

How to find and get sequence data



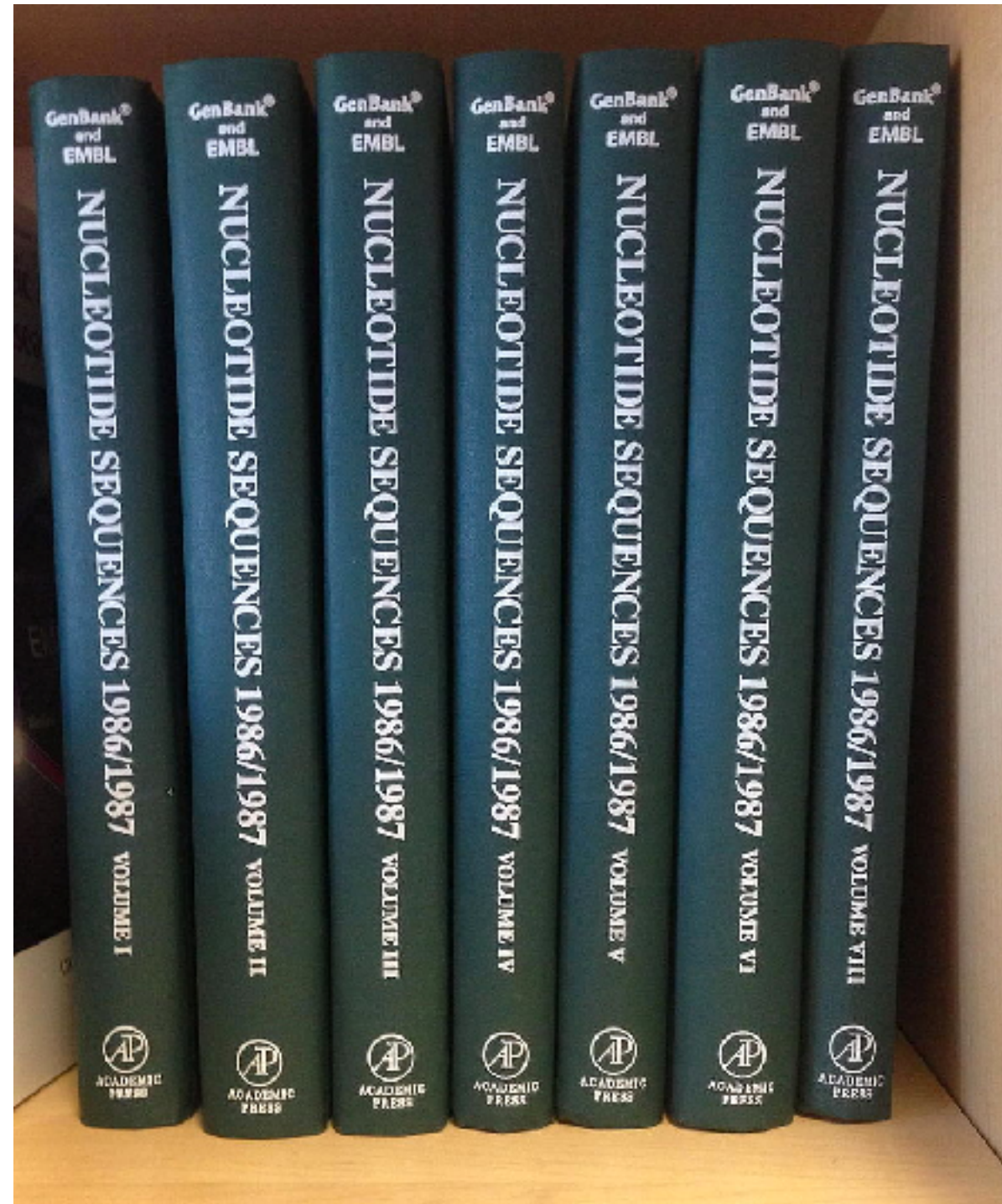
Computational Biology
Workshop

Todos Santos Center
May 9-12, 2022

Mark Stenglein, PhD
Associate Professor
Center for Vector-Borne Infectious Diseases
Department of Microbiology, Immunology, and Pathology
Mark.Stenglein@colostate.edu
StengleinLab.org

GenBank was one of the earliest sequence databases.

