



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL



**World Health
Organization**
Philippines



KDCA

Korea Disease Control and
Prevention Agency

Genetic Databases

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Philippine Genome Center
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April 18, 2024



**CENTRE FOR
PATHOGEN
GENOMICS**

 **Doherty
Institute**

A joint venture between The University of Melbourne and The Royal Melbourne Hospital



The Royal
Melbourne
Hospital

Objectives



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- To familiarize with genetic sequence databases:
NCBI, GISAID
- To search sequence data
- To retrieve sequences
- To do a BLAST search
- To download sequences and metadata files

What is a genetic database?



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- A collection of DNA or RNA sequences that have been determined and stored for research and analysis purposes.
- These databases serve as repositories of genetic information and provide valuable resources for scientists and researchers in various fields, such as genomics, genetics, and bioinformatics.

Moore's Law and Carlson Curve

Moore's Law: The number of transistors on microchips doubles every two years

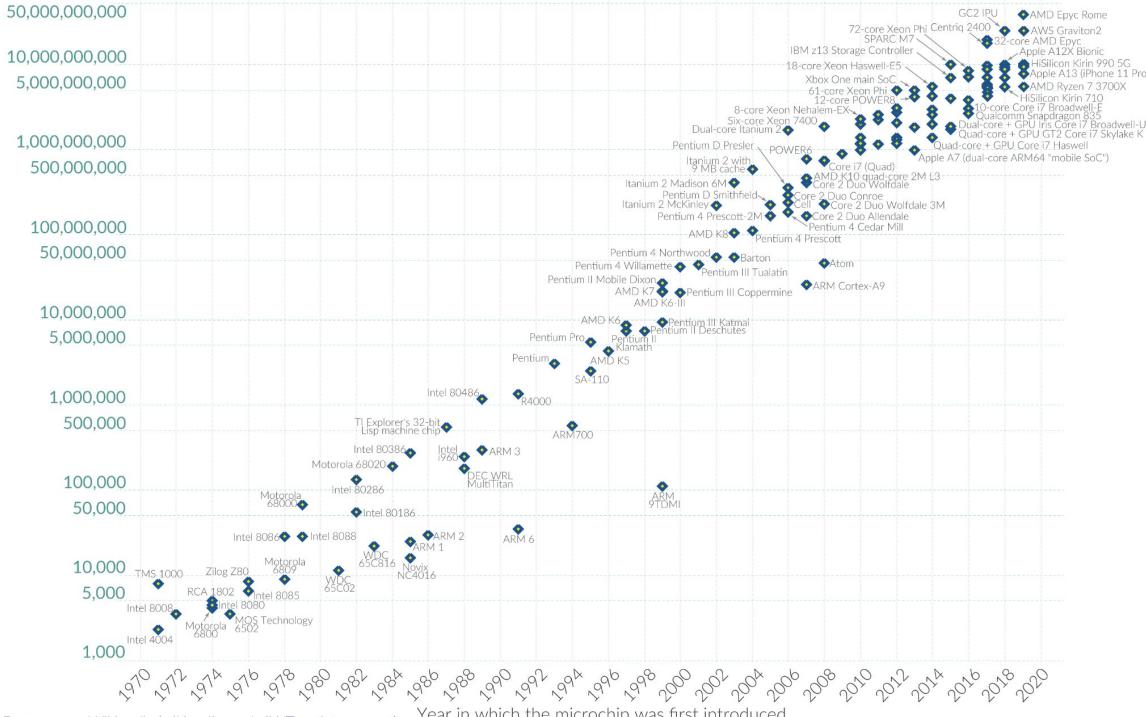
Moore's law describes the empirical regularity that the number of transistors on integrated circuits doubles approximately every two years. This advancement is important for other aspects of technological progress in computing – such as processing speed or the price of computers.



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Our World
in Data

Transistor count

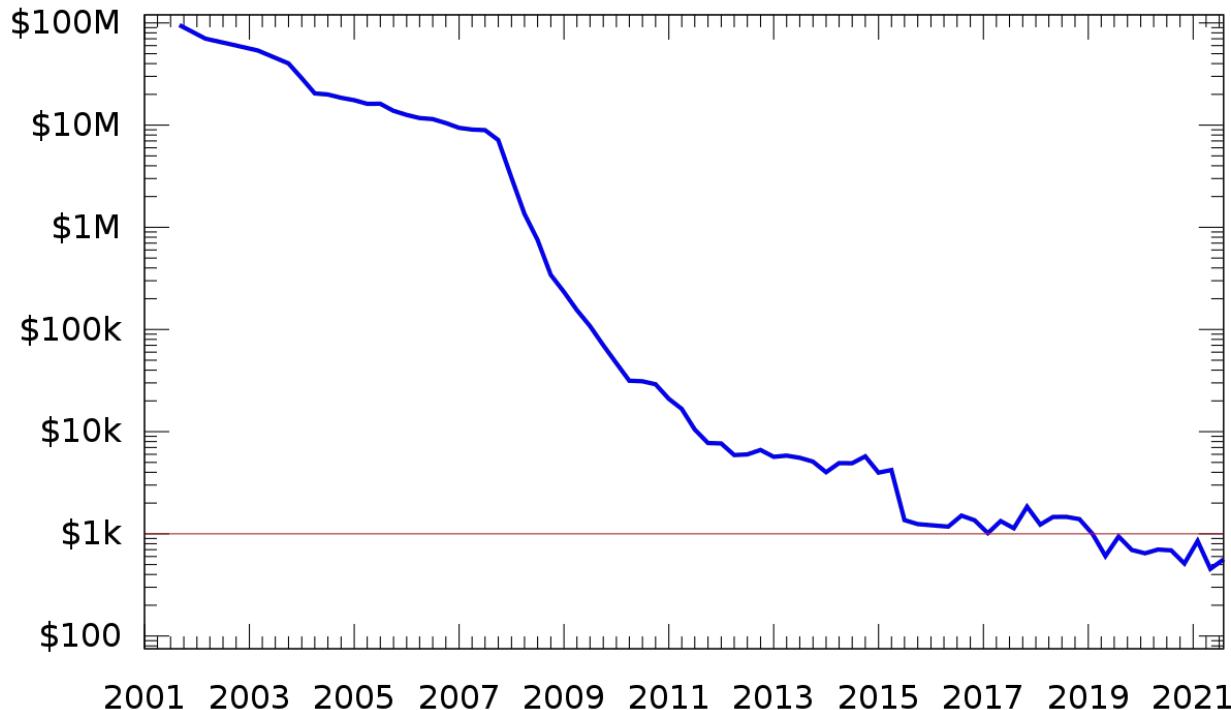


Moore's Law and Carlson Curve

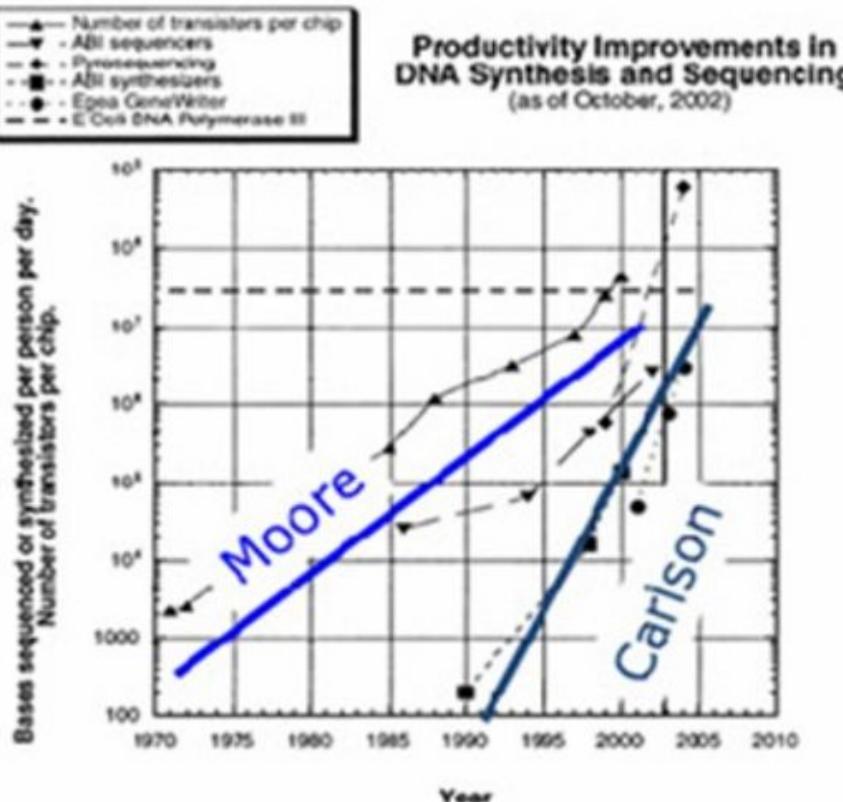


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Cost to sequence a human genome (USD)



Moore's Law and Carlson Curve



Why use genetic databases?



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- Data access and sharing
- Comparative genomics for evolutionary studies
- Gene identification and annotation
- Submission of sequences is a requirement for publication

An official website of the United States government [Here's how you know](#)

NIH National Library of Medicine

National Center for Biotechnology Information

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Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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Easy Access to Genetic Test Information with the NIH Genetic Testing Registry (GTR)

09 Apr 2024

[We have made some exciting updates to](#)

MedGen Users, We Want Your Feedback!

28 Mar 2024

Do you use NCBI's MedGen? If so, then you probably know it's NCBI's one-stop

Changes to SRA Data Access on the Google Cloud Platform (GCP)

20 Mar 2024

← → C https://www.ncbi.nlm.nih.gov/genomes/FLU/Database/nph-select.cgi?go=database

NCBI Resources How To Sign in to NCBI HHS Vulnerability Disclosure

Influenza Virus Resource

Information, Search and Analysis

Influenza Virus Database

Related links New features How to cite Contact us Help

Overview Database Genome Set BLAST Annotation Submission FTP Virus resources ▾

Protein or nucleotide sequences can be retrieved from the database using GenBank accession numbers or search terms. Multiple queries can be built by clicking the "Add Query" button every time a new query is made, and queries in any combination from the Query Builder can be selected to get sequences in the database. Sequences can be downloaded, and it is possible to analyze them using the multiple sequence alignment or tree building tool integrated to the database.

Get sequences by accession

Enter a comma or space separated list of sequence accessions or upload text file with this list.

No file selected.

