 -177.5456744456943 65.66560363769531 -174.34678649902344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
338.36985964891886, 146.74117996456573)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">PTGS2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">
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<path d="M -75.39561462402344 -213.0774688720703 C -75.39561462402344 -
202.58405862528525 -83.90220437723836 -194.0774688720703 -94.39561462402344 -
194.0774688720703 C -104.88902487080851 -194.0774688720703 -113.39561462402344 -
202.58405862528525 -113.39561462402344 -213.0774688720703 C -113.39561462402344 -
223.57087911885537 -104.88902487080851 -232.0774688720703 -94.39561462402344 -
232.0774688720703 C -83.90220437723836 -232.0774688720703 -75.39561462402344 -
223.57087911885537 -75.39561462402344 -213.0774688720703 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -75.39561462402344 -213.0774688720703 C -75.39561462402344 -
202.58405862528525 -83.90220437723836 -194.0774688720703 -94.39561462402344 -
194.0774688720703 C -104.88902487080851 -194.0774688720703 -113.39561462402344 -
202.58405862528525 -113.39561462402344 -213.0774688720703 C -113.39561462402344 -
223.57087911885537 -104.88902487080851 -232.0774688720703 -94.39561462402344 -
232.0774688720703 C -83.90220437723836 -232.0774688720703 -75.39561462402344 -
223.57087911885537 -75.39561462402344 -213.0774688720703 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
269.82245702733906, 134.97247921871877)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">IL1A</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 160.66680908203125 -129.9437255859375 C 160.66680908203125 -
119.45032376634893 152.1602176209182 -110.94374084472656 141.66680526733398 -
110.94374084472656 C 131.17339291374978 -110.94374084472656 122.66680145263672 -
119.45032376634893 122.66680145263672 -129.9437255859375 C 122.66680145263672 -
140.43712740552607 131.17339291374978 -148.94371032714844 141.66680526733398 -
148.94371032714844 C 152.1602176209182 -148.94371032714844 160.66680908203125 -
140.43712740552607 160.66680908203125 -129.9437255859375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 160.66680908203125 -129.9437255859375 C 160.66680908203125 -
119.45032376634893 152.1602176209182 -110.94374084472656 141.66680526733398 -
110.94374084472656 C 131.17339291374978 -110.94374084472656 122.66680145263672 -
119.45032376634893 122.66680145263672 -129.9437255859375 C 122.66680145263672 -
140.43712740552607 131.17339291374978 -148.94371032714844 141.66680526733398 -
148.94371032714844 C 152.1602176209182 -148.94371032714844 160.66680908203125 -
140.43712740552607 160.66680908203125 -129.9437255859375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 380.5810089414065,

173.30591759981468)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">IL6</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 41.12532424926758 -132.73666381835938 C 41.12532424926758 -130.40388099198668 39.23423012251527 -128.51278686523438 36.90144729614258 -128.51278686523438 C 34.568664469769885 -128.51278686523438 32.67757034301758 -130.40388099198668 32.67757034301758 -132.73666381835938 C 32.67757034301758 -135.06944664473207 34.568664469769885 -136.96054077148438 36.90144729614258 -136.96054077148438 C 39.23423012251527 -136.96054077148438 41.12532424926758 -135.06944664473207 41.12532424926758 -132.73666381835938 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 41.12532424926758 -132.73666381835938 C 41.12532424926758 -130.40388099198668 39.23423012251527 -128.51278686523438 36.90144729614258 -128.51278686523438 C 34.568664469769885 -128.51278686523438 32.67757034301758 -130.40388099198668 32.67757034301758 -132.73666381835938 C 32.67757034301758 -135.06944664473207 34.568664469769885 -136.96054077148438 36.90144729614258 -136.96054077148438 C 39.23423012251527 -136.96054077148438 41.12532424926758 -135.06944664473207 41.12532424926758 -132.73666381835938 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 327.542263554784, 165.2047298024834)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">ICAM1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M -77.45582580566406 -126.29110336303711 C -77.45582580566406 -115.7976910094529 -85.96241555887899 -107.29109954833984 -96.45582580566406 -107.29109954833984 C -106.94923605244914 -107.29109954833984 -115.45582580566406 -115.7976910094529 -115.45582580566406 -126.29110336303711 C -115.45582580566406 -136.7845157166213 -106.94923605244914 -145.29110717773438 -96.45582580566406 -145.29110717773438 C -85.96241555887899 -145.29110717773438 -77.45582580566406 -136.7845157166213 -77.45582580566406 -126.29110336303711 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -77.45582580566406 -126.29110336303711 C -77.45582580566406 -

115.7976910094529 -85.96241555887899 -107.29109954833984 -96.45582580566406 -
107.29109954833984 C -106.94923605244914 -107.29109954833984 -115.45582580566406 -
115.7976910094529 -115.45582580566406 -126.29110336303711 C -115.45582580566406 -
136.7845157166213 -106.94923605244914 -145.29110717773438 -96.45582580566406 -
145.29110717773438 C -85.96241555887899 -145.29110717773438 -77.45582580566406 -
136.7845157166213 -77.45582580566406 -126.29110336303711 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
267.74988752359377, 174.990171432594)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CCL3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 133.66091918945312 -192.0173797607422 C 133.66091918945312 -
189.1582258137765 131.34312379125353 -186.84042358398438 128.48397827148438 -
186.84042358398438 C 125.6248327517152 -186.84042358398438 123.30703735351562 -
189.1582258137765 123.30703735351562 -192.0173797607422 C 123.30703735351562 -
194.87653370770786 125.6248327517152 -197.1943359375 128.48397827148438 -197.1943359375
C 131.34312379125353 -197.1943359375 133.66091918945312 -194.87653370770786
133.66091918945312 -192.0173797607422 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 133.66091918945312 -192.0173797607422 C 133.66091918945312 -
189.1582258137765 131.34312379125353 -186.84042358398438 128.48397827148438 -
186.84042358398438 C 125.6248327517152 -186.84042358398438 123.30703735351562 -
189.1582258137765 123.30703735351562 -192.0173797607422 C 123.30703735351562 -
194.87653370770786 125.6248327517152 -197.1943359375 128.48397827148438 -197.1943359375
C 131.34312379125353 -197.1943359375 133.66091918945312 -194.87653370770786
133.66091918945312 -192.0173797607422 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 371.8869960475716,
138.3095222720604)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CSF3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -334.3772277832031 -39.54112243652344 C -334.3772277832031 -
37.25984663515938 -336.22656721621405 -35.41050720214844 -338.5078430175781 -
35.41050720214844 C -340.7891188189422 -35.41050720214844 -342.6384582519531 -
37.25984663515938 -342.6384582519531 -39.54112243652344 C -342.6384582519531 -
41.8223982378875 -340.7891188189422 -43.67173767089844 -338.5078430175781 -

```
43.67173767089844 C -336.22656721621405 -43.67173767089844 -334.3772277832031 -
41.8223982378875 -334.3772277832031 -39.54112243652344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -334.3772277832031 -39.54112243652344 C -334.3772277832031 -
37.25984663515938 -336.22656721621405 -35.41050720214844 -338.5078430175781 -
35.41050720214844 C -340.7891188189422 -35.41050720214844 -342.6384582519531 -
37.25984663515938 -342.6384582519531 -39.54112243652344 C -342.6384582519531 -
41.8223982378875 -340.7891188189422 -43.67173767089844 -338.5078430175781 -
43.67173767089844 C -336.22656721621405 -43.67173767089844 -334.3772277832031 -
41.8223982378875 -334.3772277832031 -39.54112243652344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
157.32710354875212, 208.13472446638923)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">MX2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 40.57882785797119 -52.49871635437012 C 40.57882785797119 -44.30233971300474
33.93436627904401 -37.65786361694336 25.73800754547119 -37.65786361694336 C
17.541648811898373 -37.65786361694336 10.897187232971191 -44.30233971300474
10.897187232971191 -52.49871635437012 C 10.897187232971191 -60.6950929957355
17.541648811898373 -67.33956909179688 25.73800754547119 -67.33956909179688 C
33.93436627904401 -67.33956909179688 40.57882785797119 -60.6950929957355
40.57882785797119 -52.49871635437012 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 40.57882785797119 -52.49871635437012 C 40.57882785797119 -44.30233971300474
33.93436627904401 -37.65786361694336 25.73800754547119 -37.65786361694336 C
17.541648811898373 -37.65786361694336 10.897187232971191 -44.30233971300474
10.897187232971191 -52.49871635437012 C 10.897187232971191 -60.6950929957355
17.541648811898373 -67.33956909179688 25.73800754547119 -67.33956909179688 C
33.93436627904401 -67.33956909179688 40.57882785797119 -60.6950929957355
40.57882785797119 -52.49871635437012 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
322.36231557860776, 207.0984555453255)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL8</text>

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 142.8695526123047 -44.70391845703125 C 142.8695526123047 -39.22881945409291 138.43110791407116 -34.790374755859375 132.9560089111328 -34.790374755859375 C 127.48090990819446 -34.790374755859375 123.04246520996094 -39.22881945409291 123.04246520996094 -44.70391845703125 C 123.04246520996094 -50.17901745996959 127.48090990819446 -54.617462158203125 132.9560089111328 -54.617462158203125 C 138.43110791407116 -54.617462158203125 142.8695526123047 -50.17901745996959 142.8695526123047 -44.70391845703125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 142.8695526123047 -44.70391845703125 C 142.8695526123047 -39.22881945409291 138.43110791407116 -34.790374755859375 132.9560089111328 -34.790374755859375 C 127.48090990819446 -34.790374755859375 123.04246520996094 -39.22881945409291 123.04246520996094 -44.70391845703125 C 123.04246520996094 -50.17901745996959 127.48090990819446 -54.617462158203125 132.9560089111328 -54.617462158203125 C 138.43110791407116 -54.617462158203125 142.8695526123047 -50.17901745996959 142.8695526123047 -44.70391845703125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 373.5329991280438, 208.42067109096647)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">CCL2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 86.57278442382812 -62.517011642456055 C 86.57278442382812 -52.02360034227142 78.06619552456226 -43.51700973510742 67.57278633117676 -43.51700973510742 C 57.07937713779125 -43.51700973510742 48.57278823852539 -52.02360034227142 48.57278823852539 -62.517011642456055 C 48.57278823852539 -73.01042294264069 57.07937713779125 -81.51701354980469 67.57278633117676 -81.51701354980469 C 78.06619552456226 -81.51701354980469 86.57278442382812 -73.01042294264069 86.57278442382812 -62.517011642456055 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 86.57278442382812 -62.517011642456055 C 86.57278442382812 -52.02360034227142 78.06619552456226 -43.51700973510742 67.57278633117676 -43.51700973510742 C 57.07937713779125 -43.51700973510742 48.57278823852539 -52.02360034227142 48.57278823852539 -62.517011642456055 C 48.57278823852539 -73.01042294264069 57.07937713779125 -81.51701354980469 67.57278633117676 -81.51701354980469 C 78.06619552456226 -81.51701354980469 86.57278442382812 -73.01042294264069 86.57278442382812 -62.517011642456055 z"/>

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</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 341.6350097220206,
204.3967696951179)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CCL20</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -446.6337585449219 18.30450439453125 C -446.6337585449219 28.79791464131632
-455.1403482981368 37.30450439453125 -465.6337585449219 37.30450439453125 C -
476.12716879170694 37.30450439453125 -484.6337585449219 28.79791464131632 -
484.6337585449219 18.30450439453125 C -484.6337585449219 7.811094147746177 -
476.12716879170694 -0.69549560546875 -465.6337585449219 -0.69549560546875 C -
455.1403482981368 -0.69549560546875 -446.6337585449219 7.811094147746177 -
446.6337585449219 18.30450439453125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -446.6337585449219 18.30450439453125 C -446.6337585449219 28.79791464131632
-455.1403482981368 37.30450439453125 -465.6337585449219 37.30450439453125 C -
476.12716879170694 37.30450439453125 -484.6337585449219 28.79791464131632 -
484.6337585449219 18.30450439453125 C -484.6337585449219 7.811094147746177 -
476.12716879170694 -0.69549560546875 -465.6337585449219 -0.69549560546875 C -
455.1403482981368 -0.69549560546875 -446.6337585449219 7.811094147746177 -
446.6337585449219 18.30450439453125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 98.03046578091956,
241.66403299812234)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">ZBP1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -582.320068359375 -59.980255126953125 C -582.320068359375 -49.48684488016805
-590.8266581125899 -40.980255126953125 -601.320068359375 -40.980255126953125 C -
611.8134786061601 -40.980255126953125 -620.320068359375 -49.48684488016805 -
620.320068359375 -59.980255126953125 C -620.320068359375 -70.4736653737382 -
611.8134786061601 -78.98025512695312 -601.320068359375 -78.98025512695312 C -
590.8266581125899 -78.98025512695312 -582.320068359375 -70.4736653737382 -
582.320068359375 -59.980255126953125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
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218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -582.320068359375 -59.980255126953125 C -582.320068359375 -49.48684488016805
-590.8266581125899 -40.980255126953125 -601.320068359375 -40.980255126953125 C -
611.8134786061601 -40.980255126953125 -620.320068359375 -49.48684488016805 -
620.320068359375 -59.980255126953125 C -620.320068359375 -70.4736653737382 -
611.8134786061601 -78.98025512695312 -601.320068359375 -78.98025512695312 C -
590.8266581125899 -78.98025512695312 -582.320068359375 -70.4736653737382 -
582.320068359375 -59.980255126953125 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
31.455272370450338, 205.56648178150073)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">SMIM18</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -558.2322387695312 18.20458698272705 C -558.2322387695312 21.272759104385447
-560.7193756841675 23.7600040435791 -563.7874145507812 23.7600040435791 C -
566.855453417395 23.7600040435791 -569.3425903320312 21.272759104385447 -
569.3425903320312 18.20458698272705 C -569.3425903320312 15.136414861068655 -
566.855453417395 12.649169921875 -563.7874145507812 12.649169921875 C -
560.7193756841675 12.649169921875 -558.2322387695312 15.136414861068655 -
558.2322387695312 18.20458698272705 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -558.2322387695312 18.20458698272705 C -558.2322387695312 21.272759104385447
-560.7193756841675 23.7600040435791 -563.7874145507812 23.7600040435791 C -
566.855453417395 23.7600040435791 -569.3425903320312 21.272759104385447 -
569.3425903320312 18.20458698272705 C -569.3425903320312 15.136414861068655 -
566.855453417395 12.649169921875 -563.7874145507812 12.649169921875 C -
560.7193756841675 12.649169921875 -558.2322387695312 15.136414861068655 -
558.2322387695312 18.20458698272705 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 48.76179411788733,
235.41858627119123)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">SMIM22</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -623.9515991210938 5.019292831420898 C -623.9515991210938 10.43427484802641
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-628.3413072379872 14.82398509979248 -633.7562866210938 14.82398509979248 C -
639.1712660042003 14.82398509979248 -643.5609741210938 10.43427484802641 -
643.5609741210938 5.019292831420898 C -643.5609741210938 -0.39568918518461427 -
639.1712660042003 -4.785399436950684 -633.7562866210938 -4.785399436950684 C -
628.3413072379872 -4.785399436950684 -623.9515991210938 -0.39568918518461427 -
623.9515991210938 5.019292831420898 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -623.9515991210938 5.019292831420898 C -623.9515991210938 10.43427484802641
-628.3413072379872 14.82398509979248 -633.7562866210938 14.82398509979248 C -
639.1712660042003 14.82398509979248 -643.5609741210938 10.43427484802641 -
643.5609741210938 5.019292831420898 C -643.5609741210938 -0.39568918518461427 -
639.1712660042003 -4.785399436950684 -633.7562866210938 -4.785399436950684 C -
628.3413072379872 -4.785399436950684 -623.9515991210938 -0.39568918518461427 -
623.9515991210938 5.019292831420898 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
18.248156182514272, 231.29813716918937)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">SMIM5</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 201.6436309814453 54.856056213378906 C 201.6436309814453 65.34946646016398
193.13704122823037 73.8560562133789 182.6436309814453 73.8560562133789 C
172.15022073466025 73.8560562133789 163.6436309814453 65.34946646016398
163.6436309814453 54.856056213378906 C 163.6436309814453 44.36264596659383
172.15022073466025 35.856056213378906 182.6436309814453 35.856056213378906 C
193.13704122823037 35.856056213378906 201.6436309814453 44.36264596659383
201.6436309814453 54.856056213378906 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 201.6436309814453 54.856056213378906 C 201.6436309814453 65.34946646016398
193.13704122823037 73.8560562133789 182.6436309814453 73.8560562133789 C
172.15022073466025 73.8560562133789 163.6436309814453 65.34946646016398
163.6436309814453 54.856056213378906 C 163.6436309814453 44.36264596659383
172.15022073466025 35.856056213378906 182.6436309814453 35.856056213378906 C
193.13704122823037 35.856056213378906 201.6436309814453 44.36264596659383
201.6436309814453 54.856056213378906 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
391.13927900135087, 258.5181629960021)">
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<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">SERPINE1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 149.5731964111328 -10.754785537719727 C 149.5731964111328 -0.26137529093465517 141.06660665791787 8.245214462280273 130.5731964111328 8.245214462280273 C 120.07978616434774 8.245214462280273 111.57319641113281 -0.26137529093465517 111.57319641113281 -10.754785537719727 C 111.57319641113281 -21.2481957845048 120.07978616434774 -29.754785537719727 130.5731964111328 -29.754785537719727 C 141.06660665791787 -29.754785537719727 149.5731964111328 -21.2481957845048 149.5731964111328 -10.754785537719727 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 149.5731964111328 -10.754785537719727 C 149.5731964111328 -0.26137529093465517 141.06660665791787 8.245214462280273 130.5731964111328 8.245214462280273 C 120.07978616434774 8.245214462280273 111.57319641113281 -0.26137529093465517 111.57319641113281 -10.754785537719727 C 111.57319641113281 -21.2481957845048 120.07978616434774 -29.754785537719727 130.5731964111328 -29.754785537719727 C 141.06660665791787 -29.754785537719727 149.5731964111328 -21.2481957845048 149.5731964111328 -10.754785537719727 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 373.87432544017906, 228.26462788964514)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">IL1B</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 122.01114654541016 82.6584701538086 C 122.01114654541016 86.73563209252374 118.70596741098231 90.04082489013672 114.62882232666016 90.04082489013672 C 110.551677242338 90.04082489013672 107.24649810791016 86.73563209252374 107.24649810791016 82.6584701538086 C 107.24649810791016 78.58130821509344 110.551677242338 75.27611541748047 114.62882232666016 75.27611541748047 C 118.70596741098231 75.27611541748047 122.01114654541016 78.58130821509344 122.01114654541016 82.6584701538086 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 122.01114654541016 82.6584701538086 C 122.01114654541016 86.73563209252374 118.70596741098231 90.04082489013672 114.62882232666016 90.04082489013672 C

```
110.551677242338 90.04082489013672 107.24649810791016 86.73563209252374
107.24649810791016 82.6584701538086 C 107.24649810791016 78.58130821509344
110.551677242338 75.27611541748047 114.62882232666016 75.27611541748047 C
118.70596741098231 75.27611541748047 122.01114654541016 78.58130821509344
122.01114654541016 82.6584701538086 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 362.5047193871935,
265.9810525776978)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">NFKBIA</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 90.403564453125 23.563573837280273 C 90.403564453125 34.05698408406535
81.89697555385914 42.56357383728027 71.40356636047363 42.56357383728027 C
60.91015716708812 42.56357383728027 52.403568267822266 34.05698408406535
52.403568267822266 23.563573837280273 C 52.403568267822266 13.0701635904952
60.91015716708812 4.563573837280273 71.40356636047363 4.563573837280273 C
81.89697555385914 4.563573837280273 90.403564453125 13.0701635904952 90.403564453125
23.563573837280273 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 90.403564453125 23.563573837280273 C 90.403564453125 34.05698408406535
81.89697555385914 42.56357383728027 71.40356636047363 42.56357383728027 C
60.91015716708812 42.56357383728027 52.403568267822266 34.05698408406535
52.403568267822266 23.563573837280273 C 52.403568267822266 13.0701635904952
60.91015716708812 4.563573837280273 71.40356636047363 4.563573837280273 C
81.89697555385914 4.563573837280273 90.403564453125 13.0701635904952 90.403564453125
23.563573837280273 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
340.94277418141735, 244.08902093411925)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">TNFAIP3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 121.18714904785156 219.0633544921875 C 121.18714904785156 229.55676473897256
112.68055929463664 238.0633544921875 102.18714904785156 238.0633544921875 C
91.69373880106649 238.0633544921875 83.18714904785156 229.55676473897256
83.18714904785156 219.0633544921875 C 83.18714904785156 208.56994424540244
91.69373880106649 200.0633544921875 102.18714904785156 200.0633544921875 C
112.68055929463664 200.0633544921875 121.18714904785156 208.56994424540244
```

```
121.18714904785156 219.0633544921875 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 121.18714904785156 219.0633544921875 C 121.18714904785156 229.55676473897256
112.68055929463664 238.0633544921875 102.18714904785156 238.0633544921875 C
91.69373880106649 238.0633544921875 83.18714904785156 229.55676473897256
83.18714904785156 219.0633544921875 C 83.18714904785156 208.56994424540244
91.69373880106649 200.0633544921875 102.18714904785156 200.0633544921875 C
112.68055929463664 200.0633544921875 121.18714904785156 208.56994424540244
121.18714904785156 219.0633544921875 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 357.6053478734133,
334.2350892022534)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">SOCS3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 208.70346069335938 246.904052734375 C 208.70346069335938 257.39746298116006
200.19686752434816 265.904052734375 189.70345306396484 265.904052734375 C
179.21003860358152 265.904052734375 170.7034454345703 257.39746298116006
170.7034454345703 246.904052734375 C 170.7034454345703 236.41064248758994
179.21003860358152 227.904052734375 189.70345306396484 227.904052734375 C
200.19686752434816 227.904052734375 208.70346069335938 236.41064248758994
208.70346069335938 246.904052734375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 208.70346069335938 246.904052734375 C 208.70346069335938 257.39746298116006
200.19686752434816 265.904052734375 189.70345306396484 265.904052734375 C
179.21003860358152 265.904052734375 170.7034454345703 257.39746298116006
170.7034454345703 246.904052734375 C 170.7034454345703 236.41064248758994
179.21003860358152 227.904052734375 189.70345306396484 227.904052734375 C
200.19686752434816 227.904052734375 208.70346069335938 236.41064248758994
208.70346069335938 246.904052734375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
394.29734244700586, 347.07259469945126)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">ANGPTL4</text>