GenBank circa 1987



~ 10,000 sequences

GenBank release 100 (1997)
distributed by CDROM

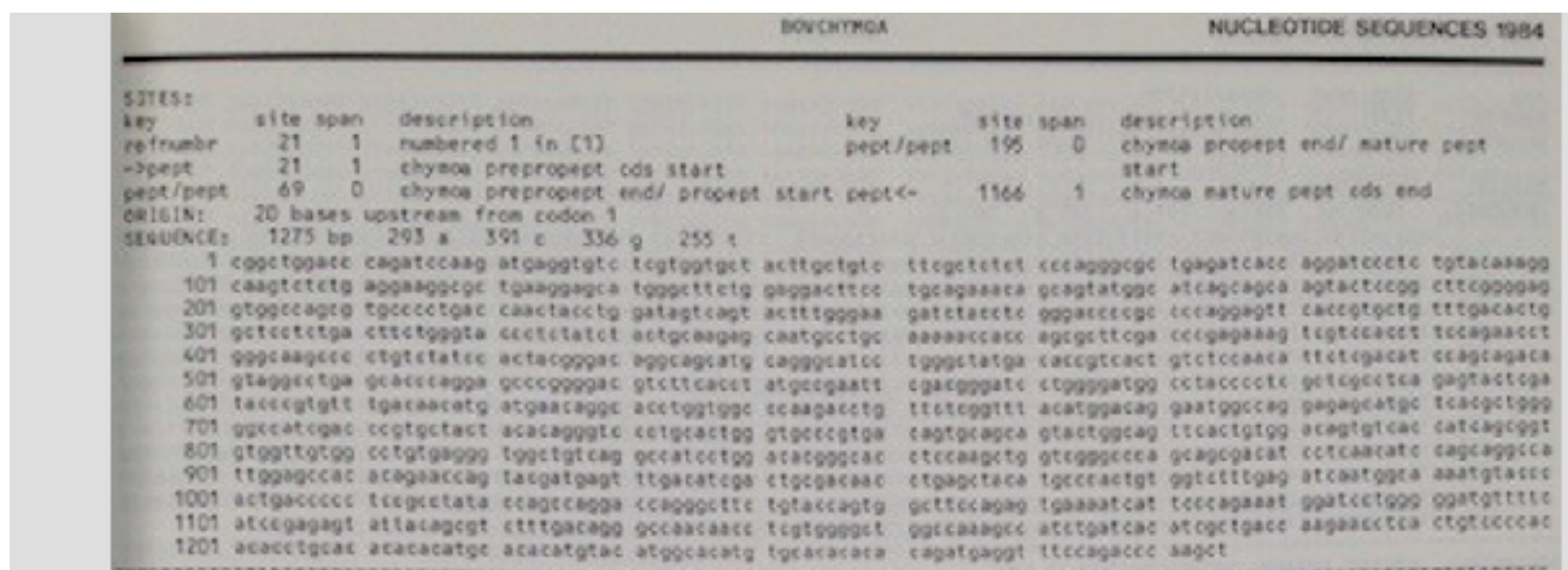


~1,300,000 sequences

Genbank today



>237,000,000 sequences



First release: 1982: 606 sequences

Today, we'll focus on NCBI databases

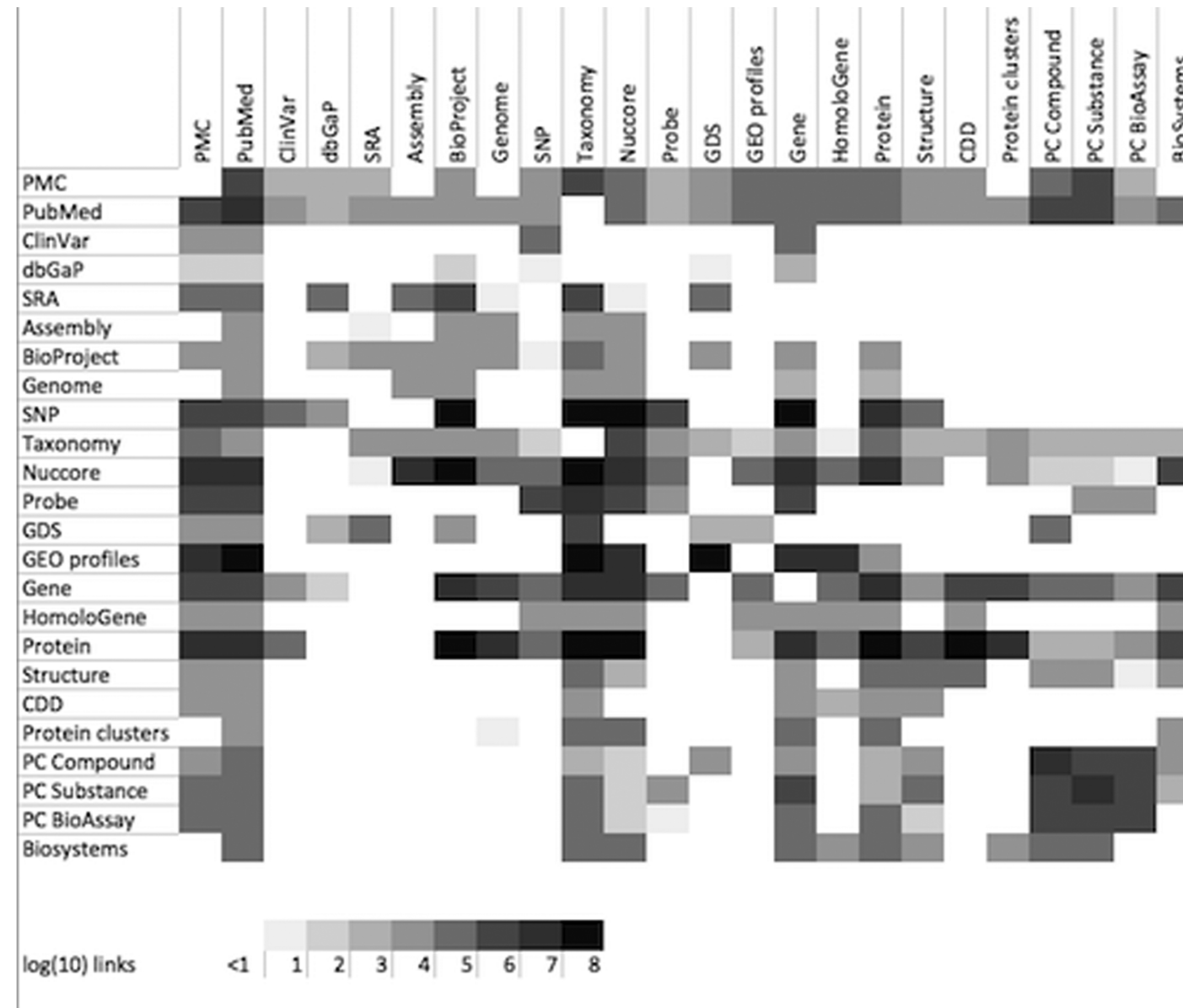
Category	Example NCBI db	Content
Literature	PubMed	Papers
Genome	Assembly	Genome assemblies
Taxonomy	Taxonomy	Information about species and higher order taxa
Proteins	Protein	Protein sequences

Plus many more...

One useful feature of NCBI databases is that they connect to each other

So, you can, for example:

- get all the sequences associated with a species or genus
- get all the protein sequences encoded by a genome
- get the SRA datasets associated with a paper



The 2020 paper containing the original sequence description of SARS-CoV-2

Article

A new coronavirus associated with human respiratory disease in China

<https://doi.org/10.1038/s41586-020-2008-3>

Received: 7 January 2020

Accepted: 28 January 2020

Published online: 3 February 2020

Open access

 Check for updates

Fan Wu^{1,7}, Su Zhao^{2,7}, Bin Yu^{3,7}, Yan-Mei Chen^{1,7}, Wen Wang^{4,7}, Zhi-Gang Song^{1,7}, Yi Hu^{2,7}, Zhao-Wu Tao², Jun-Hua Tian³, Yuan-Yuan Pei¹, Ming-Li Yuan², Yu-Ling Zhang¹, Fa-Hui Dai¹, Yi Liu¹, Qi-Min Wang¹, Jiao-Jiao Zheng¹, Lin Xu¹, Edward C. Holmes^{1,5} & Yong-Zhen Zhang^{1,4,6}✉