Select sequence type:

Protein Protein coding region Nucleotide

Search for keyword:

Keyword Search in strain name

Define search set:

Type	Host	Country/Region	Protein	Subtype
any	any	any	any	H any
A	Avian	regions	PB2	1
B	Bat	Northern temperate	PB1	2
C	Blow fly	Southern temperate	PB1-F2	3

Sequence length Collection date Release date

Min.: From: Year Month Day

Max.: To: Year Month Day

Full-length only Full-length plus

Additional filters:

Collapse identical sequences

Influenza Virus Data Hub

[Download](#) ▾

Select genus:

 Alphainfluenzavirus (A) Gammainfluenzavirus (C)
 Betainfluenzavirus (B) Deltainfluenzavirus (D)

Quick Links

[Influenza Virus BLAST](#)
[Influenza Virus Annotation Tool \(FLAN\)](#)
[Influenza Virus Articles in PubMed](#)
[Submit assembled sequences to GenBank](#)
[Submit sequence reads to SRA](#)
[Legacy Influenza Resource](#)
[Advanced Filters for GenBank Sequences](#)

Selected Results: 0

[Align](#) [Build Phylogenetic Tree](#)

ⓘ New! Randomized subsets in Downloads

You now have the option of downloading a smaller, randomized subset of the data shown in the Results table. Begin by using filters to refine your dataset, select the Nucleotide, Protein, or RefSeq Genome tab above the table for the datatype you would like to download, then follow the prompts in the Download menu. Our [Help documentation](#) has more information.

Refine Results Reset

Virus +

- Alphainfluenzavirus, taxid:197911 ✖
- Betainfluenzavirus, taxid:197912 ✖
- Gammainfluenzavirus. ✖

Expand Table

Nucleotide (1,172,924)		Protein (1,569,151)		RefSeq Genome (10)		Select Columns							
<input type="checkbox"/>	Accession ▲	<input type="checkbox"/>	Organism Name New! ▲	<input type="checkbox"/>	Submitters ▲	<input type="checkbox"/>	Organization ▲	<input type="checkbox"/>	Release Date ▲	<input type="checkbox"/>	Isolate ▲	<input type="checkbox"/>	Species
<input type="checkbox"/>	NC_036615 RefSeq	Influenza D virus (D/swine...)	Hause,B.M., et ...	<input type="checkbox"/>	National Center for Biotech...	<input type="checkbox"/>	2018-01-16	<input type="checkbox"/>		<input type="checkbox"/>	Deltainf...	<input type="checkbox"/>	Deltainf...
<input type="checkbox"/>	NC_036616 RefSeq	Influenza D virus (D/swine...)	Hause,B.M., et ...	<input type="checkbox"/>	National Center for Biotech...	<input type="checkbox"/>	2018-01-16	<input type="checkbox"/>		<input type="checkbox"/>	Deltainf...	<input type="checkbox"/>	Deltainf...
<input type="checkbox"/>	NC_036617 RefSeq	Influenza D virus (D/swine...)	Hause,B.M., et ...	<input type="checkbox"/>	National Center for Biotech...	<input type="checkbox"/>	2018-01-16	<input type="checkbox"/>		<input type="checkbox"/>	Deltainf...	<input type="checkbox"/>	Deltainf...
<input type="checkbox"/>	NC_036618 RefSeq	Influenza D virus (D/swine...)	Hause,B.M., et ...	<input type="checkbox"/>	National Center for Biotech...	<input type="checkbox"/>	2018-01-16	<input type="checkbox"/>		<input type="checkbox"/>	Deltainf...	<input type="checkbox"/>	Deltainf...



Explore Virus Data

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[West Nile virus](#)
[MERS coronavirus](#)
[SARS-CoV-2 coronavirus](#)
[Advanced Filters for GenBank Sequences](#)
[Visual Filters for GenBank Sequences ⓘ](#)

Selected Results: 0

[Align](#)
[Build Phylogenetic Tree](#)

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Refine Results [Reset](#)

Virus [+](#)

Severe acute respiratory syndrome-related coronavirus, taxid:694009 [X](#)

Accession [+](#)

Sequence Length [+](#)

Ambiguous Characters [+](#)

[Expand Table](#)

Select Columns					
Nucleotide (8,798,520)		Protein (45,007,462)		RefSeq Genome (2)	
<input type="checkbox"/>	Accession ▲	Organism Name New! ▲	Submitters ▲	Organization ▲	Release Date ▲
<input type="checkbox"/>	NC_045512 <small>RefSeq</small>	Severe acute respiratory s...	Wu,F., et al.	National Center for Biotech...	2020-01-13
<input type="checkbox"/>	NC_004718 <small>RefSeq</small>	SARS coronavirus Tor2	He,R., et al.	National Center for Biotech...	2003-04-14
<input type="checkbox"/>	PP654379	Severe acute respiratory s...	Opentrans,P.	NYC DOHMH, Bureau of th...	2024-04-12
<input type="checkbox"/>	PP654380	Severe acute respiratory s...	Opentrans,P.	NYC DOHMH, Bureau of th...	2024-04-12
<input type="checkbox"/>	PP654381	Severe acute respiratory s...	Opentrans,P.	NYC DOHMH, Bureau of th...	2024-04-12

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In Focus

16 million hCoV-19 sequences shared: Where do surveillance efforts stand?

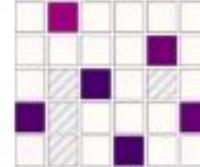
After mixed efforts in 2020, followed by a massive explosion of Omicron data generated by late 2021 from 215 countries and territories, the number of unique submitting countries, and hence, representativeness of global surveillance, today remains at early 2021 levels, and well above 2020 levels.

While the US, UK, and Germany contributed an outsized share in 2022, it is worth pointing out that increasing representation of diverse regions over time, and the timeliness of submissions are far more critical to ensure new variants are detected in real-time. The recent timely discovery of BA.2.86 and EG.5.1 are examples of continued effectiveness so far.



中国新冠疫情

Variation comparison



hCoV-19 data sharing via GISAID

16,659,235

genome sequence submissions

Phylogenetics

[hCoV-19 \(COVID-19\)](#)[Dengue](#)[Influenza](#)[MpoX](#)[RSV](#)

Tracking Variants

[hCoV-19 Variants](#)[Mpox Variants](#)[Influenza Subtypes](#)[RSV Subtypes](#)

Frequency Dashboards

[hCoV-19 \(COVID-19\)](#)[Mpox](#)[Influenza](#)[RSV](#)

GISAID Resources

Data Acknowledgement Locator

 EPI_SET ID Example ID

Register for Access Credentials

obtain free access and collaborate with tens-of-thousands of researchers

GISAID

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Pandemic coronavirus causing COVID-19

A previously unknown human coronavirus (hCoV-19) was first detected in late 2019 in patients in the City of Wuhan, who suffered from respiratory illnesses including atypical pneumonia, an illness that has become known as coronavirus disease (COVID-19). The coronavirus originated from an animal host and is closely related to the virus responsible for the Severe Acute Respiratory Syndrome coronavirus (SARS).

On 10 January 2020, the first virus genomes and associated data were publicly shared via GISAID. The World Health Organization announced on 11 March 2020 the first coronavirus pandemic. As the pandemic progresses, scientists from around the globe are tracking the virus and its genome sequences to ensure optimal virus diagnostic tests, to track and trace the ongoing outbreak and to identify potential intervention options. Several analyses to assist with these efforts are offered here, including sequence alignments, diagnostic primer and probe coordinates, 3D protein models, drug targets, phylogenetic trees and many more.

A circular phylogenetic tree centered on a 3D model of a COVID-19 spike protein. The tree branches outwards, with various colored tips representing different variants and lineages. Labels include "SARSCoV2", "SARSCoV1", "MERS", "SARS", and many specific variant names like "B.1.1.529", "B.1.1.519", etc. A vertical sidebar on the right lists "SARSCoV2", "SARSCoV1", "MERS", "SARS", and "Other".

Audacity

Audacity Instant

BLAST

CoVizue

Emerging Variants

Lineage Frequency

Official GISAID reference sequence

PrimerChecker

Submission tracker

Spike glycoprotein mutation surveillance

Wastewater

Analysis Update (2024-04-02)

Important note: In the [GISAID EpiFlu™ Database Access Agreement](#), you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the [GISAID EpiFlu™ Database Access Agreement](#) in respect of such data in the same manner as if they were data relating to influenza viruses.

v2.5.1

GISAID

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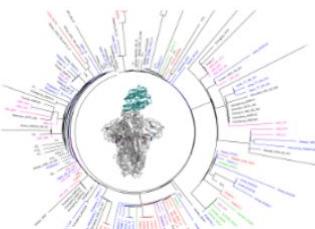
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EpiCoV™ **Search** Downloads | Upload

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[Search](#)



Audacity



AudacityInstant



BLAST



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B.1.475	0.475
B.1.476	0.476
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B.1.480	0.480
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B.1.612	0

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EPI_ISL ID	<input type="text"/>	Virus name	<input type="text"/>	EPI_SET ID	<input type="text"/>	<input type="checkbox"/> Complete ⓘ
Location	<input type="text"/>		Host	<input type="text"/>	<input type="checkbox"/> High coverage ⓘ	
Collection	<input type="text"/>	to	<input type="text"/>	Submission	<input type="text"/>	<input type="checkbox"/> Low coverage excluded ⓘ
Clade	<input type="text"/>	Lineage	<input type="text"/>	Variant	<input type="text"/>	<input type="checkbox"/> With patient status ⓘ
AA Substitutions ⓘ	<input type="text"/>		Nuc Mutations ⓘ	<input type="text"/>	<input type="checkbox"/> Collection date complete ⓘ	
						<input type="checkbox"/> Under investigation

Text Search

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission		Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0221/2024	Original	EPI_ISL_19052879	2024-04-01	2024-04-15		29,837	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0220/2024	Original	EPI_ISL_19052878	2024-03-28	2024-04-15		29,870	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0219/2024	Original	EPI_ISL_19052877	2024-03-26	2024-04-15		29,869	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0218/2024	Original	EPI_ISL_19052876	2024-03-25	2024-04-15		29,870	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0217/2024	Original	EPI_ISL_19052875	2024-03-21	2024-04-15		29,868	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0216/2024	Original	EPI_ISL_19052874	2024-03-21	2024-04-15		29,823	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0215/2024	Original	EPI_ISL_19052873	2024-03-21	2024-04-15		29,867	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0214/2024	Original	EPI_ISL_19052872	2024-03-20	2024-04-15		29,835	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0213/2024	Original	EPI_ISL_19052871	2024-03-19	2024-04-15		29,833	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0212/2024	Original	EPI_ISL_19052870	2024-03-19	2024-04-15		29,833	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0211/2024	Original	EPI_ISL_19052869	2024-03-18	2024-04-15		29,832	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0210/2024	Original	EPI_ISL_19052868	2024-03-18	2024-04-15		29,828	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0209/2024	Original	EPI_ISL_19052867	2024-03-14	2024-04-15		29,866	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0208/2024	Original	EPI_ISL_19052866	2024-03-14	2024-04-15		29,868	Human	North America / U	Mississippi