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 339.0625 163.22817993164062 C 339.0625 173.72159017842569 330.55591024678506 182.22817993164062 320.0625 182.22817993164062 C 309.56908975321494 182.22817993164062 301.0625 173.72159017842569 301.0625 163.22817993164062 C 301.0625 152.73476968485556 309.56908975321494 144.22817993164062 320.0625 144.22817993164062 C 330.55591024678506 144.22817993164062 339.0625 152.73476968485556 339.0625 163.22817993164062 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 339.0625 163.22817993164062 C 339.0625 173.72159017842569 330.55591024678506 182.22817993164062 320.0625 182.22817993164062 C 309.56908975321494 182.22817993164062 301.0625 173.72159017842569 301.0625 163.22817993164062 C 301.0625 152.73476968485556 309.56908975321494 144.22817993164062 320.0625 144.22817993164062 C 330.55591024678506 144.22817993164062 339.0625 152.73476968485556 339.0625 163.22817993164062 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 457.71228424223165, 308.4891702557282)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">IGFBP3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 32.090771198272705 30.131452560424805 C 32.090771198272705 40.62486280720988 23.584181445057776 49.131452560424805 13.090771198272705 49.131452560424805 C 2.597360951487632 49.131452560424805 -5.909228801727295 40.62486280720988 -5.909228801727295 30.131452560424805 C -5.909228801727295 19.63804231363973 2.597360951487632 11.131452560424805 13.090771198272705 11.131452560424805 C 23.584181445057776 11.131452560424805 32.090771198272705 19.63804231363973 32.090771198272705 30.131452560424805 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 32.090771198272705 30.131452560424805 C 32.090771198272705 40.62486280720988 23.584181445057776 49.131452560424805 13.090771198272705 49.131452560424805 C 2.597360951487632 49.131452560424805 -5.909228801727295 40.62486280720988 -5.909228801727295 30.131452560424805 C -5.909228801727295 19.63804231363973 2.597360951487632 11.131452560424805 13.090771198272705 11.131452560424805 C 23.584181445057776 11.131452560424805 32.090771198272705 19.63804231363973 32.090771198272705 30.131452560424805 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 316.5306026453417, 247.11750744978906)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 5.882788181304932 99.53211212158203 C 5.882788181304932 102.26899587452769 3.6640986964080335 104.48767852783203 0.9272065162658691 104.48767852783203 C -1.8096856638762957 104.48767852783203 -4.028375148773193 102.26899587452769 -4.028375148773193 99.53211212158203 C -4.028375148773193 96.79522836863637 -1.8096856638762957 94.57654571533203 0.9272065162658691 94.57654571533203 C 3.6640986964080335 94.57654571533203 5.882788181304932 96.79522836863637 5.882788181304932 99.53211212158203 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 5.882788181304932 99.53211212158203 C 5.882788181304932 102.26899587452769 3.6640986964080335 104.48767852783203 0.9272065162658691 104.48767852783203 C -1.8096856638762957 104.48767852783203 -4.028375148773193 102.26899587452769 -4.028375148773193 99.53211212158203 C -4.028375148773193 96.79522836863637 -1.8096856638762957 94.57654571533203 0.9272065162658691 94.57654571533203 C 3.6640986964080335 94.57654571533203 5.882788181304932 96.79522836863637 5.882788181304932 99.53211212158203 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 310.921913488517, 272.64257957597164)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL6</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 274.1085205078125 85.74756622314453 C 274.1085205078125 96.2409764699296 265.60193075459756 104.74756622314453 255.1085205078125 104.74756622314453 C 244.61511026102744 104.74756622314453 236.1085205078125 96.2409764699296 236.1085205078125 85.74756622314453 C 236.1085205078125 75.25415597635946 244.61511026102744 66.74756622314453 255.1085205078125 66.74756622314453 C 265.60193075459756 66.74756622314453 274.1085205078125 75.25415597635946 274.1085205078125 85.74756622314453 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 274.1085205078125 85.74756622314453 C 274.1085205078125 96.2409764699296
265.60193075459756 104.74756622314453 255.1085205078125 104.74756622314453 C
244.61511026102744 104.74756622314453 236.1085205078125 96.2409764699296
236.1085205078125 85.74756622314453 C 236.1085205078125 75.25415597635946
244.61511026102744 66.74756622314453 255.1085205078125 66.74756622314453 C
265.60193075459756 66.74756622314453 274.1085205078125 75.25415597635946
274.1085205078125 85.74756622314453 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 429.1206331561613,
272.76241528153497)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">MT2A</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 139.8866729736328 284.8885192871094 C 139.8866729736328 295.38192953389444
131.38008151251975 303.8885192871094 120.88666915893555 303.8885192871094 C
110.39325680535134 303.8885192871094 101.88666534423828 295.38192953389444
101.88666534423828 284.8885192871094 C 101.88666534423828 274.3951090403243
110.39325680535134 265.8885192871094 120.88666915893555 265.8885192871094 C
131.38008151251975 265.8885192871094 139.8866729736328 274.3951090403243
139.8866729736328 284.8885192871094 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 139.8866729736328 284.8885192871094 C 139.8866729736328 295.38192953389444
131.38008151251975 303.8885192871094 120.88666915893555 303.8885192871094 C
110.39325680535134 303.8885192871094 101.88666534423828 295.38192953389444
101.88666534423828 284.8885192871094 C 101.88666534423828 274.3951090403243
110.39325680535134 265.8885192871094 120.88666915893555 265.8885192871094 C
131.38008151251975 265.8885192871094 139.8866729736328 274.3951090403243
139.8866729736328 284.8885192871094 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 365.7576938092574,
364.5874498922693)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">FNDC1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -251.3785400390625 -349.7051696777344 C -251.3785400390625 -
339.2117594309493 -259.88512979227744 -330.7051696777344 -270.3785400390625 -
330.7051696777344 C -280.87195028584756 -330.7051696777344 -289.3785400390625 -
339.2117594309493 -289.3785400390625 -349.7051696777344 C -289.3785400390625 -

```
360.19857992451944 -280.87195028584756 -368.7051696777344 -270.3785400390625 -
368.7051696777344 C -259.88512979227744 -368.7051696777344 -251.3785400390625 -
360.19857992451944 -251.3785400390625 -349.7051696777344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -251.3785400390625 -349.7051696777344 C -251.3785400390625 -
339.2117594309493 -259.88512979227744 -330.7051696777344 -270.3785400390625 -
330.7051696777344 C -280.87195028584756 -330.7051696777344 -289.3785400390625 -
339.2117594309493 -289.3785400390625 -349.7051696777344 C -289.3785400390625 -
360.19857992451944 -280.87195028584756 -368.7051696777344 -270.3785400390625 -
368.7051696777344 C -259.88512979227744 -368.7051696777344 -251.3785400390625 -
360.19857992451944 -251.3785400390625 -349.7051696777344 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
188.02594084073849, 71.97266344885355)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">BST2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -340.1660461425781 -261.0916748046875 C -340.1660461425781 -
257.20146179313065 -343.3196868907869 -254.04782104492188 -347.20989990234375 -
254.04782104492188 C -351.1001129139006 -254.04782104492188 -354.2537536621094 -
257.20146179313065 -354.2537536621094 -261.0916748046875 C -354.2537536621094 -
264.98188781624435 -351.1001129139006 -268.1355285644531 -347.20989990234375 -
268.1355285644531 C -343.3196868907869 -268.1355285644531 -340.1660461425781 -
264.98188781624435 -340.1660461425781 -261.0916748046875 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -340.1660461425781 -261.0916748046875 C -340.1660461425781 -
257.20146179313065 -343.3196868907869 -254.04782104492188 -347.20989990234375 -
254.04782104492188 C -351.1001129139006 -254.04782104492188 -354.2537536621094 -
257.20146179313065 -354.2537536621094 -261.0916748046875 C -354.2537536621094 -
264.98188781624435 -351.1001129139006 -268.1355285644531 -347.20989990234375 -
268.1355285644531 C -343.3196868907869 -268.1355285644531 -340.1660461425781 -
264.98188781624435 -340.1660461425781 -261.0916748046875 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
151.39356157557933, 107.31980617902902)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">ISG15</text>
```

```
</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -151.77099609375 -303.6351623535156 C -151.77099609375 -293.14175210673056 -
160.27758584696494 -284.6351623535156 -170.77099609375 -284.6351623535156 C -
181.26440634053506 -284.6351623535156 -189.77099609375 -293.14175210673056 -
189.77099609375 -303.6351623535156 C -189.77099609375 -314.1285726003007 -
181.26440634053506 -322.6351623535156 -170.77099609375 -322.6351623535156 C -
160.27758584696494 -322.6351623535156 -151.77099609375 -314.1285726003007 -
151.77099609375 -303.6351623535156 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -151.77099609375 -303.6351623535156 C -151.77099609375 -293.14175210673056 -
160.27758584696494 -284.6351623535156 -170.77099609375 -284.6351623535156 C -
181.26440634053506 -284.6351623535156 -189.77099609375 -293.14175210673056 -
189.77099609375 -303.6351623535156 C -189.77099609375 -314.1285726003007 -
181.26440634053506 -322.6351623535156 -170.77099609375 -322.6351623535156 C -
160.27758584696494 -322.6351623535156 -151.77099609375 -314.1285726003007 -
151.77099609375 -303.6351623535156 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
233.95960282988582, 93.21580782460813)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">IFIT1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -201.52767944335938 -224.2325897216797 C -201.52767944335938 -
220.65673642116622 -204.4264812942131 -217.7579345703125 -208.00233459472656 -
217.7579345703125 C -211.57818789524003 -217.7579345703125 -214.47698974609375 -
220.65673642116622 -214.47698974609375 -224.2325897216797 C -214.47698974609375 -
227.80844302219316 -211.57818789524003 -230.70724487304688 -208.00233459472656 -
230.70724487304688 C -204.4264812942131 -230.70724487304688 -201.52767944335938 -
227.80844302219316 -201.52767944335938 -224.2325897216797 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -201.52767944335938 -224.2325897216797 C -201.52767944335938 -
220.65673642116622 -204.4264812942131 -217.7579345703125 -208.00233459472656 -
217.7579345703125 C -211.57818789524003 -217.7579345703125 -214.47698974609375 -
220.65673642116622 -214.47698974609375 -224.2325897216797 C -214.47698974609375 -
227.80844302219316 -211.57818789524003 -230.70724487304688 -208.00233459472656 -
```

```
230.70724487304688 C -204.4264812942131 -230.70724487304688 -201.52767944335938 -
227.80844302219316 -201.52767944335938 -224.2325897216797 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
216.79201929744175, 124.05328078723916)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">IFIT3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 161.65411376953125 -292.1676940917969 C 161.65411376953125 -
281.6742838450118 153.1475240163163 -273.1676940917969 142.65411376953125 -
273.1676940917969 C 132.1607035227462 -273.1676940917969 123.65411376953125 -
281.6742838450118 123.65411376953125 -292.1676940917969 C 123.65411376953125 -
302.66110433858194 132.1607035227462 -311.1676940917969 142.65411376953125 -
311.1676940917969 C 153.1475240163163 -311.1676940917969 161.65411376953125 -
302.66110433858194 161.65411376953125 -292.1676940917969 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 161.65411376953125 -292.1676940917969 C 161.65411376953125 -
281.6742838450118 153.1475240163163 -273.1676940917969 142.65411376953125 -
273.1676940917969 C 132.1607035227462 -273.1676940917969 123.65411376953125 -
281.6742838450118 123.65411376953125 -292.1676940917969 C 123.65411376953125 -
302.66110433858194 132.1607035227462 -311.1676940917969 142.65411376953125 -
311.1676940917969 C 153.1475240163163 -311.1676940917969 161.65411376953125 -
302.66110433858194 161.65411376953125 -292.1676940917969 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
378.42092672595396, 98.50352315301471)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CSF2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 64.28983306884766 -228.82406616210938 C 64.28983306884766 -
225.85506370876485 61.88298103000467 -223.44821166992188 58.913978576660156 -
223.44821166992188 C 55.944976123315634 -223.44821166992188 53.538124084472656 -
225.85506370876485 53.538124084472656 -228.82406616210938 C 53.538124084472656 -
231.7930686154539 55.944976123315634 -234.19992065429688 58.913978576660156 -
234.19992065429688 C 61.88298103000467 -234.19992065429688 64.28983306884766 -
231.7930686154539 64.28983306884766 -228.82406616210938 z"/>

</g> <!-- drawing style -->
```

```
</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 64.28983306884766 -228.82406616210938 C 64.28983306884766 -
225.85506370876485 61.88298103000467 -223.44821166992188 58.913978576660156 -
223.44821166992188 C 55.944976123315634 -223.44821166992188 53.538124084472656 -
225.85506370876485 53.538124084472656 -228.82406616210938 C 53.538124084472656 -
231.7930686154539 55.944976123315634 -234.19992065429688 58.913978576660156 -
234.19992065429688 C 61.88298103000467 -234.19992065429688 64.28983306884766 -
231.7930686154539 64.28983306884766 -228.82406616210938 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 337.0898683886238,
121.42946140917047)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">HCAR3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 51.60874938964844 -361.9933776855469 C 51.60874938964844 -358.82862831189794
49.043219950358676 -356.2630920410156 45.87847900390625 -356.2630920410156 C
42.713738057453824 -356.2630920410156 40.14820861816406 -358.82862831189794
40.14820861816406 -361.9933776855469 C 40.14820861816406 -365.1581270591958
42.713738057453824 -367.7236633300781 45.87847900390625 -367.7236633300781 C
49.043219950358676 -367.7236633300781 51.60874938964844 -365.1581270591958
51.60874938964844 -361.9933776855469 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 51.60874938964844 -361.9933776855469 C 51.60874938964844 -358.82862831189794
49.043219950358676 -356.2630920410156 45.87847900390625 -356.2630920410156 C
42.713738057453824 -356.2630920410156 40.14820861816406 -358.82862831189794
40.14820861816406 -361.9933776855469 C 40.14820861816406 -365.1581270591958
42.713738057453824 -367.7236633300781 45.87847900390625 -367.7236633300781 C
49.043219950358676 -367.7236633300781 51.60874938964844 -365.1581270591958
51.60874938964844 -361.9933776855469 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
331.72350208354743, 60.18775899058806)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">HSPA6</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
```

```
opacity="1" stroke="#000000">

<path d="M 8.361821174621582 -299.6146240234375 C 8.361821174621582 -295.020638977764
4.637660468341965 -291.2964782714844 0.04367542266845703 -291.2964782714844 C -
4.550309623005051 -291.2964782714844 -8.274470329284668 -295.020638977764 -
8.274470329284668 -299.6146240234375 C -8.274470329284668 -304.208609069111 -
4.550309623005051 -307.9327697753906 0.04367542266845703 -307.9327697753906 C
4.637660468341965 -307.9327697753906 8.361821174621582 -304.208609069111
8.361821174621582 -299.6146240234375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M 8.361821174621582 -299.6146240234375 C 8.361821174621582 -295.020638977764
4.637660468341965 -291.2964782714844 0.04367542266845703 -291.2964782714844 C -
4.550309623005051 -291.2964782714844 -8.274470329284668 -295.020638977764 -
8.274470329284668 -299.6146240234375 C -8.274470329284668 -304.208609069111 -
4.550309623005051 -307.9327697753906 0.04367542266845703 -307.9327697753906 C
4.637660468341965 -307.9327697753906 8.361821174621582 -304.208609069111
8.361821174621582 -299.6146240234375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 310.5415301521814,
90.14423688297444)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">DUSP2</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -450.91656494140625 -194.6586456298828 C -450.91656494140625 -
191.14158045215405 -453.7677027709521 -188.29043579101562 -457.2847595214844 -
188.29043579101562 C -460.80181627201665 -188.29043579101562 -463.6529541015625 -
191.14158045215405 -463.6529541015625 -194.6586456298828 C -463.6529541015625 -
198.17571080761158 -460.80181627201665 -201.02685546875 -457.2847595214844 -
201.02685546875 C -453.7677027709521 -201.02685546875 -450.91656494140625 -
198.17571080761158 -450.91656494140625 -194.6586456298828 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -450.91656494140625 -194.6586456298828 C -450.91656494140625 -
191.14158045215405 -453.7677027709521 -188.29043579101562 -457.2847595214844 -
188.29043579101562 C -460.80181627201665 -188.29043579101562 -463.6529541015625 -
191.14158045215405 -463.6529541015625 -194.6586456298828 C -463.6529541015625 -
198.17571080761158 -460.80181627201665 -201.02685546875 -457.2847595214844 -
201.02685546875 C -453.7677027709521 -201.02685546875 -450.91656494140625 -
198.17571080761158 -450.91656494140625 -194.6586456298828 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
100.37128658282762, 137.64091333428024)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">IFI44L</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -10.944412231445312 -428.27923583984375 C -10.944412231445312 -
417.7858255930587 -19.45100198466024 -409.27923583984375 -29.944412231445312 -
409.27923583984375 C -40.43782247823039 -409.27923583984375 -48.94441223144531 -
417.7858255930587 -48.94441223144531 -428.27923583984375 C -48.94441223144531 -
438.7726460866288 -40.43782247823039 -447.27923583984375 -29.944412231445312 -
447.27923583984375 C -19.45100198466024 -447.27923583984375 -10.944412231445312 -
438.7726460866288 -10.944412231445312 -428.27923583984375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -10.944412231445312 -428.27923583984375 C -10.944412231445312 -
417.7858255930587 -19.45100198466024 -409.27923583984375 -29.944412231445312 -
409.27923583984375 C -40.43782247823039 -409.27923583984375 -48.94441223144531 -
417.7858255930587 -48.94441223144531 -428.27923583984375 C -48.94441223144531 -
438.7726460866288 -40.43782247823039 -447.27923583984375 -29.944412231445312 -
447.27923583984375 C -19.45100198466024 -447.27923583984375 -10.944412231445312 -
438.7726460866288 -10.944412231445312 -428.27923583984375 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
294.85231682481594, 35.74171128240331)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">HSPA1A</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 118.70773315429688 -444.0585021972656 C 118.70773315429688 -
433.56509195048056 110.20114169318381 -425.0585021972656 99.70772933959961 -
425.0585021972656 C 89.2143169860154 -425.0585021972656 80.70772552490234 -
433.56509195048056 80.70772552490234 -444.0585021972656 C 80.70772552490234 -
454.5519124440507 89.2143169860154 -463.0585021972656 99.70772933959961 -
463.0585021972656 C 110.20114169318381 -463.0585021972656 118.70773315429688 -
454.5519124440507 118.70773315429688 -444.0585021972656 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 118.70773315429688 -444.0585021972656 C 118.70773315429688 -433.56509195048056 110.20114169318381 -425.0585021972656 99.70772933959961 -425.0585021972656 C 89.2143169860154 -425.0585021972656 80.70772552490234 -433.56509195048056 80.70772552490234 -444.0585021972656 C 80.70772552490234 -454.5519124440507 89.2143169860154 -463.0585021972656 99.70772933959961 -463.0585021972656 C 110.20114169318381 -463.0585021972656 118.70773315429688 -454.5519124440507 118.70773315429688 -444.0585021972656 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 354.95312450618536, 28.465801143835016)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">HSPA1B</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M -61.196903228759766 -54.55107879638672 C -61.196903228759766 -44.057668549601644 -69.70349383592377 -35.55107879638672 -80.1969051361084 -35.55107879638672 C -90.69031643629303 -35.55107879638672 -99.19690704345703 -44.057668549601644 -99.19690704345703 -54.55107879638672 C -99.19690704345703 -65.0444890431718 -90.69031643629303 -73.55107879638672 -80.1969051361084 -73.55107879638672 C -69.70349383592377 -73.55107879638672 -61.196903228759766 -65.0444890431718 -61.196903228759766 -54.55107879638672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -61.196903228759766 -54.55107879638672 C -61.196903228759766 -44.057668549601644 -69.70349383592377 -35.55107879638672 -80.1969051361084 -35.55107879638672 C -90.69031643629303 -35.55107879638672 -99.19690704345703 -44.057668549601644 -99.19690704345703 -54.55107879638672 C -99.19690704345703 -65.0444890431718 -90.69031643629303 -73.55107879638672 -80.1969051361084 -73.55107879638672 C -69.70349383592377 -73.55107879638672 -61.196903228759766 -65.0444890431718 -61.196903228759766 -54.55107879638672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 273.51511985429164, 208.0699060987576)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M -42.32565689086914 25.8951473236084 C -42.32565689086914 36.108724083411026 -50.605397635406206 44.38846397399902 -60.8189754486084 44.38846397399902 C -71.03255326181059 44.38846397399902 -79.31229400634766 36.108724083411026 -79.31229400634766 25.8951473236084 C -79.31229400634766 15.681570563805767 -

```
71.03255326181059 7.401830673217773 -60.8189754486084 7.401830673217773 C -
50.605397635406206 7.401830673217773 -42.32565689086914 15.681570563805767 -
42.32565689086914 25.8951473236084 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#9f9f9f">

<path d="M -42.32565689086914 25.8951473236084 C -42.32565689086914 36.108724083411026
-50.605397635406206 44.38846397399902 -60.8189754486084 44.38846397399902 C -
71.03255326181059 44.38846397399902 -79.31229400634766 36.108724083411026 -
79.31229400634766 25.8951473236084 C -79.31229400634766 15.681570563805767 -
71.03255326181059 7.401830673217773 -60.8189754486084 7.401830673217773 C -
50.605397635406206 7.401830673217773 -42.32565689086914 15.681570563805767 -
42.32565689086914 25.8951473236084 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 284.1822425563667,
244.93048823347058)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CCL4</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -47.20186996459961 113.39480972290039 C -47.20186996459961
123.88821786288634 -55.70846057176361 132.39480590820312 -66.20187187194824
132.39480590820312 C -76.69528317213287 132.39480590820312 -85.20187377929688
123.88821786288634 -85.20187377929688 113.39480972290039 C -85.20187377929688
102.90140158291445 -76.69528317213287 94.39481353759766 -66.20187187194824
94.39481353759766 C -55.70846057176361 94.39481353759766 -47.20186996459961
102.90140158291445 -47.20186996459961 113.39480972290039 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -47.20186996459961 113.39480972290039 C -47.20186996459961
123.88821786288634 -55.70846057176361 132.39480590820312 -66.20187187194824
132.39480590820312 C -76.69528317213287 132.39480590820312 -85.20187377929688
123.88821786288634 -85.20187377929688 113.39480972290039 C -85.20187377929688
102.90140158291445 -76.69528317213287 94.39481353759766 -66.20187187194824
94.39481353759766 C -55.70846057176361 94.39481353759766 -47.20186996459961
102.90140158291445 -47.20186996459961 113.39480972290039 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 281.7001581695334,
285.51071592945004)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CCL7</text>
```

```
</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -150.38169860839844 19.357580244541168 C -150.38169860839844
29.85099049132624 -158.88828836161338 38.35758024454117 -169.38169860839844
38.35758024454117 C -179.8751088551835 38.35758024454117 -188.38169860839844
29.85099049132624 -188.38169860839844 19.357580244541168 C -188.38169860839844
8.864169997756095 -179.8751088551835 0.3575802445411682 -169.38169860839844
0.3575802445411682 C -158.88828836161338 0.3575802445411682 -150.38169860839844
8.864169997756095 -150.38169860839844 19.357580244541168 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -150.38169860839844 19.357580244541168 C -150.38169860839844
29.85099049132624 -158.88828836161338 38.35758024454117 -169.38169860839844
38.35758024454117 C -179.8751088551835 38.35758024454117 -188.38169860839844
29.85099049132624 -188.38169860839844 19.357580244541168 C -188.38169860839844
8.864169997756095 -179.8751088551835 0.3575802445411682 -169.38169860839844
0.3575802445411682 C -158.88828836161338 0.3575802445411682 -150.38169860839844
8.864169997756095 -150.38169860839844 19.357580244541168 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
230.64209147679333, 242.14961315908997)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">CXCL10</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -180.7474365234375 70.21997833251953 C -180.7474365234375 80.7133885793046 -
189.25402627665244 89.21997833251953 -199.7474365234375 89.21997833251953 C -
210.24084677022256 89.21997833251953 -218.7474365234375 80.7133885793046 -
218.7474365234375 70.21997833251953 C -218.7474365234375 59.726568085734456 -
210.24084677022256 51.21997833251953 -199.7474365234375 51.21997833251953 C -
189.25402627665244 51.21997833251953 -180.7474365234375 59.726568085734456 -
180.7474365234375 70.21997833251953 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -180.7474365234375 70.21997833251953 C -180.7474365234375 80.7133885793046 -
189.25402627665244 89.21997833251953 -199.7474365234375 89.21997833251953 C -
210.24084677022256 89.21997833251953 -218.7474365234375 80.7133885793046 -
218.7474365234375 70.21997833251953 C -218.7474365234375 59.726568085734456 -
210.24084677022256 51.21997833251953 -199.7474365234375 51.21997833251953 C -
```

```
189.25402627665244 51.21997833251953 -180.7474365234375 59.726568085734456 -
180.7474365234375 70.21997833251953 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 218.3977910155131,
265.6025555262195)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">GPR84</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -174.94927978515625 191.22341918945312 C -174.94927978515625
201.71682943623819 -183.4558695383712 210.22341918945312 -193.94927978515625
210.22341918945312 C -204.4426900319413 210.22341918945312 -212.94927978515625
201.71682943623819 -212.94927978515625 191.22341918945312 C -212.94927978515625
180.73000894266806 -204.4426900319413 172.22341918945312 -193.94927978515625
172.22341918945312 C -183.4558695383712 172.22341918945312 -174.94927978515625
180.73000894266806 -174.94927978515625 191.22341918945312 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -174.94927978515625 191.22341918945312 C -174.94927978515625
201.71682943623819 -183.4558695383712 210.22341918945312 -193.94927978515625
210.22341918945312 C -204.4426900319413 210.22341918945312 -212.94927978515625
201.71682943623819 -212.94927978515625 191.22341918945312 C -212.94927978515625
180.73000894266806 -204.4426900319413 172.22341918945312 -193.94927978515625
172.22341918945312 C -183.4558695383712 172.22341918945312 -174.94927978515625
180.73000894266806 -174.94927978515625 191.22341918945312 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
221.97915621984623, 321.39793550080924)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">TNIP3</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -432.568359375 210.37246704101562 C -432.568359375 220.86587728780069 -
441.07494912821494 229.37246704101562 -451.568359375 229.37246704101562 C -
462.06176962178506 229.37246704101562 -470.568359375 220.86587728780069 -470.568359375
210.37246704101562 C -470.568359375 199.87905679423056 -462.06176962178506
191.37246704101562 -451.568359375 191.37246704101562 C -441.07494912821494
191.37246704101562 -432.568359375 199.87905679423056 -432.568359375 210.37246704101562
z"/>

</g> <!-- drawing style -->
```

```
</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -432.568359375 210.37246704101562 C -432.568359375 220.86587728780069 -
441.07494912821494 229.37246704101562 -451.568359375 229.37246704101562 C -
462.06176962178506 229.37246704101562 -470.568359375 220.86587728780069 -470.568359375
210.37246704101562 C -470.568359375 199.87905679423056 -462.06176962178506
191.37246704101562 -451.568359375 191.37246704101562 C -441.07494912821494
191.37246704101562 -432.568359375 199.87905679423056 -432.568359375 210.37246704101562
z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
104.41208296975081, 330.2276711964476)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">TFEC</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -282.9193420410156 -133.3740692138672 C -282.9193420410156 -
122.88065053988561 -291.42593179423056 -114.37405395507812 -301.9193420410156 -
114.37405395507812 C -312.4127522878007 -114.37405395507812 -320.9193420410156 -
122.88065053988561 -320.9193420410156 -133.3740692138672 C -320.9193420410156 -
143.86748788784877 -312.4127522878007 -152.37408447265625 -301.9193420410156 -
152.37408447265625 C -291.42593179423056 -152.37408447265625 -282.9193420410156 -
143.86748788784877 -282.9193420410156 -133.3740692138672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -282.9193420410156 -133.3740692138672 C -282.9193420410156 -
122.88065053988561 -291.42593179423056 -114.37405395507812 -301.9193420410156 -
114.37405395507812 C -312.4127522878007 -114.37405395507812 -320.9193420410156 -
122.88065053988561 -320.9193420410156 -133.3740692138672 C -320.9193420410156 -
143.86748788784877 -312.4127522878007 -152.37408447265625 -301.9193420410156 -
152.37408447265625 C -291.42593179423056 -152.37408447265625 -282.9193420410156 -
143.86748788784877 -282.9193420410156 -133.3740692138672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 174.1982710149868,
171.72418056764073)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">MX1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
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```
opacity="1" stroke="#000000">

<path d="M -202.9454345703125 -88.90166473388672 C -202.9454345703125 -
78.40825448710164 -211.45202432352744 -69.90166473388672 -221.9454345703125 -
69.90166473388672 C -232.43884481709756 -69.90166473388672 -240.9454345703125 -
78.40825448710164 -240.9454345703125 -88.90166473388672 C -240.9454345703125 -
99.3950749806718 -232.43884481709756 -107.90166473388672 -221.9454345703125 -
107.90166473388672 C -211.45202432352744 -107.90166473388672 -202.9454345703125 -
99.3950749806718 -202.9454345703125 -88.90166473388672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -202.9454345703125 -88.90166473388672 C -202.9454345703125 -
78.40825448710164 -211.45202432352744 -69.90166473388672 -221.9454345703125 -
69.90166473388672 C -232.43884481709756 -69.90166473388672 -240.9454345703125 -
78.40825448710164 -240.9454345703125 -88.90166473388672 C -240.9454345703125 -
99.3950749806718 -232.43884481709756 -107.90166473388672 -221.9454345703125 -
107.90166473388672 C -211.45202432352744 -107.90166473388672 -202.9454345703125 -
99.3950749806718 -202.9454345703125 -88.90166473388672 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
209.78189085084475, 192.23065408113374)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">AREG</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M -72.39506530761719 282.886962890625 C -72.39506530761719 293.38037313741006
-80.90165506083211 301.886962890625 -91.39506530761719 301.886962890625 C -
101.88847555440226 301.886962890625 -110.39506530761719 293.38037313741006 -
110.39506530761719 282.886962890625 C -110.39506530761719 272.39355264383994 -
101.88847555440226 263.886962890625 -91.39506530761719 263.886962890625 C -
80.90165506083211 263.886962890625 -72.39506530761719 272.39355264383994 -
72.39506530761719 282.886962890625 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M -72.39506530761719 282.886962890625 C -72.39506530761719 293.38037313741006
-80.90165506083211 301.886962890625 -91.39506530761719 301.886962890625 C -
101.88847555440226 301.886962890625 -110.39506530761719 293.38037313741006 -
110.39506530761719 282.886962890625 C -110.39506530761719 272.39355264383994 -
101.88847555440226 263.886962890625 -91.39506530761719 263.886962890625 C -
80.90165506083211 263.886962890625 -72.39506530761719 272.39355264383994 -
72.39506530761719 282.886962890625 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->
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<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
267.63561019093993, 363.6645207681756)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">WNT2B</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 374.1859436035156 -272.8877258300781 C 374.1859436035156 -262.39431558329306
365.6793538503007 -253.88772583007812 355.1859436035156 -253.88772583007812 C
344.69253335673056 -253.88772583007812 336.1859436035156 -262.39431558329306
336.1859436035156 -272.8877258300781 C 336.1859436035156 -283.3811360768632
344.69253335673056 -291.8877258300781 355.1859436035156 -291.8877258300781 C
365.6793538503007 -291.8877258300781 374.1859436035156 -283.3811360768632
374.1859436035156 -272.8877258300781 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 374.1859436035156 -272.8877258300781 C 374.1859436035156 -262.39431558329306
365.6793538503007 -253.88772583007812 355.1859436035156 -253.88772583007812 C
344.69253335673056 -253.88772583007812 336.1859436035156 -262.39431558329306
336.1859436035156 -272.8877258300781 C 336.1859436035156 -283.3811360768632
344.69253335673056 -291.8877258300781 355.1859436035156 -291.8877258300781 C
365.6793538503007 -291.8877258300781 374.1859436035156 -283.3811360768632
374.1859436035156 -272.8877258300781 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905,
475.87616038526005, 107.39362699999957)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal"
stroke="none" fill="#000000" font-size="12" x="0" y="0">HAS1</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-
opacity="1" stroke="#000000">

<path d="M 219.63026428222656 -119.37971496582031 C 219.63026428222656 -
108.88630471903524 211.12367452901162 -100.37971496582031 200.63026428222656 -
100.37971496582031 C 190.1368540354415 -100.37971496582031 181.63026428222656 -
108.88630471903524 181.63026428222656 -119.37971496582031 C 181.63026428222656 -
129.87312521260537 190.1368540354415 -138.3797149658203 200.63026428222656 -
138.3797149658203 C 211.12367452901162 -138.3797149658203 219.63026428222656 -
129.87312521260537 219.63026428222656 -119.37971496582031 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409,
218.65205957242523)">

<g fill-opacity="1" fill-rule="nonzero" stroke="none" fill="#000000">

<path d="M 219.63026428222656 -119.37971496582031 C 219.63026428222656 -108.88630471903524 211.12367452901162 -100.37971496582031 200.63026428222656 -100.37971496582031 C 190.1368540354415 -100.37971496582031 181.63026428222656 -108.88630471903524 181.63026428222656 -119.37971496582031 C 181.63026428222656 -129.87312521260537 190.1368540354415 -138.3797149658203 200.63026428222656 -138.3797149658203 C 211.12367452901162 -138.3797149658203 219.63026428222656 -129.87312521260537 219.63026428222656 -119.37971496582031 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 405.82680800846083, 178.17705046844006)">

<text fill-opacity="1" font-style="normal" font-family="Helvetica" font-weight="normal" stroke="none" fill="#000000" font-size="12" x="0" y="0">SELE</text>

</g> <!-- transform -->

<g transform="matrix(0.46110573037801905, 0, 0, 0.46110573037801905, 319.2792479517409, 218.65205957242523)">

