

The instructions below show how to access to NCBI SARS-CoV-2 Resources:

Step 1: Visit <https://www.ncbi.nlm.nih.gov/sars-cov-2/>

**NIH** National Library of Medicine  
National Center for Biotechnology Information

Search NCBI Search

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

## NCBI SARS-CoV-2 Resources

**Quick Navigation Guide**

- Sequence Submission
- Literature
- Sequence-Related Resources
- Clinical Resources
- Other Websites

### SARS-CoV-2 Data

<b>1,203,728</b> <a href="#">SRA runs</a>	<b>1,701,368</b> <a href="#">Nucleotide records</a>	<b>6,665</b> <a href="#">ClinicalTrials.gov</a>
<b>182,933</b> <a href="#">PubMed</a>	<b>211,947</b> <a href="#">PMC</a>	

Step 2: Click on Nucleotide records, you will access to the Data:

**SARS-CoV-2 Data Hub**  
Download ▾

Quick Links  
Betacoronavirus BLAST  
CDC Outbreak Information  
SARS-CoV-2 Articles in PubMed  
SRA Data  
NCBI SARS-CoV-2 Resources  
Datasets command line

**Tabular View** Dashboard Visualizations Mutations in SRA Complete Tree

Selected Results: 0 [Align](#) [Build Phylogenetic Tree](#)

**Refine Results** [Reset](#)

Virus +  
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), taxid:2697049 x

Accession +

Sequence Length +

Ambiguous Characters [New!](#) +

Sequence Type +

Nucleotide (1,701,368)	Protein (9,390,894)	RefSeq Genome (1)	Select Columns
<input type="checkbox"/> Accession ▾	<input type="checkbox"/> Submitters ▾	<input type="checkbox"/> Release Date ▾	<input type="checkbox"/> Pangolin ▾
<input type="checkbox"/> <a href="#">NC_045512</a> <a href="#">RefSeq</a>	Wu,F., et al.	2020-01-13	B
<input type="checkbox"/> <a href="#">MZ317675</a>	Keller,M., e...	2021-09-29	
<input type="checkbox"/> <a href="#">OK326756</a>	Siu,G.K.-H.,...	2021-09-29	
<input type="checkbox"/> <a href="#">OK326757</a>	Siu,G.K.-H.,...	2021-09-29	
<input type="checkbox"/> <a href="#">OK326758</a>	Siu,G.K.-H.,...	2021-09-29	
<input type="checkbox"/> <a href="#">OK326759</a>	Siu,G.K.-H.,...	2021-09-29	

Expand Table

Wuhan-Hu-1  
NW-FLI-0721  
HKPU-00188  
HKPU-00189  
HKPU-00190  
HKPU-00191

Step 3: [Optional] On the left panel, you can refine search results using different criteria. For example, you can refine using Sequence Length from 28,000 to 35,000 and Submit:

Selected Results: 0

Align Build Phylogenetic Tree

Refine Results [Reset](#)

Virus [+](#)

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), taxid:2697049 [×](#)

Accession [+](#)

Sequence Length [+](#)

Min: 28000 Max: 35000 [×](#)

Ambiguous Characters [New!](#) [+](#)

Sequence Type [+](#)

RefSeq Genome Completeness [+](#)

Nucleotide Completeness [+](#)

Pango lineage [New!](#) [+](#)

Expand Table

Nucleotide (1,698,136)	Protein (0)	RefSeq Genome (0)	<a href="#">Select Columns</a>		
<input type="checkbox"/> Accession	<input type="checkbox"/> Submitters	<input type="checkbox"/> Release Date	<input type="checkbox"/> Pangolin	<input type="checkbox"/> Isolate	
<input type="checkbox"/> <a href="#">NC_045512</a> <a href="#">RefSeq</a>	Wu,F., et al.	2020-01-13	B	Wuhan-	
<input type="checkbox"/> <a href="#">MZ317675</a>	Keller,M., e...	2021-09-29		NW-FLI-	
<input type="checkbox"/> <a href="#">OK326756</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326757</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326758</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326759</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326760</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326761</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326762</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	
<input type="checkbox"/> <a href="#">OK326763</a>	Siu,G.K.-H.,...	2021-09-29		HKPU-C	

[Download](#)

Step 4: You can select multiple individual records you want to download and hit the Download button:

SARS-CoV-2 Data Hub

Quick Betacoronavirus BLAST SARS-CoV-2 Articles in NCBI SARS-CoV-2  
CDC Outbreak PubMed Resources  
Datasets command line

Download ▾

Tabular View [31](#)

Selected Results: 5

Refine Results

Virus

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), taxid:2697049

Accession

Sequence Length

Min: 28000 Max: 35000 [×](#)

Ambiguous Characters [New!](#) [+](#)

Build Phylogenetic Tree

[Select Columns](#)

Pangolin Isolate

Wuhan-

NW-FLI-

HKPU-C

HKPU-C

HKPU-C

[Feedback](#)

Download Results [×](#)

Step 1 of 3: Select Data Type

Sequence data (FASTA Format)	Accession List	Current table view result
<input checked="" type="radio"/> Nucleotide	<input type="radio"/> Nucleotide	<input type="radio"/> CSV format
<input type="radio"/> Coding Region	<input type="radio"/> Protein	<input type="radio"/> XML format
<input type="radio"/> Protein	<input type="radio"/> Assembly	

[Next](#)

Step 5: Select the type of data you want to download. Here, I'm selecting Nucleotide, and hit Next:

The screenshot shows the SARS-CoV-2 Data Hub interface. A modal dialog titled "Download Results" is open, displaying "Step 2 of 3: Select Records". The dialog has two radio button options: "Download Selected Records" (which is selected) and "Download All Records". At the bottom of the dialog are "Back" and "Next" buttons. The background interface shows a list of search results with columns for selection, accession number, author, date, and location. The first four rows are selected with checkmarks.