Emerging infectious diseases, such as severe acute respiratory syndrome (SARS) and Zika virus disease, present a major threat to public health^{1–3}. Despite intense research efforts, how, when and where new diseases appear are still a source of considerable uncertainty. A severe respiratory disease was recently reported in Wuhan, Hubei province, China. As of 25 January 2020, at least 1,975 cases had been reported since the first patient was hospitalized on 12 December 2019. Epidemiological investigations have suggested that the outbreak was associated with a seafood market in Wuhan. **Here we study a single patient who was a worker at the market and who was admitted to the Central Hospital of Wuhan on 26 December 2019 while experiencing a severe respiratory syndrome that included fever, dizziness and a cough.** Metagenomic RNA sequencing⁴ of a sample of bronchoalveolar lavage fluid from the patient identified a new RNA virus strain from the family *Coronaviridae*, which is designated here ‘WH-Human 1’ coronavirus (and has also been referred to as ‘2019-nCoV’). Phylogenetic analysis of the complete viral genome (29,903 nucleotides) revealed that the virus was most closely related (89.1% nucleotide similarity) to a group of

The pubmed record for that paper

← → ↻ <https://pubmed.ncbi.nlm.nih.gov/32015508/>

Most Visited blastn blastx blastp NCBI Tax Genbank SRA PubMed FoCo W ggplot theme Kuali CO-COVID_stats Pre-K Saliva Nextflow :: Anacond...

National Library of Medicine
National Center for Biotechnology Information Log in

Search

[Advanced](#) [User Guide](#)

Save Email Send to Display options

[Case Reports](#) > [Nature](#). 2020 Mar;579(7798):265-269. doi: 10.1038/s41586-020-2008-3.
Epub 2020 Feb 3.

A new coronavirus associated with human respiratory disease in China

Fan Wu ^{# 1}, Su Zhao ^{# 2}, Bin Yu ^{# 3}, Yan-Mei Chen ^{# 1}, Wen Wang ^{# 4}, Zhi-Gang Song ^{# 1}, Yi Hu ^{# 2}, Zhao-Wu Tao ², Jun-Hua Tian ³, Yuan-Yuan Pei ¹, Ming-Li Yuan ², Yu-Ling Zhang ¹, Fa-Hui Dai ¹, Yi Liu ¹, Qi-Min Wang ¹, Jiao-Jiao Zheng ¹, Lin Xu ¹, Edward C Holmes ^{1 5}, Yong-Zhen Zhang ^{6 7 8}

Affiliations [+ expand](#)

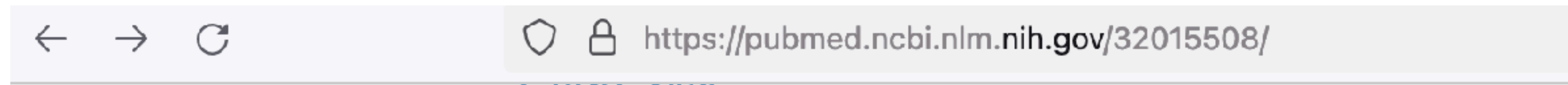
FULL TEXT LINKS



ACTIONS



At the bottom of the pubmed page: related information links



Related information

[Assembly](#)

[Cited in Books](#)

[Domains](#)

[Gene](#)

[MedGen](#)

[Nucleotide](#)

[Nucleotide](#)

[Nucleotide \(Weighted\)](#)

[Protein](#)

[Protein \(RefSeq\)](#)

[Protein \(Weighted\)](#)

[Related Project](#)

[SRA](#)

[Taxonomy via GenBank](#)



Click this link to get to the actual virus genome sequence

We've jumped to the NCBI nucleotide database (Genbank)

The screenshot shows the NCBI GenBank interface for the SARS-CoV-2 genome. At the top, there is a search bar with 'Nucleotide' selected and a 'Search' button. Below the search bar is a 'COVID-19 Information' banner with links to CDC, NIH, SARS-CoV-2 data, HHS, and Spanish. The main content area displays the title 'Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome' and the NCBI Reference Sequence: NC_045512.2. There are links for 'FASTA' and 'Graphics'. A 'Go to:' dropdown is visible. The main text block contains the following information:

LOCUS NC_045512 29903 bp ss-RNA linear VRL 18-JUL-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-CoV-2)
ORGANISM Severe acute respiratory syndrome coronavirus 2
Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes; Nidovirales; Coronidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus.
REFERENCE 1 (bases 1 to 29903)
AUTHORS Wu, F., Zhao, S., Yu, B., Chen, Y.M., Wang, W., Song, Z.G., Hu, Y., Tao, Z.W., Tian, J.H., Pei, Y.Y., Yuan, M.L., Zhang, Y.L., Dai, F.H., Liu, Y., Wang, Q.M., Zheng, J.J., Xu, L., Holmes, E.C. and Zhang, Y.Z.
TITLE A new coronavirus associated with human respiratory disease in China

On the right side, there are several utility sections: 'Change region shown', 'Customize view', 'Analyze this sequence' (with sub-links for Run BLAST, Pick Primers, Highlight Sequence Features, and Find in this Sequence), 'NCBI Virus' (with a description: Retrieve, view, and download SARS-CoV-2 coronavirus genomic and protein sequences.), and 'Related information' (with sub-links for Assembly, BioProject, Protein, and PubMed). A blue arrow points to the 'Protein' link in the 'Related information' section.

Click this link to get to the protein sequences encoded by this genome

Exercise: download all the *protein* sequences encoded by this SARS-CoV-2 genome

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Help

Advanced

COVID-19 Information

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

GenBank Send to: Change region shown Customize view

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

NCBI Reference Sequence: NC_045512.2

[FASTA](#) [Graphics](#)

Go to:

LOCUS NC_045512 29903 bp ss-RNA linear VRL 18-JUL-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-CoV-2)

ORGANISM *Severe acute respiratory syndrome coronavirus 2*
Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes; Nidovirales; Coronidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus.