Total: 16,659,891 viruses

<< < **1** 2 3 4 5 > >>

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Pandemic coronavirus causing COVID-19

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Emerging Variants

Lineage Frequency

Official GISAID reference sequence

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Spike glycoprotein mutation surveillance

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Analysis Update (2024-04-02)

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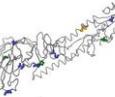
Emerging Variants



EpiCharts



PrimerChecker



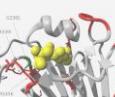
FluSurver



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Submission Tracker



HA Mutation Surveillance



Subtype / Clade Frequency



Vaccine Reference Sequences



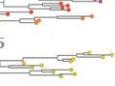
Phylogenetics Global H3N2



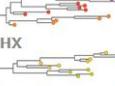
Phylogenetics Global H1N1



Phylogenetics Global B Vic



Phylogenetics Global H5



Phylogenetics Global HX

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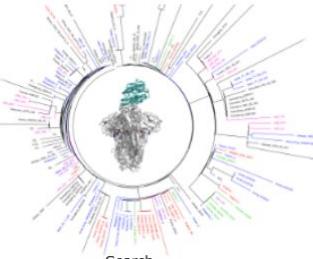
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Emerging Variants



Lineage Frequency



Official GISAID reference sequence



PrimerChecker



Submission tracker



Spike glycoprotein mutation surveillance



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Global Phylogeny

Audacity v1.33

Color by
Continent | All

By continent

- Europe
- North America
- Asia
- South America
- Oceania
- Africa
- Other



Newick tree

The global phylogeny of hCoV-19 data is made available as a Newick tree file. The tree uses 12,627,040 high quality genomes. The analysis is carried out with the most recent sequences. To access older versions please use the calendar to the right.

14 April 2024

To access older versions of the tree please use the calendar above.

[DOWNLOAD TREE](#)

Zipped Newick tree and CSV metadata,
181.7MB



A joint venture between The University of Melbourne and The Royal Melbourne Hospital

AudacityInstant (v5.1.0)

Feedback

Find the genomes that are closely related to your hCoV-19 sequences

AudacityInstant searches the entire EpiCoV database to find closely related sequences, providing valuable metadata about each related sequence, such as their Clade, Lineage, Location, Variant, and Collection Date.

Paste sequences in FASTA format

No files chosen.

BROWSE FILES

or upload FASTA file

Try with an example sequence

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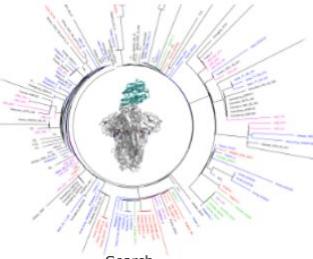
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 CoVizue



 Emerging Variants



 Lineage Frequency



 Official GISAID reference sequence



 PrimerChecker



 Submission tracker



 Spike glycoprotein mutation surveillance



 Wastewater

Analysis Update (2024-04-02)

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BLAST (v1.2.2)

BLAST searches against sequences collected during the last three months.

Use AudacityInstant to search for closely-related sequences against all sequences in the EpiCoV database.

For further questions and suggestions contact [audacity1support@gisaid.org].

> Paste up to 10 FASTA-Sequences here

Submit hCoV-19 BLAST

BLAST (v1.2.2)

BLAST searches against sequences collected during the last three months.

Use AudacityInstant to search for closely-related sequences against all sequences in the EpiCoV database.

For further questions and suggestions contact audacityIsupport@gisaid.org.

[Submit hCoV-19 BLAST](#)

Nucleotide BLAST 2.6.0+ | 297,370 sequences | Updated 16 hour(s) and 0 minute(s) ago

1. Query:

Subject collection date prior to query collection date

HSPs ▾



1. Subject: hCoV-19/England/CJ TMB-CM7YE1HM/2024 Download HSP(s)

EPT TSI 18860928 Location Europe / United Kingdom / England Collection Date 2024-01-21 Length 29.765bp

HSP 1 | Identity 99.73%, Score 4711, Bit-Score 8700.69, eValue 0, Length 4739, Gaps 0, From (Query/Subject) 16413/16367, To (Query/Subject) 21151/21105

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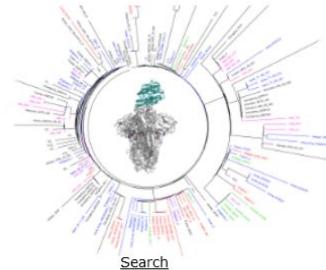
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Emerging Variants


Lineage Frequency


Official GISAID reference sequence


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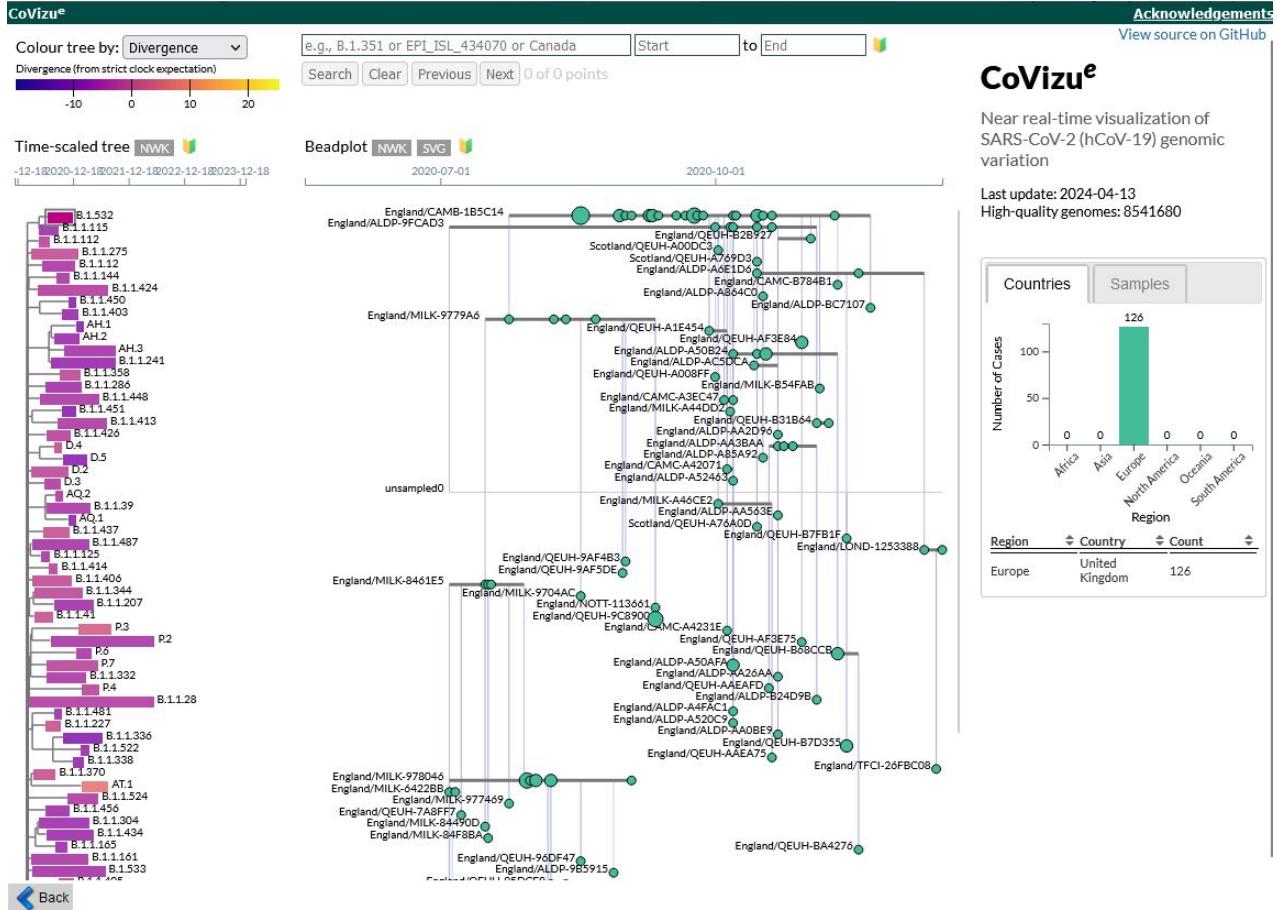

Spike glycoprotein mutation surveillance


Wastewater

Analysis Update (2024-04-02)

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A circular phylogenetic tree centered on a 3D model of a COVID-19 spike protein. The tree branches outwards, with labels for various SARS-CoV-2 variants and their source locations. A vertical scroll bar on the right side of the tree indicates it can be viewed in full.

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Emerging Variants



Lineage Frequency



Official GISAID reference sequence



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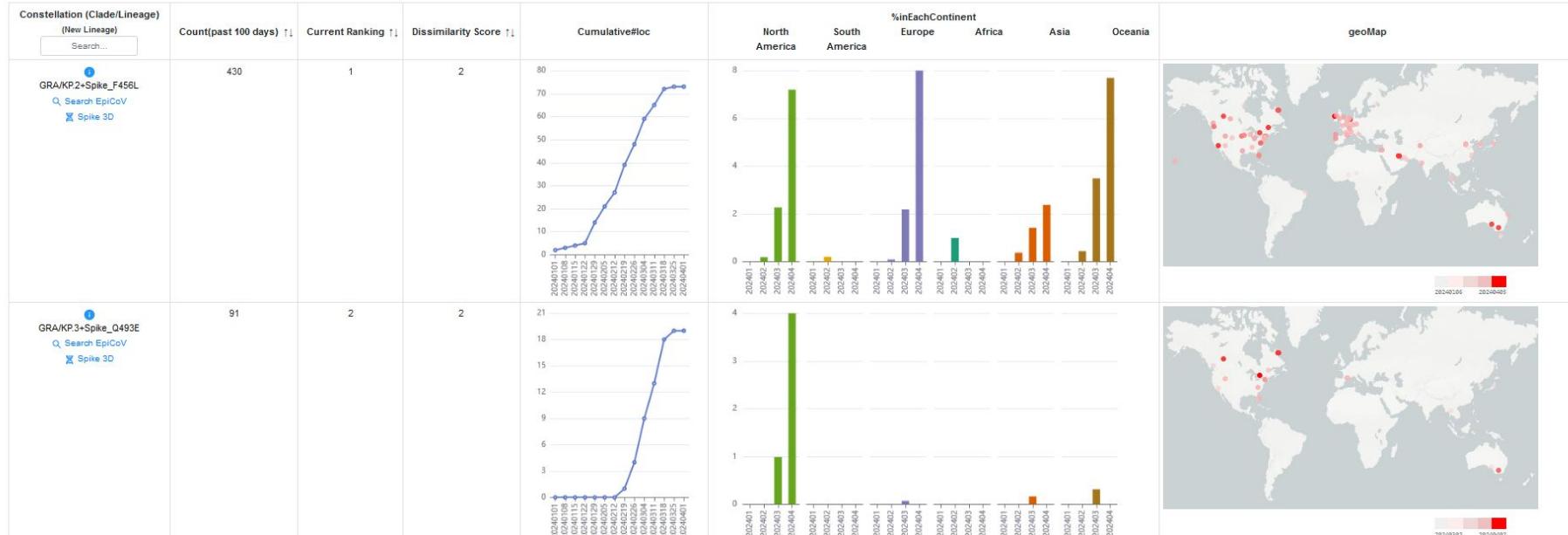
Emerging Variants (v1.22.01)

Spread Acceleration

This site helps to monitor emerging hCoV-19 variants that could become relevant due to signs of increased spread (estimated by change in number of locations) combined with potential effects on receptor or antibody binding as annotated in CoVsurer. Please click [here](#) for a more detailed method description.

