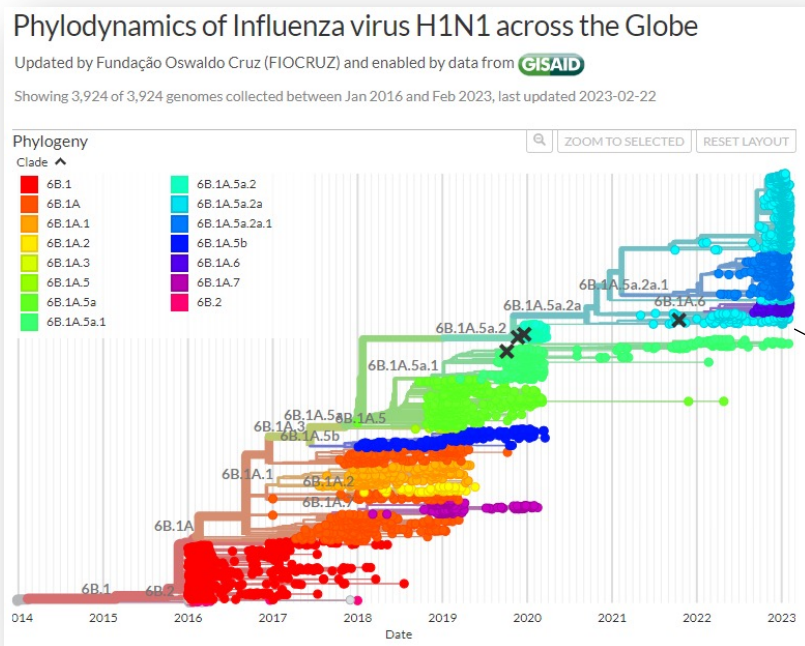


GISAID

Data Science Initiative



Seamless integration of tools inside the GISAID platform (log-in once) provides you comprehensive views from multiple angles and all info in one place



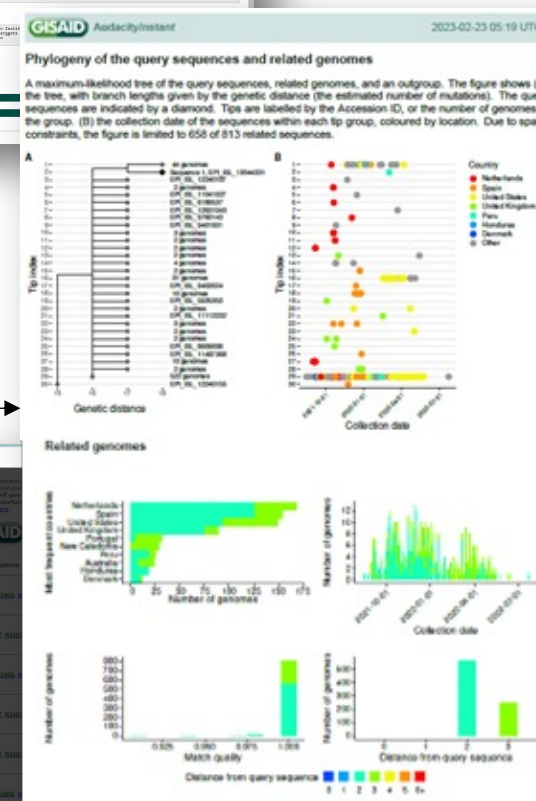
Subsampled summary tree

Full entry meta-data

A/Norway/01839/2023

Collection date	2023-01-26
Submitting laboratory	Norwegian Institute of Public Health
Continent	Europe
Host	Human
Country	Norway
Gender	Male
GISAID ID	EPI_ISL_16986282
Originating laboratory	Norwegian Institute of Public Health
Clade	6B.1A.5a.2a.1
Age	65 Y

Accession	Accession: EPI_ISL_16986282	Type	A/INFLU	
Accession ID	EPI_ISL_16986282	Change	0/0/0	
Parent accession	EPI_ISL_16986282	Change	0/0/0	
Sample information	Collection date	2023-01-26	Location	Norway
	Site	Norway	Additional location	
	Additional host	Human	Other age	65 Y
	Sex	Male	Gender	Male
	Zip code		Country	Norway
	Parent code		Specimen	
	Lab protocol		Specimen source	
	Pathogen type			
Submitting laboratory	Originating lab	Norwegian Institute of Public Health	Address	Norwegian Institute of Public Health Middelthunsgate 17 0407 Oslo Norway
	Sample ID given to the submitting laboratory		Address	
	Submitting lab	Norwegian Institute of Public Health		
	Submitting lab	Norwegian Institute of Public Health		
Sample ID given to the submitting laboratory	Accession ID	EPI_ISL_16986282	Accession ID	EPI_ISL_16986282
	Accession ID	EPI_ISL_16986282	Accession ID	EPI_ISL_16986282
	Accession ID	EPI_ISL_16986282	Accession ID	EPI_ISL_16986282
Phylogenetic	Phylogenetic	Unspecified		
Metadata	Metadata	Unspecified		
Download	Download	Unspecified		
View related sequences	View related sequences	Unspecified		