REFERENCE 1 (bases 1 to 29903)

AUTHORS Wu, F., Zhao, S., Yu, B., Chen, Y.M., Wang, W., Song, Z.G., Hu, Y., Tao, Z.W., Tian, J.H., Pei, Y.Y., Yuan, M.L., Zhang, Y.L., Dai, F.H., Liu, Y., Wang, Q.M., Zheng, J.J., Xu, L., Holmes, E.C. and Zhang, Y.Z.

TITLE A new coronavirus associated with human respiratory disease in China

Related information

- Assembly
- BioProject
- Protein**
- PubMed

Click this link to get to the protein sequences encoded by this genome

Now we've jumped to the NCBI protein database

← → ↻ https://www.ncbi.nlm.nih.gov/protein?LinkName=nucore_protein&from_uid=1798174254 ☆ 📄 📧 ↶

Sequence length
Custom range...

Molecular weight
Custom range...

Release date
Custom range...

Revision date
Custom range...

[Clear all](#)

[Show additional filters](#)

- [ORF7b \[Severe acute respiratory syndrome coronavirus 2\]](#)
 1. Accession: GI: 1820616061
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)
- [ORF1a polyprotein \[Severe acute respiratory syndrome coronavirus 2\]](#)
 2. Accession: GI: 1802476803
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)
- [ORF10 protein \[Severe acute respiratory syndrome coronavirus 2\]](#)
 3. **38 aa protein**
Accession: YP_009725255.1 GI: 1798174256
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)
- [nucleocapsid phosphoprotein \[Severe acute respiratory syndrome coronavirus 2\]](#)
 4. **419 aa protein**
Accession: YP_009724397.2 GI: 1798174255
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)
- [ORF8 protein \[Severe acute respiratory syndrome coronavirus 2\]](#)
 5. **121 aa protein**
Accession: YP_009724396.1 GI: 1796318604
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)
- [ORF7a protein \[Severe acute respiratory syndrome coronavirus 2\]](#)
 6. **121 aa protein**
Accession: YP_009724395.1 GI: 1796318603
[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

Find related data ▲

Database:

Recent activity ▲

[Turn Off](#) [Clear](#)

- [Protein Links for Nucleotide \(Select 1798174254\) \(12\)](#) Protein
- [Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, c](#) Nucleotide
- [Protein Links for Nucleotide \(Select 1798172431\) \(10\)](#) Protein
- [Nucleotide \(Weighted\) Links for PubMed \(Select 32015508\) \(411230\)](#) Nucleotide
- [Nucleotide Links for PubMed \(Select 32015508\) \(2\)](#) Nucleotide

[See more...](#)

You could click on these sequences one at a time to access them

← → ↻ https://www.ncbi.nlm.nih.gov/protein/YP_009724390.1

surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]

NCBI Reference Sequence: YP_009724390

[Identical Proteins](#) [FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS	YP_009724390	1273 aa	linear	VRL 18-JUL-2020
DEFINITION	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2].			
ACCESSION	YP_009724390			
VERSION	YP_009724390.1			
DBLINK	BioProject: PRJNA485481			
DBSOURCE	REFSEQ: accession NC_045512.2			
KEYWORDS	RefSeq.			
SOURCE	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)			
ORGANISM	Severe acute respiratory syndrome coronavirus 2 Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes; Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus.			
REFERENCE	1 (residues 1 to 1273)			
AUTHORS	Wu, F., Zhao, S., Yu, B., Chen, Y.M., Wang, W., Song, Z.G., Hu, Y., Tao, Z.W., Tian, J.H., Pei, Y.Y., Yuan, M.L., Zhang, Y.L., Dai, F.H., Liu, Y., Wang, Q.M., Zheng, J.J., Xu, L., Holmes, E.C. and Zhang, Y.Z.			
TITLE	A new coronavirus associated with human respiratory disease in China			
JOURNAL	Nature 579 (7798), 265–269 (2020)			
PUBMED	32015508			
REMARK	Erratum: [Nature 2020 Apr; 580(7803):E7 PMID: 32206181]			

Or you can download them all at once, in various formats

Summary ▾ 20 per page ▾ Sort by Default order ▾

Items: 12

✖ There were some problems retrieving the sequence. GI: 1820616061

✖ There were some problems retrieving the sequence. GI: 1802476803

[ORF7b \[Severe acute respiratory syndrome coronavirus 2\]](#)

1. Accession: GI: 1820616061

[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)

[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

[ORF1a polyprotein \[Severe acute respiratory syndrome coronavirus 2\]](#)

2. Accession: GI: 1802476803

[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)

[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

[ORF10 protein \[Severe acute respiratory syndrome coronavirus 2\]](#)

3. 38 aa protein

Accession: YP_009725255.1 GI: 1798174256

[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)

[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

[nucleocapsid phosphoprotein \[Severe acute respiratory syndrome coronavirus 2\]](#)

4. 419 aa protein

Accession: YP_009724397.2 GI: 1798174255

[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)

[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

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 Collections Analysis Tool

Download 12 items.

Format

- Summary
- GenPept
- GenPept (full)
- FASTA**
- ASN.1
- XML
- INSDSeq XML
- TinySeq XML
- Feature Table
- FASTA CDS
- Accession List
- GI List
- GFF3

Recent activity

🔍 Protein Links for Nucleotide 1798174254) (12)

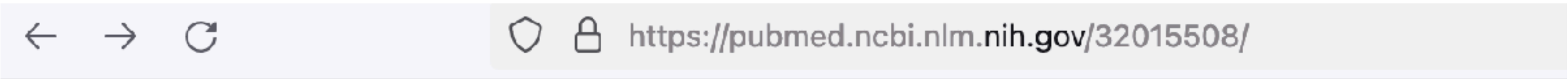
📄 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan

🔍 Protein Links for Nucleotide 1798172431) (10)

🔍 Nucleotide (Weighted) Link (Select 32015508) (411230)

🔍 Nucleotide Links for PubMed 32015508) (2)

At the bottom of the pubmed page: related information links



Related information

[Assembly](#)

[Cited in Books](#)

[Domains](#)

[Gene](#)

[MedGen](#)

[Nucleotide](#)

[Nucleotide](#)

[Nucleotide \(Weighted\)](#)

[Protein](#)

[Protein \(RefSeq\)](#)

[Protein \(Weighted\)](#)

[Related Project](#)

[SRA](#)



Click this link to get to the NGS data from this paper

[Taxonomy via GenBank](#)

The NCBI SRA database contains NGS datasets

The screenshot shows the NCBI SRA database interface. At the top, there is a navigation bar with "NCBI Resources" and "How To" menus, and a "Sign in to NCBI" link. Below this is a search bar with "SRA" selected in a dropdown menu and a "Search" button. A "Help" link is also visible.