<g stroke-linejoin="round" stroke-width="2" stroke-linecap="round" fill="none" stroke-opacity="1" stroke="#000000">

<path d="M 208.72535705566406 -402.9059753417969 C 208.72535705566406 -392.4125650950118 200.21876730244912 -383.9059753417969 189.72535705566406 -383.9059753417969 C 179.231946808879 -383.9059753417969 170.72535705566406 -392.4125650950118 170.72535705566406 -402.9059753417969 C 170.72535705566406 -413.39938558858194 179.231946808879 -421.9059753417969 189.72535705566406 -421.9059753417969 C 200.21876730244912 -421.9059753417969 208.72535705566406 -413.39938558858194 208.72535705566406 -402.9059753417969 z"/>

</g> <!-- drawing style -->

</g> <!-- transform -->

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324.32806396484375 C 246.83123982940128 -324.32806396484375 248.62210083007812 -
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318.1189249655206 240.62210083007812 -320.32806396484375 C 240.62210083007812 -
322.5372029641669 242.41296183075494 -324.32806396484375 244.62210083007812 -
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215.7622833251953 -188.18603515625 C 215.7622833251953 -198.67944540303506
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```

```
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108.38344198818788 287.25701904296875 -118.87685012817383 C 287.25701904296875 -
129.37025826815977 295.7636087961837 -137.87684631347656 306.25701904296875 -
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225.62596130371094 -42.791954040527344 C 225.62596130371094 -53.28536428731242
234.13255447272215 -61.791954040527344 244.62596893310547 -61.791954040527344 C
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225.62596130371094 -42.791954040527344 C 225.62596130371094 -53.28536428731242
234.13255447272215 -61.791954040527344 244.62596893310547 -61.791954040527344 C
```

