

A dummy's guide to using the NIH
database to evaluate homology
between HIV and SARS-CoV-2

This power point is based in part on instructions provided in this substack article by Dr. Syed

Arkmedic's blog

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Absolute proof: The Gp-120 sequences prove beyond all doubt that "COVID-19" was man-made

The "missing link" was there in Pradhan's paper all along, we just needed to ask the right question: "where are the genome sequences for the Gp-120 inserts"



Dr Ah Kahn Syed

Apr 10

♡ 98 💬 78 ↗

https://arkmedic.substack.com/p/absolute-proof-the-gp-120-sequences?utm_source=%2Fprofile%2F41910983-dr-ah-kahn-syed&utm_medium=reader2&s=r

You will be evaluating the following sequences from a preprint previously posted on BioRxiv

Motifs	Virus Glycoprotein	Motif Alignment	HIV protein and Variable region	HIV Genome Source Country/subtype	Number of Polar Residues	Total Charge	pI Value
Insert 1	2019- nCoV (GP) HIV1(GP120)	71 76 TNGTKR TNGTKR 404 409	gp120- V4	Thailand */ CRF01_1 AE	5 5	2 2	11 11
Insert 2	2019- nCoV (GP) HIV1(GP120)	145 150 HKNNKS HKNNKS 462 467	gp120- V5	Kenya*/ G	6 6	2 2	10 10
Insert 3	2019- nCoV (GP) HIV1(GP120)	245 256 RSYL----TPGDSSSG RTYL FNET TRGNSSSG 136 150	gp120- V1	India*/C	8 10	2 1	10.84 8.75
Insert 4	2019- nCoV (Poly P) HIV1(gag)	676 684 QTNS-----PRRA QTNS SILMQRSNFKG PRRA 366 384	Gag	India*/C	6 12	2 4	12.00 12.30

The preprint was mysteriously removed from BioRxiv only three days after it was posted on January 2020.

Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag

Prashant Pradhan^{§1,2}, Ashutosh Kumar Pandey^{§1}, Akhilesh Mishra^{§1}, Parul Gupta¹, Praveen Kumar Tripathi¹, Manoj Balakrishnan Menon¹, James Gomes¹, Perumal Vivekanandan*¹ and Bishwajit Kundu*¹

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This power point was prepared so non-biologists can decide for themselves whether or not this removal was justified.

Click on the following link
to open the NIH database

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

The top of your page will appear like this

Make sure this tab is highlighted in order to focus your search on amino acid sequences

BLASTP programs search protein databases using a protein query. [more...](#)

[Reset page](#)

[Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Query subrange [?](#)

From

To

Or, upload file

No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Place cursor in the “Enter Query Sequence” box
and enter the first sequence: TNGTKR

Standard Protein BLAST

[blastn](#) **[blastp](#)** [blastx](#) [tblastn](#) [tblastx](#)

BLASTP programs search protein databases using a protein query. more...

[Reset page](#)

[Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

TNGTKR

Query subrange [?](#)

From

To

Or, upload file

No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Scroll down to near the bottom

Enter the term “viridae” into this box

Click on “BLAST”

Choose Search Set

Databases Standard databases (nr etc.): New Experimental databases

Compare Select to compare standard and experimental database ?

Standard

Database Non-redundant protein sequences (nr) ?

Organism exclude

Exclude Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm Quick BLASTP (Accelerated protein-protein BLAST)
 blastp (protein-protein BLAST)
 PSI-BLAST (Position-Specific Iterated BLAST)
 PHI-BLAST (Pattern Hit Initiated BLAST)
 DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm ?

Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

Your query may take a few minutes

The top of your new page will appear like this

The screenshot shows the top portion of a web browser displaying the NCBI BLAST results page. The browser's address bar shows the URL: `https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=QueryResults&PROGRAM=blastn&QUERY=FPVYJ7VE013`. The page header includes the NIH logo and the text "U.S. National Library of Medicine National Center for Biotechnology Information". A "Log in" button is visible in the top right corner. Below the header, there is a "COVID-19 Information" banner with links to "Public health information (CDC)", "Research information (NIH)", "SARS-CoV-2 data (NCBI)", "Prevention and treatment information (HHS)", and "Español". The main content area shows the search results for "RID-FPVYJ7VE013". The search parameters are displayed in a table on the left, and the "Filter Results" section is on the right. The "Filter Results" section includes a search box for organisms, a "Filter" button, and a "Reset" button. The "Filter Results" section also includes a "Percent Identity" filter, an "E value" filter, and a "Query Coverage" filter.

