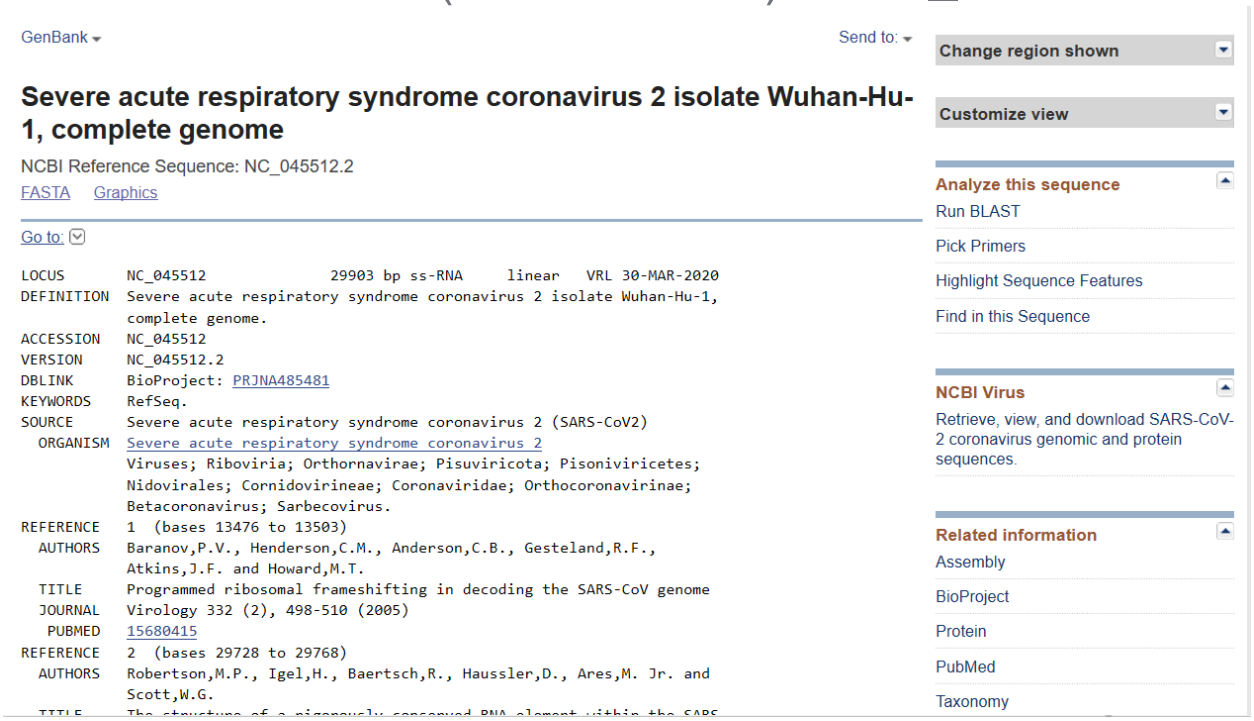
SARS CoV-2 ENVELOPE GLYCOPROTEIN SEQUENCE HOMOLOGY WITH HUMAN IMMUNODEFICIENCY VIRUS (HIV) + ROLES OF REV & TAT PROTEINS.

The Genbank reference sequence number for the novel coronavirus (SARS-CoV-2) is **NC_045512.2**



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Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