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z"/>

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</g> <!-- transform -->

</g> <!-- default stroke -->

</svg> <!-- bounding box -->
```

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Peter Koper[pkoper1@gmail.com]
Sent: Fri 4/17/2020 3:00:24 PM (UTC-05:00)
Subject: Media interview request - Dr. Menachery

Dear Dr. Menachery:

My name is Peter Koper. I am a writer for the arts/essay website SpliceToday (https://www.splicetoday.com/)

I am preparing an article about molecules and their role in humans' lives.

The piece is for a general audience.
Your expertise and communication skills make you an ideal source.

I would like to have a short email interview with you.

I thank you in advance for your reply.

Regards,

Peter Koper

--

Koper Heavy Industries, ltd.

To: Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]; 'Erdman Dean'[derdman05@gmail.com]; Murphy, Frederick A.[famurphy@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; 'Denison Mark'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rollin Pierre'[pierrerollin2019@gmail.com]; 'Tesh Robert'[rbtesh22@gmail.com]; Weaver, Scott[sweaver@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Menachery, Vineet[vimenach@UTMB.EDU]; 'Folks Thomas'[Virusdoctom@aol.com]; 'Nichol Stuart'[stn1@CDC.GOV]; 'Spiropoulou Christina (CDC/CCID/NCZVED)'[ccs8@cdc.gov]; Keiser, Philip[phkeiser@UTMB.EDU]; Karl Johnson[microcaddis@gmail.com]; Doug Watts[dwatts2@utep.edu]; Ian Lipkin[wil2001@columbia.edu]
From: calisher@cybersafe.net[calisher@cybersafe.net]
Sent: Sun 4/26/2020 1:14:07 PM (UTC-05:00)
Subject: RE: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Want to weigh something large? Put it on one end of a teeter-totter (a seesaw). Then balance that with a large rock on the other end. Now all you need do is weight the rock.

One way to determine the quality of these newly developed assays is to (a) find someone who knows what the hell they are doing and have them (b) test by MACELISA and IgGelisa, then (c) test by NEUTRALIZATION. Without the latter, I ain't buying it. In the current situation, who cares whether a person has antibody, to SARS-CoV-2, unless that antibody is helpful in determining protection. Jordi Casals and Bob Shope must be turning in their graves.

Now W.H.O. is saying that the presence of antibody is not indicative of protection from a second exposure to SARS-CoV-2. No shit, Sherlock.

Charlie

-----Original Message-----
From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Saturday, April 25, 2020 10:42 PM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Erdman Dean <derdman05@gmail.com>; Murphy, Frederick A. <famurphy@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Denison Mark <mark.denison@vanderbilt.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Rollin Pierre <pierrerollin2019@gmail.com>; Tesh Robert <rbtesh22@gmail.com>; Weaver, Scott <sweaver@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Folks Thomas <Virusdoctom@aol.com>; Calisher Charles <calisher@cybersafe.net>; Nichol Stuart <stn1@CDC.GOV>; Spiropoulou Christina (CDC/CCID/NCZVED) <ccs8@cdc.gov>; Keiser, Philip <phkeiser@UTMB.EDU>
Subject: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Coronavirus Antibody Tests: Can You Trust the Results?
https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nytimes.com%2F2020%2F04%2F24%2Fhealth%2Fcoronavirus-antibody-tests.html%3Fre&data=02%7C01%7Cvimenach%40utmb.edu%7Cb7a778805eed40da80aa08d7ea0d9da6%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637235216509928652&sdata=L3FF1NQ4CtLxXWtalyuJFjH6AL4EN1cMLPuw08BszwE%3D&reserved=0

ferringSource=articleShare

Tom Ksiazek

Sent from a portable device

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Gurumurthy, Channabasavaiah B[cgurumurthy@unmc.edu]
Sent: Tue 6/9/2020 10:11:37 PM (UTC-05:00)
Subject: Re: COVID-19 mouse models

Dear Dr. Menachery,
I thought to re-send my previous email as I guess it may not have reached you the first time, or you may be busy.
I hope to hear from you.
Best Regards,
Guru

From: Channabasavaiah Gurumurthy <cgurumurthy@unmc.edu>
Date: Saturday, June 6, 2020 at 7:21 PM
To: "vimenach@utmb.edu" <vimenach@utmb.edu>
Subject: COVID-19 mouse models

Dear Dr. Menachery,

First, congratulations on your multiple papers and preprints on SARS-CoV2 including the recent *Science* Perspectives!

I would like to introduce myself. My name is Guru. I am a mouse molecular geneticist and a genome editing technology developer.

I serve as the director of the transgenic core facility at the University of Nebraska. I have developed a couple breakthrough CRISPR genome editing technologies called Easi-CRISPR and i-GONAD. I have included links to a few papers on these contributions below my signature.

I have designed strategies for developing over 20 mouse models for COVID-19. They are various kinds of knock-in models (that can be developed using Easi-CRISPR approach).

I have applied for a supplemental award through my R21 with NIAID for developing 6 of those models, which is currently under review. I have been in communication with the program officer who suggested that I should also consider applying for emergency R21 or R01 to develop these models.

PAR-20-177 https://grants.nih.gov/grants/guide/pa-files/PAR-20-177.html [grants.nih.gov]
PAR-20-178, https://grants.nih.gov/grants/guide/pa-files/PAR-20-178.html [grants.nih.gov]

I am reaching out to you to ask if you would be interested in joining with me in a grant submission. I am planning to submit either R21 (just to develop the models and distribute to the community) or R01 to develop and characterize models, if I can collaborate with experts like yourself who are actively working on SARS-Virology (my PHD in virology was on molecular epidemiology of foot-and-mouth disease virus but I am a genome editor since about 10 years!).

I have written the model generation part (for about 10 models), which is nearly ready for submitting as an R21 grant. If you can join me, we can easily add a few more designs and convert the grant into an R01 as multiple-PIs. I will develop all the models(as a genome editing expert), and as an infectious disease expert you could characterize and evaluate the models.

My list also includes immunocompromised strain background such as NSG, which are likely to develop more severe symptoms suitable for many studies. Some of the models I have designed (such as Cre-LoxP and Tet inducible knock-ins) in C57BL/6J (and NSG backgrounds) could be particularly useful for your aging related studies, where you can turn on the genes at different time points before infecting the mice.

If you are interested I would be happy to share more information. Also, it would great if you are available for a phone call anytime that works for you (weekend is fine). Please feel free to call 402 707 3035.

I look forward to hearing from you.

Best Regards,
Guru

C.B. Gurumurthy, BVSC, MVSC, PhD, Exec. MBA
Associate Professor, Pharmacology and Experimental Neuroscience.
Director, Mouse Genome Engineering Core Facility,
University of Nebraska Medical Center,
DRC II Room 1030,
Omaha, NE. 68106-5915
Phone: 402 559 8187 (Lab)
https://www.unmc.edu/pharmacology/faculty/primary-faculty/gurumurthy/index.html
Twitter: CRISPRGuru
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1220-4
https://www.nature.com/articles/nprot.2017.153
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-018-1400-x
https://www.nature.com/articles/s41596-019-0187-x
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1776-2

To: Ramos, Analaura[anramos@utmb.edu]; Beasley, David W.[dwbeasle@UTMB.EDU]; Brasel, Trevor[trbrasel@UTMB.EDU]; Bente, Dennis A.[dabente@UTMB.EDU]; Boldogh, Istvan[sboldogh@UTMB.EDU]; Cross, Robert W.[rwcross@UTMB.EDU]; Eaves-Pyles, Tonyia D.[tdeavesp@UTMB.EDU]; Endsley, Janice J.[jjendsle@utmb.edu]; Endsley, Mark A.[maendsle@utmb.edu]; Hosakote madaiah, Yashoda[yahosako@utmb.edu]; Lee, Sunhee[sunhlee@UTMB.EDU]; Hu, Haitao[haihu@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Mire, Chad[chmire@UTMB.EDU]; Sha, Jian[jisha@UTMB.EDU]; Soong, Lynn[lysoong@UTMB.EDU]; Sun, Jiaren[jisun@UTMB.EDU]; Terasaki, Kaori[katerasa@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]
Cc: Speakes, Shannon D.[sdspeake@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 8/10/2020 9:08:10 AM (UTC-05:00)
Subject: Re: APT FY 20

From: Ramos, Analaura <anramos@utmb.edu>
Sent: Thursday, August 6, 2020 1:27 PM
To: Beasley, David W. <dwbeasle@UTMB.EDU>; Brasel, Trevor <trbrasel@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; Boldogh, Istvan <sboldogh@UTMB.EDU>; Cross, Robert W. <rwcross@UTMB.EDU>; Eaves-Pyles, Tonyia D. <tdeavesp@UTMB.EDU>; Endsley, Janice J. <jjendsle@utmb.edu>; Endsley, Mark A. <maendsle@utmb.edu>; Hosakote madaiah, Yashoda <yahosako@utmb.edu>; Lee, Sunhee <sunhlee@UTMB.EDU>; Hu, Haitao <haihu@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Sha, Jian <jisha@UTMB.EDU>; Soong, Lynn <lysoong@UTMB.EDU>; Sun, Jiaren <jisun@UTMB.EDU>; Terasaki, Kaori <katerasa@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>
Cc: Speakes, Shannon D. <sdspeake@UTMB.EDU>
Subject: FW: APT FY 20

Friendly reminder to please send us your materials.

Thank you
Ana Laura Ramos

From: Ramos, Analaura
Sent: Wednesday, June 17, 2020 2:04 PM
Subject: APT FY 20

Dear Faculty,

APT FY20 blank faculty activity reports have been updated and placed in your S drive faculty folder under **S:\Faculty\Your Name\APT 2020.** (templates attached)

Those faculty who are up for post-tenure review have a 6 year activity report to complete which has been saved to your respective faculty folder on the S drive.

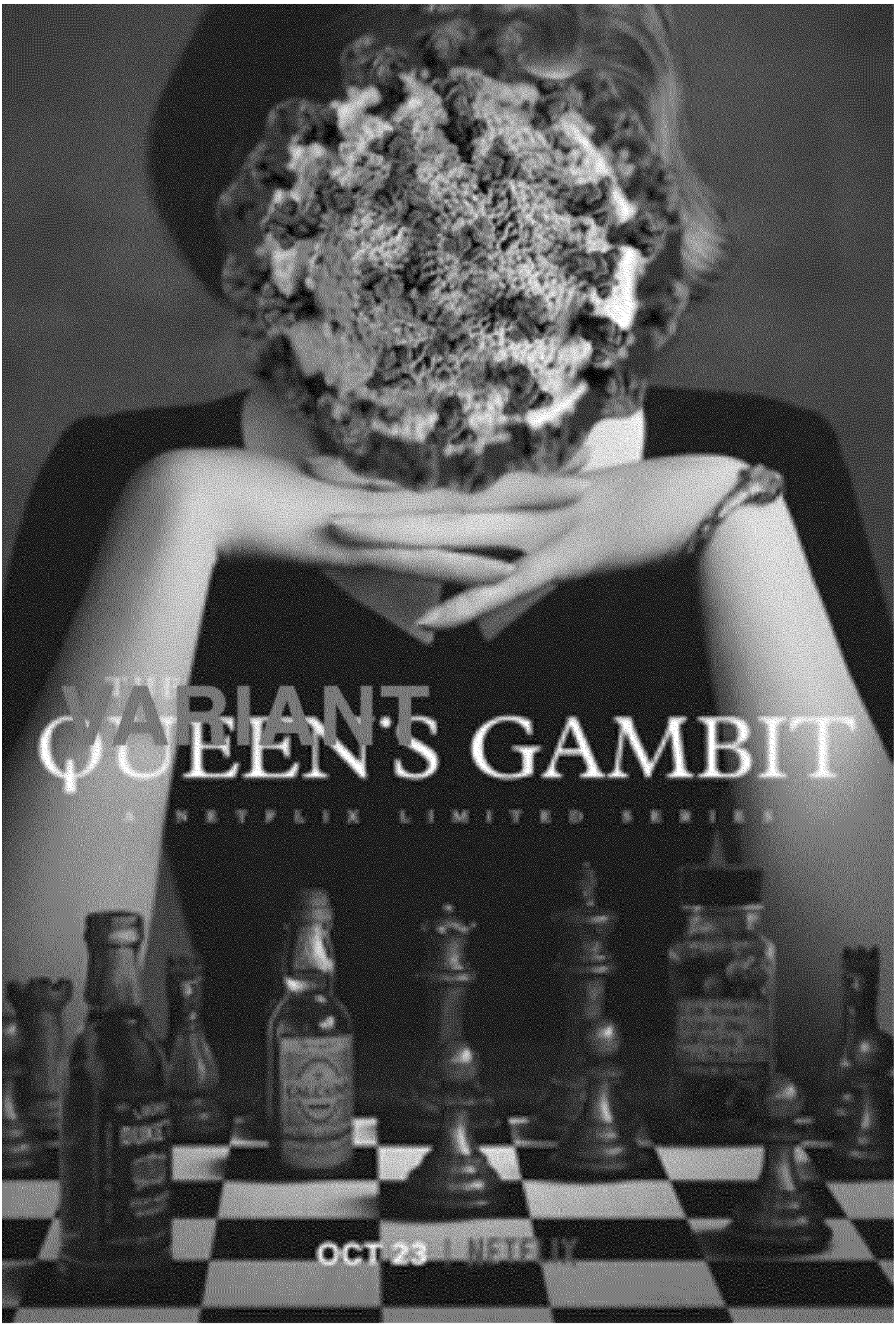
Please update your CV and make sure it's in the UTMB format (template attached).
Also, please turn in teaching evaluations or materials you would like the committee to review.

If you are on the non-tenure track, please request a letter from your supervisor evaluating your FY20 performance to be sent to the administrative office.
For faculty holding administrative titles, please request a letter from your administrative superior to be sent to the administrative office.

Let me know if you have any questions. Please turn in the reports by **August 1st** to the administrative office.

Thank you
Ana Laura Ramos
Sr. Administrative Manager
Microbiology & Immunology
301 University Blvd., Galveston, TX 77555-1019
P 409.772-2724
F 409.772-2366 E anramos@utmb.edu

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: vineet menachery[vineet.menachery@gmail.com]
Sent: Mon 2/22/2021 3:50:52 PM (UTC-06:00)



To: Speakes, Shannon D.[sdspeake@UTMB.EDU]; Beasley, David W.[dwbeasle@UTMB.EDU]; Bente, Dennis A.[dabente@UTMB.EDU]; Boldogh, Istvan[sboldogh@UTMB.EDU]; Chopra, Ashok[achopra@UTMB.EDU]; Cong, Yingzi[yicong@UTMB.EDU]; Cross, Robert W.[rwcross@UTMB.EDU]; Dickson, Laura[ldickson@UTMB.EDU]; Eaves-Pyles, Tonyia D.[tdeavesp@UTMB.EDU]; Endsley, Janice J.[jjendsle@utmb.edu]; Endsley, Mark A.[maendsle@utmb.edu]; Gagnon, Matthieu[magagnon@UTMB.EDU]; Garg, Nisha[nigarg@utmb.edu]; Giraldo Giraldo, Maria I.[migirald@UTMB.EDU]; Geisbert, Thomas W.[twgeisbe@UTMB.EDU]; Hosakote madaiah, Yashoda[yahosako@utmb.edu]; Hu, Haitao[haihu@UTMB.EDU]; Huda, Ruksana[rhuda@UTMB.EDU]; Lawrence, William S.[wslawren@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Lee, Sunhee[sunhlee@UTMB.EDU]; Liang, Yuejin[yu2liang@UTMB.EDU]; Makino, Shinji[shmakino@UTMB.EDU]; Mire, Chad[chmire@UTMB.EDU]; Rajsbaum, Ricardo[rirajsba@UTMB.EDU]; Sha, Jian[jisha@UTMB.EDU]; Soong, Lynn[lysoong@UTMB.EDU]; Sun, Jiaren[jisun@UTMB.EDU]; Sun, Keer[kesun@UTMB.EDU]; Terasaki, Kaori[katerasa@UTMB.EDU]; Torres, Alfredo G.[altorres@utmb.edu]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Wang, Tian[ti1wang@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Yao, Suxia[suyao@UTMB.EDU]; Yi, Minkyung[miyi@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 1/20/2021 1:39:07 PM (UTC-06:00)
Subject: Re: **IMPORTANT**Departmental Review 2014-2020**INFORMATION NEEDED**

From: Speakes, Shannon D. <sdspeake@UTMB.EDU>
Sent: Friday, January 8, 2021 10:48 AM
To: Beasley, David W. <dwbeasle@UTMB.EDU>; Bente, Dennis A. <dabente@UTMB.EDU>; Boldogh, Istvan <sboldogh@UTMB.EDU>; Chopra, Ashok <achopra@UTMB.EDU>; Cong, Yingzi <yicong@UTMB.EDU>; Cross, Robert W. <rwcross@UTMB.EDU>; Dickson, Laura <ldickson@UTMB.EDU>; Eaves-Pyles, Tonyia D. <tdeavesp@UTMB.EDU>; Endsley, Janice J. <jjendsle@utmb.edu>; Endsley, Mark A. <maendsle@utmb.edu>; Gagnon, Matthieu <magagnon@UTMB.EDU>; Garg, Nisha <nigarg@utmb.edu>; Giraldo Giraldo, Maria I. <migirald@UTMB.EDU>; Geisbert, Thomas W. <twgeisbe@UTMB.EDU>; Hosakote madaiah, Yashoda <yahosako@utmb.edu>; Hu, Haitao <haihu@UTMB.EDU>; Huda, Ruksana <rhuda@UTMB.EDU>; Lawrence, William S. <wslawren@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Lee, Sunhee <sunhlee@UTMB.EDU>; Liang, Yuejin <yu2liang@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Mire, Chad <chmire@UTMB.EDU>; Rajsbaum, Ricardo <rirajsba@UTMB.EDU>; Sha, Jian <jisha@UTMB.EDU>; Soong, Lynn <lysoong@UTMB.EDU>; Sun, Jiaren <jisun@UTMB.EDU>; Sun, Keer <kesun@UTMB.EDU>; Terasaki, Kaori <katerasa@UTMB.EDU>; Torres, Alfredo G. <altorres@utmb.edu>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Wang, Tian <ti1wang@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Yao, Suxia <suyao@UTMB.EDU>; Yi, Minkyung <miyi@UTMB.EDU>
Subject: **IMPORTANT**Departmental Review 2014-2020**INFORMATION NEEDED**

Good morning,

We are currently working on the departmental review for period 2014-2020.

I'm asking all faculty to send a brief description of your research project in the following format:

- Description should be 12-15 (maximum) lines
- 0.05" margin
- Arial 11 font

Also, please let me know if you have been promoted during this period.

Please submit requested material to me by Friday, January 15th.

Thank you,

Shannon Speakes
McLaughlin Program Coordinator
The University of Texas Medical Branch
Microbiology & Immunology
Medical Research Bldg. rm 4.142
301 University Blvd., Galveston, TX. 77555-0610
Office: 409-772-8140
Email:sdspeake@utmb.edu

To: Katerina TILIAKOU[Katerina.TILIAKOU@trtworld.com]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 1/21/2020 1:21:28 PM (UTC-06:00)
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

0044798 695 7447

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 1:17 PM
To: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

I'm ready now.

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 11:59 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

Could you please call me at 00447986957447 or please let me know what time can I call you?

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 3:29 PM
To: Katerina TILIAKOU
Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

I am about to head into the containment lab this morning. Best time would be when I get out, perhaps around 1pm New York time.

My office number is 001-409-772-9713. You can also email me the questions if that is preferable.

VDM

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:54 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

That's great! What's the best number and time that I can reach out to you today in order to let you know about the questions?

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:52 PM
To: Katerina TILIAKOU
Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Ok. I can be available for that.

My Skype email is Vineet.Menachery@gmail.com

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:49 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

The interview will be for 5 minutes. You have to be available from 2.15pm New York time to do a Skype test call.

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Katerina TILIAKOU
Sent: Tuesday, January 21, 2020 2:20 PM
To: Menachery, Vineet
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

That's great news. We would love to have you today at 14:30pm New York time.

Could you please send me the best number and time that I can reach out for a pre-interview today as well?

Please feel free to message me at 00447986957447.

Best regards,

Katerina

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:09 AM
To: Katerina TILIAKOU
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Katerina,

I am a bit confused on the time. Would you like me to Skype tomorrow (January 21st) at 1400?

I should be available. Please let me know the parameters (how long I should set aside?).

Thanks

Vineet D. Menachery

Vineet D. Menachery, Ph.D.
Assistant Professor

Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Monday, January 20, 2020 8:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Dear Dr Menachery,

This is Katerina from TRT World, an international news broadcasting channel based in London.

We are running a story on Coronavirus today at 19G (14.00pm New York time) for our news bulletin and I was wondering if you could join us as guest via Skype.

Please feel free to message me at 00447986957447.

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

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To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Thomas Danielian[Thomas.Danielian@global.com]
Sent: Mon 1/27/2020 5:55:14 AM (UTC-06:00)
Subject: Fw: [External] Re: UK LBC Radio Interview request

Dear Dr. Menachery,

I hope you are well. Please see my below correspondence with Dr. Danthi. Would you be available to speak to us?

Many thanks!

Thomas

From: Danthi, Pranav <pdanthi@indiana.edu>
Sent: Monday, January 27, 2020 11:48 AM
To: Thomas Danielian <Thomas.Danielian@global.com>
Cc: vimenach@utmb.edu <vimenach@utmb.edu>
Subject: Re: [External] Re: UK LBC Radio Interview request

Hi Thomas,
Thanks for reaching out. I dont have sufficient expertise on coronaviruses. You could ask Dr. Menachery at UTMB. I cc'd him here.
Pranav Danthi

www.indiana.edu/~reovirus

On Jan 27, 2020, at 5:52 AM, Thomas Danielian <Thomas.Danielian@global.com> wrote:

Dear Dr. Danthi,

To clarify, these times are ET

Many thanks!

Thomas

From: Thomas Danielian
Sent: Monday, January 27, 2020 10:47 AM
To: pdanthi@indiana.edu <pdanthi@indiana.edu>
Subject: UK LBC Radio Interview request

Dear Dr. Danthi,

I hope you are well. This is Thomas from LBC Radio in the UK.

I was wondering if you might be available to talk about the latest news surrounding the Coronavirus tonight? If not you do you know if any of your colleagues from Indiana or ASV might be able to help?

Would be an over the phone or Facetime Audio interview. It is for our overnight show, so it would be a live interview anytime at 8.30pm, 8.50pm, 9.30pm or 9.50pm.

Hope you you can help!

Many thanks,

Thomas

30 LEICESTER SQUARE,
LONDON WC2H 7LA

Part of Global, the Media & Entertainment Group
@global global.com

Thomas Danielian
Senior Producer of Overnight with Darren Adam, Steve Allen's Early Breakfast & Steve Allen In Conversation
+44 (0) 7889 734 446 (Signal & WhatsApp)
thomas.danielian@global.com
thomasdanielian@gmail.com

Global is the trading name for Global Media & Entertainment Limited and associated companies. You can contact us at 30 Leicester Square, London, WC2H 7LA, Tel: 020 7766 6000, Email: info@global.com or, for further information about our companies and brands, please go to www.global.com. This email is confidential. If it has been sent to you in error, please notify the sender and delete the email and any attachments; please do not copy, disclose or use in any way this email or its contents.

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Brent Bearden[Brent@Atlasbio.com]
Sent: Mon 3/23/2020 1:48:36 PM (UTC-05:00)
Subject: Atlas Bio Serum

Vineet,

just left you a voicemail. I AM TRYING TO HELP!

I am one of the Owners of Atlas Biologicals and I am trying to help you. **We have a bovine serum product that works exceptionally well with VERO cells and I am certain it will help you in your COVID Research.**

The product is called **EQUALFETAL** and it is a product that we manufacture and sell mostly to the vaccine and human cell therapy markets. It is also used in large scale Monoclonal antibody production.

I am 100% certain it will work for you and SAVE you a tremendous amount of money compared to your use of traditional FBS. *I believe FBS will start to get harder to find and this is a solution for you if it does.*

Have your lab manager request a sample.

***I will send you a FREE SAMPLE IMMEDIATELY if you want to try it.*

***The serum is only $220.00 per 500mL*

Looking forward to your reply,

ATLAS BIOLOGICALS

Brent Bearden
Vice President & Owner

T: 970-494-2051
E: brent@atlasbio.com
W: www.atlasbio.com

To: Shi, Pei yong[peshi@UTMB.EDU]; McLellan, Susan[sumclell@UTMB.EDU]; Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; calisher, C (calisher@cybersafe.net)[calisher@cybersafe.net]; Cross, Robert W.[rwcross@UTMB.EDU]; Erdman,D (derdman05@gmail.com)[derdman05@gmail.com]; Folks, Thomas (Virusdoctom@aol.com)[Virusdoctom@aol.com]; Holubar, Connie J.[cjholuba@UTMB.EDU]; Plante, Kenneth S.[ksplante@UTMB.EDU]; Laposata, Michael[milaposa@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; Mark R. Denison[mark.denison@vanderbilt.edu]; Murphy, Frederick A.[famurphy@UTMB.EDU]; Pyles, Richard B.[rbpyles@UTMB.EDU]; Rollin,P (pierrerollin2019@gmail.com)[pierrerollin2019@gmail.com]; Tesh,R(Home)[rbtesh22@gmail.com][rbtesh22@gmail.com]; Tesh, Robert B.[rtesh@UTMB.EDU]; tpmonath@gmail.com[tpmonath@gmail.com]; Trumble, Julie M.[jtrumble@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Weaver, Scott[sweaver@UTMB.EDU]; Cajimat, Maria N.[nbcajirm@UTMB.EDU]; Judy, Barbara M.[bmjudy@utmb.edu]; Milazzo, Marylou[mamilazz@UTMB.EDU]; Newman, Patrick C.[pcnewman@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 4/1/2020 2:19:21 PM (UTC-05:00)
Subject: Re: Grady 2020 reference from my EndNote library

My bet is it could delay antibody response and yeild, but not block completely.

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Wednesday, April 1, 2020 2:19 PM
To: McLellan, Susan <sumclell@UTMB.EDU>; Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; calisher, C (calisher@cybersafe.net) <calisher@cybersafe.net>; Cross, Robert W. <rwcross@UTMB.EDU>; Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; Folks, Thomas (Virusdoctom@aol.com) <Virusdoctom@aol.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>; Laposata, Michael <milaposa@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Mark R. Denison <mark.denison@vanderbilt.edu>; Murphy, Frederick A. <famurphy@UTMB.EDU>; Pyles, Richard B. <rbpyles@UTMB.EDU>; Rollin,P (pierrerollin2019@gmail.com) <pierrerollin2019@gmail.com>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tesh, Robert B. <rtesh@UTMB.EDU>; tpmonath@gmail.com <tpmonath@gmail.com>; Trumble, Julie M. <jtrumble@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Cajimat, Maria N. <nbcajirm@UTMB.EDU>; Judy, Barbara M. <bmjudy@utmb.edu>; Milazzo, Marylou <mamilazz@UTMB.EDU>; Newman, Patrick C. <pcnewman@UTMB.EDU>
Subject: RE: Grady 2020 reference from my EndNote library

How much immune suppression could chloroquine do in human?
Once animal models have been established, this could be experimentally tested.
Thanks.

- Pei-Yong

From: McLellan, Susan <sumclell@UTMB.EDU>
Sent: Wednesday, April 1, 2020 2:11 PM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; calisher, C (calisher@cybersafe.net) <calisher@cybersafe.net>; Cross, Robert W. <rwcross@UTMB.EDU>; Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; Folks, Thomas (Virusdoctom@aol.com) <Virusdoctom@aol.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>; Laposata, Michael <milaposa@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Mark R. Denison <mark.denison@vanderbilt.edu>; Murphy, Frederick A. <famurphy@UTMB.EDU>; Pyles, Richard B. <rbpyles@UTMB.EDU>; Rollin,P (pierrerollin2019@gmail.com) <pierrerollin2019@gmail.com>; Shi, Pei yong <peshi@UTMB.EDU>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tesh, Robert B. <rtesh@UTMB.EDU>; tpmonath@gmail.com; Trumble, Julie M. <jtrumble@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Cajimat, Maria N. <nbcajirm@UTMB.EDU>; Judy, Barbara M. <bmjudy@utmb.edu>; Milazzo, Marylou <mamilazz@UTMB.EDU>; Newman, Patrick C. <pcnewman@UTMB.EDU>
Subject: RE: Grady 2020 reference from my EndNote library

An interesting question was brought up in our ID section – could chloroquine, in it's immune mediating capacity, reduce immune response to point where people don't develop neutralizing / protective Ab? So they would be higher risk for getting infected again? Even worse, getting infected with minimal symptoms but able to transmit again? Are we creating a pool of people who will not develop immunity hence increasing our pool of susceptibles for the future?

Susan McLellan, MD MPH
Infectious Diseases
UTMB

From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Wednesday, April 1, 2020 1:11 PM
To: calisher, C (calisher@cybersafe.net) <calisher@cybersafe.net>; Cross, Robert W. <rwcross@UTMB.EDU>; Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; Folks, Thomas (Virusdoctom@aol.com) <Virusdoctom@aol.com>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Plante, Kenneth S. <ksplante@UTMB.EDU>; Laposata, Michael <milaposa@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Mark R. Denison <mark.denison@vanderbilt.edu>; Murphy, Frederick A. <famurphy@UTMB.EDU>; Pyles, Richard B. <rbpyles@UTMB.EDU>; Rollin,P (pierrerollin2019@gmail.com) <pierrerollin2019@gmail.com>; Shi, Pei yong <peshi@UTMB.EDU>; McLellan, Susan <sumclell@UTMB.EDU>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tesh, Robert B. <rtesh@UTMB.EDU>; tpmonath@gmail.com; Trumble, Julie M. <jtrumble@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Weaver, Scott <sweaver@UTMB.EDU>; Cajimat, Maria N. <nbcajirm@UTMB.EDU>; Judy, Barbara M. <bmjudy@utmb.edu>; Milazzo, Marylou <mamilazz@UTMB.EDU>; Newman, Patrick C. <pcnewman@UTMB.EDU>
Subject: Grady 2020 reference from my EndNote library

Grady D. (2020, 20200401). **Malaria Drug Helps Virus Patients Improve, in Small Study.** NYTimes Retrieved 0401, 2020,

To: Martin, Chris E[Chris.Martin@charter.com]; 'Vineet.Menachery@gmail.com'[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 6/8/2020 5:00:33 PM (UTC-05:00)
Subject: Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

From: Martin, Chris E <Chris.Martin@charter.com>
Sent: Monday, June 8, 2020 4:57 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; 'Vineet.Menachery@gmail.com' <Vineet.Menachery@gmail.com>
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Here I am

Here what I need for this tomorrow

Skype Handle:
Phone #:
Location: Town / City calling from

From: Martin, Chris E
Sent: Monday, June 08, 2020 9:35 AM
To: 'vimenach@utmb.edu' <vimenach@utmb.edu>; 'Vineet.Menachery@gmail.com' <Vineet.Menachery@gmail.com>
Subject: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Greetings Dr. Menachery,

I am an Executive producer with Spectrum News in Austin for our nightly Texas politics and public affairs program 'Capital Tonight' hosted by Karina Kling.

I would like to speak with you about coming on our show via Skype tomorrow Tuesday 6.9 at 130p to discuss the progression of the coronavirus.

Would it be possible to schedule a brief call with you to discuss your work with the coronavirus?

The best way to reach me these days is on my mobile phone 201-417-9413.

Thank you Dr. Menachery.

Chris Martin
Executive Producer
News, Documentary and Long-Form Programming
Spectrum Networks
1708 Colorado St. | Austin, TX 78701
o 512.531.1205 | c **201.417.9413**

To: Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; Raimer, Ben G.[bgraimer@UTMB.EDU]; Patel, Janak A.[jpatel@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Keiser, Philip[phkeiser@UTMB.EDU]; Sharma, Gulshan[gusharma@UTMB.EDU]
Cc: Makino, Shinji[shmakino@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 4/9/2020 9:05:26 AM (UTC-05:00)
Subject: Re: (BN) Coronavirus May 'Reactivate' in Cured Patients, Korean CDC

There are many of these reports that have trickled out of patients testing positive again and worthy of follow up and monitoring.

However, I have not seen any reports that live virus was collected from these people who were reactivated/reinfected. The ones I have seen have all been PCR based tests. I can think of a few reasons this could occur.

1) Patients may not have truly cleared virus to begin with. COVID-19 patients have been going through waves of disease symptoms with people seemingly getting better and regressing a few days later. This may be happening in these studies and may be exacerbated in patients with milder disease.
2) PCR positive testing may be a product of clearing cells/debris. As the airway repairs itself, debris from infected cells may still contain the viral RNA and end with a positive test. The stability of small pieces of viral RNA and the abundance of the targets (depending on PCR) make this a potential outcome. Without the PCR data, it is hard to judge and cutoffs will be important.
3) The virus has gone dormant and reactivated in some way like a herpes viruses. This has never been seen before with a coronavirus. I am doubtful that this is what is happening.

My best bet is a combination of 1/2 are occurring. Without the data, it is hard to decipher if this is real. The CT values on the PCR test would be informative here and if they are on the low end (>30CT), my bet is the #2 is what is happening.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>
Sent: Thursday, April 9, 2020 9:00 AM
To: Raimer, Ben G. <bgraimer@UTMB.EDU>; Patel, Janak A. <jpatel@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Keiser, Philip <phkeiser@UTMB.EDU>; Sharma, Gulshan <gusharma@UTMB.EDU>
Cc: Menachery, Vineet <vimenach@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>
Subject: Re: (BN) Coronavirus May 'Reactivate' in Cured Patients, Korean CDC

Dear Ben

This is a serious concern – I add Vineet Menachery and Shinji Makino since they are our two most expert coronavirologists at UTMB to see if they have an insights from the virus side.

It could very well be a testing problem, however. The PCR test based on nasal or throat swabs alone is spotty at best from day 6 post symptoms onwards – see paper from Germany in Nature attached. Caveat to this paper is that these were all mild cases – nonetheless an important study. I have not looked at the data in great detail but believe one could see whether patients oscillated between negative and positive status.

If useful to you I can check with my friend Dr. Antonio Dajer (Cornell ED) – he was highlighted in the New Yorker recently for his work with COVID-19 patients. He can tell me if they have seen anything like this

Mariano

Mariano A. Garcia-Blanco MD PhD

Professor and Chair
Biochemistry and Molecular Biology
Professor
Internal Medicine
Mildred H Vacek and John R Vacek Distinguished Chair in Honor of President Truman G. Blocker, Jr.
University of Texas Medical Branch
Galveston TX USA
maragarc@utmb.edu
https://bmb.utmb.edu/faculty/garcia-blanco.asp
https://bmb.utmb.edu/MGB-Bradrick/

Adjunct Professor
Emerging Infectious Diseases
Duke-NUS Medical School
Singapore
mariano.garciablanco@duke-nus.edu.sg
https://www.duke-nus.edu.sg/content/garcia-blanco-mariano

From: "Raimer, Ben G." <bgraimer@UTMB.EDU>
Date: Thursday, April 9, 2020 at 8:52 AM
To: "Patel, Janak A." <jpatel@UTMB.EDU>, "LeDuc, James W." <jwleduc@UTMB.EDU>, "Garcia-Blanco, Mariano A." <maragarc@UTMB.EDU>, "Keiser, Philip" <phkeiser@UTMB.EDU>, "Sharma, Gulshan" <gusharma@UTMB.EDU>
Subject: FW: (BN) Coronavirus May 'Reactivate' in Cured Patients, Korean CDC

What do you guys make of this?

Subject: (BN) Coronavirus May 'Reactivate' in Cured Patients, Korean CDC

(BN) Coronavirus May 'Reactivate' in Cured Patients, Korean CDC Says

Coronavirus May 'Reactivate' in Cured Patients, Korean CDC Says
2020-04-09 04:25:07.356 GMT

By Kyunghee Park
(Bloomberg) -- The coronavirus may be "reactivating" in people who have been cured of the illness, according to Korea's Centers for Disease Control and Prevention.
About 51 patients classed as having been cured in South Korea have tested positive again, the CDC said in a briefing on Monday. Rather than being infected again, the virus may have been reactivated in these people, given they tested positive

again shortly after being released from quarantine, said Jeong Eun-kyeong, director-general of the Korean CDC.