All countries

Input comma separated mutations here for search, then press Enter...



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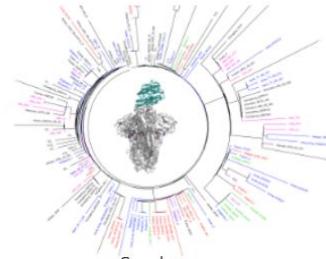
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A circular phylogenetic tree centered on the SARS-CoV-2 virus. The tree branches out into various lineages, each represented by a different color. Labels on the branches include names like Alpha, Beta, Gamma, Delta, Epsilon, Zeta, Eta, Iota, Kappa, Mu, Nu, Omicron, and Pi. The tree is densely labeled with numerous individual variant names and numbers.

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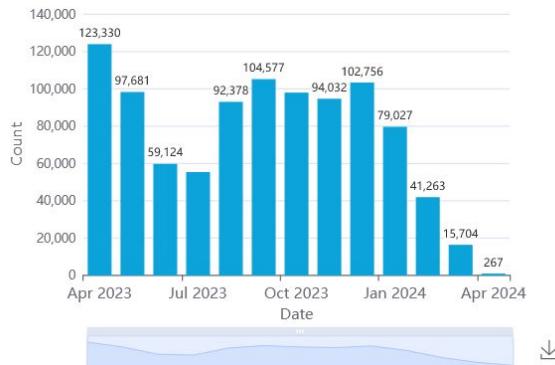
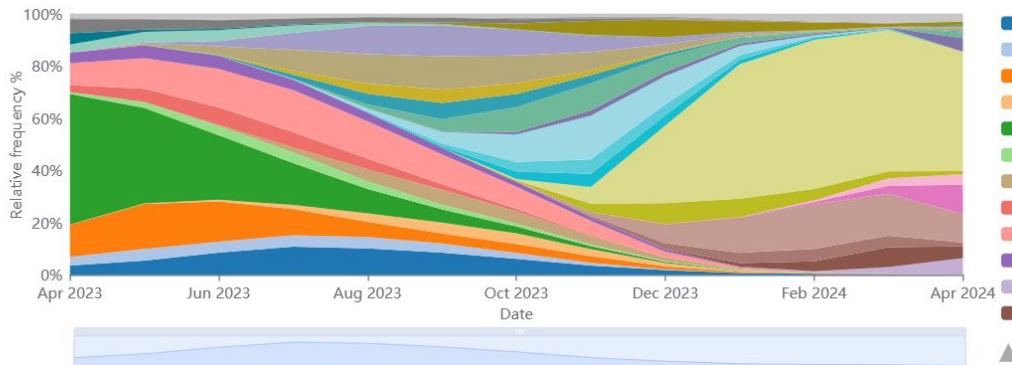
Lineage Frequency

Acknowledgements

Data to produce the charts was updated on 15 April 2024 16:00UTC. Lineages below 4% are combined and counted as part of their parental lineages.

Lineage Relative Frequencies Over Time

All Countries



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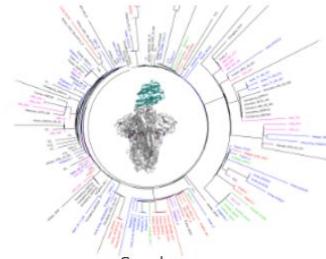
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hCoV-19/Wuhan/WIV04/2019 (**WIV04**) is the official reference sequence employed by GISAID (EPI_ISL_402124). WIV04 was chosen because of its high-quality genome sequence and because it represented the consensus of a handful of early submissions for the betacoronavirus responsible for COVID-19. (Pilailuk et al 2020)

WIV04 is representative of and identical to the early outbreak sequences. WIV04 was isolated by the Wuhan Institute of Virology from a clinical sample of a bronchoalveolar lavage fluid (BALF) collected at the Wuhan Jinyintan Hospital in Hubei Province on 30th December 2019 from a symptomatic patient, a retailer working at the Huanan Seafood Wholesale Market.

BALF was used for RNA extraction and metagenomic next-generation sequencing (NGS). The consensus sequence was obtained by de-novo assembly. (Zheng-Li Shi et al 2020)



ORF1ab

Position 266 to 21555, length: 21289nt
(ribosomal frameshift at position 13468)

Proteins

1. ORF1ab polyprotein
7096 AA
2. Protein by proteolytic cleavage: Nonstructural protein NSP1
180 AA (1Met-Gly180)
3. Protein by proteolytic cleavage: Nonstructural protein NSP2
638 AA (181Ala-Gly818)
4. Protein by proteolytic cleavage: Nonstructural protein NSP3
1944 AA (819Ala-Gly2763)
5. Protein by proteolytic cleavage: Nonstructural protein NSP4
499 AA (2764Lys-Gln3263)
6. Protein by proteolytic cleavage: Nonstructural protein NSP5
605 AA (3264Ser-Gln3569)
7. Protein by proteolytic cleavage: Nonstructural protein NSP6
289 AA (3570Ser-Gln3859)
8. Protein by proteolytic cleavage: Nonstructural protein NSP7
82 AA (3860Ser-Gln3942)

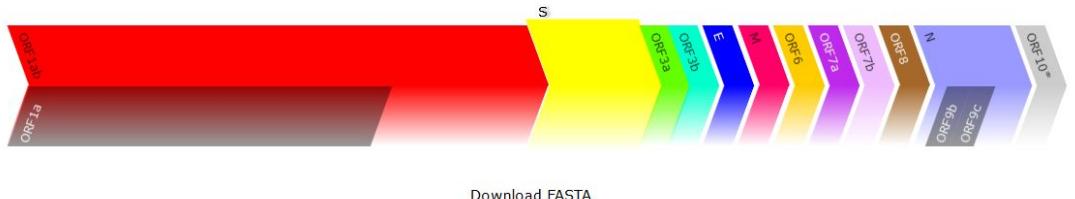
Evidence in the Literature

1. Denisa Bojkova KK, Koch B, Widera M, Krause D, Ciesek S, Cinatl J, Münch C. SARS-CoV-2 infected host cell proteomics reveal potential therapy targets. *Nature* (2020) DOI: [10.21203/rs.3.rs-17218/v1](https://doi.org/10.21203/rs.3.rs-17218/v1)
2. Davidson, A.D., Williamson, M.K., Lewis, S. et al. Characterisation of the transcriptome and proteome of SARS-CoV-2 reveals a cell passage induced in-frame deletion of the furin-like cleavage site from the spike glycoprotein. *Genome Med* 12, 68 (2020) DOI: [10.1186/s13073-020-00763-0](https://doi.org/10.1186/s13073-020-00763-0)
3. Wu, F., Zhao, S., Yu, B. et al. A new coronavirus associated with human respiratory disease in China. *Nature* 579, 265–269 (2020) DOI: [10.1038/s41586-020-2008-3](https://doi.org/10.1038/s41586-020-2008-3)

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S

Position 21563 to 25384, length: 3821nt
(Protein: Spike glycoprotein Length: 1273 AA)

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1. Denisa Bojkova KK, Koch B, Widera M, Krause D, Ciesek S, Cinati J, Münch C. SARS-CoV-2 infected host cell proteomics reveal potential therapy targets. *Nature* (2020) DOI: [10.1126/science.abb3718/v1](#)
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Nucleotide Sequence

Click sequence to download FASTA

```
ATGTTGTTTCTGTTTGTCCACTAGTCAGTGTTAACTTACAACAGAACTCAATTCCCCGCATACATAATTCTTACAGCTGGTTTATTACCTCGACAAAGTTTCAGATCTCAGTTT
AATTCCAACTCAGGACTTGTCTTACCTTCTTCAATGTTACTTGGTTCATGCTATACATGCTCTGGGACCAATGGTACTAAAGGGTTGATAACCTGTCCTACCATTAATGAGTTTATTGTC
AGAAGCTTAACTATAAAGGAGCTGATTTTGACTCTTAGATTGCGAACAGCTTCACTTAACTTGTAAATACGCTACTAATGTTTAAAGGTTGTAATTTGTCAGGTTTAACTTGTAAATGATGTCATTTGGGTTG
TATTGCTTAAAGAATATTGATGTTATTAAAATATTTCTAAGCACAGCCCTTAATTGCGCTGATCTCCCTCAGGGTTTGGCTTAGACCAATTGCTAGATTGCTCAATAGTTAACATCACTAGTTT
AAACTTACTTGTGACTTACATGAAGTTTGTGACTCTGGTGTATTCTTCACTGAGCTTAAATTGTGGTTATCTTCAACCTAGGGACTTTTATTAAAATATAATGAAAAGGAAACATTACA
GATGCTGAGCTGACTCTGGCCTCTCAGAAACAAAGTGTACGGTAAATCTTCACTGAGATACTTGTGAGCTTACAGCAACTGTTGCTGATTTCTGCTTCTATAATTCGCACTTTCACCTTAAAGTGTATGGAG
TGTCTCTACTAAATTAATGATCTCTGTTTACTAATGCTATGCAAGATTCTGTAATAGAGGTGATGAAGTCAGACAAATGCTCAGGGCAAACCTGAAAGATTGCTGATTATAATTAAACAGATGATT
ACAGGTGCGTTAGCTGGATTCTAACATCTGTAAGGTTGGTAATTATAATTCTGTATAGATTGTTAGGAAGTCTAATCTAACACCTTGGAGAGAGATTTCACTGAAATCTATCAGGCCGTAG
```

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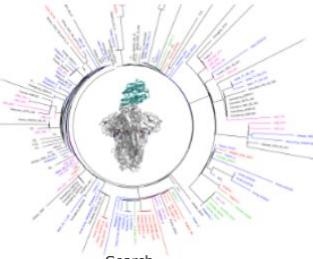
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Methodology

PrimerChecker uses the `blastn` algorithm from Basic Local Alignment Search Tool (BLAST) with parameters for short sequence matches to search primers against high quality sequences within GISAID's database. A high-quality genome is defined as <1% Ns and <0.05% unique non-synonymous mutations. The result provided is a list of virus sequences with one or more mutations in either forward, probe or reverse primer region with interactive display of time and location of the respective samples. This does not necessarily indicate a primer would not function but serves as a guide to variability of the targeted region.