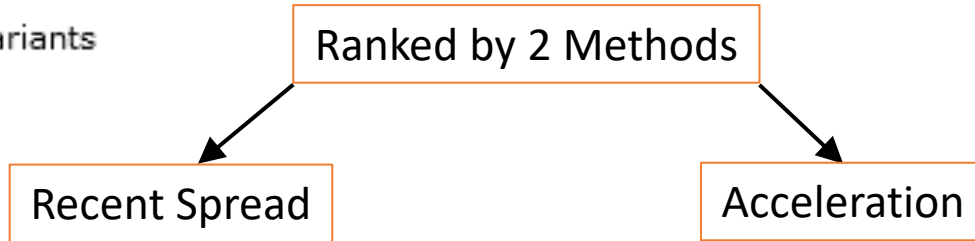
Full list and summary of all related sequences in the database (not just subsample)

Full mutation phenotype annotation



Emerging Variants Tracker

Monitoring emerging Fast Spreading hCoV-19 variants



CoVsurver

356 antibody binding sites

2388 literature entries
(antibody escape, ACE2 binding, Spike expression and stability)

Monitor AA changes with potential effects on receptor or antibody binding as annotated in CoVsurver

Constellation

E_T11A, N_P13L, Spike_D405N, Spike_D614G, Spike_D796Y, Spike_E484A, Spike_G257S, Spike_G339H, Spike_G446S, Spike_K147E, Spike_K417N, Spike_N440K, Spike_N460K, Spike_N501Y, Spike_P681H, Spike_Q498R, Spike_R408S, Spike_S371F, Spike_S373P, Spike_S375F, Spike_S477N, Spike_T376A, Spike_T478K, Spike_W152R, Spike_Y505H

All countries

Filter by Country

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

Filter by Mutation

Constellation (Clade/Lineage) (New Lineage)	Count(past 100 days) ↑↓	Current Ranking ↑↓	Dissimilarity Score ↑↓	Cumulative#loc	%inEachContinent					geoMap	
					North America	South America	Europe	Africa	Asia		Oceania
BA.2.75											
GRA/BA.2.75+Spike_F 486S+Spike_R346T	652	3	4								

View mutations in Spike 3D Structure

Search GISAID EpiCoV database

Tool to see new variants before they have a lineage name

CoVsurver real-time surveillance for mutations that can affect viral fitness

3D structural visualization of the spike glycoprotein with mutations identified in the query sequences shown as colored balls

Spin ON Spin OFF Save IMAGE

Spike glycoprotein (PDB: 6acc, EM 3.6 Angstrom) with RBD in down conformation.

Spike glycoprotein (PDB: 6acc, EM 4.2 Angstrom) in complex with host cell receptor ACE2 (green ribbon).

% AA identity: 99.843%

List of variations displayed in structure (nearest residue if in loop/termini region)

Query	Clade	Best reference hit	%id	%coverage	#mut:	List of mutations
NSP1 hCoV-19/Wuhan/WIV04/2019		NSP1 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP2 hCoV-19/Wuhan/WIV04/2019		NSP2 hCoV-19/Wuhan/WIV04/2019	99.8%	100%	1	I120F
NSP3 hCoV-19/Wuhan/WIV04/2019		NSP3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP4 hCoV-19/Wuhan/WIV04/2019		NSP4 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP5 hCoV-19/Wuhan/WIV04/2019		NSP5 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP6 hCoV-19/Wuhan/WIV04/2019		NSP6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP7 hCoV-19/Wuhan/WIV04/2019		NSP7 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP8 hCoV-19/Wuhan/WIV04/2019		NSP8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP9 hCoV-19/Wuhan/WIV04/2019		NSP9 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP10 hCoV-19/Wuhan/WIV04/2019		NSP10 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP11 hCoV-19/Wuhan/WIV04/2019		NSP11 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP12 hCoV-19/Wuhan/WIV04/2019		NSP12 hCoV-19/Wuhan/WIV04/2019	99.9%	100%	1	P223L
NSP13 hCoV-19/Wuhan/WIV04/2019		NSP13 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP14 hCoV-19/Wuhan/WIV04/2019		NSP14 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP15 hCoV-19/Wuhan/WIV04/2019		NSP15 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NSP16 hCoV-19/Wuhan/WIV04/2019		NSP16 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
Spike hCoV-19/Wuhan/WIV04/2019		Spike hCoV-19/Wuhan/WIV04/2019	99.8%	100%	2	S477N D614G
NS3 hCoV-19/Wuhan/WIV04/2019		NS3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
E hCoV-19/Wuhan/WIV04/2019		E hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
M hCoV-19/Wuhan/WIV04/2019		M hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NS6 hCoV-19/Wuhan/WIV04/2019		NS6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NS7a hCoV-19/Wuhan/WIV04/2019		NS7a hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NS7b hCoV-19/Wuhan/WIV04/2019		NS7b hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
NS8 hCoV-19/Wuhan/WIV04/2019		NS8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
N hCoV-19/Wuhan/WIV04/2019		N hCoV-19/Wuhan/WIV04/2019	99.5%	100%	2	R203K G204R