NCBI Reference Sequence: NC_045512.2

FASTA Graphics

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LOCUS       NC_045512              29903 bp ss-RNA     linear   VRL 30-MAR-2020
DEFINITION  Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1,
            complete genome.
ACCESSION   NC_045512
VERSION     NC_045512.2
DBLINK      BioProject: PRJNA485481
KEYWORDS    RefSeq.
SOURCE      Severe acute respiratory syndrome coronavirus 2 (SARS-CoV2)
  ORGANISM  Severe acute respiratory syndrome coronavirus 2
            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
            Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae;
            Betacoronavirus; Sarbecovirus.
REFERENCE   1  (bases 13476 to 13503)
  AUTHORS   Baranov,P.V., Henderson,C.M., Anderson,C.B., Gesteland,R.F.,
            Atkins,J.F. and Howard,M.T.
  TITLE     Programmed ribosomal frameshifting in decoding the SARS-CoV genome
  JOURNAL   Virology 332 (2), 498-510 (2005)
   PUBMED   15680415
REFERENCE   2  (bases 29728 to 29768)
  AUTHORS   Robertson,M.P., Igel,H., Baertsch,R., Haussler,D., Ares,M. Jr. and
            Scott,W.G.
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NCBI Virus

Retrieve, view, and download SARS-CoV-2 coronavirus genomic and protein sequences.

Related information

Assembly

BioProject

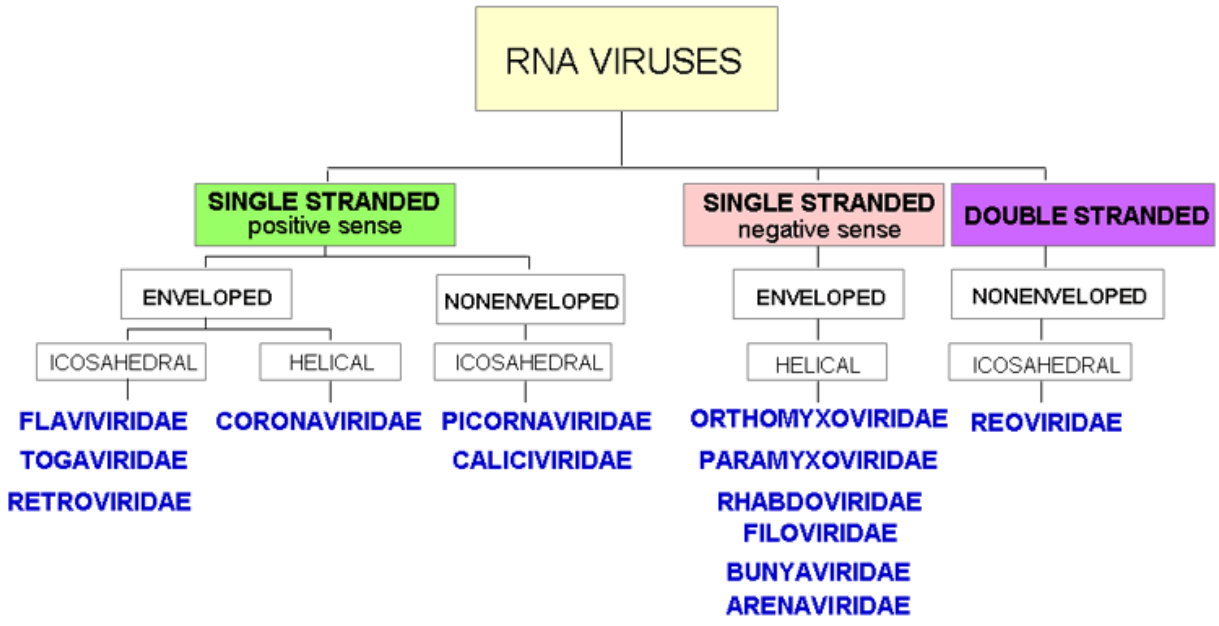
Protein

PubMed

Taxonomy

When running a BLAST (basic local alignment search tool) to find a SARS CoV-2 sequence homology within other referenced viruses (such as the coronaviruses involved in pneumonia, SARS, MERS, etc) this program is able to find sequence similarities in ALL families of viruses, especially between different RNA viruses, of which coronavirus is one, as they are inherently different than their