FASTA Sequence

Select from a list of public primers or paste your own primer FASTA below.

Due to a technical limitation, we have temporarily restricted queries to primer sequences of 19bp or longer.

- >fwd
GTGAAATGGTCATGTGTGGCGG
- >rev
TATGCTAATAGTGTAAAAACATTG
- >prb
CAGGTGGAACCTCATCAGGAGATGC

[Use Sample Input](#) [Clear Input](#)

Select analysis time period. Longer time periods take longer to analyse.

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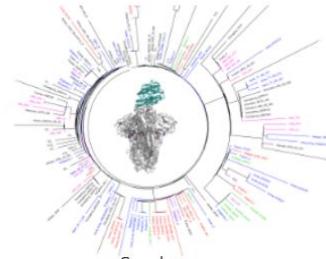
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A circular phylogenetic tree centered on a 3D model of a COVID-19 spike protein. The tree branches outwards, with various colored tips representing different SARS-CoV-2 variants and strains. Labels on the branches include "Alpha", "Beta", "Gamma", "Delta", "Epsilon", "Mu", "Nu", "Omicron", and "Lambda". A vertical sidebar on the right lists "SARSCoV2 variants" and "SARSCoV2 lineage".


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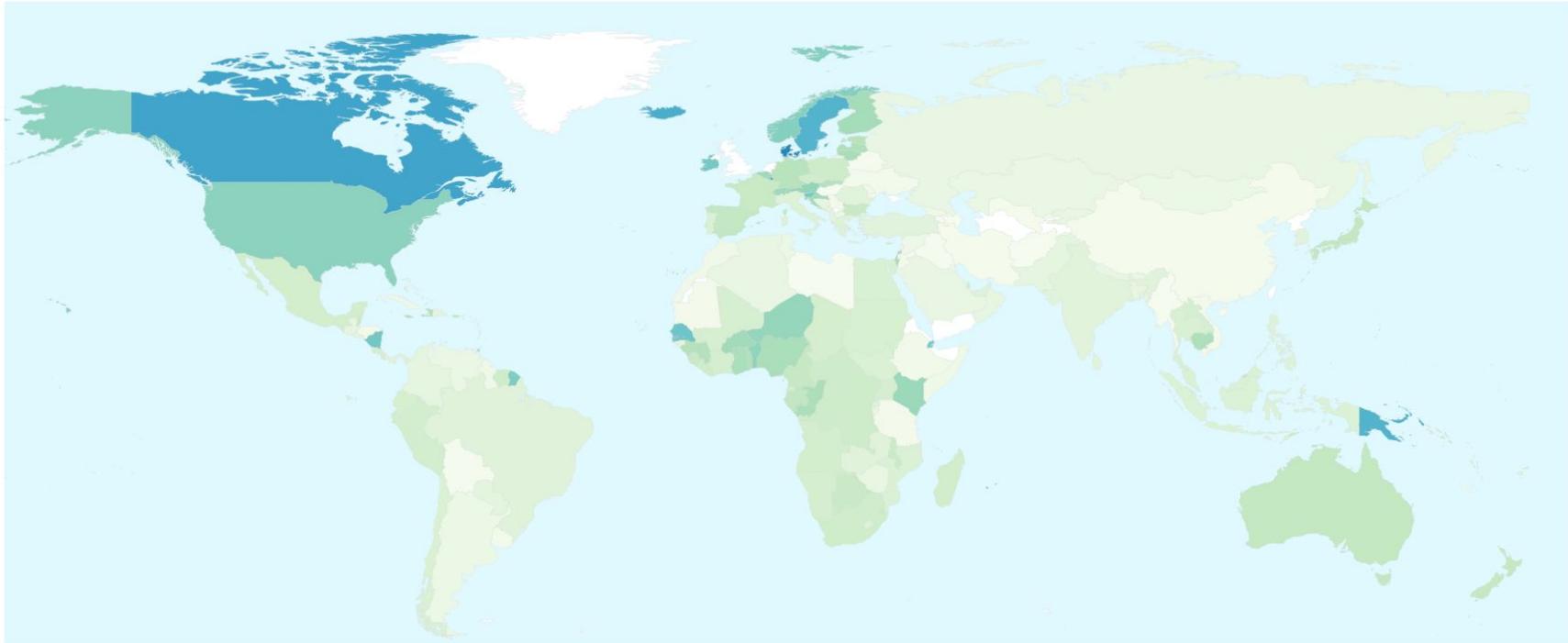

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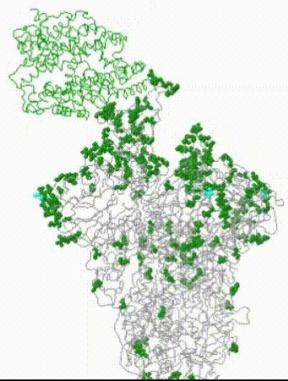
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- ACE2 human host receptor
 - CoV spike glycoprotein trimer
 - Spike glycoprotein variation occurring 100 times or less
 - Spike glycoprotein variation occurring greater than 100 times
- lineage defining muts:** aa changes found in >=10% of sequences in the lineage

- Spike glycoprotein variation found in >=10% of sequences from the lineage
 - Spike glycoprotein variation near host receptor, or other functional annotation
 - Insertion/deletion
 - Spike glycoprotein variation altering potential N-glycosylation sites
- lineage emerging muts:** aa changes found in <10% of sequences in the lineage that are also found in top 50 emerging constellations by Spread and top 20 emerging constellations by Acceleration (See emerging variant analysis for details)

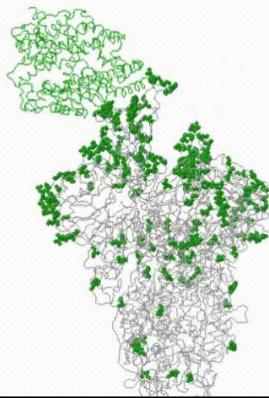
KP.2 defining muts: **ins16MPLF T19I R21T L24del P25del P26del A27S S50L H69del V70del V127F G142D Y144del F157S R158G N211del L212I V213G L216F H245N A264D I332V G339H R346T K356T S371F S373P S375F T376A R403K D405N R408S K417N N440K V445H G446S N450D L452W L455S F456L F456L N460K S477N T478K N481K V483del E484K F486P Q493E Q498R N501Y Y505H E554K A570V D614G P621S H655Y N679K P681R N764K D796Y S939F Q954H N969K V1104L P1143L**
KP.2 emerging muts: **H146Q S255del S256del G257del**

2024-04-16



KP.3 defining muts: **ins16MPLF T19I R21T L24del P25del P26del A27S S50L H69del V70del V127F G142D Y144del F157S R158G N211del L212I V213G L216F H245N A264D I332V G339H K356T S371F S373P S375F T376A R403K D405N R408S K417N N440K V445H G446S N450D L452W L455S F456L N460K S477N T478K N481K V483del E484K F486P Q493E Q498R N501Y Y505H E554K A570V D614G P621S H655Y N679K P681R N764K D796Y S939F Q954H N969K V1104L P1143L V1228A**
KP.3 emerging muts:

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This subset comprises entries from wastewater surveillance, and includes entries with substantially lower sequence coverage that may result in incomplete annotations for variant, clade, lineage and AA substitutions.

EPI_ISL ID	Virus name	EPI_SET ID	<input type="checkbox"/> Complete <small>?</small>
Location			<input type="checkbox"/> High coverage <small>?</small>
Collection	to	Submission	<input type="checkbox"/> Low coverage excluded <small>?</small>
Clade	all	Lineage	<input type="checkbox"/> With patient status <small>?</small>
AA Substitutions <small>?</small>	Nucl Mutations <small>?</small>		<input type="checkbox"/> Collection date complete <small>?</small>
<input type="checkbox"/> Under investigation			

Text Search

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission date	<small>i</small>	Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/env/Ukraine/85262/2024	Original	EPI_ISL_19032008	2024-02-01	2024-04-05	<small>▲</small>	29,691	Environment	Europe / Ukraine	Reference I
<input type="checkbox"/>	hCoV-19/env/Ukraine/85231/2024	Original	EPI_ISL_19032007	2024-02-22	2024-04-05	<small>▲</small>	29,548	Environment	Europe / Ukraine	Reference I
<input type="checkbox"/>	hCoV-19/env/Czech Republic/NRL_w435/20	Original	EPI_ISL_19031901	2023-12-05	2024-04-05	<small> ⓘ</small>	29,310	Environment	Europe / Czech F	National Ins
<input type="checkbox"/>	hCoV-19/env/Czech Republic/NRL_w426/20	Original	EPI_ISL_19031900	2023-11-28	2024-04-05	<small> ⓘ</small>	29,294	Environment	Europe / Czech F	National Ins
<input type="checkbox"/>	hCoV-19/env/Ukraine/84940/2024	Original	EPI_ISL_18985928	2024-02-01	2024-03-16	<small> ⓘ</small>	29,559	Environment	Europe / Ukraine	Reference I
<input type="checkbox"/>	hCoV-19/env/Ukraine/84930/2024	Original	EPI_ISL_18985927	2024-01-11	2024-03-16	<small> ⓘ</small>	29,753	Environment	Europe / Ukraine	Reference I
<input type="checkbox"/>	hCoV-19/env/Ukraine/84923/2023	Original	EPI_ISL_18985926	2023-12-28	2024-03-16	<small>▲</small>	29,700	Environment	Europe / Ukraine	Reference I

Total: 12,637 viruses

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Retrieving a sequence

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

The screenshot shows the GISAID website interface. At the top, there is a navigation bar with links for Registered Users, EpiFlu™, EpiCoV™ (which is highlighted with a red box), EpiPox™, EpiArbo™, and My Profile. Below the navigation bar, the main content area features a heading "Pandemic coronavirus causing COVID-19". A text block describes the discovery of hCoV-19 in Wuhan and its relation to SARS. To the right of this text is a circular phylogenetic tree centered on a green COVID-19 genome icon. Below the tree is a "Search" button. The main content area also includes a section titled "Analysis Update (2024-04-02)" and a note about accepting terms and conditions for viewing influenza virus data.