NCBI Blast:Nucleotide Sequenc x US9216205B2 - Modified polynucle The USPTO Publication Site for Issu +

NIH U.S. National Library of Medicine
National Center for Biotechnology Information [Log in](#)

! **COVID-19 Information** [Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

BLAST® » blastn suite » results for RID-FPVYJ7VE013 [Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

[< Edit Search](#) [Save Search](#) [Search Summary](#) [How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

i Your search parameters were adjusted to search for a short input sequence.

Job Title	Nucleotide Sequence
RID	FPVYJ7VE013 <small>Search expires on 07-25 09:41 am</small> Download All v
Program	BLASTN ? Citation v
Database	nt See details v
Query ID	lc Query_24129
Description	None
Molecule type	nucleic acid
Query Length	19
Other reports	Distance tree of results MSA viewer ?

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to **E value** to **Query Coverage** to

[Filter](#) [Reset](#)

Scroll down to see matches to your query

All these matches correspond to SARS-CoV-2

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download Select columns Show ?

select all *100 sequences selected* GenPept Graphics Distance tree of results Multiple alignment MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain B, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2554	100.00%	1380	7LX5_B
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1310	7SBS_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1310	7KRQ_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1310	7SBP_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1310	6XR8_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1308	7SBK_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1307	7LQV_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1305	7N1Q_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1305	7N1U_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1298	7FCD_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1298	7FAE_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	7LYK_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	6XKL_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	7SXU_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	7SXT_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	6VSB_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	7KDK_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute res...	21.4	21.4	100%	2555	100.00%	1288	7SXS_A

Go back to the initial page for searching

Click on the box that says “add organism”

Choose Search Set

Databases Standard databases (nr etc.): New Experimental databases

Compare Select to compare standard and experimental database [?](#)

Standard

Database Non-redundant protein sequences (nr) [?](#)

Organism exclude **Add organism**  [?](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm

- Quick BLASTP (Accelerated protein-protein BLAST)
- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)
- DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm [?](#)

BLAST Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

[< Try experimental clustered nr database](#) [?](#)
For more info see [What is clustered nr?](#)

This will result in the addition of a second box

Choose Search Set

Databases Standard databases (nr etc.): **New** Experimental databases

Compare Select to compare standard and experimental database ?

Standard

Database Non-redundant protein sequences (nr) ?

Organism Optional

Viridae (taxid:10239) exclude **Add organism**

Enter organism name or id--completions will be suggested exclude ←

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. ?

Exclude Optional

Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm

Quick BLASTP (Accelerated protein-protein BLAST)

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm ?

BLAST Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

Try experimental clustered nr database ?
For more info see [What is clustered nr?](#)

Enter the term “coronaviridae”

Check the “exclude” box on the right

Click on “BLAST”

Choose Search Set

Databases Standard databases (nr etc.): **New** Experimental databases

Compare Select to compare standard and experimental database ?

Standard

Database Non-redundant protein sequences (nr) ?

Organism Optional

Viridae (taxid:10239) exclude **Add organism**

Coronaviridae (taxid:11118) exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. ?

Exclude Optional

Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm

Quick BLASTP (Accelerated protein-protein BLAST)

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm ?

BLAST Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

On the next page enter “synthetic” in this box

Check on the “exclude” box

Enter “100” here to exclude imperfect matches

Click on “Filter”

[← Edit Search](#)

[Save Search](#)

[Search Summary](#) ▾

[? How to read this report?](#)

[▶ BLAST Help Videos](#)

[↶ Back to Traditional Results Page](#)

i Your search parameters were adjusted to search for a short input sequence.
Your search is limited to records that include: Viridae (taxid:10239) ; and exclude: Coronaviridae (taxid:11118)

Job Title	Protein Sequence
RID	7GPJ8W5J016 Search expires on 05-10 08:03 am Download All ▾
Program	BLASTP ? Citation ▾
Database	nr See details ▾
Query ID	lcl Query_15014
Description	unnamed protein product
Molecule type	amino acid
Query Length	6
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

