

## **Proof that the SARS-CoV-2 coronavirus is a man-made, genetically-modified virus, and NOT the result of a natural mutation.**

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In the very early days of the coronavirus making the news (late January 2020), a study was pre-published (awaiting official publishing and peer-review) which suggested that the coronavirus may be man-made (*Pradhan et al. 2020*). The authors of the study performed an analysis of the genome of the virus, and found it was mostly based on the 2002 SARS virus, but also allegedly found to have 4x insertions of the HIV virus in its genetic code. Such genetic differences could not have happened naturally. This caused a major stir at the time, and the scientists were criticised as perhaps mocking the seriousness of the new epidemic (as a pandemic hadn't been announced at that time), and the authors of the study withdrew it from publishing due to pressure from the scientific community. The authors intended to revise the study and perhaps republish it.

Many rumours and debates have persisted as to the origins of the virus - did it come from bats or another animal, how did it cross over into humans, and was this a natural process or man-made?

A few months have passed and more studies have been published on many aspects of the coronavirus. The official line from the WHO and our governments is that the coronavirus was a natural development or mutation, from a still-unknown animal source, and some studies have published these findings.

But governments and their agencies lie. They all do. All the time.

I've not believed a lot of the scary information in the media since day 1 of this infection. I've looked into the statistics of it and why they do not make any sense and cannot be believed. The testing of the virus is questionable and inaccurate, and the classification of deaths is a rort - a process recommended by the WHO to falsely inflate death rates, which has so many people unnecessarily scared of this virus, leading to politicians making disruptive and damaging policy changes which have affected us all. For what intents and purposes we still do not fully understand, but a lot of things in this pandemic stink of untruths. Especially on the issue of whether the virus is man-made or not.

A pivotal new study was published in the prestigious *Nature Medicine* journal (*Andersen et al., 2020*). The authors investigated the genetic code of a key part of the coronavirus and compared this to other known coronaviruses, to come to a conclusion that the new coronavirus was a natural mutation from one of several possible animal sources, of which

still has not been identified. Their conclusion was pretty definitive. Except their conclusion and theories were not supported by their own results, but it helped negate many "conspiracy-theory" social media posts and instead supported the narrative of the media and governments and their health departments.

The following figure from the Andersen study clearly shows the genetic code differences between the different animal coronavirus types and the 2002 SARS coronavirus too. The marked and different coloured areas show the genetic differences. A major problem with the scientists' conclusions is the INSERTION of a 12-nucleotide section in the "Human-SARS-CoV-2" coronavirus sequence (notes with a star in the figure) which is COMPLETELY MISSING from every other coronavirus type known. Such a large genetic difference cannot happen randomly or naturally. It's not even in the alleged bat coronavirus as the source of this pandemic. The coronavirus didn't come from bats. Such an insertion can only come from a lab.