"While we are putting more weight on reactivation as the possible cause, we are conducting a comprehensive study on this," Jeong said. "There have been many cases when a patient during treatment will test negative one day and positive another."

A patient is deemed fully recovered when two tests conducted with a 24-hour interval show negative results.

The Korean CDC will conduct an epidemiological probe into the cases, Jeong said.

South Korea was one of the earliest countries to see a large-scale coronavirus outbreak, but the country has seen just 200 deaths and a falling new case tally since peaking at 1,189 on Feb. 29. One of the world's most expansive testing programs and a tech-driven approach to tracing infections has seen Korea contain its epidemic without lockdowns or shuttering businesses.

Fear of re-infection in recovered patients is also growing in China, where the virus first emerged last December, after reports that some tested positive again -- and even died from the disease -- after supposedly recovering and leaving hospital. There's little understanding of why this happens, although some believe that the problem may lie in inconsistencies in test results.

Read more about Korea's CDC chief: The Virus Hunter Showing the World How to Fight an Epidemic

As of Wednesday, South Korea had 10,384 virus cases, with 6,776 released from hospital, according to data compiled by Johns Hopkins University and Bloomberg News.

Epidemiologists around the world are in a race to find out more about the virus that causes Covid-19. The pathogen's rapid global spread has recently seen the focus shift to patients who contract the virus but display few or atypical symptoms. Korea has been at the forefront of tracking these cases, which are causing particular concern in China, where the epidemic is showing signs of coming under control.

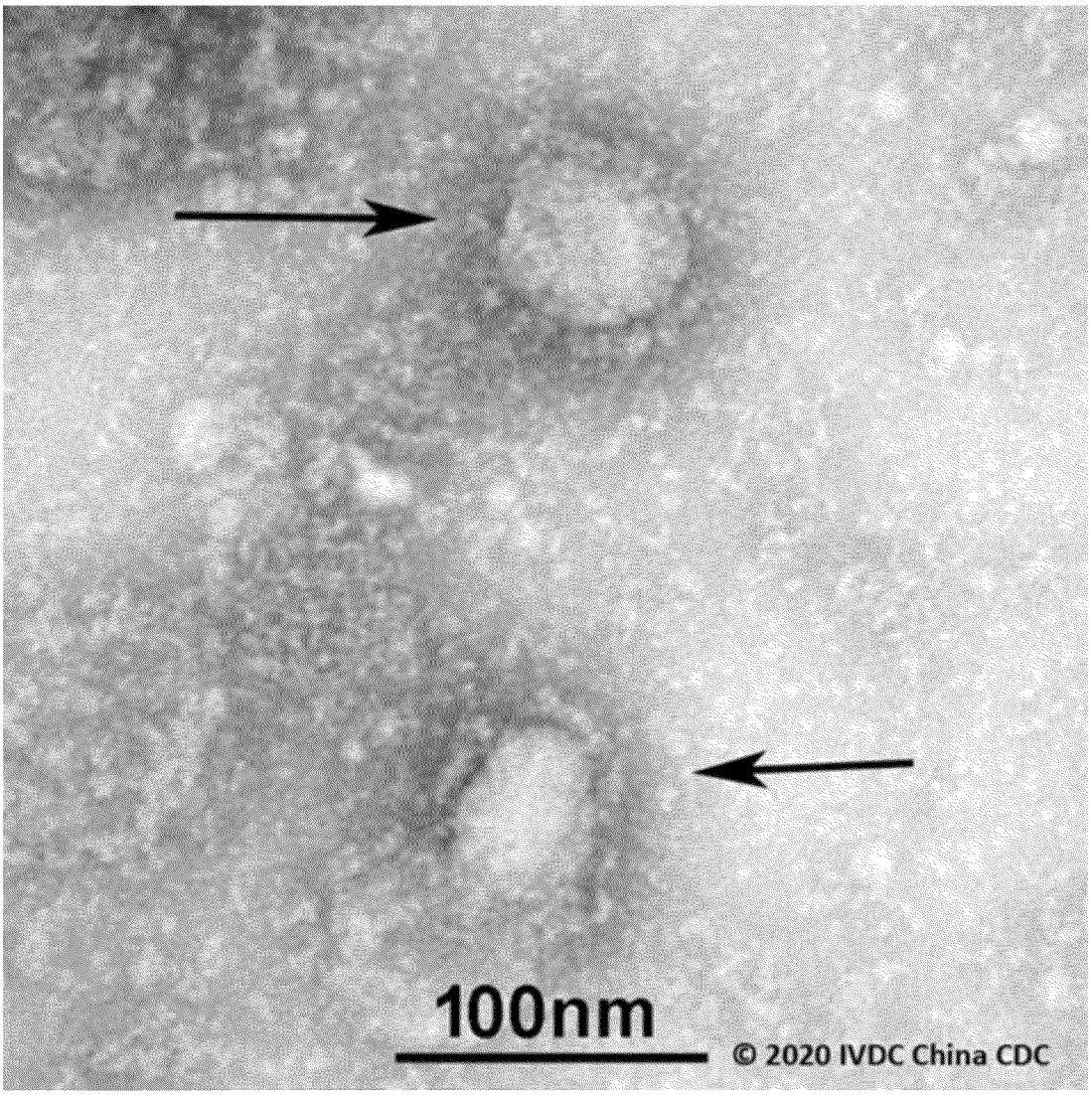
To contact the reporter on this story:
Kyunghee Park in Singapore at kpark3@bloomberg.net
To contact the editors responsible for this story:
Young-Sam Cho at ycho2@bloomberg.net
Emma O'Brien, Rachel Chang

To: Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; Erdman,D (derdman05@gmail.com)[derdman05@gmail.com]; LeDuc, James W.[jwleduc@UTMB.EDU]; Shi, Pei yong[peshi@UTMB.EDU]; Tesh,R(Home)[rbtesh22@gmail.com][rbtesh22@gmail.com]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 1/21/2020 5:00:40 PM (UTC-06:00)
Subject: Re: EM Image of 2019-nCoV

From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Tuesday, January 21, 2020 5:00 PM
To: Erdman,D (derdman05@gmail.com) <derdman05@gmail.com>; LeDuc, James W. <jwleduc@UTMB.EDU>; Shi, Pei yong <peshi@UTMB.EDU>; Tesh,R(Home)[rbtesh22@gmail.com] <rbtesh22@gmail.com>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: EM Image of 2019-nCoV

I guess that means they do have an isolate? It's hard to tell sometimes these days with folks equating having a PCR hit with an isolate…

From: Dean Erdman [mailto:derdman05@gmail.com]
Sent: 21 January, 2020 16:16
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Subject: EM Image of 2019-nCoV



To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Inderjeet Phd2014[inderjeet@nii.ac.in]
Sent: Wed 5/5/2021 11:16:49 AM (UTC-05:00)
Subject: looking for postdoc position

Dear Dr Vineet,
Greetings!

I`m Inderjeet Kalia, recently I have completed my PhD from the National Institute of Immunology, New Delhi, India. I visited your lab profile and fascinated by your research on SARS and MERS-CoV. Without stretching this mail very long, I want to ask if any postdoc position is available in your lab. I`m very eager to apply to your lab. Waiting for your reply, thank you.

Inderjeet Kalia, PhD
National Institute of Immunology
Aruna Asif Ali Road, JNU campus
New Delhi - 110067

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: vaisakh e h[vaisakh.lit@gmail.com]
Sent: Sun 5/30/2021 10:26:24 PM (UTC-05:00)
Subject: MEDIA: REQUEST FOR INTERVIEW

Hi Vineet,
This is Vaisakh E. Hari, a journalist with THE WEEK magazine in India, one of the largest circulated English-language news weeklies in the country, published by the Malayala Manorama group. Speaking as someone who has been following your work for some time, it is a pleasure to make your acquaintance.

We were working on a cover story on the ongoing coronavirus pandemic, which has unfortunately hit very close to home for many of us in India, and we would very much appreciate it if you could share your expertise with us on the subject.

Some topics we mean to explore:

1. The feelings of the medical community on the origins of the pandemic, now that both the US President Joe Biden and the UK intelligence agencies have lent credence to the "lab-leak" hypothesis. Does such a theory have legs to stand on?

2. Emergence of the variants of coronavirus, and what does it mean going forward?

3. Are vaccines the only hedge against (what you described in an interview as) "worst-case outcomes"?

4. Evaluation of the situation in India.

Would it be possible to schedule an interview? Our magazine goes to print by 10pm IST Tuesday.

Our website: https://www.theweek.in/home.html

Regards,

Vaisakh E. Hari

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Inderjeet Phd2014[inderjeet@nii.ac.in]
Sent: Tue 6/1/2021 7:26:38 AM (UTC-05:00)
Subject: Re: looking for postdoc position

Dear Dr. Vineet,

About a month ago, I sent you an email regarding my interest in your research work. I`m looking for a suitable Postdoc position in the infection biology area and I would love to discuss ongoing projects in your lab if you can find some spare time. I will also send you my CV, I think my experience and expertise would be a good fit for your lab. Thank you so much.
Have a nice day.

Best regards
Inderjeet Kalia, Ph.D.
National Institute of Immunology
Aruna Asif Ali Road, JNU campus
New Delhi - 110067

On Wed, May 5, 2021 at 9:46 PM Inderjeet Phd2014 <inderjeet@nii.ac.in> wrote:

> Dear Dr Vineet,
> Greetings!
>
> I`m Inderjeet Kalia, recently I have completed my PhD from the National Institute of Immunology, New Delhi, India. I visited your lab profile and fascinated by your research on SARS and MERS-CoV. Without stretching this mail very long, I want to ask if any postdoc position is available in your lab. I`m very eager to apply to your lab. Waiting for your reply, thank you.
>
> **Inderjeet Kalia, PhD**
> National Institute of Immunology
> Aruna Asif Ali Road, JNU campus
> New Delhi - 110067

To: Menachery, Vineet[vimenach@UTMB.EDU]; Wendy.Menachery@gmail.com[Wendy.Menachery@gmail.com]; vineet.menachery@gmail.com[vineet.menachery@gmail.com]
From: Brian Kelly[kelly@washucsc.org]
Sent: Mon 6/14/2021 1:38:57 PM (UTC-05:00)
Subject: Hello from CSC @ WashU/Meeting

Good Afternoon Wendy and Vineet,
I hope this email finds you both well!

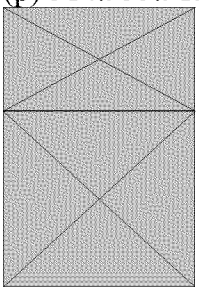
I started at the CSC about nine months ago and have been spending a lot of time meeting members of our community. Would both of you be willing to meet via Zoom or phone sometime? It would be great to share a few updates on the CSC and hear about your experiences here.

Please let me know a date or time that works best for you. Aside from Tuesdays, my schedule is flexible. Thank you both for your time!

Blessings,

Brian

--
Brian Kelly
Director of Advancement
Catholic Student Center at Washington University
(p) 314.935.9191 ext. 202



To: Menachery, Vineet[vimenach@UTMB.EDU]; vineet.menachery@gmail.com[vineet.menachery@gmail.com]
From: Abhijith V. N[abhijithekv@gmail.com]
Sent: Thur 3/26/2020 4:53:46 AM (UTC-05:00)
Subject: UV rays to inactivate SARS-CoV2.

Greetings Sir.
I am contacting you for further specific information regarding the mention on UV rays to kill the Corona Virus you made for the Washington Post dated 23 March 2020.

I have learned that SARS (2003) could be killed using UV rays of 254nm and I reckon that studies are still happening on what would be the wavelength of UV required to inactivate the SARS-CoV2.

I'm a Bachelor of Engineering in Electrical and Electronics student from Bangalore, India and the scare is on the rise here in India.

Inorder to combat this situation the All India Council for Technical Education (AICTE) has called all the innovators to contribute to flatten the curve.

From the many problem statements given by the event organisers, there is one which mentions about the need for disinfecting the currency notes. So for this need I'd like to know what must be the wavelength of the UV.

From your expertise, can you please clarify that will UV of 254nm be sufficient for the SARS-CoV2 because of the similarities it shares with the SARS (2003). Since there is no studies yet to confirm this, you could potentially tell me if 254nm would work because SARS-CoV2 is a cousin of SARS (2003).

Expecting a reply at the earliest.

Thank you and have a great day.
Abhijith V. Narayan

To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Vineet D. Menachery[vineet.menachery@gmail.com]
Sent: Mon 4/13/2020 4:29:10 PM (UTC-05:00)
Subject: Fwd: CBS National News Request

---------- Forwarded message ---------
From: **Amorebieta, Maite** <AmorebietaM@cbsnews.com>
Date: Mon, Apr 13, 2020 at 1:04 PM
Subject: CBS National News Request
To: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>

Dear Vineet Menachery,

Hope this note finds you well.
I am a producer at *CBS This Morning*, the national morning show in the United States co-hosted by Gayle King, Anthony Mason and Tony Dokoupil.

I am researching a piece about whether someone could be infected with COVID-19 more than once, and I would appreciate your insight.

Do you have a few minutes for a quick call on background?

Thanks and best,

Maite Amorebieta

C: +1 973 219 3031

--

Vineet D. Menachery

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: ashley.york@nature.com[ashley.york@nature.com]
Sent: Tue 5/19/2020 7:55:42 AM (UTC-05:00)
Subject: Strictly confidential invitation to review a manuscript for Nature Reviews Microbiology

Dear Dr. Menachery,

Manuscript number: NRMICRO-20-199V4
Title: COVID-19: Mechanisms of vaccination and immunity
Author(s): Daniel Speiser and Martin Bachmann
Manuscript type: Proposal review

I hope you are well. Nature Reviews Microbiology has recently received this Proposal review article to be considered for publication. The article abstract is included at the end of this email for your information. As you are an expert in this field, I would like to invite you to act as a referee.

We are keen to ensure that the review process is both rigorous and swift, but we understand that the ongoing COVID-19 pandemic is causing severe disruption and are very aware that many researchers will have difficulty in meeting the timelines associated with our peer review process. If you accept this invitation, I would like to receive your comments within 10 working days, but please do contact me if you need additional time, we intend to be highly flexible at this time. If you are unable to review this paper, we would be grateful if you could suggest potential alternative reviewers, keeping in mind that Nature-branded journals strive toward an equitable demographic representation within our reviewer pool, for example, with respect to gender and geography. More information about our commitment to diversity can be found here.

Please respond to this invitation within 2 working days to let me know whether or not you would like to act as a referee for this article. We use an online submission and peer review system, so please reply by clicking on the following link:
https://mts-nrmicro.nature.com/cgi-bin/main.plex?el=A4Z1PiR6D1edX5F5A9ftdULOkyssKLKjdQI7XHTzdAZ

Do you want to involve one of your trainees in the peer-review process?
The Nature Reviews journals are committed to facilitating training in peer review and to ensuring that everyone involved in our peer-review process is appropriately recognised. We have therefore started an initiative to allow and encourage established referees to involve one early-career researcher in our peer-review process. If you participate in this trial, you will remain the primary contact and you will submit the final report, but the review that you compile together will be considered a co-review, meaning that both of you receive recognition for your contributions. We will send instructions to your co-reviewer and ensure that their referee activity is logged on our systems so that they are recognised for their review activity. **If you would like to participate, please reply to this email with the name and contact details of the researcher you'd like to co-review with within 48 hrs of accepting this invitation.** We cannot accept the addition of a co-reviewer after submission of the report and reserve the right to exclude the suggested co-reviewer if a conflict of interest is detected.

You should let us know if, on initial inspection and despite our efforts to avoid it, you realize that you have a competing or financial interest in the article's content. For further guidance, please take a look at our competing interests policy. We ask all referees to inform us of any interest that might be perceived as relevant. The content of this article must be kept in strict confidence, and you should not make use of it in your own research before it is published. In the interest of transparency, we are asking authors to declare any financial and non-financial competing interests. We hope this will aid in your evaluation of the paper.

I hope to hear from you soon.

Best wishes,
Ashley

Ashley York, D.Phil.
Senior Editor

Nature Reviews Microbiology
4 Crinan Street
London
N1 9XW

e-mail: ashley.york@nature.com
tel: +44 (0)20 7418 5903
http://www.nature.com/nrmicro

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* * * * * *

Vaccines are needed to induce immunity to SARS-CoV-2, the virus causing COVID-19. Vaccines that induce large quantities of high affinity virus-neutralizing antibodies and T helper type 1 responses may optimally prevent infection, and avoid unfavorable effects. Vaccination trials require precise clinical management, complemented with detailed serology testing for protective virus-neutralizing antibodies and unwanted disease enhancing antibodies. Here we review pros and cons of available vaccine platforms, and options to accelerate vaccine development towards rapid immunization of the world's population against SARS-CoV-2. Broad use of carefully selected favorable vaccines may be critical for limiting harm and enabling long-term return to normal public life and economy.

COVID 19 and impact on peer review
As a result of the significant disruption that is being caused by the COVID-19 pandemic we are very aware that many researchers will have difficulty in meeting the timelines associated with our peer review process during normal times. Please do let us know if you need additional time. Our systems will continue to remind you of the original timelines but we intend to be highly flexible at this time.
This email has been sent through the Springer Nature Tracking System NY-610A-NPG&MTS

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: rudraneil S[rudraneil@gmail.com]
Sent: Tue 5/26/2020 6:11:34 AM (UTC-05:00)
Subject: Re: Interview request from Hindustan Times India

Hello Dr Menachery,
Thought I would try my luck one final time with my interview request!
Best wishes,
Neil

On Fri, May 22, 2020 at 4:46 PM rudraneil S <rudraneil@gmail.com> wrote:

> Dear Dr Menachery,
> Hope you are well.
> I am a journalist with Hindustan Times, one of the leading English dailies in India, and I specialize in longform stories.
> I am very keen to do an interview with you about your work at the Menachery Lab, and your thoughts on the current pandemic and the development of vaccines.
> Would you kindly consider a telephonic interview (at a time convenient to you) where you would be able to spare 30 minutes?
> I would be most grateful.
> I have been trying to reach you on your UTMB mail for the past two weeks without success, and I'm hoping that I'll have more luck with gmail!
>
> Here are links to some of my work:
> www.hindustantimes.com/india-news/humans-provide-the-conditions-for-epidemics-to-flourish-frank-snowden/story-u9sTv3lMa3IuWj5gNsgwwN.html
>
> www.hindustantimes.com/india-news/india-under-lockdown-migrant-labourer-peddles-1-700-km-in-7-days-to-reach-home/story-FTrl4Jlc0K7HOxO63cyonM.html
>
> https://www.livemint.com/Politics/Lofa7q6gweBypR05IoERrO/The-autopsy-report.html
>
> https://www.livemint.com/Science/9JRNZtcy8r8BnBjtzJJliO/Manu-Prakash-A-pocketful-of-inventions.html
>
> https://www.livemint.com/Politics/WC5Ey3efB2xcZ7XMeW6X5K/The-badlands-of-Delhi.html
>
> Warmest wishes
> Rudraneil Sengupta
> +919899692300

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: 金遠凡[googling0204@gmail.com]
Sent: Sun 6/7/2020 8:04:48 PM (UTC-05:00)
Subject: Inquiry for the availability for new Ph.D. student in 2021
CV_Yuanfan_2020.pdf

Dear Professor Menachery,

My name is Yuan fan working full-time in the Institute of Preventive Medicine (IPM) in Taiwan, and I am applying to the University of Texas Medical Branch for the Ph.D. program in 2021. I have learned that the research of your lab associates with high-risk, zoonotic viruses, and their pathogenesis by using the cutting edge platforms. One of your aim of the study is to obtain mechanistic information and develop an alternative approach of antiviral treatment, which attract me the most. I have found that you have made a lot of great effort into researching the mechanisms and improving the animal model for investigating the conspiracy of the viruses. Your recent effort in constructing an infectious clone of SARS-CoV-2 and a thorough understanding and reviewing of the virus caught my attention exceedingly.

Furthermore, I am always looking forward to dedicating on the research and work in zoonotic viruses, such as SARS-CoV-2, not just I have gained related experience in the institute, but also, I think it could be one of the most influential studies around the world. It can shed light on the incremental emerging diseases for humans to understand.

Besides, I am interested in virology, emerging viruses, viral evolution, and high containment pathogens. Therefore, *I am writing to ask about that would your laboratory receive new Ph.D. students next year, 2021?* If I could have the fortune to get the admission for this program, I would like to receive the intensive training and leading-edge knowledge under your supervision. Also, the scholarship from my institute would cover my tuition fees and living costs, which means I can fully concentrate on doing research.

In terms of my background, I am a biomedical, military officer dedicated me both in biomedical science and my beloved country, Taiwan, for many years. I have awarded the full scholarship to cover my expenses of studying abroad, including tuition fees and living costs. Therefore, I am planning to apply for the Ph.D. program in the Graduate School of Biomedical Science at the University of Texas Medical Branch.

Here are my brief academic background and research experience. I have earned a master's degree in Microbiology and Immunology. Under the supervise of Prof. Chung in National Defense Medical Center (NDMC) in Taiwan, I studied the pathogenesis of *Streptococcus pneumonia* by using RNA-sequencing to investigate its gene expression profile when exposed to human serum. I have developed a hypothesis that the competence phase could be the critical status for this bacterium to cause invasive disease.

Now, I work as a research assistant at the Institute of Preventive Medicine (IPM), which is an essential facility in Taiwan, responsible for biodefense and biomedical research. I am in the group whose mission is to culture and detect the unknown samples of patients from the hospital or the field. Under the supervision of Dr. Kao and Chang that are our group leaders, I conduct and design the experiments in BSL-4. Recently, I have been working on two projects. One is for studying the essential viral characteristics of SARS-CoV-2, including the replication cycle on different MOI, the growth curve among three different strains, and constructing the viral protein for generating antibodies. Also, the animal model for investigating the pathogenesis of SARS-CoV-2 is under development to ask further questions. The other is for developing platform identifying potential interactive host protein when infected with Enterovirus-D68, EV-D68 by using ascorbate peroxidases, APEX biotin labeling under the supervise of Dr. Kao and Dr. Tsai. Being aware that the zoonotic virus could be the next emerging disease, I have a strong sense of duty for Taiwan and a keen interest in studying virology to become a virologist.

Attachment to this letter is my CV.

I am looking forward to your reply.

Please be feel free to ask me any questions.
Thank you

Best Wishes

Yuanfan

==========
國防醫學院 預防醫學研究所
研究助理員 金遠凡
(02)8177-7038#19808

Institute of Preventive Medicine, National Defense Medical Center, Taiwan
Research Assistant
Yuanfan Chin
==========

CHIN-YUAN FAN

googling0204@gmail.com • +886-922-905-081 • Taiwan (ROC)

Curriculum Vitae

Education

National Defense Medical Center (NDMC)

Master of Science (MS)

Graduate Institute of Microbiology and Immunology — 2016-2018
Academic ranking: 1st place in the class
GPA 4.0/4.0, 25 credits.

Bachelor of Science (BS)

School of Public Health — 2010-2014
Academic ranking: 1st place in the class
GPA 4.0/4.0, 138 credits.
Emergency Medical Technician level-2 Certification

Work, Research and Teaching Experience

Institute of Preventive Medicine (IPM)

Research Assistant — 2014-2016 & 2018 to date

- Investigated the essential viral characteristics and pathogenesis of SARS-CoV-2, including developing the animal model
- Establishment and Development of the Diagnostic System for RG-4 and the Other Highly Pathogenic Pathogens in the BSL-4 laboratory
- Development of novel recombinant ascorbate peroxidases (APEX) fusion protein as a platform to analyze host-virus protein interaction networks in living cells
- Work experience: being shadowing member in lab of Dr. Holly Shelton for influenza research in the Pirbright Institute in England
- Investigated the role of viral polymerase A (PA) protein in influenza virus-induced apoptosis
- Prepared the anti-influenza serum in the ferret animal model
- Assessed the efficiency of the baculovirus protein expression system in the mosquito cell
- Used gold nanorod to improve the SERS (Surface-Enhanced Raman Scattering) detection method

High Containment lab assistant manager; Department of purchasing supervisor — 2018 to date

- Assisted lab manager in maintaining high containment lab working, managing documents, and setting SOP.
- Conducted regular drills of biological protection, managed equipment and participated in bio-protection training
- Reviewed purchasing documents, handled superior supervision in purchasing materials, and organized procurement cases

National Defense Medical Center (NDMC)

Master of Science, Graduate Institute of Microbiology and Immunology

Human sera induced competence and fratricide in *Streptococcus pneumoniae.* (Thesis, supervised by Prof. Chung) — 2016-2018

Teaching Assistant, *School of Microbiology and Immunology*

Emergency Medical Technician level2 certificate, *School of Public Health* — 2012-2013

The college research project, *School of Public Health*

Subsidy project from Ministry of Science and Technology, Taiwan (ROC)

Using bioinformatics method to Annotate Nitric Oxide Synthase in *Trichomonas Vaginalis* — 2011-2012

Awards and Honors

Institute of Preventive Medicine (IPM) Scholarship — 2020
(Studying Abroad Scholarship)

NDMC Outstanding Student, Mr. Shou Lian Scholarship — 2018
(Academic Excellence Award)

NDMC Alumni association Scholarship — 2017

NDMC Military Medical Research Symposium - Excellent work — 2015
(Poster Presentation)

NDMC Outstanding Student, Liu Yanfeng Scholarship — 2014
(Academic Excellence Award)

NDMC Alumni association Scholarship — 2013

The College Student Research Scholarship — 2011
Ministry of Science and Technology, Taiwan (ROC)

Skills

- Biochemistry and molecular biology skills:
  - RNA-sequencing, PCR.
  - Western blotting, ELISA, protein purification & quantification.
  - DNA quantification & electrophoresis, nucleic acid extraction.
  - IFA, cell culture, flow cytometry, cloning.
- Microbiology skills, including virology and bacteriology.
- Image analysis: TEM, fluorescence microscopy.
- Qualitative analysis: UV, SERS.
- Synthesis and characterization of nanoparticle skills.
- Bioinformatic skills: necessary python coding & using biostatistics software
- Certificate in laboratory animal care & conducting experiments in BSL-3 & 4 laboratories
- Other: Emergency Medical Technician level2.

To: Menachery, Vineet[vimenach@UTMB.EDU]; 'Vineet.Menachery@gmail.com'[Vineet.Menachery@gmail.com]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Mon 6/8/2020 9:35:23 AM (UTC-05:00)
Subject: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Greetings Dr. Menachery,

I am an Executive producer with Spectrum News in Austin for our nightly Texas politics and public affairs program 'Capital Tonight' hosted by Karina Kling.

I would like to speak with you about coming on our show via Skype tomorrow Tuesday 6.9 at 130p to discuss the progression of the coronavirus.

Would it be possible to schedule a brief call with you to discuss your work with the coronavirus?

The best way to reach me these days is on my mobile phone 201-417-9413.

Thank you Dr. Menachery.

Chris Martin
Executive Producer
News, Documentary and Long-Form Programming
Spectrum Networks
1708 Colorado St. | Austin, TX 78701
o 512.531.1205 | c **201.417.9413**

Charter
COMMUNICATIONS

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Tue 6/9/2020 7:35:47 AM (UTC-05:00)
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Thanks so much Dr. Menachery

Please let me know if you have any questions.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Monday, June 08, 2020 9:59 PM
To: Martin, Chris E <Chris.Martin@charter.com>; Vineet.Menachery@gmail.com
Subject: [EXTERNAL] Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Vineet.menachery@gmail.com
552.117
Galveston Texas

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Martin, Chris E <Chris.Martin@charter.com>
Sent: Monday, June 8, 2020 9:36 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Dr. Menachery

I would be grateful to get this info ASAP... so I may get all of our operations folks set for tomorrow's interview, please.

Chris Martin
Executive Producer
Spectrum News
201-417-9413 (m)

On Jun 8, 2020, at 4:57 PM, Martin, Chris E <Chris.Martin@charter.com> wrote:

Here I am

Here what I need for this tomorrow

Skype Handle:
Phone #:
Location: Town / City calling from

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To: Reyes, Raul[rareyes@UTMB.EDU]; Menachery, Vineet[vimenach@UTMB.EDU]; 'Vineet.Menachery@gmail.com'[Vineet.Menachery@gmail.com]
Cc: Holubar, Connie J.[cjholuba@UTMB.EDU]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Tue 6/9/2020 6:17:17 PM (UTC-05:00)
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Hi

I just wanted to thank you for your time today. I thought the interview was excellent.

Extremely appreciative.

I hope we can do it again sometime.

From: Martin, Chris E
Sent: Tuesday, June 09, 2020 11:27 AM
To: 'Reyes, Raul' <rareyes@UTMB.EDU>; 'Menachery, Vineet' <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com
Cc: Holubar, Connie J. <cjholuba@UTMB.EDU>
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Hello again Mr. Reyes and Dr. Menachery

I was wondering if you might have some B-Roll of the Menachery Lab. All purpose Lab footage of Dr. Menachery and colleagues at work??

Any chance you could shoot it my way?

From: Reyes, Raul [mailto:rareyes@UTMB.EDU]
Sent: Monday, June 08, 2020 1:25 PM
To: Martin, Chris E <Chris.Martin@charter.com>
Cc: Holubar, Connie J. <cjholuba@UTMB.EDU>
Subject: [EXTERNAL] RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Thank you for your inquiry. Your request is one of many today that our office is considering.

Thank you,

Raul

Raul Reyes
Director of Media Relations
Department of Marketing and Communications

The University of Texas Medical Branch
301 University Blvd., Galveston, TX 77555-0128
Office 409 747 0794

Cell 409 771 7841

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Working together to work wonders.™

From: Martin, Chris E <Chris.Martin@charter.com>
Sent: Monday, June 8, 2020 1:18 PM
To: Reyes, Raul <rareyes@UTMB.EDU>
Subject: FW: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Greetings Mr. Reyes

I was reaching out to Dr. Menachery to discuss the possibility of having him on our program tomorrow to discuss COVID.

See my email to him below. Happy to discuss – Mobile is best 201-417-9413

Thank you

From: Martin, Chris E
Sent: Monday, June 08, 2020 9:35 AM
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To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; DL-News-TX-AUS-Ingest[DL-News-TX-AUS-Ingest@charter.com]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Tue 6/9/2020 7:51:16 AM (UTC-05:00)
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Dr. Menachery

Would it be possible to do a quick test call this morning?? We have had trouble in the past with guests calling from inside facilities like UTMB.

Reminder – Skype for business won't work in this case. You'll need regular, personal Skype.

Thank you.

From: Menachery, Vineet [mailto:vimenach@UTMB.EDU]
Sent: Monday, June 08, 2020 9:59 PM
To: Martin, Chris E <Chris.Martin@charter.com>; Vineet.Menachery@gmail.com
Subject: [EXTERNAL] Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Vineet.menachery@gmail.com
552.117
Galveston Texas

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

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Spectrum News
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o 512.531.1205 | c **201.417.9413**

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To: Reyes, Raul[rareyes@UTMB.EDU]; Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
Cc: Holubar, Connie J.[cjholuba@UTMB.EDU]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Tue 6/9/2020 11:27:24 AM (UTC-05:00)
Subject: RE: Media Request / Spectrum News / Skype Interview Tuesday 6.9

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Raul

Raul Reyes
Director of Media Relations
Department of Marketing and Communications

The University of Texas Medical Branch
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Office 409 747 0794
Cell 409 771 7841

utmb Health

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The contents of this e-mail message and

To: DL-News-TX-AUS-Ingest[DL-News-TX-AUS-Ingest@charter.com]; DL-News-TX-AUS-Operations[DL-News-TX-AUS-Operations@charter.com]; Kling, Karina M[Karina.Kling@charter.com]; Mizroch, Marissa H[Marissa.Mizroch@charter.com]; Lipkin, Ariana R[Ariana.Lipkin@charter.com]; 'Vineet.Menachery@gmail.com'[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]; Thompson, Blake B[Blake.Thompson@charter.com]; Fields, Chris J[Chris.Fields@charter.com]; Reyes, Raul[rareyes@UTMB.EDU]
From: Martin, Chris E[Chris.Martin@charter.com]
Sent: Tue 6/9/2020 7:45:10 AM (UTC-05:00)
Subject: TUESDAY 6.9.2020, Time: 130p CT, Capital Tonight Skype Interview with Virologist Dr. Vineet Menachery

Capital Tonight Skype Interview

Dr. Vineet D. Menachery, Virologist - University of Texas Medical Branch at Galveston

Tuesday 6.9.2020
Time: 130p CT

You will be speaking to 'Capital Tonight' Political Anchor Karina Kling

Ingest – please record an ISO of Dr. Menachery

Guest Skype Address:
live:.cid.253368b2ae6259c7 // Vineet.menachery@gmail.com

Austin Ingest Skype address
austiningest

Cell for any technical issues: **552.117**

Exact location where Skype is originating: Galveston

Dr. Menachery: Can you please Skype call US at around 120p so we can do any troubleshooting and get you checked-in??

Please contact Chris Martin, Capital Tonight Executive Producer with any issues. 201-417-9413

Thank you

Chris Martin
Executive Producer
News, Documentary and Long-Form Programming
Spectrum Networks
1708 Colorado St. | Austin, TX 78701
o 512.531.1205 | c **201.417.9413**

Charter
COMMUNICATIONS

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Chhanda Das[cdas@aai.org]
Sent: Thur 2/18/2021 3:05:20 PM (UTC-06:00)
Subject: FW: AAI Travel Award reimbursement - Outstanding Check

Please see the email below,

Thank you

Chhanda Das