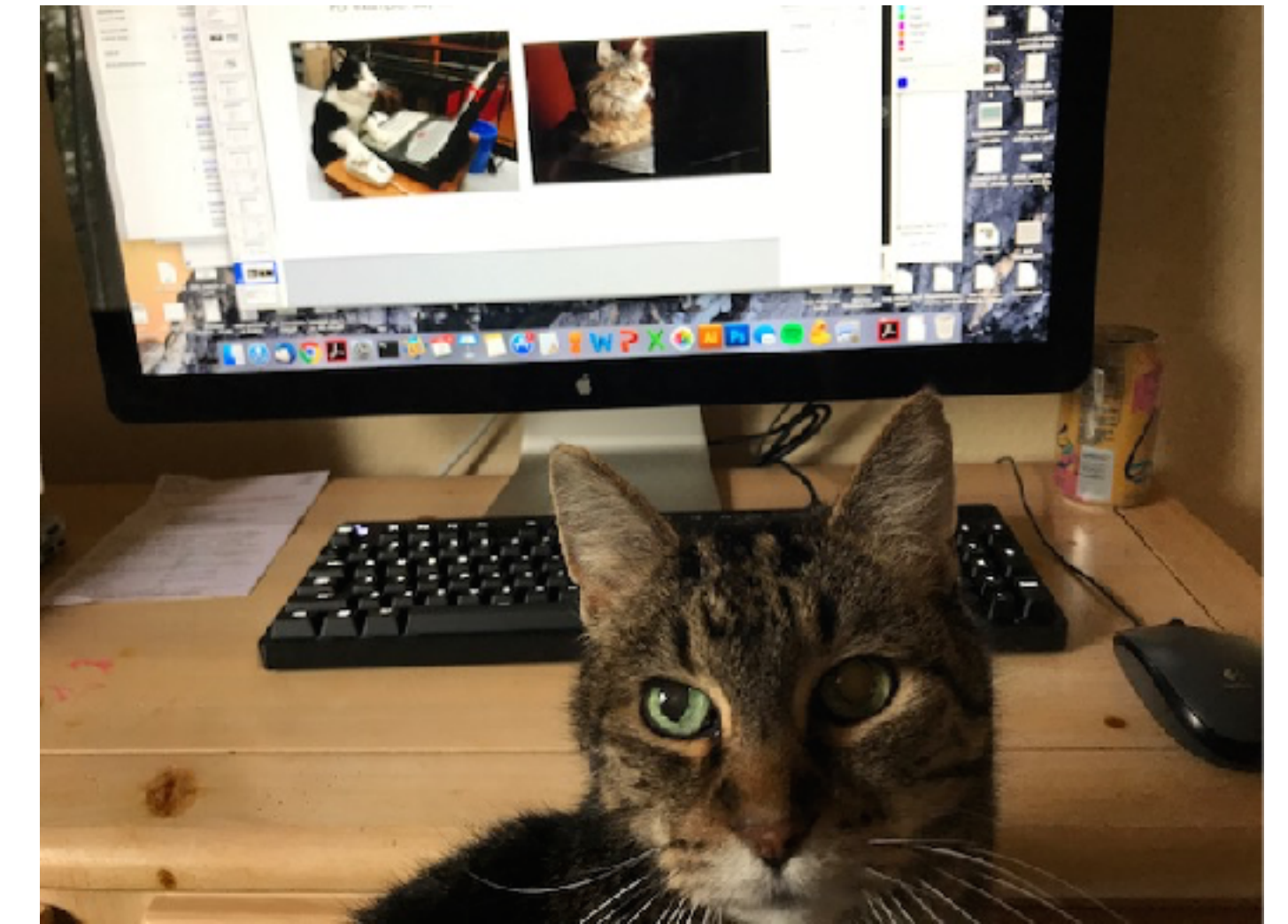
A prominent orange banner at the top of the main content area contains "COVID-19 Information" with a close button (X) and several links: [Public health information \(CDC\)](#), [Research information \(NIH\)](#), [SARS-CoV-2 data \(NCBI\)](#), [Prevention and treatment information \(HHS\)](#), and [Español](#).

The main content area is divided into two columns. The left column displays search results for the query "SRX7636886". It includes a "Full" dropdown menu and a "Send to:" dropdown menu. The results section is titled "Links from PubMed" and lists the entry "SRX7636886: Complete genome of a novel coronavirus associated with severe human respiratory disease in Wuhan, China". Below this, it provides technical details: "1 ILLUMINA (Illumina MiniSeq) run: 28.3M spots, 8G bases, 2.6Gb downloads". A "Design:" section describes the RNA extraction and sequencing process. A "Submitted by:" section identifies the Shanghai Public Health Clinical Center & School of Public Health, Fudan University. A "Study:" section provides a link to the complete genome. A "Sample:" section lists the accession number SAMN13922059 and the organism "human lung metagenome". A "Library:" section lists various parameters such as Name, Instrument, Strategy, Source, Selection, and Layout.

The right column contains two sections: "Related Information" and "Recent activity". The "Related Information" section lists links to BioProject, BioSample, PMC, PubMed, and Taxonomy. The "Recent activity" section shows a list of recent searches, including "SRA Links for PubMed (Select 32015508) (1)", "Protein Links for Nucleotide (Select 1798174254) (12)", "Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-HU-1, c Nucleotide", "Protein Links for Nucleotide (Select 1798172431) (10)", and "Nucleotide (Weighted) Links for PubMed (Select 32015508) (411230)".