Organism only top 20 will appear

exclude

synthetic construct (taxid:32630)

[+ Add organism](#)

Percent Identity

100 to 100

E value

to

Query Coverage

100 to 100

[Filter](#)

[Reset](#)

These sequences match the 2nd query

Most matches will correspond to HIV

Some synthetic sequences will get past the filter

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	synthetic SARS-CoV-2 spike glycoprotein [Measles morbillivirus]	Measles morbillivirus	21.4	21.4	100%	292	100.00%	1273	QOT47607.1
<input checked="" type="checkbox"/>	NSP3-P2A-SARS CoV-2/S1 [Rotavirus A]	Rotavirus A	21.4	21.4	100%	293	100.00%	1046	QPJ72397.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	867	UBW84093.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	863	AFU28737.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	863	AFU28711.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	863	AFU28717.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	858	AFU28733.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	858	AFU28693.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	857	AFU28721.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	857	AFU28699.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	857	AFU28729.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	857	AFU28705.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	100%	293	100.00%	857	AFU28725.1
<input checked="" type="checkbox"/>	NSP3-P2A-SARS CoV-2/NTD [Rotavirus A]	Rotavirus A	21.4	21.4	100%	294	100.00%	641	QPJ72395.1
<input checked="" type="checkbox"/>	terminase large subunit [Streptococcus phage Javan411]	Streptococcus phage Javan411	21.4	21.4	100%	294	100.00%	570	QBX18329.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: Terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	294	100.00%	570	DAJ23136.1

Go back to the starting link for searching
and enter these terms in your boxes

This narrows the search to coronaviruses
that exclude sequences for SARS-CoV-2

Click on “BLAST”

Choose Search Set

Databases Standard databases (nr etc.): **New** Experimental databases

Compare Select to compare standard and experimental database

Standard

Database

Organism exclude

exclude

Exclude Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm Quick BLASTP (Accelerated protein-protein BLAST)

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

On the next page enter “100” in these boxes

Click on “Filter”

[← Edit Search](#)

[Save Search](#)

[Search Summary](#) ▾

[? How to read this report?](#)

[▶ BLAST Help Videos](#)

[↶ Back to Traditional Results Page](#)

i Your search parameters were adjusted to search for a short input sequence.
Your search is limited to records that include: Coronaviridae (taxid:11118) ; and exclude: SARS-2 (taxid:2697049)

Job Title	Protein Sequence
RID	70F6WXB3013 <small>Search expires on 05-04 04:19 am</small> Download All ▾
Program	BLASTP ? Citation ▾
Database	nr See details ▾
Query ID	lcl Query_43484
Description	unnamed protein product
Molecule type	amino acid
Query Length	6
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity

100 to 100

E value

to

Query Coverage

100 to 100

[Filter](#)

[Reset](#)

Scroll down and you will find the few sequences that match the criteria for your 3rd query

Click on the “Accession” link to get the date

All these accession dates are 2021 or later

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Select columns Show 100 ?

select all 3 sequences selected [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome coronavirus	21.4	21.4	100%	6.8	100.00%	1283	TX08_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome-related coronavirus]	Severe acute respiratory syndrome-related cor...	21.4	21.4	100%	6.8	100.00%	1261	TW <small>Show re</small>
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome coronavirus	21.4	21.4	100%	6.8	100.00%	1258	TWVN_A

Repeat the entire query procedure
for the second sequence: HKNNKS

Standard Protein BLAST

[blastn](#) **[blastp](#)** [blastx](#) [tblastn](#) [tblastx](#)

BLASTP programs search protein databases using a protein query. [more...](#)

[Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

HKNNKS

Query subrange [?](#)

From

To

Or, upload file

No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

This is the result for your 1st query for HKNNKS

All these matches correspond to SARS-CoV-2

Sequences producing significant alignments

Download

Select columns

Show

100



select all 100 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1273	100.00%	1298	7FCD_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1286	7AKD_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1285	7LWS_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1284	7R12_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1283	7EJ4_A
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1282	BCN86353.1
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1281	7MTE_A
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1278	ULB48625.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1277	UDN18211.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG28329.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UJP49095.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG30177.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKD44401.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG28978.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG35749.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKS94618.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG34905.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	22.3	22.3	100%	1274	100.00%	1276	UKG35809.1

