Analysis by and presented on behalf of GISAID by

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Deputy Executive Director (Research)

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and Research
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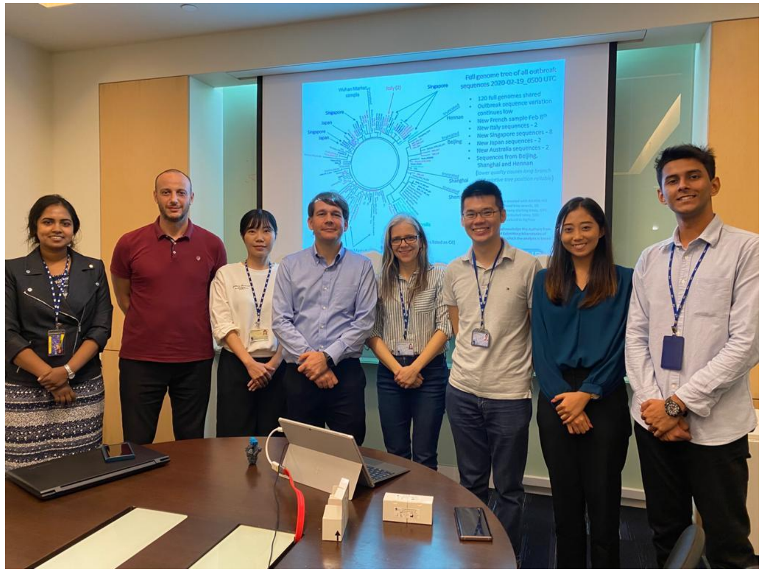
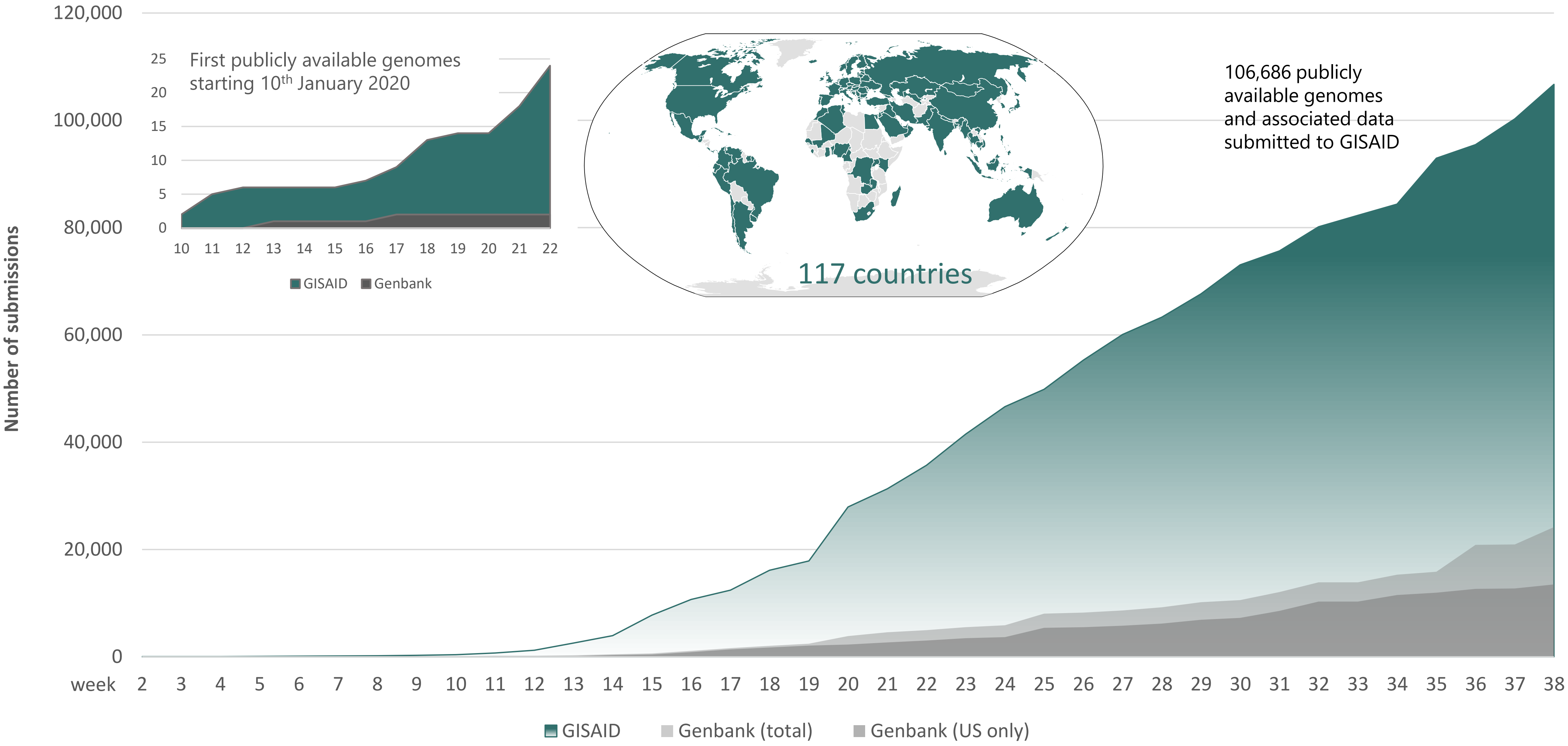