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EPI_ISL ID	Virus name	EPI_SET ID	<input type="checkbox"/> Complete ⓘ
Location		Host	<input type="checkbox"/> High coverage ⓘ
Collection	to	Submission	<input type="checkbox"/> Low coverage excluded ⓘ
Clade	all	Lineage	<input type="checkbox"/> With patient status ⓘ
AA Substitutions ⓘ	Nuc Mutations ⓘ		<input type="checkbox"/> Collection date complete ⓘ
			<input type="checkbox"/> Under investigation

Text Search

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission		Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0221/2024	Original	EPI_ISL_19052879	2024-04-01	2024-04-15		29,837	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0220/2024	Original	EPI_ISL_19052878	2024-03-28	2024-04-15		29,870	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0219/2024	Original	EPI_ISL_19052877	2024-03-26	2024-04-15		29,869	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0218/2024	Original	EPI_ISL_19052876	2024-03-25	2024-04-15		29,870	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0217/2024	Original	EPI_ISL_19052875	2024-03-21	2024-04-15		29,868	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0216/2024	Original	EPI_ISL_19052874	2024-03-21	2024-04-15		29,823	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0215/2024	Original	EPI_ISL_19052873	2024-03-21	2024-04-15		29,867	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0214/2024	Original	EPI_ISL_19052872	2024-03-20	2024-04-15		29,835	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0213/2024	Original	EPI_ISL_19052871	2024-03-19	2024-04-15		29,833	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0212/2024	Original	EPI_ISL_19052870	2024-03-19	2024-04-15		29,833	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0211/2024	Original	EPI_ISL_19052869	2024-03-18	2024-04-15		29,832	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0210/2024	Original	EPI_ISL_19052868	2024-03-18	2024-04-15		29,828	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0209/2024	Original	EPI_ISL_19052867	2024-03-14	2024-04-15		29,866	Human	North America / U	Mississippi
<input type="checkbox"/>	hCoV-19/USA/MS-MSPHL-0208/2024	Original	EPI_ISL_19052866	2024-03-14	2024-04-15		29,868	Human	North America / U	Mississippi

Total: 16,659,891 viruses << < 1 2 3 4 5 > >> Charts EPI_SET Selected Analysis Download

Important note: In the [GISaid EpiFlu™ Database Access Agreement](#), you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the [GISaid EpiFlu™ Database Access Agreement](#) in respect of such data in the same manner as if they were data relating to influenza viruses.

Retrieving a sequence

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EPI_ISL ID: Virus name: hCoV-19/Philippines/PH-PGC-113286/2022 EPI_SET ID:
Location: Host:
Collection: to Submission: to
Clade: all Lineage: Variant:
AA Substitutions: Nucl Mutations:
 Complete [?](#) High coverage [?](#) Low coverage excluded [?](#)
 With patient status [?](#) Collection date complete [?](#) Under investigation

Text Search

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission date	Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/Philippines/PH-PGC-113286/2022	Original	EPI_ISL_17388963	2022-03-31	2023-04-04	ML	29,842	Human	Asia / Philippines PHILIPPINE

Total: 1 viruses << < 1 > >>

[Charts](#) [EPI_SET](#) [Select](#) [Analysis](#) [Download](#)

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Virus detail

updated 2023-04-16

Virus name: hCoV-19/Philippines/PH-PGC-113286/2022

Accession ID: EPI_ISL_17388963.2 ▾

Type: betacoronavirus

Clade: GRA

Pango Lineage: B.1.1.529 (Pango v.4.3.1 consensus call), Delta (B.1.617.2-like) +K417N (Scorpio)

AA Substitutions:
Spike D405N, Spike D614G, Spike E156G, Spike E484A, Spike F157del, Spike G339D, Spike H655Y, Spike K417N, Spike L452R, Spike N501Y, Spike N679K, Spike P681H, Spike Q498R, Spike R158del, Spike R408S, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike T19R, Spike T95I, Spike T376A, Spike T478K, Spike T859N, Spike V213G, Spike Y505H, M D3G, M I82T, N D63G, N D377Y, N R203M, NS3 D155Y, NS3 S26L, NS3 Y189C, NS7a A105V, NS7a T120I, NSP1 E102K, NSP3 P153S, NSP3 P82L, NSP3 T724I, NSP4 A446V, NSP6 T181I, NSP6 V149A, NSP12 G671S, NSP12 L829F, NSP12 P323L, NSP13 P77L

Nucl Mutations:
G210T, C241T, G569A, C3037T, C3176T, C4890T, C5184T, C9891T, T11418C, C11514T, C13019T, C13072T, C14408T, G15451A, C15925T, C16466T, A18366G, C21618G, C21846T, del22028_22033, A22034G, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22917G, G22992A, C22995A, A23013C, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C24138A, C25469T, G25855T, A25958G, A26530G, T26767C, C27707T, C27752T, del28248_28253, del28271_28271, A28461G, G28881T, G29402T, A29631G, G29742T

Variant: Former VOC Omicron GRA (B.1.1.529+BA.1*) first detected in Botswana/Hong Kong/South Africa

Passage details/history: Original

Sample information

Collection date: 2022-03-31

Location: Asia / Philippines / National Capital Region

Host: Human

Additional location information:

Gender: Male

Patient age: 28

Patient status: Recovered

Specimen source: Nasopharyngeal swab

Additional host information:

Sampling strategy: Geographic Representativeness

Outbreak:

Last vaccinated:

Treatment:



Contact Submitter

Metadata

FASTA

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It appears to contain markers of multiple lineages from both Delta and Omicron variants

Institute information

Originating lab: PHILIPPINE GENERAL HOSPITAL (PGH)
Address: Taft Ave, Ermita, Manila, 1000 Metro Manila
Sample ID given by the originating laboratory:
Submitting lab: Philippine Genome Center
Address: A. Ma. Regidor Street, National Science Complex , U.P. Campus , University of the Philippines , 1101, Quezon City, Metro Manila

Authors: Elcid Aaron R. Pangilinan, John Michael C. Egana, Renato Jacinto Q. Mantaring, Alyssa Joyce E. Telles, Francis A. Tablizo, Carlo M. Lapid, El King D. Morado, Maria Sofia L. Yangzon, Joshua Jose S. Endozo, Karol Sophia Agape R. Padilla, Jarvin E. Nipales, Lindsay Clare D.L. Carandang, Zipporah Mariebelle R. Enriquez, Tricia Anne U. Barot, Romano A. Manlimos, Kelly Nicole P. Mangonon, Ma. Exanil L. Plantig, Shiela Mae M. Araiza, Jo-Hannah S. Llamas, Kris P. Punayan, Rachelle P. Serrano, Anne M. Druco, Honeylett T. Lagnas, Philip A. Bistayan, Aristio C. Aguilar, Joie G. Charisse Apo, Yvonne Valerie D. Austria, Niña Francesca M. Bustamante, Alyssa Jamila R. Caelian, Rudy E. Fernandez, Xerxanne A. Galilea, Marielle M. Gamboa, Clarence Jane A. Gervacio, Zyrel V. Mollejon, Joshua Paul N. Pineda, Kristel B. Rico, Jan Michael C. Yap, Ma. Celeste S. Abad, Benedict A. Maralit, Marc Edsel C. Ayes, Eva Marie Cutiongco-de la Paz, Cynthia P. Saloma, Razel Nikka M. Hao, Devon Ray Pacial, Juan Antonio R. Magalang, Henrietta Marie Rodriguez, Chelsea Joy Galutan, Maria Rosario Singh-Vergeire, Alethea R. de GuzmanElcid Aaron R. Pangilinan, John Michael C. Egana, Renato Jacinto Q. Mantaring, Alyssa Joyce E. Telles, Francis A. Tablizo, Carlo M. Lapid, El King D. Morado, Maria Sofia L. Yangzon, Joshua Jose S. Endozo, Karol Sophia Agape R. Padilla, Jarvin E. Nipales, Lindsay Clare D.L. Carandang, Zipporah Mariebelle R. Enriquez, Tricia Anne U. Barot, Romano A. Manlimos, Kelly Nicole P. Mangonon, Ma. Exanil L. Plantig, Shiela Mae M. Araiza, Jo-Hannah S. Llamas, Kris P. Punayan, Rachelle P. Serrano, Anne M. Druco, Honeylett T. Lagnas, Philip A. Bistayan, Aristio C. Aguilar, Joie G. Charisse Apo, Yvonne Valerie D. Austria, Niña Francesca M. Bustamante, Alyssa Jamila R. Caelian, Rudy E. Fernandez, Xerxanne A. Galilea, Marielle M. Gamboa, Clarence Jane A. Gervacio, Zyrel V. Mollejon, Joshua Paul N. Pineda, Kristel B. Rico, Jan Michael C. Yap, Ma. Celeste S. Abad, Benedict A. Maralit, Marc Edsel C. Ayes, Eva Marie Cutiongco-de la Paz, Cynthia P. Saloma, Razel Nikka M. Hao, Devon Ray Pacial, Juan Antonio R. Magalang, Henrietta Marie Rodriguez, Chelsea Joy Galutan, Maria Rosario Singh-Vergeire, Alethea R. de Guzman

Submitter information

Submitter: Egana, John Michael
Submission Date: 2023-04-04

Addressee:

Polaris

>hCoV-19/Philippines/PH-PGC-113286/2022|EPI_ISL_17388963.2|2022-03-31
TCTGGTTTACCTCCCGAACAAACCAACTCTGATCTGTCTCTTAAACGAACTTAAAAA
TCTGGTGGCTGTCAGCTGGCTCAGCTGGTCACTCAGCAGTATAATTAACTAACTACTCTGCTTGACAGGAC



Contact Submitter

 Metadata

FASTA

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Virus detail

updated 2023-04-16

Virus name:	hCoV-19/Philippines/PH-PGC-113286/2022
Accession ID:	EPI_ISL_17388963.2 ▾
Type:	betacoronavirus
Clade:	GRA
Pango Lineage:	B.1.1.529 (Pango v.4.3.1 consensus call), Delta (B.1.617.2-like) +K417N (Scorpio)
AA Substitutions:	Spike D405N, Spike D614G, Spike E156G, Spike E484A, Spike F157del, Spike G339D, Spike H655Y, Spike K417N, Spike L452R, Spike N501Y, Spike N679K, Spike P681H, Spike Q498R, Spike R158del, Spike R408S, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike T19R, Spike T95I, Spike T376A, Spike T478K, Spike T859N, Spike V213G, Spike Y505H, M D3G, M I82T, N D63G, N D377Y, N R203M, NS3 D155Y, NS3 S26L, NS3 Y189C, NS7a A105V, NS7a T120I, NSP1 E102K, NSP3 P153S, NSP3 P82L, NSP3 T724I, NSP4 A446V, NSP6 T181I, NSP6 V149A, NSP12 G671S, NSP12 L829F, NSP12 P323L, NSP13 P77L
Nucl Mutations:	G210T, C241T, G569A, C3037T, C3176T, C4890T, C5184T, C9891T, T11418C, C11514T, C13019T, C13072T, C14408T, G15451A, C15925T, C16466T, A18366G, C21618G, C21846T, del22028_22033, A22034G, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22917G, G22992A, C22995A, A23013C, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C24138A, C25469T, G25855T, A25958G, A26530G, T26767C, C27707T, C27752T, del28248_28253, del28271_28271, A28461G, G28881T, G29402T, A29631G, G29742T
Variant:	Former VOC Omicron GRA (B.1.1.529+BA.1) first detected in Botswana/Hong Kong/South Africa
Passage details/history:	Original