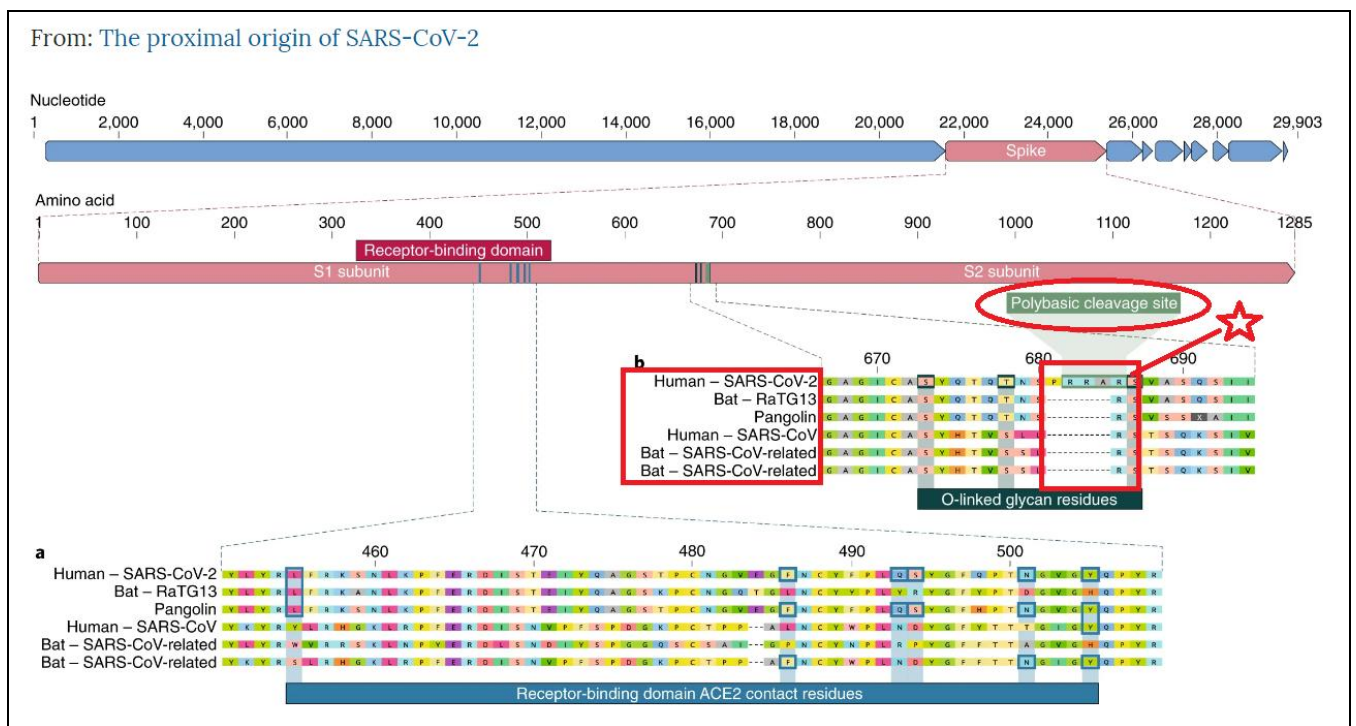


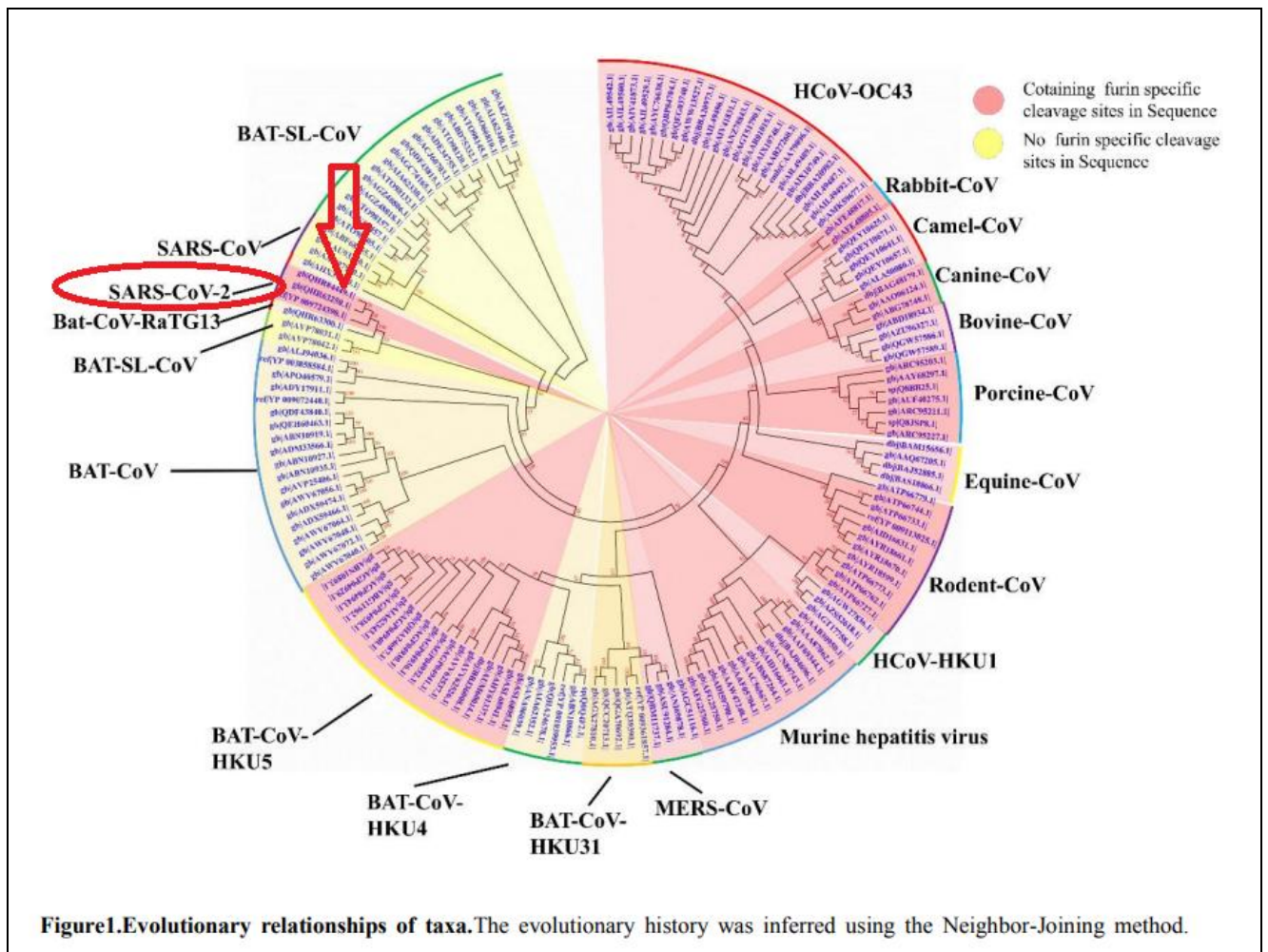
Figure 1 - Comparison of coronavirus types and genetic differences (Andersen et al., 2020)

The scientists claim the impact of this inserted sequence is unknown but that it appears to enhance infection in human cells. But they still claim that the virus is of natural origin!

The details of one study is not be enough proof to make an assertion that the coronavirus is man-made...

In a another recent pre-published study (*Wu et al., 2020*), the scientists compared the genetic code of the new coronavirus with the earlier SARS and MERS pandemic viruses, and a bat coronavirus too. They also looked at the equivalent of the genetic family tree of the coronavirus, with respect to a major component of the virus - its spike protein that is used to attach to and infect a cell. It was found that the coronavirus was closest to the 2002 SARS

virus and the bat coronavirus, with some major differences. Some minor mutations were found to exist between the current coronavirus and SARS coronavirus, and the virus binds more strongly to ACE-2 receptors (and other receptors) on human cells than SARS, hence why it can infect more people. See the phylogenetic tree diagram below.



**Figure 2 - Phylogenetic tree diagram of the coronavirus family (Wu et al., 2020)**

The phylogenetic tree diagram (a genetic evolutionary family tree) for the coronaviruses starts in the 12 o'clock position and progresses clockwise to newer generations of coronaviruses. Notice that the new coronavirus (SARS-CoV-2) is more recent. Early coronaviruses are highlighted in pink, as containing a particular location or sequence, called a "furin cleavage site", in its spike protein. The furin cleavage site disappeared several generations ago in the coronavirus family tree, but somehow magically reappears again in this new coronavirus genetic code. The ACE-2 and furin binding sites on cells throughout the body (not just in the lungs) increases the infection of this virus throughout the body to affect more organs as has been seen. This study also noted the addition of the same 12-nucleotide section of genetic code noted in the previous study that was missing from other coronavirus strains. This insertion is thought to be a reason why this virus is stronger than SARS. The study also found and recommended many medications, nutrients and herbals which would be effective against the furin site of the virus - including 4 HIV medications which is significant given the earlier finding of the alleged HIV insertions in the coronavirus

genetic code. The WHO have announced trials of HIV drugs to determine their effectiveness against this virus (*Kupferschmidt & Cohen, 2020*).

