

**To:** (b) (6) DOE HQ USA GOV <(b) (6)>; (b) (6) DOE HQ USA GOV  
<(b) (6)>  
**Cc:** (b) (6) DOE HQ USA GOV <(b) (6)>  
**Subject:** LANL Comments on Furin Paper

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(b) (6) ,

The following are (b) (6) comments on the Furin paper. (b) (5)

(b) (5), (b) (6) (b) (5)

Let me know if you think I  
should take a different course of action.

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(U) (b) (5)

[REDACTED]

(b) (1) (A)

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

(b) (1) (A)

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

(U) Even the recent Eddie Holmes et al. paper claiming "critical review" has (at least in the preprint stage) some quantification of the prevalence of CGG codons in CoV genomes. (b) (1) (A)

[REDACTED]

[REDACTED]

[REDACTED]

[REDACTED]

(U) It is vital to note here that Boni (and less stringently the Korber, Georgi, et al. paper) indicate no recent recombination with non-sarbecoviruses in SARS-CoV-2's recent genetic history. (b) (1) (A)

[REDACTED]

(b) (1) (A)

(b) (1) (A)

(U) Re: the small alignment in the memo:

1. (U) There is lots of evidence for recombination in the SARS-CoV-2 genome, for instance the ZXC21/ZC45 sequences and probably other sarbecoviruses; however this snippet of a sequence alignment gives no indication that HKU1 and OC43 are *very distantly* related to SARS-CoV-2 in comparison with RaTG13 and ZXC21/ZC45. The omission of flanking sequence seems either a large mistake or *disingenuous*
2. (U) We strongly appreciate that post-pandemic CoV sequences are not in in the alignment.

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