Sample information

Collection date:	2022-03-31
Location:	Asia / Philippines / National Capital Region
Host:	Human
Additional location information:	
Gender:	Male
Patient age:	28
Patient status:	Recovered
Specimen source:	Nasopharyngeal swab
Additional host information:	
Sampling strategy:	Geographic Representativeness
Outbreak:	
Last vaccinated:	

Treatment



Contact Submitter | Metadata | Fasta

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Virus detail

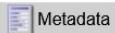
updated 2023-04-16

Virus name:	hCoV-19/Philippines/PH-PGC-113286/2022
Accession ID:	EPI_ISL_17388963.2 ▾
Type:	betacoronavirus
Clade:	GRA
Pango Lineage:	B.1.1.529 (Pango v.4.3.1 consensus call), Delta (B.1.617.2-like) +K417N (Scorpio)
AA Substitutions:	Spike D405N, Spike D614G, Spike E156G, Spike E484A, Spike F157del, Spike G339D, Spike H655Y, Spike K417N, Spike L452R, Spike N501Y, Spike N679K, Spike P681H, Spike Q498R, Spike R158del, Spike R408S, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike T19R, Spike T95I, Spike T376A, Spike T478K, Spike T859N, Spike V213G, Spike Y505H, M D3G, M I82T, N D63G, N D377Y, N R203M, NS3 D155Y, NS3 S26L, NS3 Y189C, NS7a A105V, NS7a T120I, NSP1 E102K, NSP3 P153S, NSP3 P82L, NSP3 T724I, NSP4 A446V, NSP6 T181I, NSP6 V149A, NSP12 G671S, NSP12 L829F, NSP12 P323L, NSP13 P77L
Nucl Mutations:	G210T, C241T, G569A, C3037T, C3176T, C4890T, C5184T, C9891T, T11418C, C11514T, C13019T, C13072T, C14408T, G15451A, C15925T, C16466T, A18366G, C21618G, C21846T, del22028_22033, A22034G, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22917G, G22992A, C22995A, A23013C, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C24138A, C25469T, G25855T, A25958G, A26530G, T26767C, C27707T, C27752T, del28248_28253, del28271_28271, A28461G, G28881T, G29402T, A29631G, G29742T
Variant:	Former VOC Omicron GRA (B.1.1.529+BA.1) first detected in Botswana/Hong Kong/South Africa
Passage details/history:	Original

Sample information

Collection date:	2022-03-31
Location:	Asia / Philippines / National Capital Region
Host:	Human
Additional location information:	
Gender:	Male
Patient age:	28
Patient status:	Recovered
Specimen source:	Nasopharyngeal swab
Additional host information:	
Sampling strategy:	Geographic Representativeness
Outbreak:	
Last vaccinated:	

Treatment:



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EPI_ISL ID: Virus name: hCoV-19/Philippines/PH-PGC-11; EPI_SET ID:
Location: Host:
Collection: to Submission: to
Clade: all Lineage: Variant:
AA Substitutions: Nucl Mutations:
 Complete ⓘ High coverage ⓘ Low coverage excluded ⓘ
 With patient status ⓘ Collection date complete ⓘ Under investigation

Text Search:

<input type="checkbox"/>	Virus name	Passage de	Accession ID	Collection dat	Submission d	i	Length	Host	Location	Originating
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-PGC-113286/2022	Original	EPI_ISL_17388963	2022-03-31	2023-04-04	ML	29,842	Human	Asia / Philippines	PHILIPPINE

A red arrow points to the checkbox in the first column of the table row for the virus entry.

Total: 1 viruses << < 1 > >> Charts EPI_SET Select Analysis Download

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- Nucleotide Sequences (FASTA)
- Patient status metadata
- Sequencing technology metadata

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- Sequencing technology metadata

Replace spaces with underscores in FASTA header

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new 2 gisaid_hcov-19_2024_04_16_02.fasta

```
>hcov-19/Philippines/PH-PGC-113286/2022|EPI_ISL_17388963|2022-03-31
1 TAAAGGTTTACCTCCAGGTAAACAAACCAACCTTCGATCTTGATGACTGGTCTCTAAACGAACCTTTAAAA
2 TCTGTGTGGCTCACTCGGCTGCATGCTTAGTGCACCTCACGAGTATAATTAAATAATTACTGTCGGTACAGGAC
3 ACGAGTAACCTGCTATCTCTGCAGGCTGCTTACGGTTTCTGGCTTACGCCATCAGCACACATAGGTTTG
4 TCCGGGTGACCGAAAGGTAAGATGGAGAGGCCGTTGCCCTGGTTAACGAGAAAACACACGCTCAAACAGTTGCCT
5 GTTTACAGGTCGCGACGTGCTCGTACGTGGCTTGAGACTCCGGAGGAGGCTTATCAGAGGCACGTCAAACATCT
6 TAAAGATGGCACTTGTGGCTTAGTAGAAGATTGAAAAAGGCGTTTGCCTCAACTGAAACAGCCCTATGTGTTCATCAAAC
7 GTTGGATGGTCACTGCACCTCATGGTCATGTTATGGTGGAGCTGGTAGCAGAAACTCGAAGGCATTCACTGACGGTGT
8 AGTGGTAAGACACTGGTGCCTCATGGTCATGGCGAAATACCAGTGGCTTACCGCAAGGTTCTTCGTAAGAA
9 CGGTAAAGGAGACTGGTGCCTCATGGTCATGGCGAAATACCAGTGGCTTACCGCAAGGTTCTTCGTAAGAA
10 CTTATGAAGATTTCAGGAAACTTGGAAACACTAAACATAGCAGTGGTACCCGTGAACCTCATGCGTGAGCTTAACGGA
11 GGGGCATACACTCGCTATCGATAACAACACTTGTGCCCTGATGGCTACCCCTTGAGTGCATTAAGACCTCTAGC
12 ACGTGCTGGTAAAGCTTACGCACTTGTCCGAACAACACTGGACTTATTGACACTAAGAGGGGTGTAACTGTCGCCGTG
13 AACATGAGCATGAAATTGCTGGTACACGGAACGTTCTGAAAAGAGCTATGAATTGCGACACACCTTTGAAATTAAATTG
14 GCAAGGAAATTGACACCTCAATGGGAATGTCACATTGCAATTTCGATTTCCCTTAATTCCATAATCAAGACTATTCACCC
15 AAAGGTTGAAAAGAAAAAGCTTGTGCTTATGGTAGAATTGCACTGATCTGTCTATCCAGTTGCGTCACCAAAATGAATGCA
16 ACCAAATGTGCCCTTCAACTCTCATGAAAGTGTGATCATTGTGGTAAACCTCATGGCAGACGGGCGATTGTTAAAGCC
17 ACTTGGCAATTGGTGGCAGATAAGGAAATTGACTAAAGAAGGCCACTACTGTGGTTACTTACCCCCAAATGCTGTGT
18 TAAAAATTATTGTCAGCATGTCACAAATCAGAAAGTAGGACTGAGCATAGTCTGCCGAATACATAATGAATCTGGCT
19 TGAAAACCATCTCGTAAGGGTGGTGCACATTGCCCTTGGAGGCTGTGTGTTCTTATGGTTGCCATAACAG
20 TGTGCCTATTGGGTTCCACGTGCTAGCGCTAACATAGGTTGTAACCATACAGGTGTTGGAGAAGGTTCCGAAGGTCT
21 TAATGACAAACCTCTTGGCAATTGGCTTACAGTGGAAACTGTGAAAGGTTGGATTATAAGCATTTC
22 TCGCCATTATTGGCATTTCTGCCAACAGTGTGTTTGAGGAAACTGTGAAAGGTTGGATTATAAGCATTTC
23 AAAACAAATTGTAATCTGTGGTATTTAAAGTCAAAAGGAAAGCTAAAAAGGTGCTGGAATTGGTGAACAA
24 GAAATCAATACTGAGTCCTTATGCAATTGCACTGAGGGCTGCTCGTGTGACTCAATTCTCCCGCACTCTG
25 AAACGTCTCAAAATTCTGTGCGTGTGGCTAACAGAAGGCCACTAACAAATACTGAGTGGAAATTTCACAGTATTCACTGAGA
26 CTCATTGATGCTATGATGTCACATGCTTGGCTAACAAATCTGTTGTAATGGCCTACATACAGGTGGTGT
27 TCAGTTGACTTCGCACTGCTAACATCTTGGCACTGTTATGAAAAAAACTCAAAACCCGTCCTTGATGGCTTGAAG
28 AGAAGTTAAAGGAAGGGTGTAGAGTTCTAGAGACGGTTGGGAAATTGTTAAATTCTCAACCTGTGCTTGTGAAATT
29 GTCAGGTTGGGAAATTGCTTGGGAAATTGCTTGGGAAATTGTTAAATTCTCAACCTGTGCTTGTGAAATT
30 GTCAGGTTGGGAAATTGCTTGGGAAATTGCTTGGGAAATTGCTTGGGAAATTGCTTGTGAAATT
```

Normal text file length : 30,284 lines : 376 Ln : 1 Col : 1 Pos : 1 Unix (LF) UTF-8 INS

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- Sequencing technology metadata

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EPI_ISL ID Virus name EPI_SET ID Complete⑦

Location Host

Collection to Submission to

Clade Lineage Variant

AA Substitutions⑦ Nucl Mutations⑦

Text Search

<input type="checkbox"/>	Virus name	Passage de	Accession ID	Collection dat	Submission d		Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/Australia/VICMelbourne475/2021	Original	EPI_ISL_7271188	2021	2021-12-07		29,813	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VICMelbourne476/2021	Original	EPI_ISL_7271157	2021-03-28	2021-12-07		29,865	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VICParaguay2152x/2021	Original	EPI_ISL_7271145	2021-03	2021-12-07		29,813	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VICMelbourne390/2021	Original	EPI_ISL_7271131	2021	2021-12-07		29,873	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VIC14/2021	Original	EPI_ISL_7271116	2021	2021-12-07		29,864	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VIC17/2021	Original	EPI_ISL_7271097	2021	2021-12-07		29,818	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VICAnzarkTest13/2021	Original	EPI_ISL_7271089	2021	2021-12-07		29,865	Human	Oceania / Austral	Bio1 Mel
<input type="checkbox"/>	hCoV-19/Australia/VICAnzarkTest12/2021	Original	EPI_ISL_7271068	2021	2021-12-07		29,862	Human	Oceania / Austral	Bio1 Mel