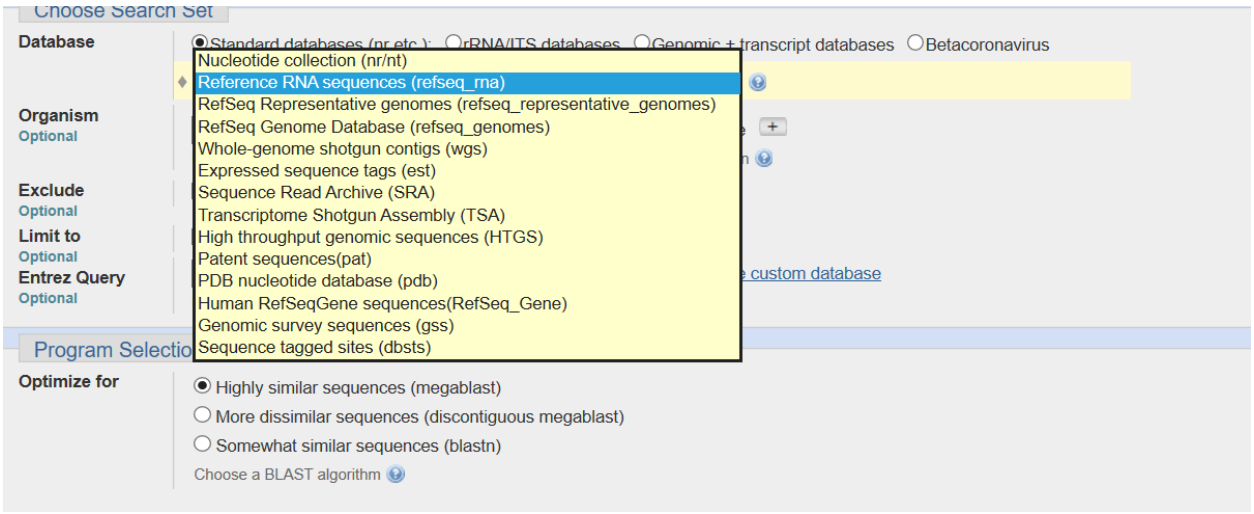
DNA-based (purported) ancestral derivatives or cousins. It just so happens that the HIV virus is also an RNA-based virus, and thus, through referencing RNA sequences individually with a BLAST tool, we are able to determine which parts of its genome would have been genetically borrowed and inserted into its DNA from that of the HIV virus, again using cutting-edge molecular machinery that puts even CRISPR to shame.

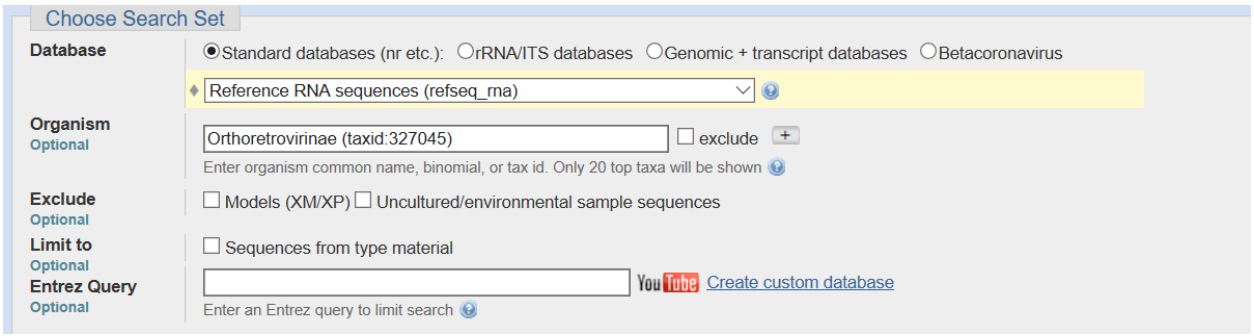


Modified from Volk et al., Essentials of Medical Microbiology, 4th Ed. 1991

Thus, it would be remarkably simple, with respect to the gene-editing tools (i.e. CRISPR and other protein constructing and editing factories) and other

molecular machinery at the disposal of the industries involved, to selectively impart phenotypic viral characteristics in bio-weaponized chimeras such as is the case with SARS CoV-2 through genotypic reconstruction/alteration. This is also yet another case for the argument that the novel coronavirus could not have come into existence by natural means. HIV is in the lentivirirus genus and retrovirus family, and as shown by the viral phylogeny above, they are significantly more closely related to coronaviruses than to other DNA viruses, differing mainly in their viral envelope symmetries, but this crucial difference is what ultimately makes their possibility of cross-linkage mutations or antigenic-drift nearly impossible.