Spike S477N

Key to alternative position numbering:
 477 hCoV-19 numbering
 464 SARS numbering

Chosen reference: Spike hCoV-19/Wuhan/WIV04/2019
 Position in reference: 477
 AA in reference: S
 AA in query: N

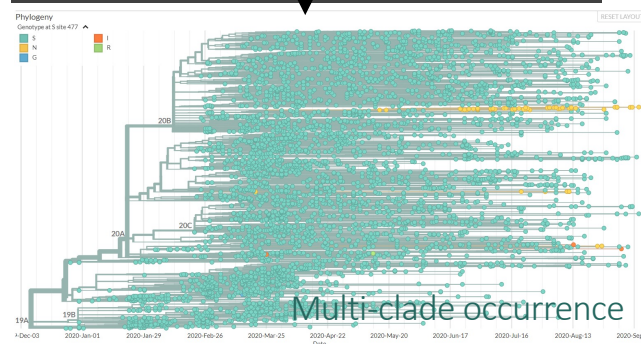
Mutation Spike S477N already occurred 4128 times (3.98% of all samples with Spike sequence) in 6 countries. The first strain with this mutation, collected in 2020, was hCoV-19/Australia/VIC5321/2020. The mutation most recently occurred in strain hCoV-19/Australia/NSW-SAVID-2752/2020, collected in September 2020. ([see map](#))
[See detailed global statistics for this position](#)

A mutation at the position equivalent to **Spike 477** has been reported in the literature to be related to **Host Change and Others**.

As seen in resolved structures of proteins from related strains, the Spike position equivalent to this mutation is involved in:
[Antibody Recognition Sites](#)
[Host Cell Receptor Binding](#)
[Viral Oligomerization Interfaces](#)

[PubMed search for this mutation](#)

NEW: [Occurrence and phylogenetic context of mutation at CoV-GLUE](#)
[Phylogenetic context for this mutation at Nextstrain](#)

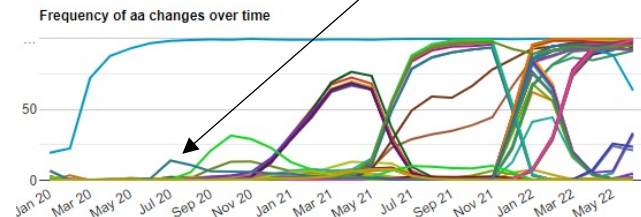
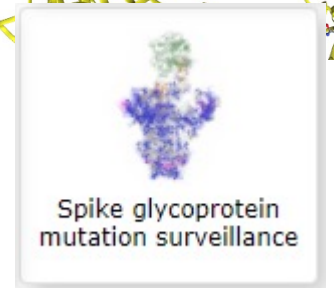
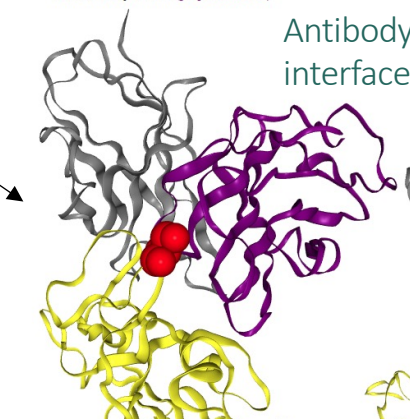


Protein: Spike
 Coronavirus type: Yeast SARS-CoV-2 (2019)
 Mutation (as in paper): S477N
 neutral AA: S
 neg. eff. AA: N
 Effect: Host Change

Receptor binding

Comment:
 In a deep mutational scanning experiment that expresses Spike RBD in a yeast-display platform, S477N mildly increases the binding to ACE2 (apparent dissociation constant delta-log10 value: 0.06)
[Literature reference](#)
 (Mutation S477N in the paper is at an equivalent position of the mutation in your query)

Antibody interaction: The mutation position (red atoms) corresponds to position 477 on viral chain E (yellow backbone) of protein entry 6xcn, originating from Severe acute respiratory syndrome coronavirus 2 and with a label of Spike glycoprotein. The mutation is within 6 Å from antibody chain F (purple backbone).



<https://gisaid.org/covsurver>

Literature-curated mutation effect database
 >2400 entries

drug resistance	7
virulence	23
antigenic drift / escape mutant	1336
host specificity change/shift	369
Other (enzyme activity, affects protein accumulation/ stability/function)	496

3D structure interaction mutation position database
 >3800 entries

self/oligomerization	2686
small ligand	497
antibody	356
host protein	241
host cell receptor	46

Tool to judge relevance of new mutations in variants