This is the result for your 2nd query for HKNNKS

Note how the HIV sequence matches perfectly

Sequences producing significant alignments

Download ▾

Select columns ▾

Show 100 ▾



select all 0 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	synthetic SARS-CoV-2 spike glycoprotein [Measles morbillivirus]	Measles morbillivirus	22.3	22.3	100%	142	100.00%	1273	QOT47607.1
<input type="checkbox"/>	NSP3-P2A-SARS CoV-2/S1 [Rotavirus A]	Rotavirus A	22.3	22.3	100%	142	100.00%	1046	QPJ72397.1
<input type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	22.3	22.3	100%	142	100.00%	865	ALB06757.1
<input type="checkbox"/>	NSP3-P2A-SARS CoV-2/NTD [Rotavirus A]	Rotavirus A	22.3	22.3	100%	143	100.00%	641	QPJ72395.1
<input type="checkbox"/>	hypothetical protein [Tupanvirus soda lake]	Tupanvirus soda lake	22.3	22.3	100%	144	100.00%	387	QKU35608.1
<input type="checkbox"/>	mg301 protein [Tupanvirus deep ocean]	Tupanvirus deep ocean	22.3	22.3	100%	144	100.00%	383	QKU34642.1
<input type="checkbox"/>	b144 [Murid betaherpesvirus 8]	Murid betaherpesvirus 8	22.3	22.3	100%	144	100.00%	382	AKB93327.1
<input type="checkbox"/>	e144 [Murid betaherpesvirus 8]	Murid betaherpesvirus 8	22.3	22.3	100%	144	100.00%	382	YP_007016531.1
<input type="checkbox"/>	RNA-dependent RNA polymerase [Mitovirus sp.]	Mitovirus sp.	22.3	22.3	100%	144	100.00%	354	QDH88597.1
<input type="checkbox"/>	hypothetical protein Va1_239 [Vibrio phage Va1]	Vibrio phage Va1	22.3	22.3	100%	145	100.00%	203	QAU04534.1
<input type="checkbox"/>	hypothetical protein [Vibrio phage phiKT1024]	Vibrio phage phiKT1024	22.3	22.3	100%	145	100.00%	202	UOK16774.1
<input type="checkbox"/>	TPA: MAG TPA: hypothetical protein [Myoviridae sp.]	Myoviridae sp.	22.3	22.3	100%	150	100.00%	97	DAH83395.1
<input type="checkbox"/>	hypothetical protein Hokovirus_3_227 [Hokovirus HKV1]	Hokovirus HKV1	19.7	51.1	100%	1165	100.00%	2689	ARF10954.1

This is the result for your 3rd query for HKNNKS

All these accession dates are 2021 or later

Descriptions

Graphic Summary

Alignments

Taxonomy

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain A_Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome cor...	22.3	22.3	100%	3.4	100.00%	1283	TX08_A
<input checked="" type="checkbox"/>	Spike Protein of RaTG13 Bat Coronavirus in Closed Conformation [Bat coronavirus RaTG...	Bat coronavirus RaTG13	22.3	22.3	100%	3.4	100.00%	1283	6ZGF_A
<input checked="" type="checkbox"/>	spike glycoprotein [Bat coronavirus RaTG13]	Bat coronavirus RaTG13	22.3	22.3	100%	3.4	100.00%	1269	QHR63300.2
<input checked="" type="checkbox"/>	Chain A_Spike glycoprotein [Bat coronavirus RaTG13]	Bat coronavirus RaTG13	22.3	22.3	100%	3.4	100.00%	1267	7CN4_A
<input checked="" type="checkbox"/>	Chain A_Spike glycoprotein [Severe acute respiratory syndrome-related coronavirus]	Severe acute respiratory syndrome-rela...	22.3	22.3	100%	3.4	100.00%	1261	7W98_A
<input checked="" type="checkbox"/>	Chain A_Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome cor...	22.3	22.3	100%	3.4	100.00%	1258	7WVN_A