GISAID provisions for analysing Spike mutations

- Single comprehensive source of all outbreak genomes
- Summary and report of clade trends and associated mutations
- Enabling all registered users through dedicated download of all current Spike proteins as well as complete genome alignment
- Spike protein mutation annotation for all entries, common ones in drop down
- Integrated mutation analysis tool CoVsurver:
  - 3D structure mapping
  - Host receptor interaction
  - Antibody interaction
  - Literature phenotype annotation
  - Geotemporal frequency and phylogenetic distribution
- Upcoming: live dashboard for spike mutations
- Needed in near future: serological panel data linked to sequences

Real-time data sharing is not achieved by governmental Regulations

it is incentivized by the confidence in trusted sharing mechanisms



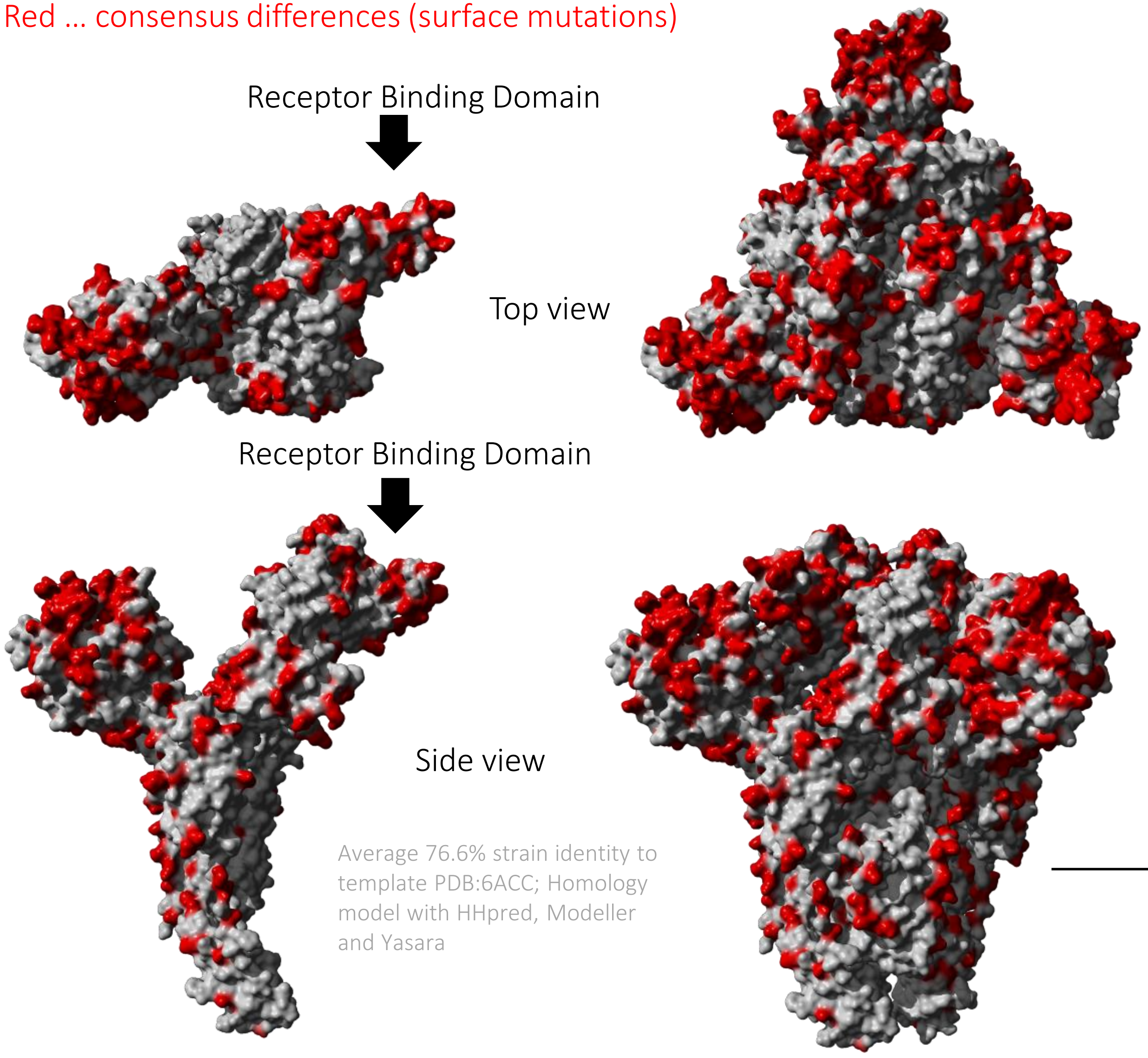
Spike mutations summary (9 months, >100k genomes)

