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So this is a sequence with 8782T, 18060T, 28144C and 29095T.

[academic.oup.com/bioinformatics...](https://academic.oup.com/bioinformatics...)

Note that 29095T is another site that is conserved in all other Sarbecoviruses. This is a descendent of an lineage that is even earlier than

<https://www.ncbi.nlm.nih.gov/nuccore/MT628174.1?report=GenBank><https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&RID=638ZU415114><https://academic.oup.com/bioinformatics/advance-article/doi/10.1093/bioinformatics/btac186/6553661>

USA-WA-1, or Guangdong-HKU/SZ. This may be what TopHap talked about for the “one more mutation earlier into the progenitor of SARS-CoV-2”.

Left:29095. Right:18060. Both are against all other Sarbecoviruses.

Now this is two solid mutations further from lineage A at the lineage A/ lineage B divergence point, 4 from the (verified) Huanan market sequences. Late sampling mean some orthogonal mutations have accumulated, but it diverged before the 29095 mutated on WA-1 or the 18060 mutated

On Guangzhou/HKU-SZ. Note that 29095T is also seen in the deleted dataset of the Renmin hospital of Wuhan university (Wuchang).

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Another one in the same cluster!

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[ncbi.nlm.nih.gov/pmc/articles/P...](https://ncbi.nlm.nih.gov/pmc/articles/P...) Note that the 2 nsp13 mutations there are recurrent—it actually recurred to the G614(B.1) lineage genomes as well. In contrast none of the 4 ancestral sites are recurrent across year 2020.



**Infectivity of SARS-CoV-2: there Is Something More than D614G?**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7490321/#!po=18.4211>

They are located on the RNA binding surface of the nsp13 protein and appears to confer some resistance to a human RNA-binding immune protein. Confers the most advantage when 18060 is a T.

[trace.ncbi.nlm.nih.gov/Traces/sra/?ru...](https://trace.ncbi.nlm.nih.gov/Traces/sra/?ru...)

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29095T is found in SRR11278166 at 10x above noise background. This is USA-WA16/UW12.

compared to SRR11278167 or USA-WA15/UW11 where there is little to no T in 29095.

If you recall the article where this come from,



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These SRA datasets contained fractions that lacked the v1 and v2 mutations. This indicate that some of the 29095T positions are already present in the quasispecies as a minor fraction in the USA/WA cluster.

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[ncbi.nlm.nih.gov/biosample/SAMN...](https://ncbi.nlm.nih.gov/biosample/SAMN...)

[trace.ncbi.nlm.nih.gov/Traces/sra/?ru...](https://trace.ncbi.nlm.nih.gov/Traces/sra/?ru...)

And look at that. P4 stock of WA1 derived from ATCC P3 (but not their own P4 which have been plaque purified) stock gives approximately 10x noise level and about 1/1000 in the quasispecies of 29095T. Which confirms that the



<https://www.ncbi.nlm.nih.gov/biosample/SAMN14384141>



<https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR11393704>

Ancestral strain without v1-v2 is found in the U.S at the quasispecies level at time of sampling.

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May 4

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@BiophysicsFL [archive.ph/dsJ15](https://archive.ph/dsJ15) FCS that can't survive in a reservoir or reinfect in the presence of an immune system especially for D614, [archive.ph/TrTW5](https://archive.ph/TrTW5) VERO E6-specific HV6970, [zenodo.org/record/5702700...](https://zenodo.org/record/5702700...) [archive.ph/yXjt4](https://archive.ph/yXjt4) Dishonesty by main players in the virology field

@BiophysicsFL Especially shi, [archive.ph/0JvfP](https://archive.ph/0JvfP) [researchgate.net/publication/35...](https://researchgate.net/publication/35...) Evidence of circulation before Huanan being covered up, [archive.ph/dmOXT](https://archive.ph/dmOXT) [archive.ph/VXtu9](https://archive.ph/VXtu9)

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May 4

@R\_H\_Ebright

@R\_H\_Ebright

@R\_H\_Ebright [archive.ph/DJwOj](https://archive.ph/DJwOj) Seems to be too much pressure for at least some of them to continue defending GOF as “useful and safe”?

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which is by default without any pre-adaptation.

Also, propaganda pieces are propaganda pieces. The Chinese researchers working for EHA and Shi don't wear PPE when catching bats.

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May 2

The BSL-4 training lab and the outskirts of the BSL-4 jiangxia facility is what they were allowed to look into, alongside with an interview of Shi for her oral statement.

[archive.ph/FEgLQ](#) None of the experiments ongoing or previous, the lab books, the databanks or the vast archive of “more than 1500 strains of virus” were made available to the WHO team. [archive.ph/0JvfP](#) As for their bank of “22000+ viruses”? Daszak claimed to have

“Not asked for it”. [archive.ph/dx9dc](#)

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May 1

[journals.asm.org/doi/10.1128/mB...](#) [vox.com/platform/amp/f...](#) Just going to say that reality trumps arguments of safety based on the idealized, best-case scenario of everything working exactly as according to the WHO “biosafety planning standards” without any [archive.ph/iO5sh](#)

real-world imperfections or shortcomings that are typical to that of the Wuhan institute of virology or any Chinese labs. Or an unexpectedly transmissible virus that was only ever tested in cell culture before. [sciencedirect.com/topics/biochem...](#)

[archive.ph/2AOgn](#)

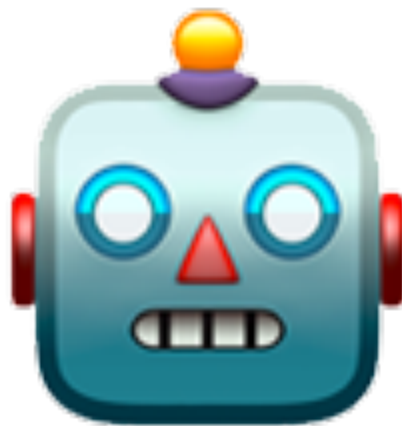
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