	Accession	Author	Date	Location
<input checked="" type="checkbox"/>	<a href="#">MZ317675</a>	Keller,M., e...	2021-09-29	NW-FLI
<input checked="" type="checkbox"/>	<a href="#">OK326756</a>	Siu,G.K.-H.,...	2021-09-29	HKPU-C
<input checked="" type="checkbox"/>	<a href="#">OK326757</a>	Siu,G.K.-H.,...	2021-09-29	HKPU-C
<input checked="" type="checkbox"/>	<a href="#">OK326758</a>	Siu,G.K.-H.,...	2021-09-29	HKPU-C

Step 6: You now have the option to download the selected records, or all records and click Next:

The screenshot shows the same SARS-CoV-2 Data Hub interface. The modal dialog is now at "Step 3 of 3: Select FASTA definition line". It has two radio button options: "Use default : Accession GenBank Title" (which is selected) and "Build custom". At the bottom are "Back" and "Download" buttons. The background interface remains the same, showing the list of search results.

Step 7: You can select the information you want to download, and click Download:

Step 8: You can open the downloaded FASTA file, and it looks like this:

```

>MZ317675.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/Felis Catus/DEU/NW-FLI-0721/2021, complete genome
TGAATAAGGTTTATACCTTCCAGGTAACAAACCAACCACTTTTCGATCTCTTGTAGATC
TGTTCTCTAAACGAACTTTAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGAC
TCACGAGTATAATTAATAACTAATTAATGTCGTTGACAGGACACGAGTAACCTGCTCAT
CTTCTGACGGCTGCTTACGGTTTCGTCCTGTTGACGCGCATCATCAGCACATCTAGGTT
TCGTCGGGTGTGACCGAAAGGTAGATGGAGAGCCTTGCCCTGGTTTCAACGAGAAAA
CACACGTCCAACCTAGTTGCCTGTTTACAGGTTTCGCGACGTGCTCGTACGTGGCTTTG
GAGACTCCGTGGAGGAGGTCTTATCAGAGGCAGCTCAACATCTTAAAGATGGCACTTGTG
GCTTAGTAGAAGTTGAAAAAGGCGTTTTCCTCAACTTGAACAGCCCTATGTGTTATCA
AACGTTGCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGCAGAA
TCGAAGGCATTTCAGTACGGTCTGATGTTGAGACACTTGGTGCTTGTCTCTCATGTGG
GCGAAATACCACTGGCTTACCGCAAGGTTCTTCTCGTAAGAACGGTAATAAAGGAGCTG
GTGGCCATAGTTACGGCGCCGATCTAAAGTCATTGACTTAGGCGACGAGCTTGGCACTG
ATCCTTATGAAGATTTTCAAGAAACTGGAACACTAAACATAGCAGTGGTGTACCCGTG
AACTCATGCGTGAGCTTAACGAGGGGCATACACTCGCTATGTCGATAACAACTTCTGTG
GCCCTGATGGCTACCTCTTGTAGTGCATTAAAGACCTTCTAGCACGTGCTGGTAAAGCTT
CATGCACCTTTGTCTGAACAACTGGACTTTATTGACACTAAGAGGGGTGTACTGCTGCC
GTGAACATGAGCATGAAATTGCTTGGTACACGGAACGTTCTGAAAAGAGCTATGAATTGC
AGACACCTTTTGAATTAATTTGGCAAGAAATTTGACACCTTCAATGGGGAATGTCCAA
ATTTGTGATTTCCCTTAAATTCATAATCAAGACTATTCAACCAAGGGTTGAAAAGAAAA
AGCTTGATGGCTTATGGGTAGAATTCGATCTGTCTATCCAGTTGCGTCACCAATGAAT
GCAACCAATGTGCTTTCAACTCTCATGAAGTGATCATTGTGGTGAACATTCATGGC
AGACGGGCGATTTTGTAAAGCCACTTGCGAATTTTGTGGCACTGAGAATTTGACTAAAG
AAGGTGCGCACTTGTGTTACTTACCCCAAAATGCTGTTGTTAAATTTATTGTCCAG
CATGTCACAATTGAGAGTAGGACCTGAGCATAGTCTTGCCGAATACCATAATGAATCTG
GCTTGAAACCACTTCTCGTAAGGGTGGTCGCACTATTGCCTTTGGAGGCTGTGTTCT
CTTATGTTGGTTGCCATAACAAGTGTGCCATTGGGTTCCAGTGCTAGCGCTAACATAG
GTTGTAACCATACAGGTGTTGTTGGAGAAGGTTCCGAAGGCTTAAATGACAACCTTCTTG
AAATACTCCAAAAAGAGAAAGTCTACATCAATATTGTTGGTGACTTTAACTTAATGAAG
AGATCGCATTTATTTGGCATCTTTTCTGCTTCCACAAGTGCTTTTGTGGAAACTGTGA
AAGGTTTGGATTATAAGCATTCAACAAATTTGTAATCCTGTGGTAATTTAAAGTTA
CAAAAGGAAAAGCTAAAAAGGTGCCTGGAATATTGGTGAACAGAAATCAATACTGAGTC

```

This file contains multiple records, one after another. If you scroll down, you will see data of the next records