- **Spike similarity to other Coronaviruses**
- Spike similarity within the outbreak
    - Frequency and trends of most common spike mutations
    - Host receptor binding mutations
    - Antibody binding mutation tool
    - Reinfection pairs comparison

Spike similarity to other coronaviruses

Spike glycoprotein hCoV-19 vs SARS

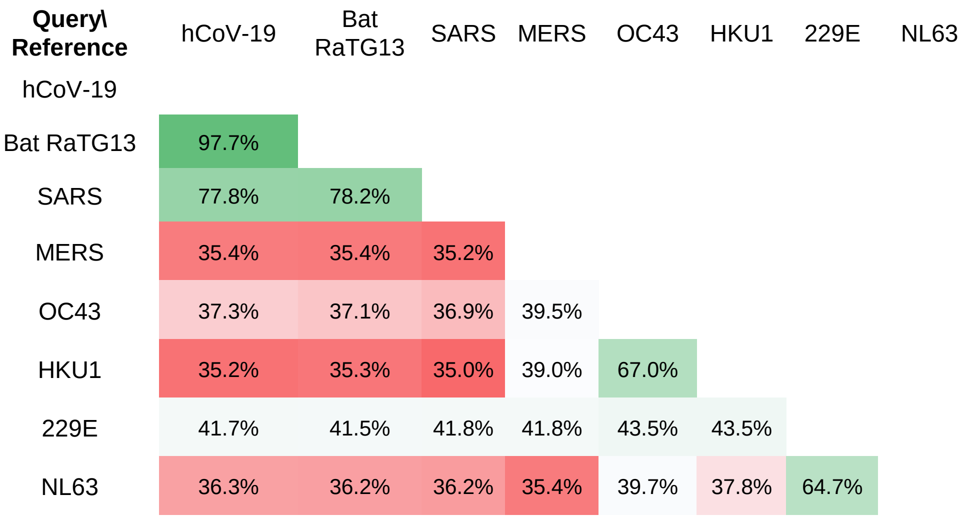
Red … consensus differences (surface mutations)



Average 76.6% strain identity to template PDB:6ACC; Homology model with HHpred, Modeller and Yasara

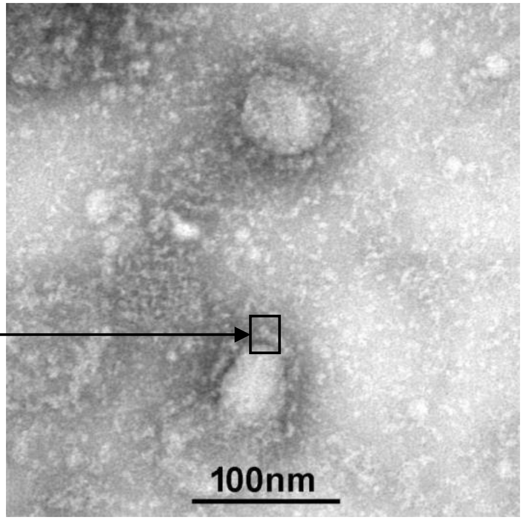
Monomer

Trimer



Query\ Reference	hCoV-19	Bat RaTG13	SARS	MERS	OC43	HKU1	229E	NL63
hCoV-19								
Bat RaTG13	97.7%							
SARS	77.8%	78.2%						
MERS	35.4%	35.4%	35.2%					
OC43	37.3%	37.1%	36.9%	39.5%				
HKU1	35.2%	35.3%	35.0%	39.0%	67.0%			
229E	41.7%	41.5%	41.8%	41.8%	43.5%	43.5%		
NL63	36.3%	36.2%	36.2%	35.4%	39.7%	37.8%	64.7%	