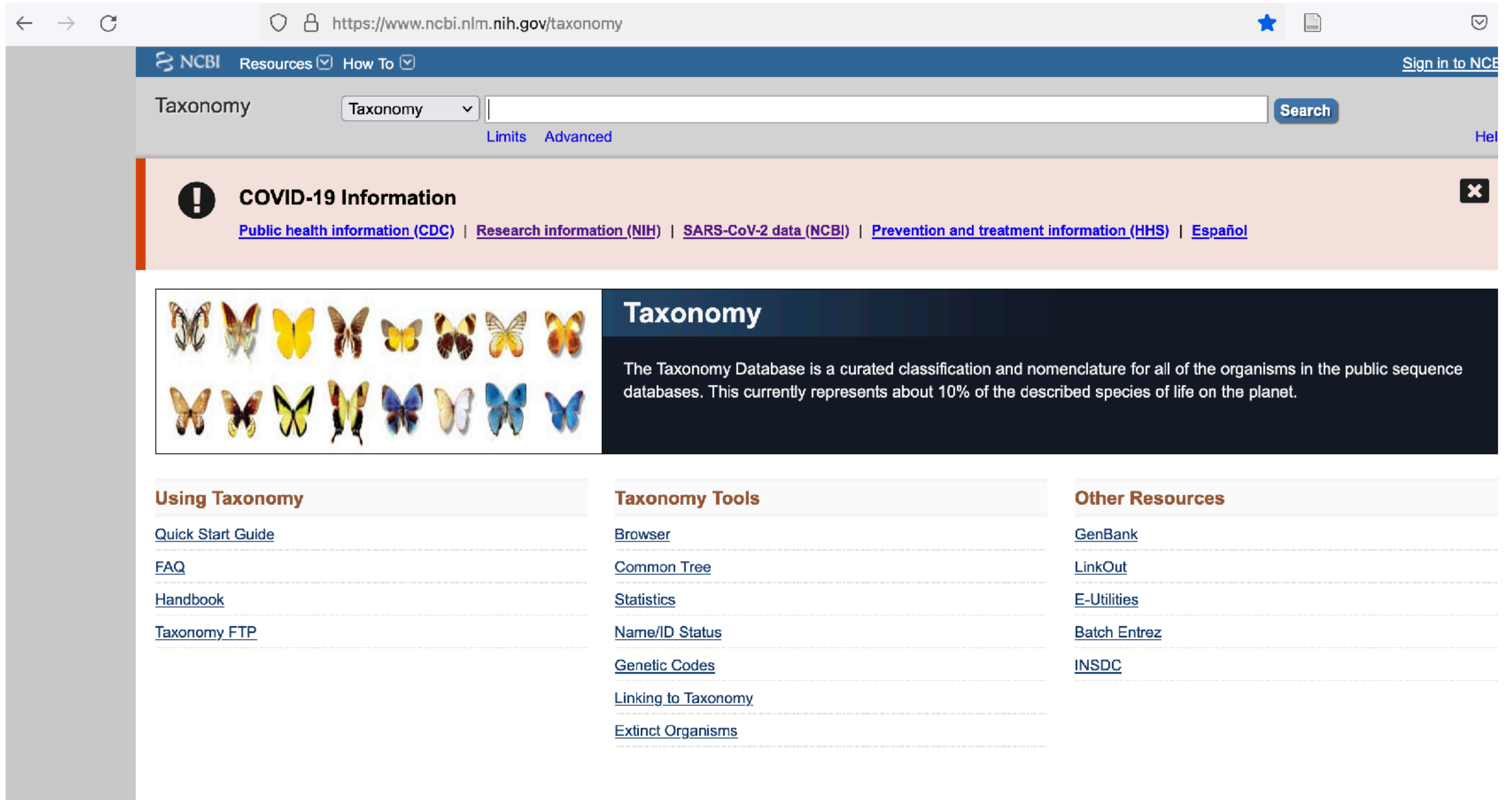
A great way to find sequence data for an organism you are interested in is via the NCBI Taxonomy database

For example, say we want to download the cat (*Felis catus*) genome



Kirby

The Taxonomy database



← → ↻ <https://www.ncbi.nlm.nih.gov/taxonomy> ★ 📄

NCBI Resources ▾ How To ▾ [Sign in to NCBI](#)

Taxonomy Taxonomy ▾ Search

[Limits](#) [Advanced](#) [Help](#)

COVID-19 Information ✕

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

Taxonomy

The Taxonomy Database is a curated classification and nomenclature for all of the organisms in the public sequence databases. This currently represents about 10% of the described species of life on the planet.

Using Taxonomy

- [Quick Start Guide](#)
- [FAQ](#)
- [Handbook](#)
- [Taxonomy FTP](#)

Taxonomy Tools

- [Browser](#)
- [Common Tree](#)
- [Statistics](#)
- [Name/ID Status](#)
- [Genetic Codes](#)
- [Linking to Taxonomy](#)
- [Extinct Organisms](#)

Other Resources

- [GenBank](#)
- [LinkOut](#)
- [E-Utilities](#)
- [Batch Entrez](#)
- [INSDC](#)

The Taxonomy page for *Felis catus*

Search for as complete name lock
Display levels using filter:

Felis catus

Taxonomy ID: 9685 (for references in articles please use NCBI:txid9685)

current name

Felis catus Linnaeus, 1758
homotypic synonym: *Felis silvestris catus*
includes: *Korat cats* L.

Genbank common name: **domestic cat**
NCBI BLAST name: **carnivores**
Rank: **species**
Genetic code: [Translation table 1 \(Standard\)](#)
Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)
Other names:

heterotypic synonym

Felis domesticus

common name(s)

cat, cats

Entrez records	
Database name	Direct links
Nucleotide	92,472
Protein	58,274
Structure	21
Genome	1
Popset	207
GEO Datasets	277
PubMed Central	3,386
Gene	46,051
SRA Experiments	2,492
Protein Clusters	12
Identical Protein Groups	45,451
Bio Project	110
Bio Sample	1,649
Bio Systems	495
Assembly	8
Probe	2,877
PubChem BioAssay	1,118
Taxonomy	1

← genome

← SRA datasets

[Lineage \(full\)](#)
[cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Dipnotetrapodomorpha](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Boreoeutheria](#); [Laurasiatheria](#); [Carnivora](#); [Feliformia](#); [Felidae](#); [Felinae](#); [Felis](#)

Felis catus in the NCBI genome database

Genome [Create alert](#) [Limits](#) [Advanced](#) [Help](#)