Accounting Assistant
The American Association of Immunologists
1451 Rockville Pike, Suite 650
Rockville, MD 20852
Phone: 301-634-7784

From: Chhanda Das
Sent: Wednesday, October 21, 2020 3:14 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com
Cc: Mary Litzinger <mlitzinger@aai.org>
Subject: AAI Travel Award reimbursement - Outstanding Check

Dear Dr. Menachery,

I'm writing to you regarding an outstanding check from The American Association of Immunologists for 2019 AAI Travel Award reimbursement– the check is outstanding as of October20, 2020.
Please confirm if you have or have not received the check matching the information below:

Check #: *41480*
Date: *01/30/2020*
Amount: *$1250*

If you have not received this check, we can reissue it for you. Please confirm the mailing address to ensure that the check is sent to the correct location:

Vineet D. Menachery

552.117

Please let me know if you have any questions or concerns,

Thank you,
Chhanda Das
Accounting Assistant
The American Association of Immunologists
1451 Rockville Pike, Suite 650
Rockville, MD 20852
Phone: 301-634-7784

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

Location: https://www.zoomgov.com/j/1611090134?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV2 Variant Testing Discussion

Start Time: Thur 1/28/2021 7:00:00 AM (UTC-06:00)

End Time: Thur 1/28/2021 8:00:00 AM (UTC-06:00)

Required Attendees: Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; AlessandroSette; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
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Passcode: **552.136**

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Tanimoto, Yukari[yukari.tanimoto@kaneka.com]
Sent: Mon 8/17/2020 1:50:43 PM (UTC-05:00)
Subject: FW: Kaneka Sodium Surfactin, inquiry related to your article in the Journal of Virology
KANEKA Surfactin-COSMOS-160728.pdf

Dr. Menachery,

As per my original email below, we are a manufacturer of Sodium Surfactin produced by fermentation using bacillus subtilis. I wanted to see if you've had a chance to review our information and whether you would be interested in using our Sodium Surfactin in further evaluations particularly in relation to the COVID-19 pandemic.

I am attaching the data sheet here for your information.

I look forward to hearing from you.

Best regards,

Yukari
Yukari Tanimoto Guevara
Market Development Manager
Kaneka Americas Holding, Inc.

Yukari.tanimoto@kaneka.com
Cell: 832-741-3858
Based in Southern California

From: Tanimoto, Yukari
Sent: Friday, March 20, 2020 11:57 AM
To: Vineet.Menachery@gmail.com
Subject: Kaneka Sodium Surfactin, inquiry related to your article in the Journal of Virology

Dr. Menachery,

I've sent an email to your utmb account but thought I'd send you one here just in case.

I am a Market Development Manager with Kaneka Americas. We manufacture Sodium Surfactin produced by fermentation using bacillus subtilis. Your article in the Journal of Virology was of keen interest to us and we are looking for partners to assess whether our Sodium Surfactin could be part of a solution to the current Covid-19 Pandemic. I am attaching a data sheet for your information. Is this something that would be of interest to you?

Best regards,

Yukari
Yukari Tanimoto Guevara
Market Development Manager
Kaneka Americas Holding, Inc.

Yukari.tanimoto@kaneka.com
Cell: 832-741-3858
Based in Southern California

Best regards,

Yukari
Yukari Tanimoto Guevara
Market Development Manager
Kaneka Americas Holding, Inc.

Yukari.tanimoto@kaneka.com
Cell: 832-741-3858
Based in Southern California

KANEKA Surfactin

Biosurfactant made by fermentation technology of KANEKA

- High performance (CMC:0.0003%) -
  > 3000 times more effective than lecithin
- Low irritation and easy biodegradation -
  > Human and environmental friendly

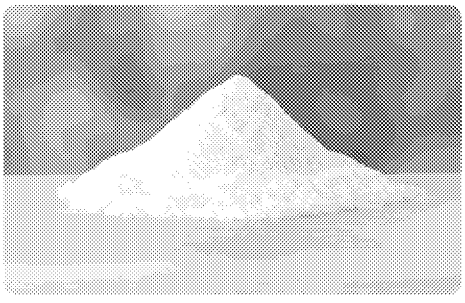
Approved by ECOCERT RAW MATERIAL

COSMOS APPROVED

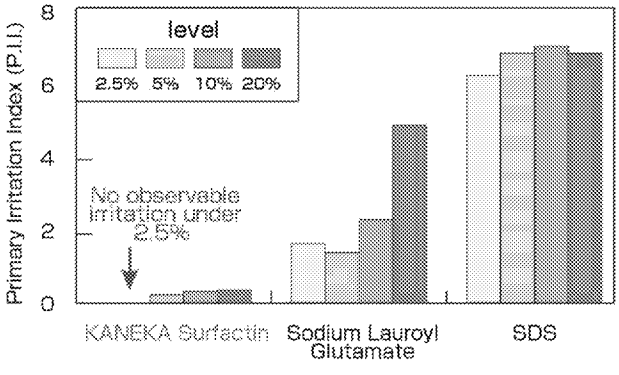
Comparison of Surfactants

Surfactants	Performance	
	Critical Micelle Concentration (CMC) [%]	Vs. SF
KANEKA Surfactin	0.0003	1
Lecithin(Natural Prod.)	1	1/3000
SDS(Synthetic Prod.)	0.1	1/300

KANEKA Surfactin (White powder)

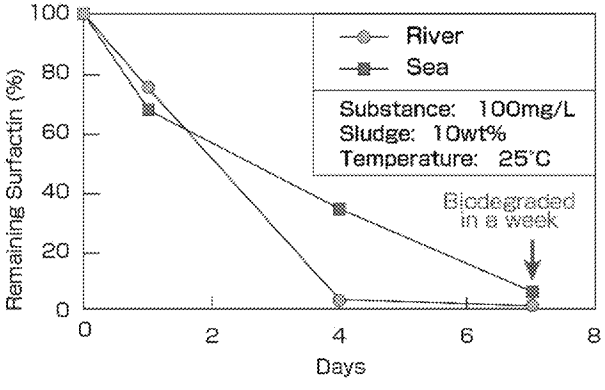


Primary skin irritation test



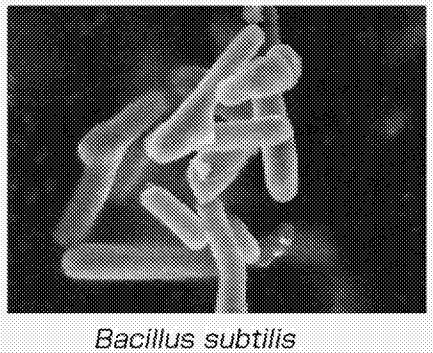
Biodegradation test

(MITI test : easily biodegradable)

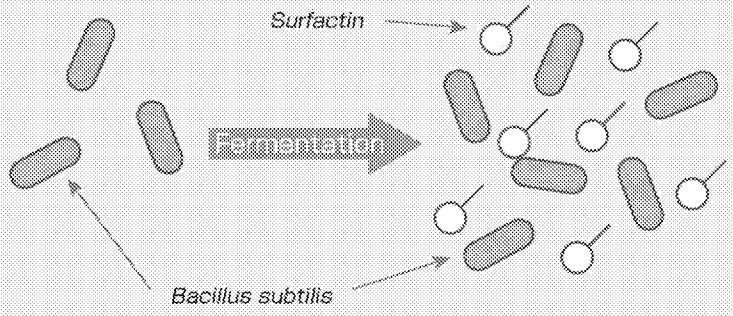


Surfactin is produced by natural fermentation.

- Found in the culture broth of *Bacillus subtilis* in 1968
- Sustainable products by fermentation under mild condition



Bacillus subtilis



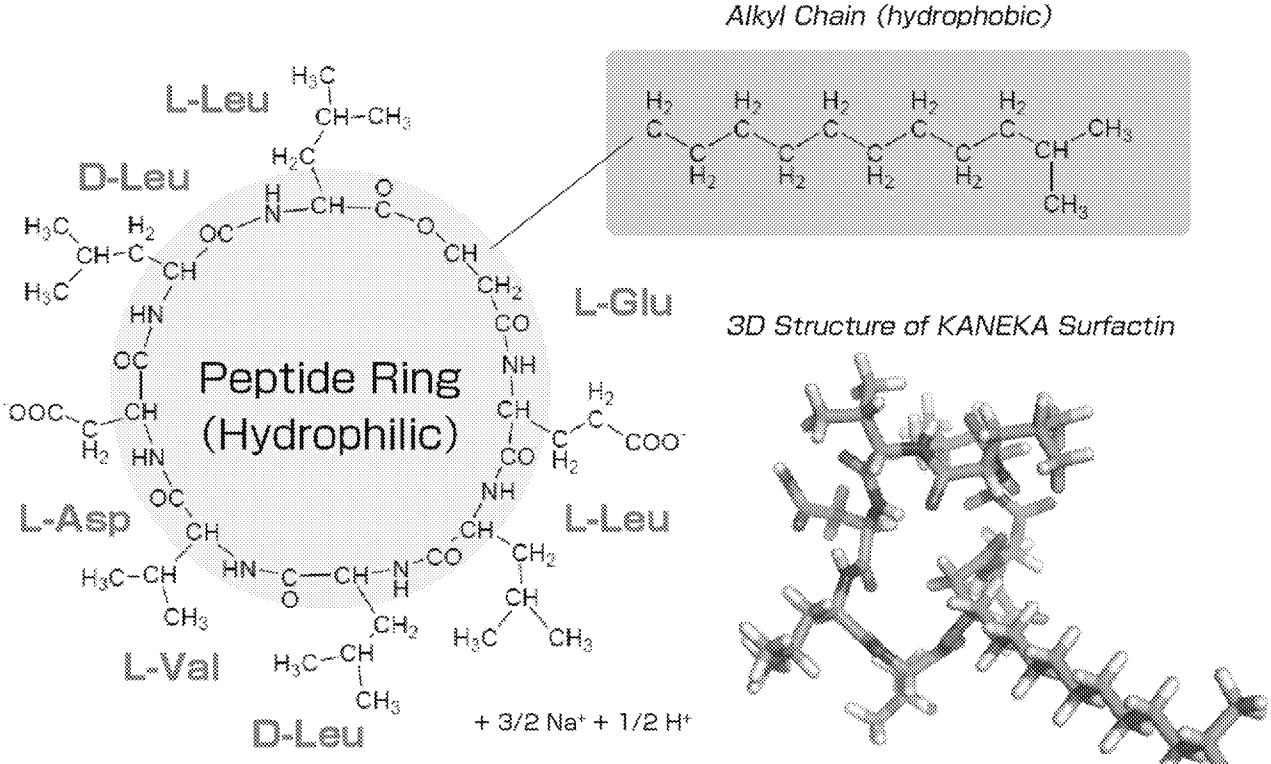
★ The data is based on limited test conditions and not guaranteed.

<Data>

Name	KANEKA Surfactin
INCI name	Sodium Surfactin
CAS No.	302933-83-1
Appearance	white powder
Stability	stable: heat treatment; acidic to weak alkaline conditions not stable: strong alkaline conditions (pH > 10)
Solubility	soluble in aqueous solvents. precipitation at acidic pH or with alkaline earth metal ions (Mg^{2+}, Ca^{2+}).
pH	pH 6.5-8.0
Use	a cosmetic ingredient worldwide since 2001
Regulation	Registration complete in Japan, Europe, Unite States and China

<Chemical Structure>

KANEKA Surfactin has an unique structure including a hydrophilic cyclic peptide part constructed by seven amino acids and a hydrophobic hydrocarbon chain.



kaneka
The Dreamology Company
---Make your dreams happen---

Contact Information
Address: Kaneka Corporation, New Business Development Division
2-3-18, Nakanoshima, Kita-ku, Osaka, 530-8288, Japan
E-Mail: surfactin@kn.kaneka.co.jp

★ The data is based on limited test conditions and not guaranteed

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Rickey Shah[rshah@broadinstitute.org]
Sent: Fri 8/21/2020 10:22:59 PM (UTC-05:00)
Subject: Prospective MD/PhD student lab interest

Dear Professor Menachery,
I hope this message finds you well.

My name is Rickey Shah and I am a prospective MD/PhD student at UTMBSOM. I earned my masters degree from Harvard Extension School and did my master thesis research in Pardis Sabeti's Lab. My project focused on high-throughput inactivation and nucleic acid extraction of biosafety level 4 pathogens. I also was appointed as a non-tenured track faculty member at Harvard University to help co-teach an introductory genetics course. In addition to this, I was a co-instructor for a genetics training program offered through the African Centres for Excellence in Genomics of Infectious diseases (ACEGID) hosted at Harvard University.

I grew up in the suburbs of Chicago and went to The University of Illinois at Chicago for my undergraduate studies. I moved back home to help my mom through a liver transplant and fell in love with medicine and became inspired to pursue a career as a physician scientist. I am currently applying to MSTP programs and am extremely interested in learning more about the projects your lab is currently working on and which projects you will be working on in the future.

I look forward to hearing back from you.

Sincerely,
Rickey Shah

P.S. I love your lab logo!

To: Cesar Munoz-Fontela[munoz-fontela@bnitm.de]; Adolfo García-Sastre[adolfo.garcia-sastre@mssm.edu]; Mariano Esteban Rodriguez[mesteban@cnb.csic.es]; Mela[mcarmen.rivas@usc.es]; guenther@bni.uni-hamburg.de Gunther[guenther@bni.uni-hamburg.de]; Addo, Marylyn Martina[m.addo@uke.de]; Lawrence Banks[banks@icgeb.org]; Delgado Vazquez.Rafael[rafael.delgado@salud.madrid.org]; McElroy, Anita Katherine[MCELROYA@pitt.edu]; Prof. Dr. med. Egbert Tannich[tannich@bnitm.de]; Michael Ramharter[ramharter@bnitm.de]; muehlber@bu.edu[muehlber@bu.edu]; Diederich, Sandra[Sandra.Diederich@fli.de]; Martin Beer[Martin.Beer@fli.de]; Quim Segales[joaquim.segales@irta.cat]; Anneke Novak-Funk[novak-funk@bnitm.de]; Thomas Dobner[thomas.dobner@hpi.uni-hamburg.de]; Geisbert, Thomas W.[twgeisbe@UTMB.EDU]; Cross, Robert W.[rwcross@UTMB.EDU]; Estefania Bni[estefania.rodriguez@bnitm.de]; Feldmann, Heinrich (NIH/NIAID) [E][feldmannh@niaid.nih.gov]; Carroll, Miles[miles.carroll.phe.gov.uk@external.domain]; Florian Wurm[florian.wurm@excellgene.com]; Florian Krammer[florian.krammer@mssm.edu]; PETERPALESE[peter.palese@mssm.edu]; Osterhaus, Albert[albert.osterhaus@tiho-hannover.de]; Enjuanes_Luis[l.enjuanes@cnb.csic.es]; Rimmelzwaan, Guus[guus.rimmelzwaan@tiho-hannover.de]; B. Haagmans[b.haagmans@erasmusmc.nl]; Juliana Idoyaga[jidoyaga@stanford.edu]; Francine Ntoumi[ffntoumi@hotmail.com]; Duprex, Paul[pduprex@pitt.edu]; Christian Drosten[christian.drosten@charite.de]; becker@staff.uni-marburg.de[becker@staff.uni-marburg.de]; R.A.M. Fouchier[r.fouchier@erasmusmc.nl]; m.koopmans@erasmusmc.nl[m.koopmans@erasmusmc.nl]; marcel.mueller@charite.de[marcel.mueller@charite.de]; Hoenen, Thomas[Thomas.Hoenen@fli.de]; becker@staff.uni-marburg.de[becker@staff.uni-marburg.de]; D.A.J. van Riel[d.vanriel@erasmusmc.nl]; vankerkhovem@who.int[vankerkhovem@who.int]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Corbett, Kizzmekia (NIH/VRC) [E][kizzmekia.corbett@nih.gov]; stephanie.seifert@wsu.edu[stephanie.seifert@wsu.edu]; Letko, Michael Colin[michael.letko@wsu.edu]; Baric, Ralph[rbaric@email.unc.edu]; Alexandra Schaefer[aschaefe@email.unc.edu]; Menachery, Vineet[vimenach@UTMB.EDU]; Kanta Subbarao[kanta.subbarao@influenzacentre.org]; Leo Poon[llmpoon@hku.hk]; malik@hku.hk[malik@hku.hk]; Jon Epstein[epstein@ecohealthalliance.org]; Linfa Wang[linfa.wang@duke-nus.edu.sg]; Leendertz, Fabian[LeendertzF@rki.de]; Mettenleiter, Thomas C.[ThomasC.Mettenleiter@fli.de]; jlloydsmith@ucla.edu[jlloydsmith@ucla.edu]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Richard Webby[richard.webby@stjude.org]; Stacey Schultz-Cherry[stacey.schultz-cherry@stjude.org]; Yoshi Kawaoka[kawaokay@vetmed.wisc.edu]; Pekosz, Andrew S.[apekosz@jhsph.edu]; Lowen, Anice[anice.lowen@emory.edu]; Ben Cowling[bcowling@hku.hk]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; Matthew Frieman[mfrieman@som.umaryland.edu]; Anthony, Simon J.[sja2127@cumc.columbia.edu]; sjanthony@ucdavis.edu[sjanthony@ucdavis.edu]; Sarah Gilbert[sarah.gilbert@ndm.ox.ac.uk]; sjanthony@ucdavis.ed[sjanthony@ucdavis.ed]; Thomas Bowden[tom@strubi.ox.ac.uk]; Aartjan te Velthuis[ajwt6@cam.ac.uk]; Barouch,Dan (HMFP - Division of Vaccine Research)[dbarouch@bidmc.harvard.edu]; Michael Osterholm[mto@umn.edu]; Jesse Bloom[jesse.bloom@gmail.com]; Damon, Inger K. (CDC/DDID/NCEZID/DHCPP)[iad7@CDC.GOV]; Racaniello, Vincent R.[vrr1@cumc.columbia.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Seth Judson[sethdjudson@gmail.com]; David Veesler[dveesler@uw.edu]; Jason McLellan[jmclellan@austin.utexas.edu]; Weiss, Susan[weisssr@pennmedicine.upenn.edu]; Pierson, Theodore (NIH/NIAID) [E][piersontc@niaid.nih.gov]; from:"atakada@czc.hokudai.ac.jp"["atakada@czc.hokudai.ac.jp"]; jboon@wustl.edu[jboon@wustl.edu]; diamond@wusm.wustl.edu[diamond@wusm.wustl.edu]; w.barclay@imperial.ac.uk[w.barclay@imperial.ac.uk]; Diamond, Jeffrey (NIH/NINDS) [E][diamondj@ninds.nih.gov]; Stagliano, Katie (NIH/NIAID) [E][staglianoke@mail.nih.gov]; Geisbert, Thomas W.[twgeisbe@UTMB.EDU]; Kilmarx, Peter (NIH/FIC) [E][peter.kilmarx@nih.gov]; Falzarano, Darryl (NIH/NIAID) [F][darryl.falzarano@nih.gov]; Kobinger, Gary (Public Health Agency of Canada)[gary.kobinger@phac-aspc.gc.ca]; Bethany Hoye (hoye.bethany@gmail.com)[hoye.bethany@gmail.com]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; Edward Holmes[edward.holmes@sydney.edu.au]; Nason, Martha (NIH/NIAID) [E][mnason@niaid.nih.gov]; eric.laing@usuhs.edu[eric.laing@usuhs.edu]; Broder, Chris (USU-DoD)[christopher.broder@usuhs.edu]; from:"mark.denison@vanderbilt.edu["mark.denison@vanderbilt.edu>, " Crowe]; James " <james.crowe@vumc.org>, " volker.thiel@vetsuisse.unibe.ch " <volker.thiel@vetsuisse.unibe.ch>, " Manning; Jessica [E] <jessica.manning@nih.gov>, William Karesh <Karesh@ecohealthalliance.org>, Jonna A.K.Mazet <jkmazet@ucdavis.edu>
From: Munster, Vincent (NIH/NIAID) [E][vincent.munster@nih.gov]
Sent: Thur 10/8/2020 12:49:54 PM (UTC-05:00)
Subject: SARS-CoV-2 and other emerging virus postdoc positions at NIAID
DIR_RML_Postdoc_VEU_08-14-15_cb_ReAd_8-25-20_cc1.docx

Dear colleagues,

Please find attached an advertisement for several postdoctoral positions within the NIAIDs Virus Ecology Section. Feel free to distribute widely.

The research spans from the identification and understanding of the drivers of zoonotic transmission for emerging viruses towards the development of countermeasures. The focus of the lab is largely on emerging coronaviruses, henipaviruses and filoviruses, but recent projects have included work on monkeypox and Lassa virus.

Kind regards,

Vincent Munster, PhD
Chief Virus Ecology Section

Department of Health and Human Services
National Institutes of Health
National Institute of Allergy and Infectious Diseases

With nationwide responsibility for improving health and well-being, the Department of Health and Human Services (HHS) oversees the biomedical research programs of the National Institutes of Health (NIH) and those of NIH's research Institutes. The National Institute of Allergy and Infectious Diseases (NIAID)—a major research component of NIH and HHS—is recruiting for the following positions:

Postdoctoral intramural research training awards (IRTAs)
Rocky Mountain Laboratories (RML), Hamilton, MT

Several postdoctoral IRTA positions are available in the Virus Ecology Unit within the Laboratory of Virology at the RML campus of NIAID in Hamilton, Montana. The laboratory studies the ecology of high- and maximum-containment RNA viruses and is currently focused on the ongoing COVID-19 pandemic.

The [HYPERLINK "https://www.niaid.nih.gov/research/vincent-j-munster-phd"] is interested in the identification and understanding of the drivers of zoonotic transmission for emerging viruses. The laboratory uses a combined field ecological and experimental laboratory approach to understand the emergence of novel viruses and develop successful medical countermeasures against these viruses. Fundamental experimental approaches of the laboratory include molecular-, cellular-, and immunological-based techniques along with animal models of pathogenesis and transmission. Studies are carried out in biosafety level (BSL) 2, BSL-3, and BSL-4 laboratories. The Virus Ecology Section considers diversity and inclusion the centerpiece of the team's culture.

Successful applicants will be part of a diverse and multidisciplinary team focused on understanding the molecular and ecological determinants of spillover from bats to humans and the determinants for onward human-to-human transmission. Candidates are expected to study the underlying molecular and structural determinants involved in zoonotic and human-to-human transmission of COVID-19 and newly identified emerging viruses (including filoviruses and henipaviruses).

An overview of the Virus Ecology Section's most recent SARS-CoV-2/COVID-19 research includes:

- Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1, NEJM 2020, DOI: 10.1056/NEJMc2004973
- Respiratory disease in rhesus macaques inoculated with SARS-CoV-2, Nature 2020, DOI: 10.1038/s41586-020-2324-7
- Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses, Nature Microbiology 2020, DOI: 10.1038/s41564-020-0688-y

- A Novel Coronavirus Emerging in China — Key Questions for Impact Assessment, NEJM 2020, DOI: 10.1056/NEJMp2000929
- ChAdOx1 nCoV-19 vaccine prevents SARS-CoV-2 pneumonia in rhesus macaques, Nature 2020

Requirements
Highly motivated candidates who have a strong background in molecular biology, genomics, computational biology, disease ecology field research, and infectious disease animal modeling are encouraged to apply. Experience working in high biological containment laboratories (BSL-3 or BSL-4) and experience with molecular biology—particularly reverse genetics or field ecology experience in infectious disease (including mathematical modeling)—would be considered an advantage.

Well-developed oral and written communication skills are essential. Candidates must hold a Ph.D. in virology, molecular biology, or another appropriate discipline and have less than three years of postdoctoral experience. Applicants may be U.S. citizens, permanent residents, or international citizens (for an IRTA, visa requirements apply). Trainees will receive health insurance as well as a stipend (commensurate with experience).

To Apply
Applicants should send their curriculum vitae (CV), a letter expressing career goals and interests, and three letters of reference with contact information no later than December 30, 2020, to Kay Menk, Laboratory Operations Specialist, Laboratory of Virology, Rocky Mountain Laboratories, NIAID, NIH, 903 S 4th Street, Hamilton, MT 59840, 406-375-9624 (phone), 406-375-9620 (fax), or email [HYPERLINK "mailto:menkk@niaid.nih.gov"].

[HYPERLINK "https://www.nytimes.com/2020/05/07/opinion/coronavirus-rocky-mountain-laboratories.html"] is a NIAID campus with excellent genomic, electron microscopic, and veterinary core support that enables scientists to completely focus on their research. Located in the scenic Bitterroot valley of western Montana, RML is surrounded by some of the best hiking, skiing, kayaking, mountain biking, and trout fishing in North America.

Visit [HYPERLINK "https://www.niaid.nih.gov/about/careers-training-opportunities"] for more information about working in NIAID's dynamic atmosphere!

HHS, NIH, and NIAID are equal opportunity employers dedicated to equity, diversity, and inclusion.

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Matthew Ozug[MOzug@npr.org]
Sent: Mon 12/21/2020 1:13:39 PM (UTC-06:00)
Subject: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Hi Dr. Menachery,

Thanks so much for agreeing to be on the show today. **We are CONFIRMED for a live interview at 5pm Eastern/4pm Central.**

Technical Details:
The folks in the studio will want to connect and test your line 10-15 minutes prior.

For the connection: The ideal connection is a FaceTime audio. Do you have **Facetime** on your computer or phone? If so can you let me know that number so I can relay it to the engineers.

As a back up: since this is a live interview we will also need a back up phone for you. It could be a landline or another cellphone, but it should not be the same phone as the primary, facetime phone, ideally.

I can call you as soon as your meeting is over and talk through any technical questions.

Conversation Notes:
I'm confirming that this will be a live interview of not more than 5 minutes. The director will tell you this when you are on the line before the interview begins, but they can give you a warning in your ear near the end of time if that helps.

I am working to send along an outline of the questions Ari hopes to ask, but it will largely mirror the conversation we had this morning.

One request: since this is for a general audience, please try to limit any overly scientific or technical language, or to define the terms. Ari can also help remind you of this. We are obviously coming to you for your extensive knowledge, but we also want to make sure all listeners can follow the conversation. (I just listened to your conversation with LuLu Garcia-Navarro, so I have no doubt this will be just as great!)

Thank you! Please let me know when you can about the best way to connect with you.

Matt

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 12:13 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: Speaking to NPR's All Things Considered?

Hi Matt,

I have something scheduled from 11:30CT to 1:30CT. I can probably talk at 2CT if that works for you. Let me know.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 10:52 AM
To: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Cc: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Speaking to NPR's All Things Considered?

Dear Dr. Menachery

I'm a producer at NPR's All Things Considered and we're looking to book a guest to speak to Ari Shapiro for this evening's program on the new strain of the virus out of the UK.

This would be on what we know, and what we still hope to learn. This would be a recorded conversation - if you're available for an interview in the next 3 hours can you please let me know.

Thanks!

Matt Ozug
Producer, NPR
mozug@npr.org
cell: +1 (917) 664 2011
office: +1 (202) 513-2133
Twitter.com/Matt_Ozug

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Matthew Ozug[MOzug@npr.org]
Sent: Mon 12/21/2020 3:08:44 PM (UTC-06:00)
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Terrific thank you so much – I really appreciate it. So long as you have a headset with a built-in mic for your laptop that should work perfectly.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 4:05 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Skype ID: Vineet.Menachery@gmail.com

I will plan to take your call on facetime at 3:45 CT. I will answer on my laptop as it is linked to my iphone.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 2:42 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Hi Dr. Menachery,

As promised, here are a few examples of questions for the interview this afternoon. Ari may remind you of this as well, but please gear your answers to a general population as much as possible: Why does it appear this new variant is more contagious and does that worry you? Is there any reason to believe the vaccines being rolled out are less effective against this variant? Do we know anything about whether the new variant is more deadly? And is there any reason to believe restricting travel out of the UK would be effective at curtailing the spread of this new variant?

Finally, and I'm sorry to be harassing you, but if you can send me a skype ID to reach you at, or (if you have it) the cell number of someone else in your house, that would be great. Just because it's a live interview we try to have as many ways as possible of reaching you.

So YOU have, it the direct studio line/phone number is 202-513-3731. And you can expect a facetime audio call from NPR in a little over an hour now.

Thank you!
Matt

From: Matthew Ozug
Sent: Monday, December 21, 2020 2:12 PM
To: 'Menachery, Vineet' <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com
Subject: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY
Importance: High

Hi Dr. Menachery,

Thanks so much for agreeing to be on the show today. **We are CONFIRMED for a live interview at 5pm Eastern/4pm Central.**

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Subject: Re: Speaking to NPR's All Things Considered?

Hi Matt,

I have something scheduled from 11:30CT to 1:30CT. I can probably talk at 2CT if that works for you. Let me know.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology

University of Texas Medical Branch, Galveston, Texas
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From: Matthew Ozug <MOzug@npr.org>
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Thanks!

Matt Ozug
Producer, NPR
mozug@npr.org
cell: +1 (917) 664 2011
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Twitter.com/Matt_Ozug

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Matthew Ozug[MOzug@npr.org]
Sent: Tue 12/22/2020 1:08:02 PM (UTC-06:00)
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

May thanks again for speaking to All Things Considered. The link for sharing is here:
https://www.npr.org/2020/12/21/948873785/new-coronavirus-variant-found-in-u-k-what-does-it-mean-for-the-world

I have one more favor to ask: Could you reply to the following 4 questions? Should take no more than a minute. All Things Considered is trying to do a better job of tracking the demography of our guests we're asking everyone to answer these questions however they please:

How would you describe your gender?

How would you describe your race and your ethnicity/nationality?

How old are you?

Where do you live?

Thank you so much!

Matt

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Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

ok.

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 3:18 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

I just heard from the director that they will call you at 3:50 CT, since another piece is wrapping up just before then.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 4:05 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Skype ID: Vineet.Menachery@gmail.com

I will plan to take your call on facetime at 3:45 CT. I will answer on my laptop as it is linked to my iphone.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 2:42 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
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Twitter.com/Matt_Ozug

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Matthew Ozug[MOzug@npr.org]
Sent: Mon 12/21/2020 11:19:34 AM (UTC-06:00)
Subject: RE: Speaking to NPR's All Things Considered?

Thank you for the quick reply! I will check with my editor and see it that is a time that can work. As I'm exploring options, would you be able to speak to Ari live at 5pm Eastern/4pm Central?

I know you're about to go into a meeting but would it be possible for me to call you very quickly?

From: Menachery, Vineet <vimenach@UTMB.EDU>
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To: vineet.menachery@gmail.com[vineet.menachery@gmail.com]; Menachery, Vineet[vimenach@UTMB.EDU]
From: Kevin Townsend[ktownsend@theatlantic.com]
Sent: Tue 1/12/2021 9:58:18 AM (UTC-06:00)
Subject: Re: Interview Inquiry — Atlantic Podcast

Excellent, thank you!

Here is the Zoom link you can connect on at 4pm CT:
https://theatlantic.zoom.us/j/91085567033

You'll be on with Jim Hamblin and Katherine Wells. And so you have it in mind: the tone of the show is casual. It started essentially as Jim (a preventive medicine doctor / staff writer) fielding worried questions from Katherine. Each episode is basically a phone call between friends that adds expert voices to help answer questions. And, as I'm sure you know, the taping isn't live — if you want to correct or retake something, go right ahead and I can edit accordingly.

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Thank you again for taking the time! If you have any questions or any trouble reaching me, my cell is 650-492-0728.

- Kevin

On January 12, 2021 at 10:24:11 AM, Menachery, Vineet (vimenach@utmb.edu) wrote:

> Sure that sound fine for me.
>
> VDM

> **From:** Kevin Townsend <ktownsend@theatlantic.com>
> **Sent:** Tuesday, January 12, 2021 9:13 AM
> **To:** vineet.menachery@gmail.com <vineet.menachery@gmail.com>; Menachery, Vineet <vimenach@UTMB.EDU>
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vimenach@utmb.edu

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From: Kevin Townsend[ktownsend@theatlantic.com]
Sent: Tue 1/12/2021 12:21:33 PM (UTC-06:00)
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From: Kevin Townsend[ktownsend@theatlantic.com]
Sent: Tue 1/12/2021 5:54:08 PM (UTC-06:00)
Subject: Re: Interview Inquiry — Atlantic Podcast

Thank you again for coming on! I thought it was a great conversation.

I can share a link here tomorrow when we post it.

Good luck in your work — I hope you're able to get a vacation away from home some day soon.

All my best,
Kevin

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To: Menachery, Vineet[vimenach@UTMB.EDU]
From: Vineet D. Menachery[vineet.menachery@gmail.com]
Sent: Thur 4/18/2019 8:57:22 AM (UTC-05:00)
Subject: Fwd: Question about antibody concentration in the WIV1 paper

---------- Forwarded message ---------
From: **Matt Frieman** <matt.frieman@gmail.com>
Date: Thu, Apr 11, 2019 at 10:29 PM
Subject: Question about antibody concentration in the WIV1 paper
To: Vineet D Menachery <vineet.menachery@gmail.com>

Vineet

I talked to David Corti, he pointed me in the right direction. He gave them to a company to sell and has them in his lab. Since this is a control for a contract experiment I am going to just buy them.

In your WIV1 paper, you used 200ug of the 227.15 antibody. Did you ever try lower amounts? In the old paper by Barry, he uses 25ug and gets a reasonable couple log drop, but your dose of 200ug really kills the virus. Just wondering if you tried lower doses or if I should just buy enough for the 200ug dose.

thanks

Matt

--

Vineet D. Menachery

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Jonathan Serviss[Jonathan.Serviss@entercom.com]
Sent: Thur 3/4/2021 2:01:55 PM (UTC-06:00)
Subject: frightening reports from Brazil on a virulent new COVID strain--short, live interview today on CBS News Radio LA

Good afternoon Dr. Menachery,

I'm writing from CBS News Radio in Los Angeles, where you've been a fantastic guest for us in the past--I hope you're doing very well and staying healthy. This is admittedly a short notice request, hoping to talk with you in an hour from now, but thought it was worth a shot.

We would be very grateful to talk with you for a short, live Skype or Zoom audio interview--live today at 4:05pm ET on our news magazine program--to discuss what we know about the highly contagious new COVID strain that has sent several parts of Brazil back into lockdown, as infections and deaths are soaring again. We'd like to ask what sets this new Brazil variant of the virus apart from current COVID strains that are circulating and whether we have any idea how the current crop of COVID vaccines will work to slow down the spread.

Would only need you for about 7-minutes live today at 4:05pm ET; let me know what you think and thanks so much for your help and consideration.

Best,
Jonathan

Jonathan Serviss
producer/writer/reporter, **KNX *In Depth***

Entercom | Los Angeles
5670 Wilshire Blvd, Suite 200
Los Angeles, CA 90036
newsroom: +1 323-900-2070
cell: +1 415-497-2131
entercom.com | RADIO.COM

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Katerina TILIAKOU[Katerina.TILIAKOU@trtworld.com]
Sent: Tue 1/21/2020 9:32:40 AM (UTC-06:00)
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

No worries at all. I will call you at 1pm, as I have to write down some notes for the presenter.

I also need your mobile number so that the News Gallery will be able to call you in case the Skype does not work.

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 3:29 PM
To: Katerina TILIAKOU
Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

I am about to head into the containment lab this morning. Best time would be when I get out, perhaps around 1pm New York time.

My office number is 001-409-772-9713. You can also email me the questions if that is preferable.

VDM

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:54 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

That's great! What's the best number and time that I can reach out to you today in order to let you know about the questions?

Best regards,

Katerina

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Assistant Producer

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From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:52 PM
To: Katerina TILIAKOU
Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Ok. I can be available for that.

My Skype email is Vineet.Menachery@gmail.com

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

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Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

The interview will be for 5 minutes. You have to be available from 2.15pm New York time to do a Skype test call.

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Assistant Producer

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United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Katerina TILIAKOU
Sent: Tuesday, January 21, 2020 2:20 PM
To: Menachery, Vineet
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

That's great news. We would love to have you today at 14:30pm New York time.

Could you please send me the best number and time that I can reach out for a pre-interview today as well?

Please feel free to message me at 00447986957447.

Best regards,

Katerina

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:09 AM
To: Katerina TILIAKOU
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Katerina,

I am a bit confused on the time. Would you like me to Skype tomorrow (January 21st) at 1400?

I should be available. Please let me know the parameters (how long I should set aside?).

Thanks

Vineet D. Menachery

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Monday, January 20, 2020 8:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Dear Dr Menachery,

This is Katerina from TRT World, an international news broadcasting channel based in London.