Eight different viruses were identified by the BLAST tool as containing similar sequences to those in the SARS CoV-2 genome. The main homology exists in the viral envelope glycoprotein gene. This is interestingly the only striking difference between the two virus families and yet, it indicates that the novel coronavirus is the **only** of its kind and in its family, genus, and order to possibly contain an **icosahedral** envelope geometry, and if not, to bear one strikingly different from its close relatives.

Sequences producing significant alignments Download Manage Columns Show 100

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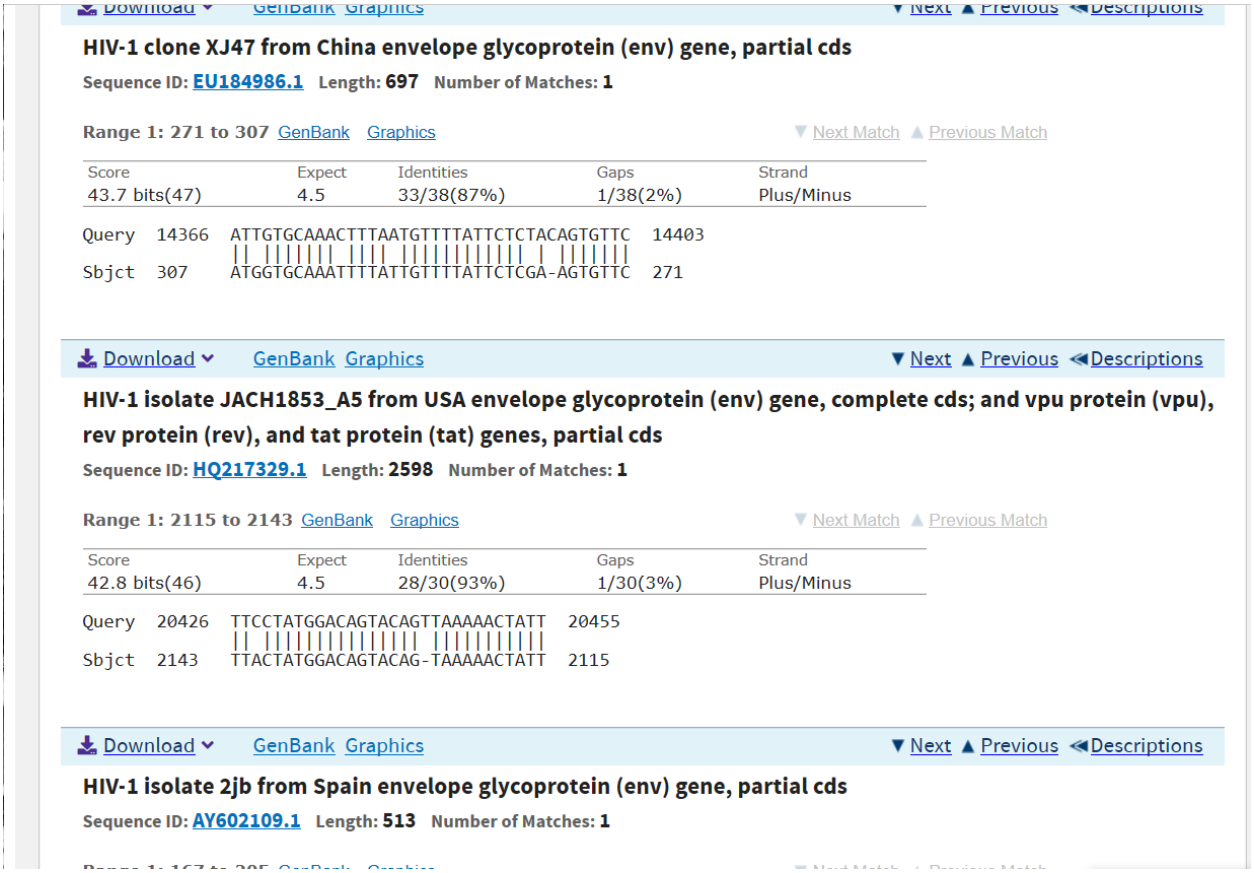
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
HIV-1 isolate XJ16-6 envelope glycoprotein (env) gene, complete cds	43.7	43.7	0%	4.5	86.84%	HQ326133.1
HIV-1 clone XJ47 from China envelope glycoprotein (env) gene, partial cds	43.7	43.7	0%	4.5	86.84%	EU184986.1
HIV-1 isolate JACH1853_A5 from USA envelope glycoprotein (env) gene, complete cds; and vpu prc	42.8	42.8	0%	4.5	93.33%	HQ217329.1
HIV-1 isolate 2jb from Spain envelope glycoprotein (env) gene, partial cds	42.8	42.8	0%	4.5	85.00%	AY602109.1
HIV-1 isolate 1jf from Spain envelope glycoprotein (env) gene, partial cds	42.8	42.8	0%	4.5	85.00%	AY602108.1
HIV-1 isolate 3jg from Spain envelope glycoprotein (env) gene, partial cds	42.8	42.8	0%	4.5	85.00%	AY602107.1
HIV-1 isolate 1ja from Spain envelope glycoprotein (env) gene, partial cds	42.8	42.8	0%	4.5	85.00%	AY602104.1
HIV-1 isolate C113 from Zimbabwe envelope glycoprotein (env) gene, partial cds	42.8	42.8	0%	4.5	88.57%	AF310652.1