Repeat the entire query procedure
for the 3rd sequence: RSYLTPGNSSSG

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RSYLTPGNSSSG

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This is the result of your 1st query for RSY...SSG

All these matches correspond to SARS-CoV-2

Sequences producing significant alignments

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	QRG14049.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	QUD15094.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	QRG14829.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	QRX42973.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	UGW53350.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	JEO85829.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	UPM67941.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	UDA89655.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	UDA79545.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	QYI91976.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1273	UGV52762.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1272	QYJ29662.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	UCX45615.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	UDK32019.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	UAU27900.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	UDH33128.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	JET41670.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	38.8	38.8	100%	0.006	100.00%	1271	JEU23913.1

For your 2nd query for RSY...SSG do not use the 100% filter

This is the result of your 2nd query for RSY...SSG

The distance tree maximum score for HIV is 26.1

Sequences producing significant alignments

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	synthetic SARS-CoV-2 spike glycoprotein [Measles morbillivirus]	Measles morbilli...	36.3	36.3	100%	0.005	91.67%	1273	QOT47607.1
<input checked="" type="checkbox"/>	NSP3-P2A-SARS CoV-2/S1 [Rotavirus A]	Rotavirus A	36.3	52.6	100%	0.005	91.67%	1046	QPJ72397.1
<input checked="" type="checkbox"/>	NSP3-P2A-SARS CoV-2/NTD [Rotavirus A]	Rotavirus A	36.3	52.6	100%	0.005	91.67%	641	QPJ72395.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Grotenhout virus]	Grotenhout virus	26.9	26.9	75%	11	88.89%	4812	ARB16032.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Norway nairovirus 1]	Norway nairovir...	26.9	26.9	75%	11	88.89%	4811	ASY03232.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37779.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Pustyn virus]	Pustyn virus	26.9	26.9	75%	11	88.89%	4811	ANJ43351.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37784.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Pustyn virus]	Pustyn virus	26.9	26.9	75%	11	88.89%	4811	QPD01613.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37782.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37780.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Norway nairovirus 1]	Norway nairovir...	26.9	26.9	75%	11	88.89%	4811	ASY03236.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37781.1
<input checked="" type="checkbox"/>	RNA-dependent RNA polymerase [Beiji nairovirus]	Beiji nairovirus	26.9	26.9	75%	11	88.89%	4811	UFP37783.1
<input checked="" type="checkbox"/>	RNA-dependent RNA-polymerase [Gakugsa tick virus]	Gakugsa tick virus	26.9	26.9	75%	11	88.89%	4811	QPD01615.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immuno...	26.1	42.8	100%	23	66.67%	223	ACL98861.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immuno...	26.1	42.8	100%	23	66.67%	223	ACL98864.1
<input checked="" type="checkbox"/>	envelope glycoprotein [Human immunodeficiency virus 1]	Human immuno...	26.1	42.8	100%	23	66.67%	223	ACL98860.1

For your 3rd query for RSY...SSG do not use the 100% filter
 This is the result of your 2nd query for RSY...SSG
 All matches entered prior to 2020 score 21.8 or lower
 This is significantly lower than the score of 26.1 for HIV