The above finding of the coronavirus specifically using the ACE-2 receptors on cell walls to infect cells is very important. Several studies have been published in recent years by scientists performing genetic modification on the SARS coronavirus and others, and even creating a chimera virus - containing genes from multiple viruses, even from different animals. In one such study by *Menachery et al. (2015)*, genes from a bat coronavirus spike protein were added to a mouse coronavirus genome and tested for its ability to infect human airway cells through their ACE-2 receptors. The man-made virus was tested in mice AND HUMANS with significant infections occurring. The study concluded that there was "a significant risk of a SARS coronavirus re-emergence". The fact that scientists are deliberately manipulating (ie, "playing with") the genetics of deadly viruses, and testing them for their ability to cause human disease, is a major concern.

This study included a Chinese Virologist, Shi Zhengli (or Zheng-Li Shi), who just happens to be the team leader of the researchers in the Wuhan Institute of Virology, a BSL-4 biowarfare lab where this study was conducted, just a few miles from the alleged epicentre of the pandemic in the Wuhan seafood market... And the study was funded by the National Institutes of Health (NIH), a US government agency.

The Chinese virologist and world expert on bat coronaviruses, Shi Zhengli, has been a part of several other published studies on coronavirus research. In another study published in 2008, Shi Zhengli and colleagues created new chimera coronavirus by "**inserting** different genetic sequences of the SARS coronavirus into different animal coronaviruses", to investigate how well the man-made virus could infect the ACE-2 receptors of human and animal cells (*Ren et al., 2008*). They found that the chimeric virus initially didn't infect human cells, so the scientists then combined a human HIV virus with it, which then DID enable it to infect human cells. Their work was to deliberately get the genetically modified virus to infect human cells. The authors wrote that this was the first time that a virus was proven to cross over from animals into humans - but was only done through deliberate genetic modification in a lab (in Wuhan).

The above studies compared a bat coronavirus to the new virus, and found a high genetic similarity of up to 96% (*Xiao and Xiao, 2020*), but more importantly are the **differences**. The bat coronavirus lacks the furin binding site, and lacks the huge gene insertion that is responsible for its infective ability in humans. According to testimonies by local Wuhan residents and those who frequented the seafood market, the bats which were found to host the bat coronavirus lived 900 kilometres away in caves, and bat was NOT traded or ever a food source in the Wuhan market (*Xiao and Xiao, 2020*).

The National Institutes of Health (NIH) have an online tool called BLAST (*NIH, 2020*) for logging, comparing and researching the genetic code of organisms. After my earlier research articles on the coronavirus topic when I questioned the government and media narrative, a follower sent me details on how to use the BLAST tool to check on the genetic code of the

SARS-CoV-2 coronavirus for similarities with the genetic code of other viruses. Using the BLAST tool, it reported 4 similar gene sequences in the coronavirus that matched other viruses - or more accurately, 4 matching gene sequences from 1 other virus. **The Human Immunodeficiency Virus, HIV type 1**. See the results in the following figure.