We are running a story on Coronavirus today at 19G (14.00pm New York time) for our news bulletin and I was wondering if you could join us as guest via Skype.

Please feel free to message me at 00447986957447.

Best regards,

Katerina

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Assistant Producer

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To: Menachery, Vineet[vimenach@UTMB.EDU]
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From: Katerina TILIAKOU[Katerina.TILIAKOU@trtworld.com]
Sent: Tue 1/21/2020 1:19:19 PM (UTC-06:00)
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Perfect. They will give you a call soon. Be available on Skype please.

Katerina TILIAKOU
Assistant Producer

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T. +44 207 580 88 84
M. +44 798 695 74 47

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 7:17 PM
To: Katerina TILIAKOU
Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

I'm ready now.

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 11:59 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

Could you please call me at 00447986957447 or please let me know what time can I call you?

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

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To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Claudia WYATT[Claudia.WYATT@trtworld.com]
Sent: Thur 1/30/2020 8:41:09 AM (UTC-06:00)
Subject: Interview request

Dear Mr Menachery,

I am a journalist working for the international English language TV channel TRT World and currently working on a segment for our news hour today on the Coronavirus.

I was wondering whether you would be available to join us via Skype this evening at 7pm UK time for an interview on the outbreak. We are expecting a WHO press conference at 6.30pm today in which they may or may not announce the declaration of global public health emergency - so it would be great to get your reaction to this.

If you would like to discuss this further, please feel free to give me a ring on +447568472474.
The interview would be no longer than 4 minutes and would be within the first 15 minutes of the programme.
Please could you let me know if you would be interested in doing this?

Many thanks in advance.

Best wishes

Claudia

Claudia WYATT
Assistant Output Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T.
M. +44 756 847 24 74

To: Menachery, Vineet[vimenach@UTMB.EDU]; wil2001@columbia.edu[wil2001@columbia.edu]; Ohad.Gal-Mor@sheba.health.gov.il[Ohad.Gal-Mor@sheba.health.gov.il]
From: Sister Abagail[tribejudahofyeshua@gmail.com]
Sent: Sat 2/15/2020 9:19:39 PM (UTC-06:00)
Subject: Another Suggestion from Sister Abagail; RE: 2019-nCoV Coronavirus
PleaseRead;Personal Observations/HypothsisOfPotential 2019-nCoV root.eml

Dear Researchers:

This is a new letter I am sending out to all the researchers I have reached out to last week, in hopes of being supportively helpful of your research work, with ideas of new research venues, in finding an effective deterrent & destroyer of the 2019-nCoV Coronavirus.

My Recent New Thoughts, Concerning Fighting the 2019-nCoV Virus:

Every LIVING Thing has required dietary needs in order to live, thrive and survive. On the flip-coin-side of that basic principle of life, is the fact that If and/or When something living is Exposed-To and/or Ingest CERTAIN Specific materials/matter/elements/plants/foods/minerals, it can deplete that living beings life-required-nutrients, potentially cause it to starve to death if it does Not possess the skills to apply the law of adaptation, and/or can cause it to Slowly and/or Quickly Die or Die off!!!!!!!!!

BASED On THIS Rudimentary Biological 2-Coin-Sided Fact, Here are my suggestions, with a HUMBLE Heart:

1. Investigate What Starves&Effects the Virus,from a Nutrutional Aspect:

(a) Study Diet of Family Member of those Effected by the 2019-nCoV Virus, but who did NOT get sick and/or die from family member exposure to the 2019-nCoV Coronavirus.
(b) Study the Diet of Those Who OVERCAME the 2019-nCoV Virus, who were effected, but did NOT Die from it, IF ANY.

2. Connect and WORK WITH Holistic Researchers & Doctors, Nutritional Therapist, AND Integrated Medicine Researchers & Doctors. Reason:
in hopes of finding a way to Starve, Attack & Destroy the 2019-nCoV Coronavirus....and potentially even future new strains of this and other viruses, bacterial infections and/or fungal infections; like the Candida Auris fungal infection that has become so deadly, in need of protection/healing intervention & Functional Medicine treatments.

LIST Of SOME Of the Main Medical Groups I Recommend, for Working WIth, From an Integrative Medicion & Nutrutional Therapy, Research and Treatment Approach:

1. Mount Sinai Integrated Medicine + Nutrition

https://www.mountsinai.org/patient-care/service-areas/community-medicine/integrative-medicine/services

2. Osher Center For Integrative Medicine, Harvard Medical School & Brigham and Women's Hospital

https://oshercenter.org/

3. The George Washington University

(a) Integrative Medicine
(b Laboratory Medicine
(c) Immunohematology & Biotechnology

https://healthsciencesprograms.gwu.edu/program/the-george-washington-university-mshs-in-integrative-medicine-master-1556891118601

4. Duke University Integrative Medicine & Nutrition

https://dukeintegrativemedicine.org/

5. YOUR Preferred Personal References List of Medical Researchers you Know and have worked with, who are Integrative Medicine, Nutritional Therapy, Functional Medicine, Immunology Researchers & Doctors.

I pray this will be of help, for pathways in the direction of Collaborating teams finding cures and helping people to overcome, live and thrive in life with great joy. Huge hugs with much gratitude for what you do to make a difference in life.

Love In ����YESHUA,
�����Sister Abagail

To: ophryp@ekmd.huji.ac.il[ophryp@ekmd.huji.ac.il]; joely@ekmd.huji.ac.il[joely@ekmd.huji.ac.il]; michalb@ekmd.huji.ac.il[michalb@ekmd.huji.ac.il]; eitansh@ekmd.huji.ac.il[eitansh@ekmd.huji.ac.il]; oraf@ekmd.huji.ac.il[oraf@ekmd.huji.ac.il]; edivon@cfhu.org[edivon@cfhu.org]; Menachery, Vineet[vimenach@UTMB.EDU]; wil2001@columbia.edu[wil2001@columbia.edu]; Ohad.Gal-Mor@sheba.health.gov.il[Ohad.Gal-Mor@sheba.health.gov.il]; NIAID Ocpostoffice (NIH/NIAID)[OCPOSTOFFICE@niaid.nih.gov]
From: Sister Abagail[tribejudahofyeshua@gmail.com]
Sent: Fri 2/28/2020 9:38:26 AM (UTC-06:00)
Subject: Potential ROOT Cause Of Mysterious COVID-19 Case in California

Dear Researchers & Scientific Medical Community:

Shalom and Boker Tov! I was reading about the "Mysterious COVID-19 Case" in California, of an infected patient who supposedly did not have Coronavirus exposure, and contracted this virus mysteriously. I have a Hypothesis of the POTENTIAL ROOT CAUSE For this mysterious California case.

According to the follow facts I have pasted below, for you to read for yourself, I believe that the mysterious patient contracted the COVID-19 Coronavirus because they were potentially exposed to marine debris carried by storm winds, that came from & carried across the Pacific Ocean; as in Plastic & Stainless Steel Particle Debris, that was Contaminated with the COVID-19 Virus! That is My Hypothesis.

Gathered Facts, Pasted below, for you to read for yourself. I pray this will be of help. ����May ELOHIM guide you by HIS wisdom, in fighting this deadly virus, and Bless you with all that you need. ⁇ I Love and respect you all, very much, as your Little Sister.

With Much Love In ELOHIM, B'Shem ⁇YESHUA,
⁇Love Sister Abagail

Mysterious California COVID-19 Coronavirus Case:

https://www.cdc.gov/media/releases/2020/s0226-Covid-19-spread.html

It is a proven FACT that a viruses CAN survive on plastic, stainless steel and other hard surfaces, for long periods of time.

https://www.mayoclinic.org/diseases-conditions/flu/expert-answers/infectious-disease/faq-20057907

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4462923/

Marine Debris, what it consist of; AND How Marine Debris is Carried by the Wind, Rivers, Ocean Currents and in Storm Winds:

https://marinedebris.noaa.gov/discover-issue/types-and-sources

https://www.weegy.com/Home.aspx?ConversationId=2PD6JLPJ&Link=i

Temperatures and Humidity Effect Virus Survival:

https://www.sciencedaily.com/releases/2010/05/100514123500.htm

Relevant Fact; Temperatures & Humidity Effect Strom Wind Speed:

https://sciencing.com/average-wind-speed-during-thunderstorm 24075.html

Current Winds Passing Over the Pacific Ocean, feeding the Storms with Strong Winds, sweeping Coast to Cost; From Satellite Radar Images - February 28, 2020:

https://www.eldoradoweather.com/current/satellite/west-us-east-pacific-geocolor.html

https://www.eldoradoweather.com/satellite/ssec/nepacific-250-850-hpa.html

Marine Debris Information/Facts:
https://marinedebris.noaa.gov/types-and-sources/sources

Jet Stream Winds Steers Atlantic Currents:

https://www.livescience.com/50998-jet-stream-controls-atlantic-climate-cycles.html

WINTER STORMS ACROSS THE PACIFIC OCEAN, Steered By The Jet Stream:

http://seasonsinthesea.com/jan-feb/phys.shtml

Relevant! Jet Stream Strong Winds, Cause Dust Bowl & Steers Weather from Location to Location:

https://www.thoughtco.com/jet-stream-and-weather-3444495

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Jonathan Serviss[Jonathan.Serviss@entercom.com]
Sent: Wed 3/10/2021 12:37:18 PM (UTC-06:00)
Subject: very concerning findings on the lethality of the UK COVID variant--talking today on CBS News Radio Los Angeles

Good morning Dr. Menachery,

I'm writing from CBS News Radio in Los Angeles, where you've been good enough to talk with us in the past--hope you're doing very well and staying healthy. We'd be grateful to have you back on our newscast for a quick interview this afternoon to discuss new research out of Great Britain on the B.1.1.7 coronavirus variant.

I'm reading about the potential for increased lethality of the so-called "UK variant" of COVID-19 and heightened risks for people who contract this variant of the virus. I'm hoping to talk with you for a brief, live Skype or Zoom audio (no video necessary) interview at 1:25pm Pacific/3:25pm Central. The interview will be quick, just about 7-minutes total, and you'd be in conversation with my two anchors; we have really simple, straight-forward questions about the potential for higher death rates associated with the UK variant of COVID.

Let me know if I can entice one of you to come back to talk with us today at 3:25pm Central and thanks so much for your help and consideration.

Best,

Jonathan

Jonathan Serviss
producer/writer/reporter, **KNX *In Depth***

Entercom | Los Angeles
5670 Wilshire Blvd, Suite 200
Los Angeles, CA 90036
newsroom: +1 323-900-2070
cell: +1 415-497-2131
entercom.com | RADIO.COM

To: Menachery, Vineet[vimenach@UTMB.EDU]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Gabriela Esquivada[gesquivada@infobae.com]
Sent: Fri 3/13/2020 1:41:12 PM (UTC-05:00)
Subject: Media inquiry / coronavirus, your 2015 paper

Vineet D. Menachery, PhD
Assistant Professor
Department of Microbiology & Immunology

Dear Professor Menachery,

I am writing on behalf of my editors at Infobae, the most visited digital media in Latin America, according to ComScore, and the second in the Spanish speaking world, after El País. We currently have 70 million unique users, as per Google Analytics, and more than 550 million page views. We have offices in Buenos Aires (headquarters), Miami and México (CDMX), and correspondents in Colombia, Uruguay, Venezuela and Chile.

We are interested in this paper you and other colleagues published in 2015:
https://www.nature.com/articles/nm.3985

Would it be possible to ask you a few questions, either via e-mail or via phone? Just in case, please let me pose a few:

I would like to understand if five years ago you predicted that something like what we are seeing now with Covid-19 might happen; in fact, the text seems to ask when, nor if. Is that so? What made you focus on coronaviruses from bats?

What is your view on the different countries of the world preparedness for this event we are living, from the perspective of someone who co-wrote that paper?

If there are 5000+ coronaviruses in bats, are there also other risks of new pathogens the human body has no antibodies for that may cause something like we are seeing today?

Thank you so much in advance. All the best,

--
Gabriela Esquivada
Infobae

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Jonathan Serviss[Jonathan.Serviss@audacy.com]
Sent: Mon 4/5/2021 11:22:03 AM (UTC-05:00)
Subject: yet more concern about yet more COVID variants--talking about a Botswana variant that's circulating in Iowa, today on CBS News Radio Los Angeles

Good morning Dr. Menachery,

It's Jonathan at CBS News Radio Los Angeles, where you've been a fantastic guest and resource on our behalf in the past--hope you're doing very well, staying healthy and coming off of a great weekend. We are following reports of several COVID outbreaks in North America, both in the U.S. and Canada, that are being traced to new variants of the virus making the rounds and becoming increasingly prevalent.

So I'm turning to you to get a better understanding about the possible impact of these variants--whether it's the Brazilian strain that's apparently been causing sizable outbreaks in British Colombia, Canada (including among the Vancouver Canucks NHL team) or the Botswana variant that's been detected among people recently infected in Iowa and the Midwest. How aggressively can we expect the novel coronavirus to continue to mutate, and how will the current crop of COVID vaccines stack up against it?

Hoping to talk with you this afternoon for a short, live Skype or Zoom audio interview somewhere within the 4-5pm ET window, depending on what your schedule allows; we'd only need you for about 7-minutes within the 4pm ET hour, where you'll be in conversation with my two anchors.

Let me know what you think and thanks again for your help and consideration.

Best,

Jonathan

Jonathan Serviss
producer/writer/reporter, **KNX *In Depth***

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5670 Wilshire Blvd, Suite 200
Los Angeles, CA 90036
newsroom: +1 323-900-2070
cell: +1 415-497-2131
entercom.com | RADIO.COM

To: ripudaman.bains@nature.com[ripudaman.bains@nature.com]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=e8de7da558c24fa08b25d7643703d2db-Menachery,]
Sent: Wed 6/30/2021 4:35:17 PM (UTC-05:00)
Subject: Re: CONFIDENTIAL and very urgent; request to review manuscript NCOMMS-20-47724A

Dr. Bains,

My apologies for the delayed response. I am currently out of the office and will not be able to complete the review.

I can recommend the following scientist for the review:

Lisa Gralinski (UNC)
Timothy Sheahan (UNC)
Rudra Channappanavar (OK State)
Tony Fehr (Kansas)

Good luck finding a suitable reviewer.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: ripudaman.bains@nature.com <ripudaman.bains@nature.com>
Sent: Monday, June 28, 2021 9:51 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: CONFIDENTIAL and very urgent; request to review manuscript NCOMMS-20-47724A

Dear Dr Menachery,

I am writing from Nature Communications with an urgent request for help with the revised version of a manuscript that we currently have under consideration. The manuscript is entitled, Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2' and it has been submitted by Professor Qin and colleagues.

We reviewed the original version of this work and the authors revised according to the comments of four referees. However, two of the referees (who are experts in animal studies and adaptation of viruses to murine hosts) are no longer responding to our requests for comments on the revised version of this work. I am emailing if you would be willing to provide us with comments on how well the authors have responded to the original concerns of Referees 2 and 3. Their comments are provided in the point-by-point response from the authors.

Additionally, we would very much appreciate your comments on the authors' data that are presented in Figures 9a and 9b and

whether there are any concerns with their presentation of growth kinetics of the murine strain in human cells, in particular if you have any concerns relating to dual use of research concern (DURC).

To provide a timely decision for the authors, we would kindly ask you to return your comments within two weeks. We are aware that the current global public health crisis is disrupting the work of many of our authors and reviewers. If you would like to assist, but would need more than 14 days to review the manuscript, please do not hesitate to let me know.

Nature Communications uses a transparent peer review system for new manuscripts submitted from January 2016. If the manuscript is accepted, the authors may agree for the reviewer comments to the authors as well as the author rebuttal letters to be published as a supplementary file associated with the paper. Any confidential comments between you and the editor will not be published. By submitting a reviewer report you agree to the publication of the comments made to the authors. Unless you sign the report with your name in those comments to the authors, we will respect and maintain your full anonymity. For more information, please refer to our FAQ page at http://www.nature.com/article-assets/npg/ncomms/authors/ncomms-transparent-peer-review.pdf

To accept or decline our request, please use the following link:
https://mts-ncomms.nature.com/cgi-bin/main.plex?el=A2S4DNL5A1JHHo7J4A9ftdwES2XWjOPHmxQegPWxrwwZ

Many thanks in advance for your help; I look forward to hearing from you.

Best regards,

Ripudaman Bains
Editor
Nature Communications

Our flexible approach during the COVID-19 pandemic
If you need more time at any stage of the peer-review process, please do let us know. While our systems will continue to remind you of the original timelines, we aim to be as flexible as possible during the current pandemic.
This email has been sent through the Springer Nature Tracking System NY-610A-NPG&MTS

To: Jonathan Serviss[Jonathan.Serviss@audacy.com]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=e8de7da558c24fa08b25d7643703d2db-Menachery,]
Sent: Tue 6/15/2021 4:04:48 PM (UTC-05:00)
Subject: Re: explaining the Delta COVID variant, back on CBS News Radio L.A. this afternoon

Hi Jonathan,

I am booked this afternoon.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Jonathan Serviss <Jonathan.Serviss@audacy.com>
Sent: Tuesday, June 15, 2021 1:01 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: explaining the Delta COVID variant, back on CBS News Radio L.A. this afternoon

Good afternoon Dr. Menachery,

It's Jonathan at CBS News Radio Los Angeles, where you've been a fantastic guest for us in the past--hope you're doing very well, staying healthy and about to embark on a somewhat, mostly normal summer! Also selfishly hoping that you're around today because we'd be very grateful to have you back on our news magazine program for a short, live interview today at 1:25pm Pacific/3:25pm Central to give us a quick tutorial on the Delta variant of the novel coronavirus.

This is because the CDC has officially labeled the Delta variant a concern, with fears that it's more contagious and likely to become the dominant COVID variant in the months ahead. What does this mean for the vaccinated and unvaccinated alike, what makes this strain more contagious and how much damage has the Delta variant already caused in other countries across the world?

Would keep this to a short and simple 6-minutes at 3:25pm Central, hopefully over a Skype or Zoom audio connection (no video necessary); let me know what's possible and thanks so much for your help and consideration.

Best,

Jonathan

Jonathan Serviss
producer/writer/reporter, **KNX *In Depth***

Entercom | Los Angeles
5670 Wilshire Blvd, Suite 200
Los Angeles, CA 90036
newsroom: +1 323-900-2070
cell: +1 415-497-2131
entercom.com | RADIO.COM

To: Halford, Bethany[B_Halford@acs.org]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Thur 4/23/2020 7:48:39 AM (UTC-05:00)
Subject: Re: Interview with C&EN

Hey Beth,

I don't have time this week to talk about it. If you wanted to try early next week, I could schedule some time then.

Apologies,

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Halford, Bethany <B_Halford@acs.org>
Sent: Thursday, April 23, 2020 7:38 AM
To: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>; Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Interview with C&EN

Hi Professor Menachery,

I'm just following up on this interview request. I understand if you don't have time for it, but would love to hear your thoughts if you do.

Thanks,
Beth

From: Halford, Bethany
Sent: Tuesday, April 21, 2020 11:47 AM
To: 'Vineet.Menachery@gmail.com' <Vineet.Menachery@gmail.com>; 'vimenach@utmb.edu' <vimenach@utmb.edu>
Subject: Interview with C&EN

Dear Professor Menachery,

I hope this note finds you well in this challenging time.

I'm a reporter with Chemical & Engineering News, a weekly newsmagazine about chemistry. I am working on a story about the discovery of EIDD-2801, a compound currently in Phase I trials for COVID-19. I've attached a recent Science Translational Medicine paper about this compound. I am looking to speak with someone about the challenges of making antivirals in general and an oral antiviral specifically. Do you have a little time to chat with me this week? I don't think it would take more than 20 minutes. Just let me know when a good time to talk might be and what is the best number to reach you.

Thanks for your help,
Beth

Bethany Halford
Senior Correspondent
Chemical & Engineering News

To: Shi, Pei yong[peshi@UTMB.EDU]; Xie, Xuping[xuxie@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Makino, Shinji[shmakino@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 4/14/2020 9:49:44 PM (UTC-05:00)
Subject: Re: Urgent Collaboration - Codon-Pair Deoptimized SARS-CoV-2 Vaccine using infectious clone

I don't have capacity at this time either.

VDM

From: Shi, Pei yong <peshi@UTMB.EDU>
Sent: Tuesday, April 14, 2020 1:14 PM
To: Xie, Xuping <xuxie@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>
Subject: RE: Urgent Collaboration - Codon-Pair Deoptimized SARS-CoV-2 Vaccine using infectious clone

Hi Vineet and Shinji,
I'm out of capacity and won't be able to take this one. Please let me know if you are interested. I will then respond.
Thanks.
Pei-Yong
-
-----Original Message-----
From: J. Robert Coleman <coleman@codagenix.com>
Sent: Tuesday, April 14, 2020 11:55 AM
To: Shi, Pei yong <peshi@UTMB.EDU>; Xie, Xuping <xuxie@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Makino, Shinji <shmakino@UTMB.EDU>
Subject: Urgent Collaboration - Codon-Pair Deoptimized SARS-CoV-2 Vaccine using infectious clone

Dear Dr. Shi and UTMB Team

I am reaching out to ask if you were interested in collaborating to make a Codon-pair deoptimized vaccine strain using your infectious clone. We have already designed deoptimized Spike and RdRNP cassettes that could be easily inserted into your WT clone. We could fund the work for the cloning and vaccine strain recovery. We have collaborated in the past with Alan BArret and Nigel Bourne at UTMB, so they are familiar with the success of our approach in Dengue. Looking forward to hearing from you soon, we can send the genes at any time. Have a good day, Regards, Robert Coleman

--

J. Robert Coleman, PhD, MBA
Chief Executive Officer
Co-founder, Codagenix, Inc.
3 Bioscience Park Drive
Farmingdale, NY 11735-0176
Phone: 516-448-5073
coleman@codagenix.com

To: Weaver, Scott[sweaver@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; McLellan, Susan[sumclell@UTMB.EDU]
Cc: Reyes, Raul[rareyes@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 5/12/2020 12:16:26 PM (UTC-05:00)
Subject: Re: Chronical series

I can participate.

VDM

From: Weaver, Scott <sweaver@UTMB.EDU>
Sent: Monday, May 11, 2020 1:52 PM
To: Holubar, Connie J. <cjholuba@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; McLellan, Susan <sumclell@UTMB.EDU>
Cc: Reyes, Raul <rareyes@UTMB.EDU>
Subject: Chronical series

Dear Susan, Vineet and Jim,

Raul Reyes has asked me to plan a series of interviews on UTMB COVID research through Nick Powel of the Houston Chronicle. I thought we might start with a high-level round table discussion of vaccine and therapeutic research, including basic and clinical, then branch out into individual projects with the lead scientists in later sessions. Let me know if you are willing to participate in the initial overview discussion.

Thanks

Scott

To: Martin, Chris E[Chris.Martin@charter.com]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 6/8/2020 10:02:25 PM (UTC-05:00)
Subject: Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

https://www.google.com/amp/s/www.washingtonpost.com/health/2020/03/10/coronavirus-is-mysteriously-sparing-kids-killing-elderly-understanding-why-may-help-defeat-virus/%3FoutputType%3Damp

https://www.statnews.com/2020/02/10/fluctuating-funding-and-flagging-interest-hurt-coronavirus-research/

https://www.google.com/amp/s/www.nytimes.com/2020/03/25/health/coronavirus-immunity-antibodies.amp.html

---

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, June 8, 2020 9:59 PM
To: Martin, Chris E <Chris.Martin@charter.com>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Vineet.menachery@gmail.com
552.117
Galveston Texas

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Martin, Chris E <Chris.Martin@charter.com>
Sent: Monday, June 8, 2020 9:36 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Dr. Menachery
I would be grateful to get this info ASAP... so I may get all of our operations folks set for tomorrow's interview, please.

Chris Martin
Executive Producer
Spectrum News
201-417-9413 (m)

On Jun 8, 2020, at 4:57 PM, Martin, Chris E <Chris.Martin@charter.com> wrote:

Here I am

Here what I need for this tomorrow

Skype Handle:
Phone #:
Location: Town / City calling from

From: Martin, Chris E
Sent: Monday, June 08, 2020 9:35 AM
To: 'vimenach@utmb.edu' <vimenach@utmb.edu>; 'Vineet.Menachery@gmail.com' <Vineet.Menachery@gmail.com>
Subject: Media Request / Spectrum News / Skype Interview Tuesday 6.9

Greetings Dr. Menachery,

I am an Executive producer with Spectrum News in Austin for our nightly Texas politics and public affairs program 'Capital Tonight' hosted by Karina Kling.

I would like to speak with you about coming on our show via Skype tomorrow Tuesday 6.9 at 130p to discuss the progression of the coronavirus.

Would it be possible to schedule a brief call with you to discuss your work with the coronavirus?

The best way to reach me these days is on my mobile phone 201-417-9413.

Thank you Dr. Menachery.

Chris Martin
Executive Producer
News, Documentary and Long-Form Programming
Spectrum Networks
1708 Colorado St. | Austin, TX 78701
o 512.531.1205 | c **201.417.9413**

<image001.png>

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=e8de7da558c24fa08b25d7643703d2db-Menachery,]
Sent: Sun 2/21/2021 9:48:22 PM (UTC-06:00)
Subject: Fw: Thank you
Covid-19 Vaccination Delays Could Bring More Virus Variants, Impede Efforts to End Pandemic - WSJ.pdf

---

From: Toy, Sarah <sarah.toy@wsj.com>
Sent: Saturday, February 20, 2021 9:28 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Thank you

Hi Dr. Menachery,
Thanks so much for your help with the article that went out today. Attaching a link and PDF here for you so you can read it. Many thanks again.

https://www.wsj.com/articles/covid-19-vaccination-delays-could-bring-more-virus-variants-impede-efforts-to-end-pandemic-11613817002

Sarah

--
Sarah Toy
REPORTER

O: 212-416-3557

E: sarah.toy@wsj.com
A: 1211 Avenue of the Americas, New York, NY 10036
T: @sarahtoy17

To: Matthew Ozug[MOzug@npr.org]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=e8de7da558c24fa08b25d7643703d2db-Menachery,]
Sent: Tue 12/22/2020 1:10:06 PM (UTC-06:00)
Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

See Below

From: Matthew Ozug <MOzug@npr.org>
Sent: Tuesday, December 22, 2020 1:08 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

May thanks again for speaking to All Things Considered. The link for sharing is here:
https://www.npr.org/2020/12/21/948873785/new-coronavirus-variant-found-in-u-k-what-does-it-mean-for-the-world

I have one more favor to ask: Could you reply to the following 4 questions? Should take no more than a minute. All Things Considered is trying to do a better job of tracking the demography of our guests we're asking everyone to answer these questions however they please:

How would you describe your gender? ***Male***

How would you describe your race and your ethnicity/nationality? Asian/Indian Subcontient

How old are you? 38

Where do you live? Galveston, Texas

Thank you so much!

Matt

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 4:29 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

ok.

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 3:18 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

I just heard from the director that they will call you at 3:50 CT, since another piece is wrapping up just before then.

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 4:05 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Skype ID: Vineet.Menachery@gmail.com

I will plan to take your call on facetime at 3:45 CT. I will answer on my laptop as it is linked to my iphone.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 2:42 PM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: RE: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY

Hi Dr. Menachery,

As promised, here are a few examples of questions for the interview this afternoon. Ari may remind you of this as well, but please gear your answers to a general population as much as possible: Why does it appear this new variant is more contagious and does that worry you? Is there any reason to believe the vaccines being rolled out are less effective against this variant? Do we know anything about whether the new variant is more deadly? And is there any reason to believe restricting travel out of the UK would be effective at curtailing the spread of this new variant?

Finally, and I'm sorry to be harassing you, but if you can send me a skype ID to reach you at, or (if you have it) the cell number of someone else in your house, that would be great. Just because it's a live interview we try to have as many ways as possible of reaching you.

So YOU have, it the direct studio line/phone number is 202-513-3731. And you can expect a facetime audio call from NPR in a little over an hour now.

Thank you!
Matt

From: Matthew Ozug
Sent: Monday, December 21, 2020 2:12 PM
To: 'Menachery, Vineet' <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com
Subject: CONFIRMING INTERVIEW WITH NPR's All Things Considered TODAY
Importance: High

Hi Dr. Menachery,

Thanks so much for agreeing to be on the show today. **We are CONFIRMED for a live interview at 5pm Eastern/4pm Central.**

Technical Details:

The folks in the studio will want to connect and test your line 10-15 minutes prior.

For the connection: The ideal connection is a FaceTime audio. Do you have **Facetime** on your computer or phone? If so can you let me know that number so I can relay it to the engineers.

As a back up: since this is a live interview we will also need a back up phone for you. It could be a landline or another cellphone, but it should not be the same phone as the primary, facetime phone, ideally.

I can call you as soon as your meeting is over and talk through any technical questions.

Conversation Notes:
I'm confirming that this will be a live interview of not more than 5 minutes. The director will tell you this when you are on the line before the interview begins, but they can give you a warning in your ear near the end of time if that helps.

I am working to send along an outline of the questions Ari hopes to ask, but it will largely mirror the conversation we had this morning.

One request: since this is for a general audience, please try to limit any overly scientific or technical language, or to define the terms. Ari can also help remind you of this. We are obviously coming to you for your extensive knowledge, but we also want to make sure all listeners can follow the conversation. (I just listened to your conversation with LuLu Garcia-Navarro, so I have no doubt this will be just as great!)

Thank you! Please let me know when you can about the best way to connect with you.