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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Chain A_Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome ...	36.3	49.2	100%	1e-04	91.67%	1283	7X08_A
<input checked="" type="checkbox"/> Spike Protein of RaTG13 Bat Coronavirus in Closed Conformation [Bat coronavirus RaTG...	Bat coronavirus RaTG13	36.3	50.5	100%	1e-04	91.67%	1283	6ZGF_A
<input checked="" type="checkbox"/> spike glycoprotein [Bat coronavirus]	Bat coronavirus	36.3	50.5	100%	1e-04	91.67%	1269	UAY13217.1
<input checked="" type="checkbox"/> spike glycoprotein [Bat coronavirus RaTG13]	Bat coronavirus RaTG13	36.3	50.5	100%	1e-04	91.67%	1269	QHR63300.2
<input checked="" type="checkbox"/> Chain A_Spike glycoprotein [Bat coronavirus RaTG13]	Bat coronavirus RaTG13	36.3	50.5	100%	1e-04	91.67%	1267	7CN4_A
<input checked="" type="checkbox"/> Chain A_Spike glycoprotein [Severe acute respiratory syndrome-related coronavirus]	Severe acute respiratory syndrome...	36.3	49.2	100%	1e-04	91.67%	1261	7W98_A
<input checked="" type="checkbox"/> Chain A_Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome ...	36.3	36.3	100%	1e-04	91.67%	1258	7WVN_A
<input checked="" type="checkbox"/> Chain A_Glycoprotein [Pangolin coronavirus]	Pangolin coronavirus	28.6	41.1	66%	0.067	100.00%	1295	7CN8_A
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	28.6	41.1	66%	0.067	100.00%	1267	QIA48614.1
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	25.2	37.8	66%	1.1	100.00%	1269	QVT76606.1
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	25.2	37.8	66%	1.1	100.00%	1269	QIQ54048.1
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	25.2	37.8	66%	1.1	100.00%	1267	QIA48632.1
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	25.2	25.2	58%	1.1	100.00%	1267	QIA48641.1
<input checked="" type="checkbox"/> spike protein [Pangolin coronavirus]	Pangolin coronavirus	25.2	37.8	66%	1.1	100.00%	1265	QIA48623.1
<input checked="" type="checkbox"/> ORF1ab polyprotein [Human coronavirus HKU1]	Human coronavirus HKU1	21.8	21.8	83%	18	70.00%	152	ACR82746.1
<input checked="" type="checkbox"/> polyprotein [Porcine epidemic diarrhea virus]	Porcine epidemic diarrhea virus	21.4	21.4	83%	26	70.00%	6781	AJD07365.1
<input checked="" type="checkbox"/> spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	20.2	20.2	75%	75	77.78%	118	BCL50733.1
<input checked="" type="checkbox"/> RNA-dependent RNA-polymerase [Bat coronavirus M.nattereri/UK/Wyt/1012B]	Bat coronavirus M.nattereri/UK/Wyt/...	20.2	20.2	83%	75	60.00%	131	AFB18248.1

Repeat the entire query procedure
for the 4th sequence: QTNSPRRA

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This is the result of your 1st query for QTNSPRRA

All these matches correspond to SARS-CoV-2

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1310	7SBS_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1310	7KRQ_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1310	6XR8_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1305	7N1Q_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1288	7KDI_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1288	7KDJ_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1287	6ZGG_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1286	7A5R_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1283	7C2L_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1283	7DX1_A
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome coronavirus	28.2	28.2	100%	15	100.00%	1283	7X08_A
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1282	BCN86353.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1282	BCN86413.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1282	CAD0240757.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1282	CAD0240766.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1282	BCN86425.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1280	QUH56559.1
<input checked="" type="checkbox"/>	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	Severe acute respiratory syndrome coronavirus 2	28.2	28.2	100%	15	100.00%	1280	QUD59342.1

For the 2nd query for QTNSPRRA do not use the 100% filter

The distance tree maximum score for HIV is 21.4

<input checked="" type="checkbox"/>	helicase [Paramecium bursaria Chlorella virus AP110A]	Paramecium bursaria Chlorella vir...	21.4	37.3	87%	470	85.71%	1122	AGE48816.1
<input checked="" type="checkbox"/>	helicase [Paramecium bursaria Chlorella virus NE-JV-1]	Paramecium bursaria Chlorella vir...	21.4	56.2	87%	470	85.71%	1120	AGE56365.1
<input checked="" type="checkbox"/>	pR31 [rat cytomegalovirus strain Maastricht]	rat cytomegalovirus strain Maastricht	21.4	21.4	87%	470	87.50%	773	NP_064136.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: Cytosine specific methyltransferase [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	87%	472	85.71%	479	DAV36400.1
<input checked="" type="checkbox"/>	PBSX family terminase large subunit [Streptococcus phage phiARI0462]	Streptococcus phage phiARI0462	21.4	21.4	100%	472	87.50%	441	YP_009324905.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	435	DAQ61591.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Bacteriophage sp.]	Bacteriophage sp.	21.4	21.4	100%	472	87.50%	435	DAX18897.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	435	DAU22005.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	435	DAP06280.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	435	DAJ84039.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp. ctSlv21]	Siphoviridae sp. ctSlv21	21.4	21.4	100%	472	87.50%	435	DAJ16098.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	435	DAK22371.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	432	DAM20207.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	432	DAS63248.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: terminase large subunit [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	100%	472	87.50%	428	DAZ60154.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: HK97 Family Phage Portal Protein [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	87%	472	85.71%	387	DAF32760.1
<input checked="" type="checkbox"/>	TPA: MAG TPA: Cytosine specific methyltransferase [Siphoviridae sp.]	Siphoviridae sp.	21.4	21.4	87%	472	85.71%	368	DAY08056.1
<input checked="" type="checkbox"/>	protease [Human immunodeficiency virus 1]	Human immunodeficiency virus 1	21.4	21.4	87%	473	87.50%	340	AAZ81655.1