COVID-19 Information

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

Felis catus (domestic cat)
Reference genome: **Felis catus (assembly Felis_catus_9.0)**
Download sequences in FASTA format for **genome, transcript, protein** ← **Download genome, transcriptome, proteome, annotation**
Download genome annotation in **GFF, GenBank** or **tabular** format
BLAST against Felis catus **genome, transcript, protein**
All 4 genomes for species:
Browse the **list**
Download sequence and annotation from **RefSeq** or **GenBank**
NEW Try **NCBI Datasets** - a new way to download genome sequence and annotation we're testing in NCBI Labs

Display Settings: Send to:

Organism Overview ; [Genome Assembly and Annotation report \[4\]](#) ; [Organelle Annotation Report \[1\]](#)



Felis catus (domestic cat)
domestic cat

Lineage: [Eukaryota\[7836\]](#); [Metazoa\[3708\]](#); [Chordata\[1775\]](#); [Craniata\[1753\]](#); [Vertebrata\[1753\]](#); [Euteleostomi\[1737\]](#); [Mammalia\[470\]](#); [Eutheria\[445\]](#); [Laurasiatheria\[255\]](#); [Carnivora\[65\]](#); [Feliformia\[24\]](#); [Felidae\[16\]](#); [Felinae\[11\]](#); [Felis\[2\]](#); [Felis catus\[1\]](#)

Felis catus, the domestic cat, provides several valuable models for infectious disease, including a model for human AIDS. With a large number of recognized breeds, the cat is also a valuable resource for studying phenotypic diversity and evolution. The cat genome will further facilitate research in human medicine as some rare diseases that occur [More...](#)

Summary

Sequence data: genome assemblies: 4; sequence reads: 2 (See [Genome Assembly and Annotation report](#))
Statistics: median total length (Mb): 2507.5
median protein count: 54726
median GC%: 41.8903

NCBI Resources

[Genome Data Viewer](#)

Tools

[BLAST Genome](#)

Related Information

[Assembly](#)

[BioProject](#)

[Gene](#)

[Components](#)

[Protein](#)

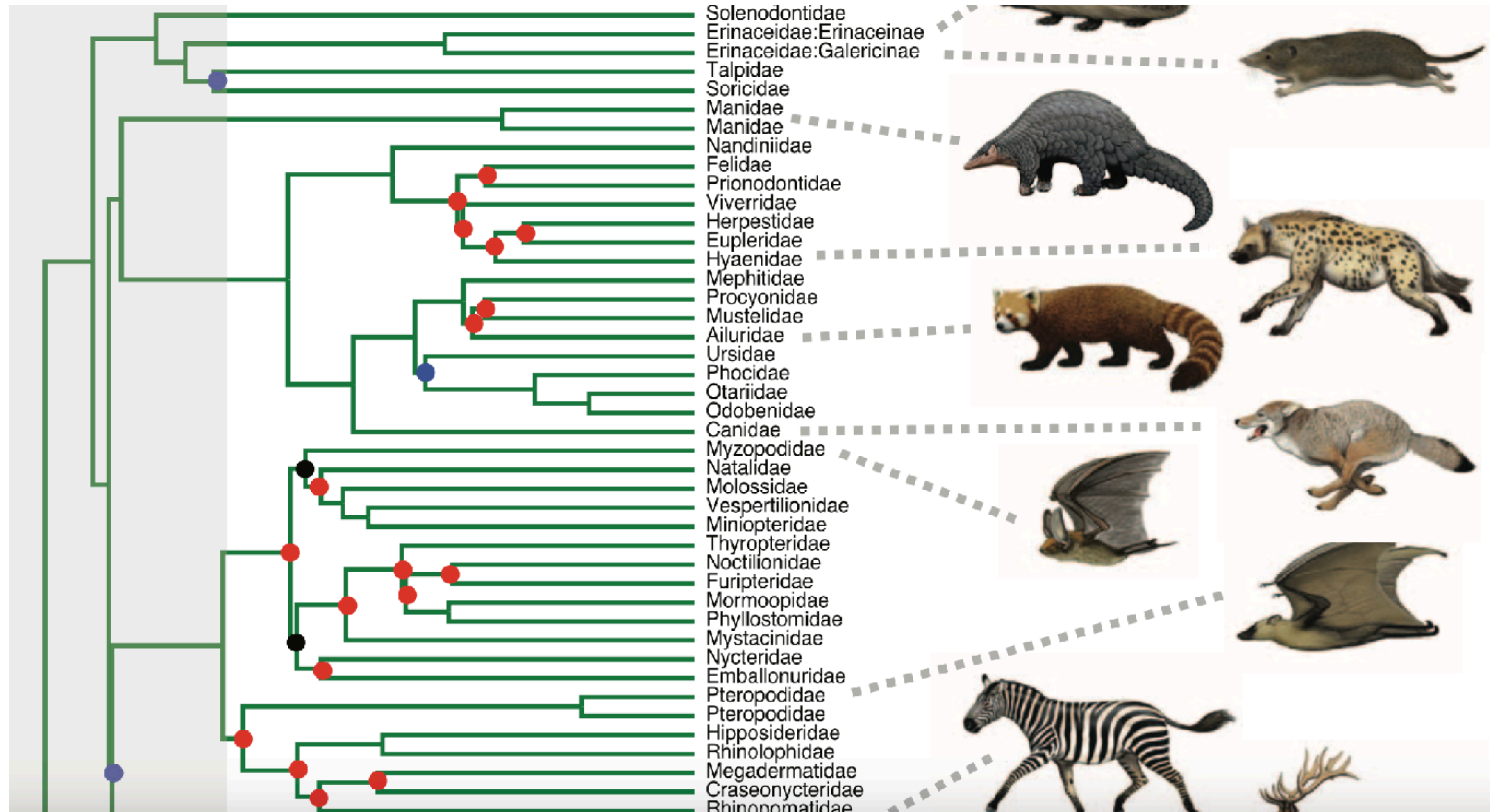
[PubMed](#)

[Taxonomy](#)

Search details

txid9685 [Organism:noexp]

The taxonomy database includes the taxonomic lineage of organisms



You can go to any point in the taxonomic tree of life in the Taxonomy db

Felis catus

Taxonomy ID: 9685 (for references in articles please use NCBI:txid9685)

current name

Felis catus Linnaeus, 1758

homotypic synonym: *Felis silvestris catus*

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Other names:

heterotypic synonym

Felis domesticus

common name(s)

cat, cats

[Lineage \(full\)](#)

[cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Dipnotetrapodomorpha](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Boreoeutheria](#); [Laurasiatheria](#); [Carnivora](#); [Feliformia](#); [Felidae](#); [Felinae](#); [Felis](#)

Eukaryotes

Mammals

Felidae

All the available genomes for species in the Felidae family

Search for as lock

Display levels using filter:

Nucleotide Protein Structure Genome Popset SNP Conserved Domains GEO Datasets PubMed Central

Gene HomoloGene SRA Experiments LinkOut BLAST GEO Profiles Protein Clusters Identical Protein Groups SPARCLE

Bio Project Bio Sample Bio Systems Assembly dbVar Genetic Testing Registry Host Viral Host Probe

PubChem BioAssay

Lineage (full): [cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Dipnotetrapodomorpha](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Boreoeutheria](#); [Laurasiatheria](#); [Carnivora](#); [Feliformia](#)

- **Felidae** (cat family) **38** ← 38 genomes for species in Felidae
 - **Acinonychinae** **1**
 - **Acinonyx** **1**
 - **Acinonyx jubatus** (cheetah) **1**
 - **Felinae** **30**
 - **Caracal** **1**
 - **Caracal caracal** **1**
 - **Catopuma** **2**
 - **Catopuma badia** (bay cat) **1**
 - **Catopuma temminckii** (Asiatic golden cat) **1**
 - **Felinae intergeneric hybrids** **1**
 - **Felis catus x Leopardis geoffroyi** **1**
 - **Felis catus x Prionailurus bengalensis**
 - **Leptailurus serval x Caracal caracal**
 - **Felis** **5**
 - **Felis catus** (domestic cat) **1**
 - **Felis chaus** (jungle cat) **1**
 - **Felis chaus x Felis catus**
 - **Felis margarita** (sand cat) **1**
 - **Felis nigripes** (black-footed cat) **1**
 - **Felis silvestris** (wild cat) **1**
 - **unclassified Felis**
 - **environmental samples**
 - **Leopardus** **7**

Felidae genomes

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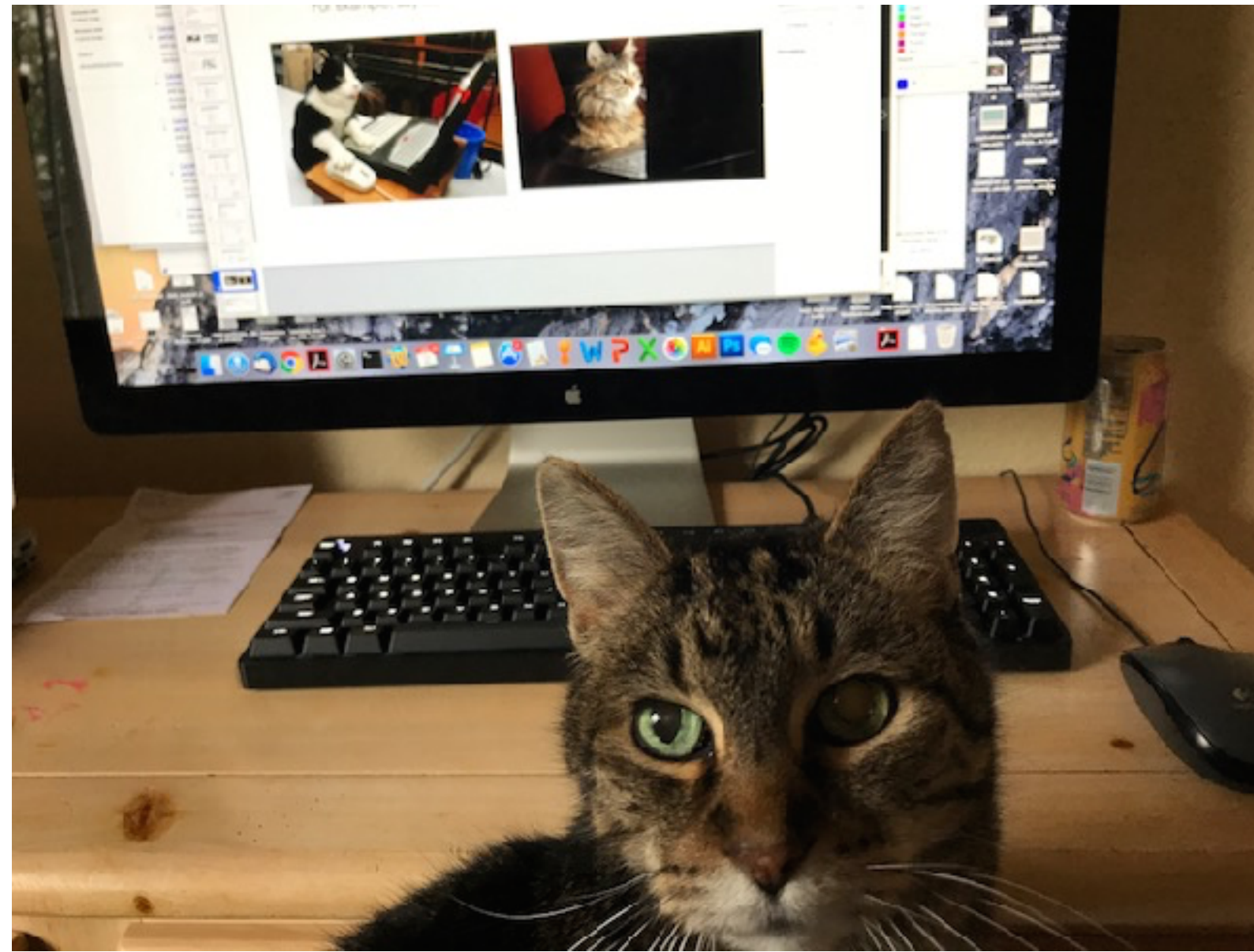
[Panthera tigris](#)

1. **tiger**
Kingdom: Eukaryota; Subgroup: Mammals
Sequence data: genome assemblies:3
Haploid chromosomes: 19; Organelles: 1
Date: 2013/09/05
ID: 10802

[Panthera leo](#)

2. **Panthera leo overview**
Kingdom: Eukaryota; Subgroup: Mammals
Sequence data: genome assemblies:3
Haploid chromosomes: 19
Date: 2019/10/01
ID: 13342

Questions?



Kirby in 2000