Matt

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Monday, December 21, 2020 12:13 PM
To: Matthew Ozug <MOzug@npr.org>; Vineet.Menachery@gmail.com
Subject: Re: Speaking to NPR's All Things Considered?

Hi Matt,

I have something scheduled from 11:30CT to 1:30CT. I can probably talk at 2CT if that works for you. Let me know.

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Matthew Ozug <MOzug@npr.org>
Sent: Monday, December 21, 2020 10:52 AM
To: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Cc: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: Speaking to NPR's All Things Considered?

Dear Dr. Menachery

I'm a producer at NPR's All Things Considered and we're looking to book a guest to speak to Ari Shapiro for this evening's program on the new strain of the virus out of the UK.

This would be on what we know, and what we still hope to learn. This would be a recorded conversation - if you're available for an interview in the next 3 hours can you please let me know.

Thanks!

Matt Ozug
Producer, NPR
mozug@npr.org
cell: +1 (917) 664 2011
office: +1 (202) 513-2133
Twitter.com/Matt_Ozug

To: Katerina TILIAKOU[Katerina.TILIAKOU@trtworld.com]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 1/21/2020 8:52:39 AM (UTC-06:00)
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Ok. I can be available for that.

My Skype email is Vineet.Menachery@gmail.com

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:49 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

The interview will be for 5 minutes. You have to be available from 2.15pm New York time to do a Skype test call.

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Katerina TILIAKOU
Sent: Tuesday, January 21, 2020 2:20 PM
To: Menachery, Vineet
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Dr Menachery,

That's great news. We would love to have you today at 14:30pm New York time.

Could you please send me the best number and time that I can reach out for a pre-interview today as well?

Please feel free to message me at 00447986957447.

Best regards,

Katerina

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:09 AM
To: Katerina TILIAKOU
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Katerina,

I am a bit confused on the time. Would you like me to Skype tomorrow (January 21st) at 1400?

I should be available. Please let me know the parameters (how long I should set aside?).

Thanks

Vineet D. Menachery

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Monday, January 20, 2020 8:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>

Subject: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Dear Dr Menachery,

This is Katerina from TRT World, an international news broadcasting channel based in London.

We are running a story on Coronavirus today at 19G (14.00pm New York time) for our news bulletin and I was wondering if you could join us as guest via Skype.

Please feel free to message me at 00447986957447.

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

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To: Katerina TILIAKOU[Katerina.TILIAKOU@trtworld.com]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Tue 1/21/2020 9:29:15 AM (UTC-06:00)
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

I am about to head into the containment lab this morning. Best time would be when I get out, perhaps around 1pm New York time.

My office number is 001-409-772-9713. You can also email me the questions if that is preferable.

VDM

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:54 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

That's great! What's the best number and time that I can reach out to you today in order to let you know about the questions?

Best regards,

Katerina

Katerina TILIAKOU
Assistant Producer

TRT WORLD UK,
5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
United Kingdom
T. +44 207 580 88 84
M. +44 798 695 74 47

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:52 PM
To: Katerina TILIAKOU

Cc: Vineet.Menachery@gmail.com
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Ok. I can be available for that.

My Skype email is Vineet.Menachery@gmail.com

VDM

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Tuesday, January 21, 2020 8:49 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Cc: Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

The interview will be for 5 minutes. You have to be available from 2.15pm New York time to do a Skype test call.

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5th Floor, 200 Grays Inn Road, London, WC1X 8XZ
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From: Katerina TILIAKOU
Sent: Tuesday, January 21, 2020 2:20 PM
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Best regards,

Katerina

From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Tuesday, January 21, 2020 2:09 AM
To: Katerina TILIAKOU
Subject: Re: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Hi Katerina,

I am a bit confused on the time. Would you like me to Skype tomorrow (January 21st) at 1400?

I should be available. Please let me know the parameters (how long I should set aside?).

Thanks

Vineet D. Menachery

Vineet D. Menachery, Ph.D.
Assistant Professor
Department of Microbiology and Immunology
University of Texas Medical Branch, Galveston, Texas
vimenach@utmb.edu

From: Katerina TILIAKOU <Katerina.TILIAKOU@trtworld.com>
Sent: Monday, January 20, 2020 8:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: TRT WORLD INTERVIEW WITH VINEET D MENACHERY/ URGENT MEDIA REQUEST - CORONAVIRUS 20/01

Dear Dr Menachery,

This is Katerina from TRT World, an international news broadcasting channel based in London.

We are running a story on Coronavirus today at 19G (14.00pm New York time) for our news bulletin and I was wondering if you could join us as guest via Skype.

Please feel free to message me at 00447986957447.

Best regards,

Katerina

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Assistant Producer

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To: Chhanda Das[cdas@aai.org]; Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
Cc: Awards[awards@aai.org]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Fri 1/24/2020 5:57:15 PM (UTC-06:00)
Subject: Re: Immunology 2019 Travel Award Reimbursement - Outstanding Check

Hi Chhanda,

I do not recall receiving the check. Can you please reissue the check? The address you have on file is accurate.

Thank you.

Vineet D. Menachery

From: Chhanda Das <cdas@aai.org>
Sent: Friday, January 24, 2020 11:26 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>; Vineet.Menachery@gmail.com <Vineet.Menachery@gmail.com>
Cc: Awards <awards@aai.org>
Subject: Immunology 2019 Travel Award Reimbursement - Outstanding Check

Dr. Menachery,

I'm writing to you regarding an outstanding check from The American Association of Immunologists for 2019 AAI Travel Award reimbursement– the check is outstanding as of January23, 2020.
Please confirm if you have or have not received the check matching the information below:
Check #: *40588*
Date: *07/19/2019*
Amount: *$1250*
If you have not received this check, we can reissue it for you. Please confirm the mailing address to ensure that the check is sent to the correct location:

Vineet D. Menachery
2227 Flower Croft Lane
League City
TX, 77573

Please let me know if you have any questions or concerns

Chhanda Das
Accounting Assistant
The American Association of Immunologists
1451 Rockville Pike, Suite 650
Rockville, MD 20852
Phone: 301-634-7784

To: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Mon 3/9/2020 1:15:05 PM (UTC-05:00)
Subject: test

afatea

To: LeDuc, James W.[jwleduc@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 3/4/2020 12:25:23 PM (UTC-06:00)
Subject: Re: Slides

Yes. Clone is with Pei Yong. Kent is doing transgenic model and I am going to try and make a non-transgenic model.

From: LeDuc, James W. <jwleduc@UTMB.EDU>
Sent: Wednesday, March 4, 2020 11:57 AM
To: Menachery, Vineet <vimenach@UTMB.EDU>
Subject: RE: Slides

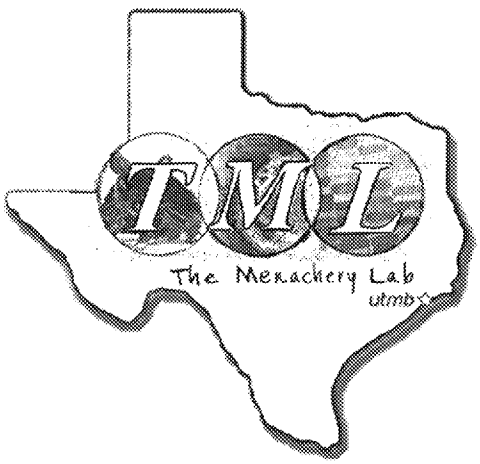
Perfect, thanks. May I assume that the infectious clone is the work being done with Pei-Yong? And the transgenic mouse model work is with Kent? I know other animals are being explored as well.

Thanks very much! Jim

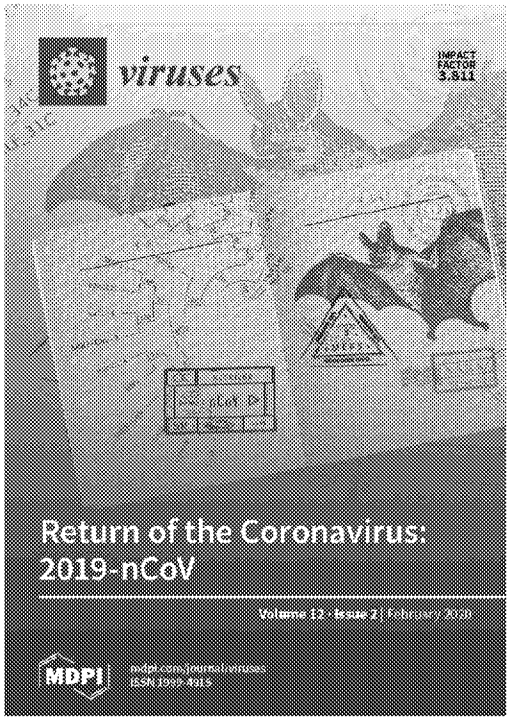
From: Menachery, Vineet <vimenach@UTMB.EDU>
Sent: Wednesday, March 04, 2020 11:48 AM
To: LeDuc, James W. <jwleduc@UTMB.EDU>
Subject: Slides

To: LeDuc, James W.[jwleduc@UTMB.EDU]
From: Menachery, Vineet[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=E8DE7DA558C24FA08B25D7643703D2DB-MENACHERY,]
Sent: Wed 3/4/2020 11:47:41 AM (UTC-06:00)
Subject: Slides
nCoV Work for Jim.pptx

Slides for Jim



Menachery Lab- Progress to Date



- Wrote initial 2019-nCoV commentary (selected for journal cover)
- Published initial characterization of the US SARS-CoV-2 strain with the CDC
- In process of submitting manuscript on sensitivity of SARS-CoV-2 to interferon treatment

Menachery Lab- Ongoing work

- Developing infectious clone for SARS-CoV-2 to generate reporter and mutant viruses
- Comparing immune responses between SARS-CoV and SARS-CoV-2 using respiratory cells
- Developing a small animal model for SARS-CoV-2 to model disease and therapeutic efficacy
- Examining CoV disease in the context of aging

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: editorial@elifesciences.org[editorial@elifesciences.org]
Sent: Mon 6/7/2021 12:04:58 PM (UTC-05:00)
Subject: Please confirm your authorship in a submission to eLife (07-06-2021-RA-eLife-71047)

Dear Vineet,

Dr. Savan has recently submitted an article, "Endomembrane targeting of human OAS1 p46 augments antiviral activity", for consideration at eLife.

* Please ensure that your name, author contributions, and competing interest statement are accurate and complete.

* Authors are responsible for disclosing all relationships and activities that might bias or be seen to bias their work, following the ICMJE's recommendations for potential conflicts of interest: http://www.icmje.org/recommendations/browse/roles-and-responsibilities/author-responsibilities--conflicts-of-interest.html

* Authors should meet the ICMJE's authorship criteria: http://www.icmje.org/recommendations/browse/roles-and-responsibilities/defining-the-role-of-authors-and-contributors.html

Please agree using the following link, to confirm that you approve of the submission of the article, its content, authorship, the order of authorship, and that you have declared any relevant conflicts of interests:

[https://submit.elifesciences.org/cgi-bin/main.plex?el=A6Hz4jNi1A1BiOk5Y5A9ftdufDtTXxyetzxL1NdzCaAZ]

A PDF of the submission can be found via the link above.

If you have an ORCID iD that isn't associated with your author profile at eLife, we would encourage you to visit https://submit.elifesciences.org/ and click on the ORCID icon under "Use an existing login" to start the process of linking the profiles together.

If you have any questions about the submission, please discuss them with the corresponding author(s).

Many thanks,

Milly

Millicent McConnell
Senior Editorial Assistant, eLife
https://elifesciences.org/
+44 (0)1223 855348

To: Menachery, Vineet[vimenach@UTMB.EDU]
Cc: Vineet.Menachery@gmail.com[Vineet.Menachery@gmail.com]
From: editorial@elifesciences.org[editorial@elifesciences.org]
Sent: Tue 6/8/2021 8:38:49 AM (UTC-05:00)
Subject: eLife review invitation (article from Skjoedt - 03-05-2021-RA-eLife-70002 - confidential)

Dear Vineet,

I'm writing in the hope that you'll be willing to review this article, "The B.1.1.7 SARS-CoV-2 variant exhibits significantly higher affinity for ACE-2 and accelerates disease severity in transgenic hACE-2 mice", for eLife, a selective journal that publishes promising research in all areas of biology and medicine. eLife is now creating public reviews for research that is reviewed by the journal - regardless of the final decision.

What changes for you as a reviewer?
We ask you to structure your review into three parts: (1) a short statement on significance and audience for this paper, (2) the public review with guidance for readers around how to interpret the work, highlighting important findings but also mentioning caveats where they exist, and (3) specific feedback to the authors stating what needs to be changed to make the manuscript acceptable for publication in eLife, or why it falls short as an eLife paper.

The intention is to post the public reviews from each reviewer alongside the preprint (on bioRxiv or medRxiv). At present, authors can opt out from posting a preprint or they can postpone the posting of the public reviews until the paper has been published elsewhere. For papers accepted for publication in eLife, the feedback for authors will be published as part of the decision letter, as before. The "recommendations for the authors" (part 3) will not be posted alongside the preprint.

eLife is taking these steps to help change how publishing works: we believe that clear public reviews should be the central mechanism by which research is evaluated.

Even if you decide to reveal your name to the authors, your name will not appear on the public review. All public reviews are signed by eLife, putting the onus on us as an organization and community to ensure that our reviews are of the highest quality and ethics.

We continue our policy of consultation between the reviewers. If you agree to review this paper, once all the reviews have been received, you will be invited to discuss your comments with the other reviewers in an online consultation session, in which the reviewers will be identified to one another, and you can recommend whether the paper should be revised for publication by eLife or rejected. Additional experiments, analyses, or data collection should only be requested if they are essential.

The abstract and information about the review process are below, and you can read what we have published so far at https://elifesciences.org.

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If you have competing interests that preclude an objective review, or you cannot otherwise provide a review of the work, you must DECLINE using the link below. Suggestions for alternatives are very welcome. (Where it's appropriate to do so, it would be helpful if you could offer a brief opinion about the work, even if you're declining to review.)

By taking on this assignment, you agree to conduct your review according to the terms in the eLife Reviewer Guide - https://submit.elifesciences.org/html/elife_reviewer_instructions.html - and you agree to our confidentiality notices below*, which help us to protect the personal data of authors, editors, and reviewers.

To respond, please use the link below and select either AGREE or DECLINE:

[https://submit.elifesciences.org/cgi-bin/main.plex?el=A3Hz5irC4A2BiOk1F5A9ftdHKHPgzQ7fBZxEiT7y1AMRwZ]

xxxxxxxxxx

Please note that we work with Publons.com to give you the opportunity to be recognised for your review, so if you agree to provide a review we will let you know how to add the details to a Publons account in the email we send at the conclusion of the review process.

We ask for comments to be returned within 14 days (although we will understand if you will need longer than usual). I'll look forward to hearing from you.

Best wishes,

Kei Sato
Reviewing Editor
eLife

xxxxxxxxxx

Title: The B.1.1.7 SARS-CoV-2 variant exhibits significantly higher affinity for ACE-2 and accelerates disease severity in transgenic hACE-2 mice

Authors: Rafael Bayarri-Olmos, Laust Johnsen, Manja Idorn, Line Reinert, Anne Rosbjerg, Cecilie Hansen, Charlotte Helgstrand, Jais Bjelke, Theresa Bak-Thomsen, Soren Paludan, Peter Garred, and Mikkel-Ole Skjoedt

Abstract:
Since the emergence of the B.1.1.7 SARS-CoV-2 lineage, it has been transmitting rapidly and accounts for the majority of new COVID-19 cases in Europe. This is likely due to a fitness advantage that could be driven by the RBD residue change (N501Y), which also developed independently in the B.1.351 and B.1.1.248/P.1 "variants-of-concern". Here we present a functional characterisation of the B.1.1.7 variant and show an eight-fold affinity increase towards human ACE-2. In accordance with this, transgenic hACE-2 mice showed a faster disease progression and severity after infection with a low dose of B.1.1.7, compared to a wild-type SARS-CoV-2 isolate. When challenged with sera from convalescent individuals or monoclonal antibodies, the N501Y variant showed a minor, but significant elevated evasion potential of RBD:ACE-2 antibody neutralisation. The data suggest that the N501Y substitution causes a remarkable rise in affinity that could explain the higher transmission rate and severity of the B.1.1.7 variant.

xxxxxxxxxx

* Confidentiality and Personal Data
We do not release the identities of the reviewers to the authors (unless requested by the reviewers themselves) but in the course of the discussion that forms part of the review process, each reviewer will know the identity of the other reviewer(s).

The review process is strictly confidential and must be treated as such by reviewers during the review process and subsequently:

1. If you agree to provide a review, we will send you the following data: author, editor and reviewer contact information, copies of submitted manuscripts and review comments and discussions arising from the review of those manuscripts, which you will handle only for the duration of the peer-review process.

2. You will only act on our written instructions when handling this personal data, you will keep the personal data secure, and not use the personal data for any other purpose than a review for eLife.

3. You will not ask anyone else to carry out this peer review for you, without our prior agreement.

4. You will assist us in allowing data subjects to exercise their rights under data protection laws, if you hold personal data relevant to them. You will also assist us in meeting our data protection obligations in relation to audits, security, notification of data breaches, and data protection impact assessments.

5. You will delete or return (at our choice) the personal data you hold on our behalf once the decision has been completed.

6. You will report any relevant personal data breaches to us immediately, as well as whether you believe our instructions in connection with the personal data infringes applicable laws.

xxxxxxxxxx

Information about Competing Interests:
Editors, reviewers, and potential reviewers are required to fully declare all potential competing interests that could lead them to be positively or negatively disposed towards an article before they agree to edit or review it. Reviewers must recuse themselves if they feel that they are unable to offer an impartial review. Common reasons for editors and reviewers to recuse themselves from the peer-review process include but are not limited to: Working at the same institution or organization as one or more of the authors, currently or recently; Having collaborated with, or served as a mentor to, one or more of the authors during the past 5 years; Having held grants with one or more of the authors, currently or recently; Having a personal relationship with an author that does not allow you to evaluate the manuscript objectively.

xxxxxxxxxx

From: Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]

Attendees: dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]

Location: https://www.zoomgov.com/j/1602664950?pwd= **552.136**

Importance: Normal

Subject: SARS-CoV-2 Variant Testing pipeline

Start Time: Fri 2/12/2021 7:00:00 AM (UTC-06:00)

End Time: Fri 2/12/2021 8:30:00 AM (UTC-06:00)

Required Attendees: dbarouch; Krogan, Nevan; Paul Thomas; stacey schultz-cherry; Post, Diane (NIH/NIAID) [E]; Stemmy, Erik (NIH/NIAID) [E]; Lampley, Rebecca (NIH/NIAID) [C]; stevens@anl.gov; jjdavis@anl.gov; Scheuermann, Richard; Eakin, Ann (NIH/NIAID) [E]; Brown, Liliana (NIH/NIAID) [E]; adam.godzik@ucr.edu; Jason McLellan; btk@lanl.gov; lmwoga@fredhutch.org; monte@duke.edu; spjwhelan@wustl.edu; Suthar, Mehul; Shi, Pei yong; McDermott, Adrian (NIH/VRC) [E]; Florian Krammer; jbloom@fredhutch.org; Julie McElrath; kawaokay@svm.vetmed.wisc.edu; Menachery, Vineet; noah.sather@seattlechildrens.org; Matthew Frieman; mrolland@hivresearch.org; Baric, Ralph; Richard Webby; Garcia-Sastre, Adolfo; malik@hku.hk; Andrew B. Ward; Ali Ellebedy; mdiamond@wustl.edu; djs200@cam.ac.uk; jboon@wustl.edu; Aubree Gordon; stanley-perlman@uiowa.edu; harm.vanbakel@mssm.edu; Graham, Barney (NIH/VRC) [E]; Schmaljohn, Connie (NIH/NIAID) [E]; Munster, Vincent (NIH/NIAID) [E]; Koup, Richard (NIH/VRC) [E]; Seder, Robert (NIH/VRC) [E]; Ghedin, Elodie (NIH/NIAID) [E]; Alessandro Sette; Adam Godzik; Embry, Alan (NIH/NIAID) [E]; Roberts, Chris (NIH/NIAID) [E]; Schotsaert, Michael; MacCannell, Duncan (CDC/DDID/NCEZID/OD); Weiss, Carol (FDA/CBER); Wentworth, David E. (CDC/DDID/NCIRD/ID); Nelson Michael; gregory.d.gromowski.civ@mail.mil; irina.maljkovicberry.ctr@mail.mil; jeffrey.r.currier.civ@mail.mil; Vincent, Leah (NIH/NIAID) [E]

Research Update Template.xlsx

Hello everyone,

Thank you for filling out the poll for times. The time that worked best for most people was **Fridays from 8 am – 9:30am ET.** For those of you who preferred the Friday 8:30am start time due to conflicts, please feel free to join when you can during the meeting.

If you have yet to fill out the capabilities sheet, please do so as soon as you can and send to me and Leah Vincent.

Finally, I wanted to let you all know that multiple B.1.1.7 and B.1.351 viruses are now available on BEI. You can find them here.

Thank you, and looking forward to speaking on Friday February 12th.

Marciela

Marciela DeGrace is inviting you to a scheduled ZoomGov meeting.

Join ZoomGov Meeting
https://www.zoomgov.com/j/1602664950?pwd=552.136

Meeting ID: 160 266 4950
Passcode: 552.136
One tap mobile
+16692545252,,1602664950#,,,,552.136 US (San Jose)
+16468287666,,1602664950#,,,,552.136 US (New York)

Dial by your location
+1 669 254 5252 US (San Jose)
+1 646 828 7666 US (New York)
+1 551 285 1373 US
+1 669 216 1590 US (San Jose)
833 568 8864 US Toll-free
Meeting ID: 160 266 4950
Passcode: 552.136
Find your local number: https://www.zoomgov.com/u/abGJeGuk6u

Join by SIP
1602664950@sip.zoomgov.com

Join by H.323
161.199.138.10 (US West)
161.199.136.10 (US East)
Meeting ID: 160 266 4950
Passcode: 552.136

		Description of resource
Reagents	Variant Virus	B.1.1.7
		B.1.351
		P.1
	Molecular clones	
	Plasmids	
	RG virus	
	Pseudovirus	
	Recombinant protein	
	Sera Panels	

		Description (ms strain, number available, etc.)
Animal Models	Mice	
	Syrian Hamster	
	NHP	

		Description of assay
	Binding	

Assays	Antibody escape	
	Neutralization - pseudovirus	
	Neutralization - live virus	
	In vitro growth	
	Structural Analysis	
	T- cell studies	

		Description of study
Epidemiology	Epidemiology	

		Description of study
Other updates	Other	

SARS-CoV-2 Variant Working Group Template

Studies Planned	Status
-	Deposited in BEI, available in 1-2 weeks
-	Deposited in BEI, available in 1-2 weeks
-	Awaiting agreements from Brazil and Japan

Studies planned	Status of animals (vaccinated, challenged, etc.)

Studies Planned	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Data source (country, etc.)	Resources needed/ potential bottlenecks

Resources needed/potential bottlenecks	Relevant pre-print(s)	

Resources needed/ potential bottlenecks	BLUF Variant Data to date	Relevant pre-print(s)

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

BLUF Variant Data to date	Relevant pre-print(s)	

To: Ksiazek, Thomas G.[tgksiaze@UTMB.EDU]; Holubar, Connie J.[cjholuba@UTMB.EDU]; 'Erdman Dean'[derdman05@gmail.com]; Murphy, Frederick A.[famurphy@UTMB.EDU]; LeDuc, James W.[jwleduc@UTMB.EDU]; Garcia-Blanco, Mariano A.[maragarc@UTMB.EDU]; 'Denison Mark'[mark.denison@vanderbilt.edu]; Shi, Pei yong[peshi@UTMB.EDU]; 'Rollin Pierre'[pierrerollin2019@gmail.com]; 'Tesh Robert'[rbtesh22@gmail.com]; Weaver, Scott[sweaver@UTMB.EDU]; Tseng, Chien-Te K.[sktseng@UTMB.EDU]; Menachery, Vineet[vimenach@UTMB.EDU]; 'Folks Thomas'[Virusdoctom@aol.com]; 'Nichol Stuart'[stn1@CDC.GOV]; 'Spiropoulou Christina (CDC/CCID/NCZVED)'[ccs8@cdc.gov]; Keiser, Philip[phkeiser@UTMB.EDU]; Karl Johnson[microcaddis@gmail.com]; Doug Watts[dwatts2@utep.edu]; Ian Lipkin[wil2001@columbia.edu]
From: calisher@cybersafe.net[calisher@cybersafe.net]
Sent: Sun 4/26/2020 1:14:07 PM (UTC-05:00)
Subject: RE: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Want to weigh something large? Put it on one end of a teeter-totter (a seesaw). Then balance that with a large rock on the other end. Now all you need do is weight the rock.

One way to determine the quality of these newly developed assays is to (a) find someone who knows what the hell they are doing and have them (b) test by MACELISA and IgGelisa, then (c) test by NEUTRALIZATION. Without the latter, I ain't buying it. In the current situation, who cares whether a person has antibody, to SARS-CoV-2, unless that antibody is helpful in determining protection. Jordi Casals and Bob Shope must be turning in their graves.

Now W.H.O. is saying that the presence of antibody is not indicative of protection from a second exposure to SARS-CoV-2. No shit, Sherlock.

Charlie

-----Original Message-----
From: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>
Sent: Saturday, April 25, 2020 10:42 PM
To: Ksiazek, Thomas G. <tgksiaze@UTMB.EDU>; Holubar, Connie J. <cjholuba@UTMB.EDU>; Erdman Dean <derdman05@gmail.com>; Murphy, Frederick A. <famurphy@UTMB.EDU>; LeDuc, James W. <jwleduc@UTMB.EDU>; Garcia-Blanco, Mariano A. <maragarc@UTMB.EDU>; Denison Mark <mark.denison@vanderbilt.edu>; Shi, Pei yong <peshi@UTMB.EDU>; Rollin Pierre <pierrerollin2019@gmail.com>; Tesh Robert <rbtesh22@gmail.com>; Weaver, Scott <sweaver@UTMB.EDU>; Tseng, Chien-Te K. <sktseng@UTMB.EDU>; Menachery, Vineet <vimenach@UTMB.EDU>; Folks Thomas <Virusdoctom@aol.com>; Calisher Charles <calisher@cybersafe.net>; Nichol Stuart <stn1@CDC.GOV>; Spiropoulou Christina (CDC/CCID/NCZVED) <ccs8@cdc.gov>; Keiser, Philip <phkeiser@UTMB.EDU>
Subject: NYTimes: Coronavirus Antibody Tests: Can You Trust the Results?

Coronavirus Antibody Tests: Can You Trust the Results?
https://nam03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.nytimes.com%2F2020%2F04%2F24%2Fhealth%2Fcoronavirus-antibody-tests.html%3Fre&data=02%7C01%7Cjwleduc%40utmb.edu%7C57b0cf1e00424438c5ed08d7ea0d9da4%7C7bef256d85db4526a72d31aea2546852%7C0%7C0%7C637235216507255047&sdata=VTrng%2B5qkZsTyex9oUJRkv90Rga4pUPzV2nldzbYYIc%3D&reserved=0

ferringSource=articleShare

Tom Ksiazek

Sent from a portable device

To: Benjamin Rusek (BRusek@nas.edu)[BRusek@nas.edu]; Dave Franz (davidrfranz@gmail.com)[davidrfranz@gmail.com]; Yuan Zhiming[yzm@wh.iov.cn]; George F GAO[gaof@im.ac.cn]; Mifang Liang[mifangl@hotmail.com]; Shi, Pei yong[peshi@UTMB.EDU]
From: LeDuc, James W.[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=937DF08E29C4439E88A04BABFFB162AD-JWLEDUC]
Sent: Tue 1/21/2020 4:33:54 PM (UTC-06:00)
Subject: Op Ed in Houston Chronicle
Chinese Response to New Virus_Le Duc 21Jan revised.docx

Ben, Dave, Zhiming, George, Mifang and Pei-Yong

The attached, slightly modified to include mention of the new case in Washington State, is scheduled to appear in Wednesday 22 Jan's Houston Chronicle. Note mention of the NASEM/CAS collaborations.

Just FYI,

Jim

James W. Le Duc, Ph.D.
Director
Galveston National Laboratory
University of Texas Medical Branch
Galveston, TX 77555-0610
(t) 409-266-6500
(f) 409-266-6810
(m) 409-789-2012

Chinese Response to New Virus: Good News/Bad News

By James W. Le Duc

Fast action and open communications by China is helping the world prepare for another potentially devastating infectious disease outbreak. While the situation is rapidly evolving, there is good news that may not make the headlines. Many will recall the dark days in the spring of 2003 when Asia and the world were threatened by the appearance of a new virus disease, Severe Acute Respiratory Syndrome, or SARS, which first appeared in southern China and quickly spread to other countries around the world, ultimately causing over 8000 cases with nearly 10% of those ending in death. SARS was caused by a novel coronavirus then unknown to medical science. There was no known cure, no diagnostic tests and little understanding of where it came from or how it was spread, although person-to-person transmission was obvious as health care workers treating the first cases were themselves among the early victims. Initially, China was reluctant to share information or alert the international community of the magnitude of the epidemic, leading to international criticism and a dangerous global health situation. Fortunately, China reversed its position, opened to collaborations with the WHO, U.S. and others, and the epidemic was eventually controlled.

Today, with another novel coronavirus discovered in China, the start is very different. In quick measure, Chinese health officials recognized that a new disease had emerged, quickly isolated patients, and instituted an impressive set of interventions in attempts to limit disease spread and characterize the new pathogen. Importantly, they have been transparent in sharing their findings with the world, thus allowing other nations to take precautions and be on the lookout for the new disease. Already, the genome of the new virus was sequenced and posted for easy access by international experts, allowing rapid exploration of possible treatments, development of diagnostics and epidemiological investigations.

China's ability to respond quickly and efficiently to this new threat is the result of nearly two decades of investments and collaborations to improve public health in China. The Chinese Centers for Disease Control incorporates many of the strengths of our own CDC, but is designed to meet the needs of a 1.4 billion plus population. In addition, China has invested in building a robust scientific capacity and partnered with containment laboratories such as ours to incorporate best practices when studying dangerous pathogens.

The current outbreak demonstrates a welcome openness to health information sharing with the global community. To diagnose an outbreak early requires astute healthcare providers able to recognize when something new or unusual is occurring; however, clinical recognition alone is meaningless if there is no capacity to investigate cases or characterize the disease-causing agent.

For the last few years, our National Academy of Science, Engineering and Medicine has worked with the Chinese Academy of Sciences to build relationships and share information on emerging diseases and advancements in vaccines and treatments. In Galveston, we welcomed leading Chinese health officials to collaborate on biocontainment facility design, biosafety training and laboratory operations. This dialogue, along with U.S.-based educational opportunities for Chinese students, benefit us all.

China's response to the new coronavirus demonstrates their investments in physical laboratories and scientific collaborations over the past decade are paying dividends, not only to China, but the entire world. Control of a new disease efficiently transmitted person-to-person is nearly impossible as we witnessed during the 2009 novel influenza pandemic and much must still be done together during this quickly evolving situation.

The outbreak is still in the early stages, but it is now clear that the new virus may be transmitted person-to-person, although the efficiency of such transmission remains in question. A few hundred patients have been identified, deaths occurred and the disease has spread from the epicenter in Wuhan to major cities in China and other Asian countries. Our CDC is now screening travelers arriving from Wuhan at U.S. airports, and the WHO is set to consider a global emergency response. With millions about to travel for the Chinese New Year, avoiding a global catastrophe must be the current goal.

The good news is that, at a time when US-China relations are being tested on many fronts, relations within the public health and scientific research arenas remain open and positive, which lays a solid foundation for curtailing this latest threat.

James Le Duc, PhD, is the Director of the Galveston National Laboratory at the University of Texas Medical Branch and a professor in UTMB's Department of Microbiology and Immunology.

705 words in body