This is truly a chimera.
What is it about the HIV virus that renders it so persistent and adaptable to our adaptive immune response? Could it be its icosahedral envelope geometry? Does it render macrophages or other lymphocytes useless due to its irregular shape? Does it evade detection by such immune cells due to its highly transient crystal envelope symmetry or rapid mutations?



Comparing the **Query** to the **Subject** we find a strong similarity in the envelope glycoprotein genes as discussed above yet also interestingly a partial similarity in the rev and tat proteins, which are also crucially important in the lentivirus (HIV) family mechanism of aggressive viral RNA transcription and consequently, replication. The **rev** protein works in the nucleus of the infected cell to regulate export of mRNA to be fully spliced and used in the production of viral structural proteins. The **tat** protein not only drastically enhances the efficiency of viral transcription, but is has also as of recently been

implicated in the pathogenesis of many HIV-related complications.

It is no surprise then that these two proteins would be included in the mad-scientist experiment that is this novel respiratory virus. The worst part; it is all so that a tyrannical government can attempt to impose mandates that violate the rights bestowed upon us by divine creation. The “solution” for this plannedemic is, as many of you are aware, an RFID microchip hypodermically adminstered through the vaccine, which will also as always be laden with heavy metals and other toxins which have been proven by hundreds of peer-reviewed studies to cause neurodegenerative disorders among literally hundreds of other illnesses.

Share the information herein with your loved ones and warn them about the mark of the beast; the microsoft-patented W02020060606 microchip vaccine (world order 2020 666) employing the luciferase enzyme… and planned to be forcibly imposed on us through house resolution #6666… it could not get any clearer.. except for the fact that its being funded and promoted by the literal gates of hell himself. The one that has told us countless times that population control and ‘producing childhood death’ is essential.

All of these indications matter not, as those who are ready to open their eyes will have the strength to open their mind for long enough to carry out independent research. There are millions of us by now, stay the course my beloved brothers and sisters.