For your 3rd query for QTNSPRRA do not use the 100% filter

All matches entered before 2020 score 19.3 or lower

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Chain A, Spike glycoprotein [Severe acute respiratory syndrome coronavirus]	Severe acute respiratory syndrome coronavirus	28.2	28.2	100%	0.041	100.00%	1283	7X08_A
<input checked="" type="checkbox"/>	nucleocapsid protein [White-eye coronavirus HKU16]	White-eye coronavirus HKU16	21.0	21.0	87%	16	85.71%	347	YP_005352842.1
<input checked="" type="checkbox"/>	S protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1169	QIQ19632.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1169	QIN55199.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50262.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50226.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50214.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50222.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50282.1
<input checked="" type="checkbox"/>	spike protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1165	AFP50202.1
<input checked="" type="checkbox"/>	S protein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	65	100.00%	1163	ARS22460.1
<input checked="" type="checkbox"/>	N protein [Myotis lucifugus coronavirus]	Myotis lucifugus coronavirus	19.3	19.3	62%	66	100.00%	425	ASL24656.1
<input checked="" type="checkbox"/>	nucleoprotein [Bat coronavirus CDPHE15/USA/2006]	Bat coronavirus CDPHE15/USA/2006	19.3	19.3	62%	66	100.00%	425	YP_008439206.1
<input checked="" type="checkbox"/>	spike glycoprotein [Infectious bronchitis virus]	Infectious bronchitis virus	19.3	19.3	62%	66	100.00%	350	API69974.1
<input checked="" type="checkbox"/>	spike glycoprotein [Rodent coronavirus]	Rodent coronavirus	18.9	18.9	62%	93	100.00%	1370	ATP66733.1
<input checked="" type="checkbox"/>	spike protein [Equine coronavirus]	Equine coronavirus	18.9	18.9	62%	93	100.00%	1363	BAN18703.1
<input checked="" type="checkbox"/>	spike protein [Equine coronavirus]	Equine coronavirus	18.9	18.9	62%	93	100.00%	1363	BAM15656.1
<input checked="" type="checkbox"/>	spike protein [Equine coronavirus]	Equine coronavirus	18.9	18.9	62%	93	100.00%	1363	BAS18866.1

What does this mean?

- 1) The 1st and 2nd sequences from SARS-CoV-2 line up perfectly with amino acid sequences on HIV.
- 2) No other virus entered into the NIH database before 2021 forms a perfect match with both the 1st and 2nd sequences.
- 3) The 3rd and 4th sequences from SARS-CoV-2 show more homology to HIV than for any virus entered prior to 2020.
- 4) The dates on these viruses are important because some viruses “found” after 2019 may have been fabricated to support the narrative that SARS-CoV-2 came from nature.
- 5) Based on computer modelling all of these inserts occur on important locations of the spike protein.
- 6) The 4th sequence is particularly important because it contains the furin cleavage site. The FCS plays a key role facilitating infection.

Statement made at Forum on Medical and Public Health Preparedness for Catastrophic Events, February 12, 2016

<https://www.ncbi.nlm.nih.gov/books/NBK349040/>

We need to increase public understanding of the need for medical counter-measures such as a pan-coronavirus vaccine.

A key driver is the media, and the economics will follow the hype.

Peter Daszak, president of EcoHealth Alliance

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Thanks to jikkyleaks (fan account) for tips on how to narrow down my search.

<https://twitter.com/Jikkyleaks>

The original power point (with animations)
can be downloaded from following website:

<https://www.firsthandsources.com/>