Total: 19 viruses << < 1 > >> Charts EPI_SET Select Analysis Download

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EPI_ISL ID	<input type="text"/>	Virus name	<input type="text"/>	EPI_SET ID	<input type="text"/>	<input checked="" type="checkbox"/> Complete <small>?</small>				
Location	Asia / Philippines			Host	<input type="text"/>	<input type="checkbox"/> High coverage <small>?</small>				
Collection	Asia / Philippines / Bangsamoro Autonomous Region in Muslim Mindanao			to	<input type="text"/>	<input type="checkbox"/> Low coverage excluded <small>?</small>				
Clade	Asia / Philippines / Bicol				<input type="text"/>	<input type="checkbox"/> With patient status <small>?</small>				
AA Substitutions <small>?</small>	Asia / Philippines / Bicol Region				<input type="text"/>	<input type="checkbox"/> Collection date complete <small>?</small>				
	Asia / Philippines / Calabarzon				<input type="text"/>	<input type="checkbox"/> Under investigation				
	Asia / Philippines / Caraga				<input type="text"/>					
	Asia / Philippines / Central Luzon				<input type="text"/>					
	Asia / Philippines / Central Visayas				<input type="text"/>					
	Asia / Philippines / Cordillera Administrative Region				<input type="text"/>					
	Asia / Philippines / Davao				<input type="text"/>					
	Asia / Philippines / Davao Region				<input type="text"/>					
<input type="checkbox"/>	Virus name	hCoV-19/Philip	Asia / Philippines / Eastern Visayas	01-17	2024-04-12	!	29,724	Human	Asia / Philippines	MARIANO I
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Ilocos	09-25	2024-03-21	!	29,425	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Metropolitan Manila	10-27	2024-03-21	!	29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Mimaropa	10-09	2024-03-21	!	29,718	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / National Capital Region	09-07	2024-03-21	!	29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Northern Mindanao	08-11	2024-03-21	!	29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Quezon City	08-30	2024-03-21	!	29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Soccoksargen							
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Western Visayas							
<input type="checkbox"/>		hCoV-19/Philip	Asia / Philippines / Zamboanga							
Total: 2,465 viruses		EPI_ISL_18998248		2023-10-31	2024-03-21	!	29,721	Human	Asia / Philippines	RITM-VIRO

<< < 1 2 3 4 5 > >>

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EPI_ISL ID Virus name EPI_SET ID Complete⑦

Location Asia / Philippines / Cordillera Administrative Region Host High coverage⑦

Collection 2023-01-01 to 2024-03-31 Submission Low coverage excluded⑦

Clade all Lineage Variant With patient status⑦

AA Substitutions⑦ Nucl Mutations⑦ Collection date complete⑦

Under investigation

Text Search

<input type="checkbox"/>	Virus name	Passage de	Accession ID	Collection dat	Submission E		Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4310/2023	Original	EPI_ISL_18998242	2023-07-06	2024-03-21		29,706	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4460/2023	Original	EPI_ISL_18998229	2023-12-18	2024-03-21		29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4215/2023	Original	EPI_ISL_18998197	2023-05-15	2024-03-21		29,721	Human	Asia / Philippines	RITM-VIRO
<input type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-302/2024	Original	EPI_ISL_18936031	2024-01-18	2024-02-27		29,732	Human	Asia / Philippines	Baguio Ger
<input type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-301/2024	Original	EPI_ISL_18936030	2024-01-18	2024-02-27		29,722	Human	Asia / Philippines	Baguio Ger
<input type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-299/2024	Original	EPI_ISL_18936029	2024-01-16	2024-02-27		29,721	Human	Asia / Philippines	Baguio Ger
<input type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-298/2024	Original	EPI_ISL_18936028	2024-01-16	2024-02-27		29,721	Human	Asia / Philippines	Baguio Ger
<input type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-297/2024	Original	EPI_ISL_18936027	2024-01-16	2024-02-27		29,721	Human	Asia / Philippines	Baguio Ger

Total: 127 viruses

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EPI_ISL ID Virus name EPI_SET ID Complete①
Location Asia / Philippines / Cordillera Administrative Region Host High coverage②
Collection 2023-01-01 to 2024-03-31 Submission Low coverage excluded③
Clade all Lineage Variant With patient status④
Substitutions⑤ Nucl Mutations⑥ Collection date complete⑦ Under investigation
Search

<input checked="" type="checkbox"/>	Virus name	Passage de	Accession ID	Collection dat	Submission C	Length	Host	Location	Originating
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4310/2023	Original	EPI_ISL_18998242	2023-07-06	2024-03-21	▲ 29,706	Human	Asia / Philippines	RITM-VIRO
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4460/2023	Original	EPI_ISL_18998229	2023-12-18	2024-03-21	▲ 29,721	Human	Asia / Philippines	RITM-VIRO
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-RITM-4215/2023	Original	EPI_ISL_18998197	2023-05-15	2024-03-21	▲ 29,721	Human	Asia / Philippines	RITM-VIRO
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-302/2024	Original	EPI_ISL_18936031	2024-01-18	2024-02-27	▲ 29,732	Human	Asia / Philippines	Baguio Ger
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-301/2024	Original	EPI_ISL_18936030	2024-01-18	2024-02-27	▲ 29,722	Human	Asia / Philippines	Baguio Ger
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-299/2024	Original	EPI_ISL_18936029	2024-01-16	2024-02-27	▲ 29,721	Human	Asia / Philippines	Baguio Ger
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-298/2024	Original	EPI_ISL_18936028	2024-01-16	2024-02-27	▲ 29,721	Human	Asia / Philippines	Baguio Ger
<input checked="" type="checkbox"/>	hCoV-19/Philippines/PH-BGHMC-5-297/2024	Original	EPI_ISL_18936027	2024-01-16	2024-02-27	▲ 29,721	Human	Asia / Philippines	Baguio Ger

Total: 127 viruses << < 1 2 3 > >> Charts EPI_SET Select Analysis **Download**

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1 >hCoV-19/Philippines/PH-RITM-4008/2023|EPI_ISL_17244997|2023-02-14
2 TTGAGATCTTCTAAACGAATTAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGAGTAT
3 AATTAATAACTAACTTACTCTGCGTGGACAGACAGAGTAACTCGTCTATCTCTGCAGGCTGCTACGGTTTCGTCG
4 TTGCAGCCGATCATCAGCACATCTAGTTTGTCCGGGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTCA
5 ACAGAACACAGTCCAACTCACTTTGCCTTTAACAGGTTCGGACAGTCTGCTGACTGGCTTGGAGACTCCGTG
6 GAGGGAGTCTTATCAGAGCACGTAACATCTAGAGATGGCACTTGCGCTTAGTAGAAGTTGAAAAGGCCTTGCC
7 TCAACTTGAACAGCCCTATGTGTTCATCAAACGTTCGGATGCTGCAACTGCACCTCATGGTATGGTGGAGCTGG
8 TAGCAGAACTCGAAGGCATTCAGTACGGTGTAGTGGTGAGACACTTGGTGTCCCTGTCCTCATGTGGCGAAATACCA
9 GTGGCTTACCGAAGGTTCTTCTCGTAAGAACGGTAATAAAGGAGCTGGTGGCATAGGTACGGCGATCTAAAGTC
10 ATTGACTTACGGCAGCAGCTGGCACTGATCCTTATGGAGATTTCAAGAAAAACTGGAAACACTAAACATAGCAGTGGTG
11 TTACCCGTGAACTCATGCGTGGACTAACGGAGGGGCATACACTCGCTATGTCGATAACAACCTCTGTGGCCCTGATGGC
12 TACCTCTTGTGAGTCATTAAGACCTCTGCGTGGTAAGCTTGTGCAACTTGTGGCAACAAACTGGACTTTAT
13 TGACACTAAAGAGGGGTGTAACTGCTGCGTAACATGAGCATGAAATTGCTGGTACACCGAACGTTCTGAAAAGAGCT
14 ATGAAATTGCGACACACCTTGTAAATTGGCAAAGAAATTGACACCTTCAATGGGAATGTCCTTAAATTGTGATTT
15 CCCTTAAATTCCATAATCAAGACTATTCAACCAAGGGTGAAAAGAAAAAGCTTGTGGCTTATGGGAGATTGATC
16 TGTCTATCCAGTGGCGTCACCAAATGAATGCAACCAAATGTGCCCTTCAACTCTCATGAAAGTGTGATATTGTGGGAA
17 CTTCTGGCACAGGGGCGATTTGTAAAGCCACTTGGCAATTGGGACTGAGAATTGACTAAAGAAGGTGCCACT
18 ACTTGGTTACTTACCCCCAAATGCTGGTTAAATTATTGTGTCAGCATGTCACAATTGAGAAGTAGGGACCTGAGCA
19 TAGCTTGGCAATACATGAAATTGCTGGTAAAGGCAATTCTCTGTAAGGGTGGCGACTATTGCCCTTGGAGGCT
20 GTGTTCTTATGGTTGCCATACAAAGTGTGCCATTGGGTCACGGCTAGCGCTAACATAGGTTGTAACCCT
21 ACAGGTGGTTGGAGAAGGTCCTAAATGACAACCTTCTGAAATACTCCAAAAGAGAAAGTCAACATCAA
22 TATTGGGGTACTTAAACCTAAATGAAAGAGATGCCATTATGGCATCTTCTGCTTCCACAAGTGTCTTGTGG
23 AAACTGTGAAAGGTTGGATTATAAGCATTCAAACAAATTGTTGAATCCTGTTGAATTAAAGTTACAAAAGGAAAA
24 GCTAAAAAAAGGTGCCGATTTGGTGAACAGAACTAAACTGAGTCCTCTTATGCAATTGCACTAGAGGCTGCTCG
25 TGTGTCAGTCATCAATTCTCCCGACTCTGGAAACTCTGCTCAAATTCTGTCGTTTACAGAAGGGCGCTATAACAA
26 TACTAGATGAAATTTCACAGTATTCACTGAGACTCATTGATGCTATGGTTCACATCTGATTTGGCTACTAACATCTA
27 GTTGAATGGCTACATACAGGTGGTGTGTCAGTTGACTTCGCGAGTGGCTAACATCTTGGCACTGTTATGA
28 AAAACTCAAACCGTCTTGTGATTGGCTTGAAGAGAAGGTTAGGAAGGTGAGAGTTCTAGAGACGTTGGGAAATTG
29 TTAAATTATCTCAACCTGTGTTGTGAAATTGTCGGGGACAAATTGTCACCTGTCACAGGAAATTAGGAGAGTGTG
30 GCTGAAATTCTGGTGTGAAATTGTCGGGGACAAATTGTCACCTGTCACAGGAAATTAGGAGAGTGTG
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