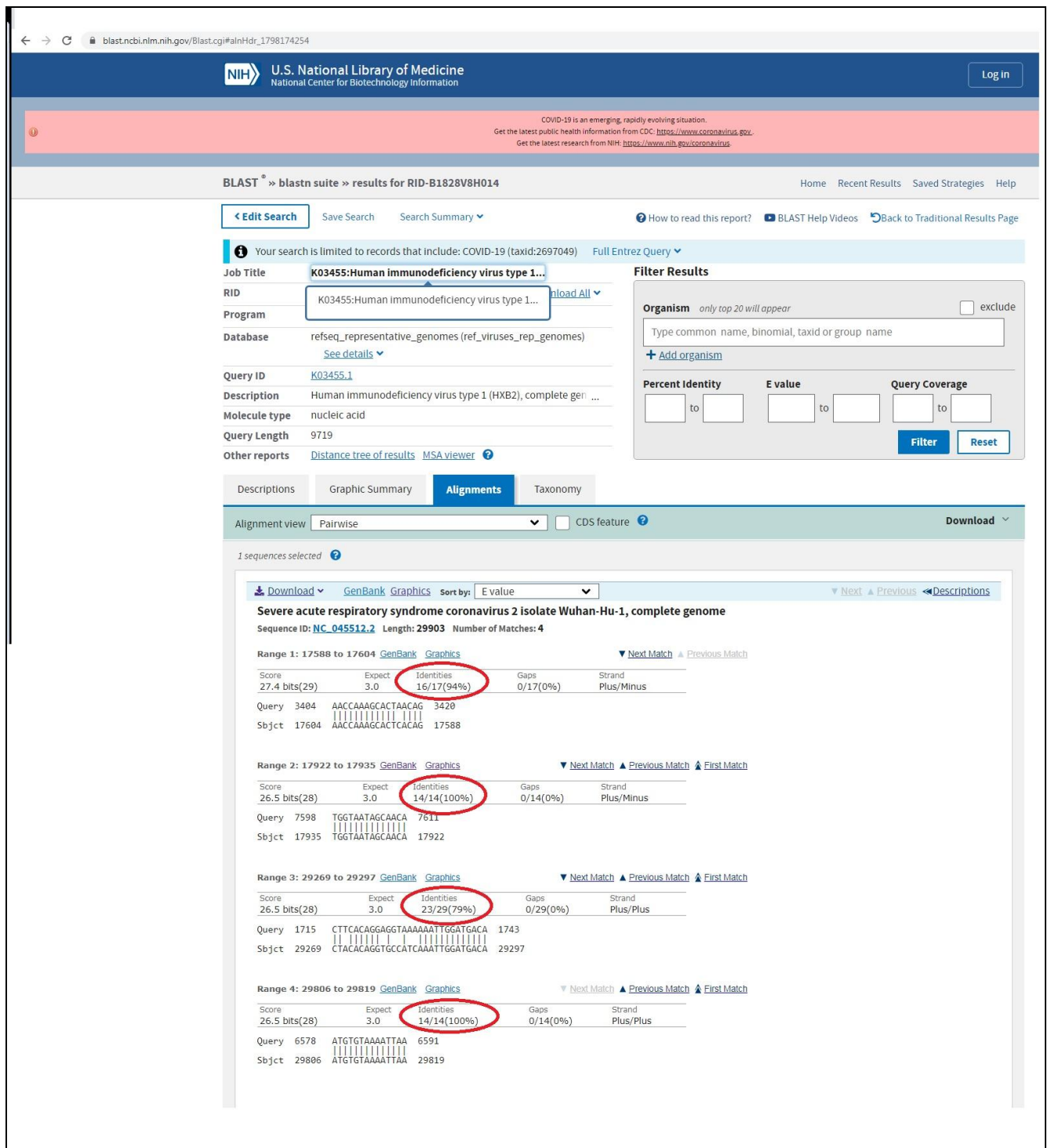


Figure 3 - BLAST results for SARS-CoV-2 (NIH, 2020)

Two of the 4 HIV sequences in the SARS-CoV-2 virus code matched 100%, one matched at 94%, and another at 79%, still being very significant. See screenshot for results. This finding does seem to confirm the finding in the original study by Pradhan and colleagues (2020), and confirm the study by Ren, Shi Zhengli and colleagues that they inserted HIV genes into a

genetically-modified SARS virus to increase its ability to infect human cells. Somehow, somewhere and by someone, accidentally or deliberately we cannot determine at this time, this genetically-modified lab-made chimeric virus escaped into the wild to infect humans. It is almost beyond any possibility that the current coronavirus was a natural mutation and animal crossover event.

Is there evidence of knowledge and technology for scientists to CREATE a virus - YES.

Is there evidence of the SARS and other animal coronaviruses being genetically modified - YES.

Is there evidence of deliberate experimentation of coronaviruses to increase their ability to infect human cells - YES.

Is there evidence of the HIV virus being used in coronavirus experiments and being found in people infected with coronavirus - YES.

Is there evidence that the coronavirus was the result of a natural mutation and crossover into humans - based on these studies and evidence, it is highly unlikely at best. I'd say NO.

Based on the evidence here, this would lead to an uncomfortable conclusion that the coronavirus is not a natural mutation of any known coronavirus strain, but in fact a man-made strain. And if it is indeed man-made, as it appears, then more uncomfortable questions need to be asked - was it released accidentally or deliberately, by whom, and for what purposes?

There have been a lot of theories labelled as "conspiracies" in this pandemic. As more evidence is found, more of those conspiracies are becoming fact.

If the virus is man-made, then anything which comes afterwards, in the form of new laws, restrictions, recommendations and mandates, must seriously be questioned and stopped.

An independent worldwide and open investigation MUST be conducted NOW to find out who is responsible for this pandemic - how the man-made coronavirus escaped from a lab, why, and for what or whose benefit. This cannot be conducted by the WHO, UN, CDC, FDA or other government or world health agencies as they are already suspiciously involved in this pandemic or involved in the suppression of scientific studies or educated voices who have questioned their actions (or lack thereof) in recent times.

Also, the genetic modification of all infective viruses and bacteria MUST STOP NOW. These dangerous practices cannot be allowed to happen again.

(Full references provided below)

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## References:

- Andersen, K.G., Rambaut, A., Lipkin, W.I., Holmes, E.C., & Garry, R.F. (2020). The proximal origin of SARS-CoV-2. *Nature Medicine*, 26, 450–452. Doi: 10.1038/s41591-020-0820-9
- Kupferschmidt, K., & Cohen, J. (2020). WHO launches global megatrial of the four most promising coronavirus treatments. *Science Magazine*. Retrieved 14th May 2020 from <https://www.sciencemag.org/news/2020/03/who-launches-global-megatrial-four-most-promising-coronavirus-treatments>
- Menachery, V.D., Yount, B.L Jr, Debbink, K., Agnihothram, S., Gralinski, L.E., Plante, J.A., Graham, R.L., Scobey, T., Ge, X-Y., Donaldson, E.F., Randell, S.H., Lanzavecchia, A., Marasco, W.A., Shi, Z-L., & Baric, R.S. (2015). A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nature Medicine*, 21, 1508–1513. Doi: 10.1038/nm.3985
- National Institutes of Health (NIH). (2020). Basic *Local Alignment Search Tool (BLAST)*. Retrieved 10th May 2020 from <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- Pradhan, P., Pandey, A.K., Mishra, A., Gupta, P., Tripathi, P.K., Menon, M.B., Gomes, J., Vivekanandan, P., & Kundu, B. (2020). Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag. *BioRxiv (preprint)*. Doi: 10.1101/2020.01.30.927871
- Ren, W., Qu, X., Li, W., Han, Z., Yu, M., Zhou, P., Zhang, S-Y., Wang, L-F., Deng, H., & Shi, Z. (2008). Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin. *Journal of Virology*, 82 (4), 1899-1907: doi:10.1128/JVI.01085-07
- Wu, C., Yang, Y., Liu, Y., Zhang, P., Wang, Y., Wang, Q., Xu, Y., Li, M., Zheng, M., Chen, L., & Li, H. (2020). *Furin, a potential therapeutic target for COVID-19*. Retrieved 14th May 2020 from <http://chinaxiv.org/user/download.htm?id=30223>
- Xiao, B., & Xiao, L. (2020). The possible origins of 2019-nCoV coronavirus. Retrieved 14th May 2020 from <https://web.archive.org/web/20200214144447/https://www.researchgate.net/publication/339070128> [The possible origins of 2019-nCoV coronavirus](https://www.researchgate.net/publication/339070128)