Percent identity of spike glycoproteins from relevant coronaviruses



Cryo-EM image IVDC, China CDC

Spike mutations summary (9 months, >100k genomes)

- Spike similarity to other Coronaviruses
- **Spike similarity within the outbreak**
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  - Host receptor binding mutations
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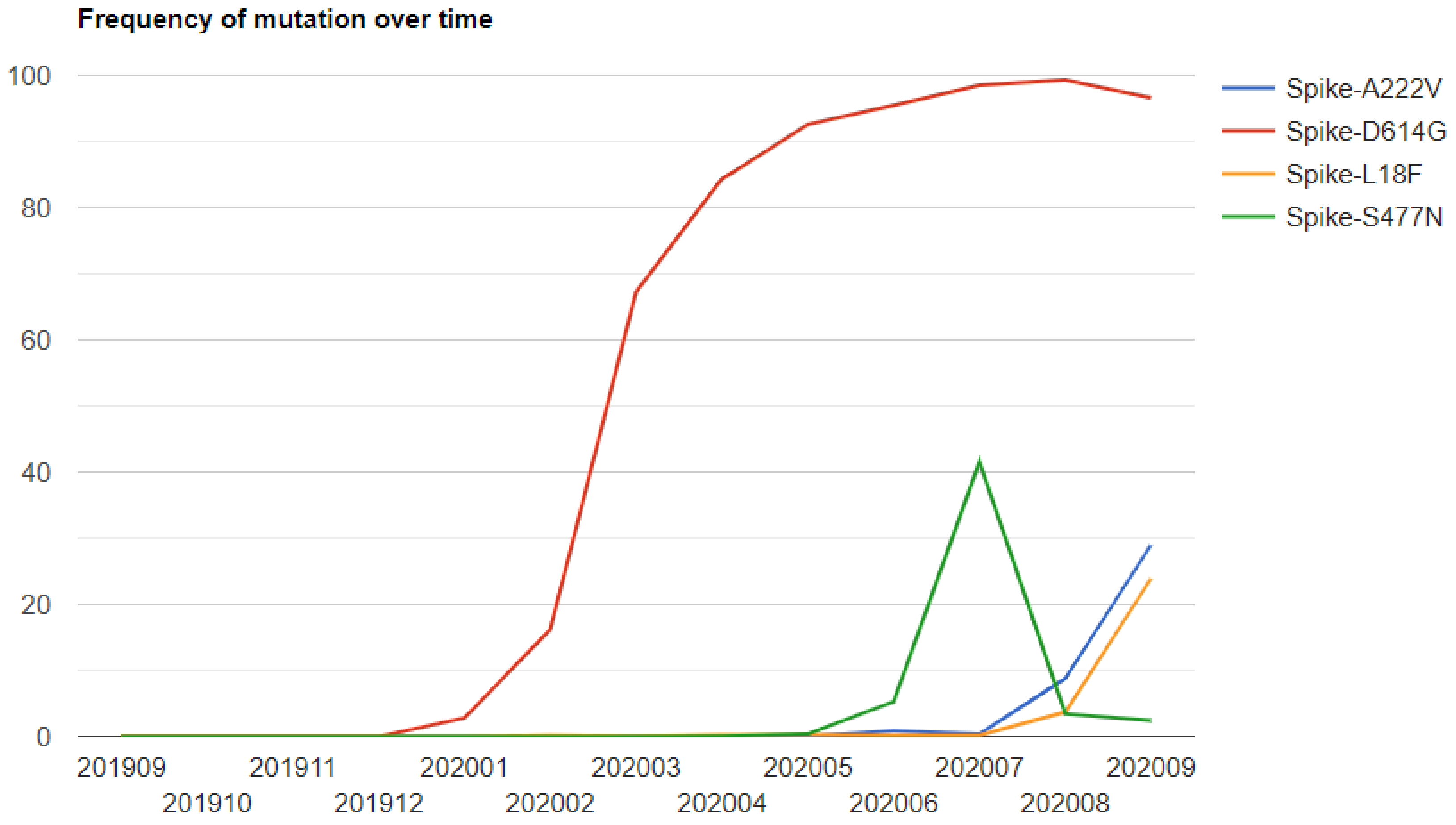
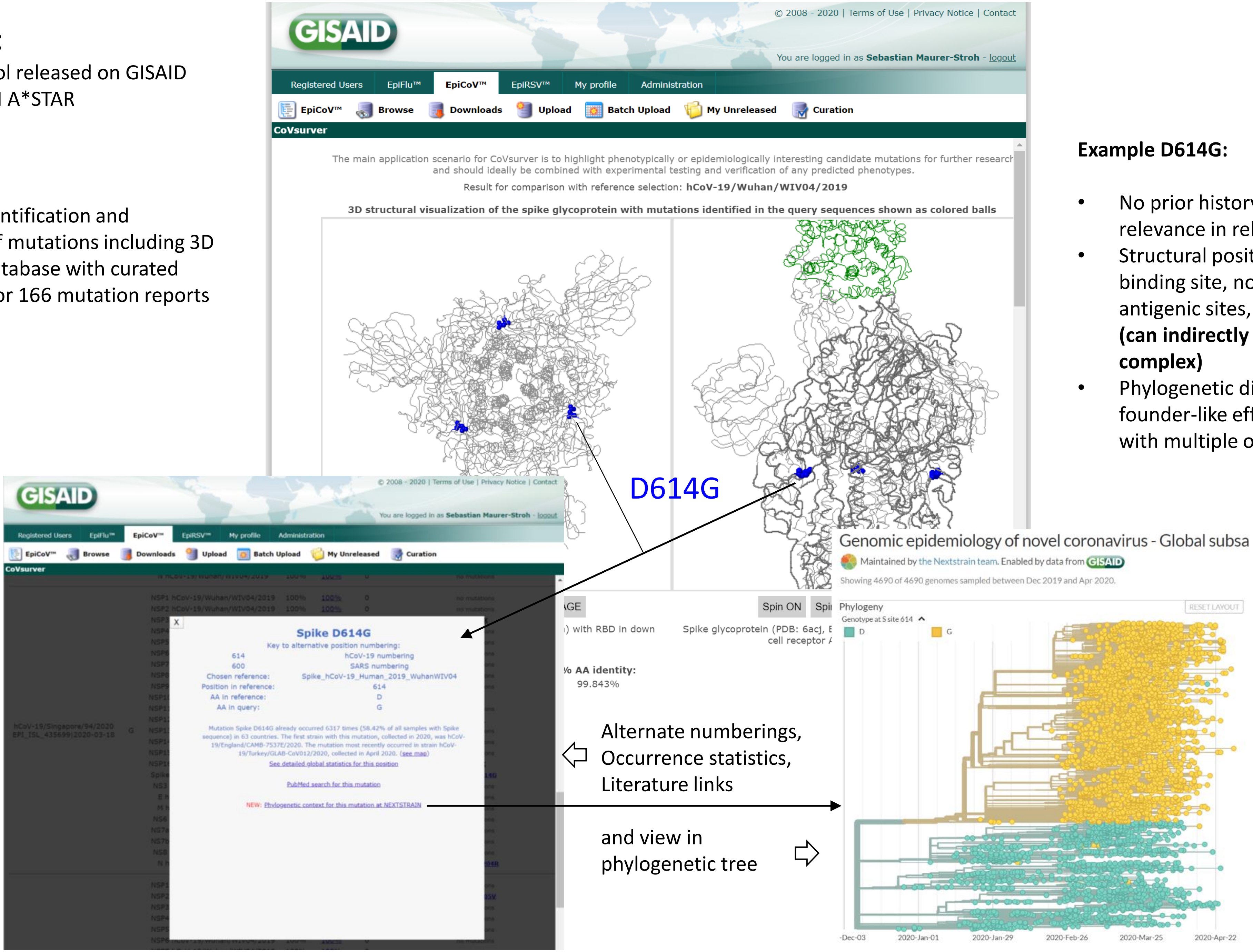
Common spike mutations within the outbreak – Sep 20 2020



CoVsurver:

New analysis tool released on GISAID developed by BII A*STAR

Capabilities: Identification and interpretation of mutations including 3D structure and database with curated literature links for 166 mutation reports



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The main application scenario for CoVsurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with experimental testing and verification of any predicted phenotypes.

Result for comparison with reference selection: **hCoV-19/Wuhan/WIV04/2019**

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

% AA identity:
99.843%

NSP1 hCoV-19/Wuhan/WIV04/2019 100% 100% 0 no mutations
NSP2 hCoV-19/Wuhan/WIV04/2019 100% 100% 0 no mutations

hCoV-19/Singapore/94/2020
EPI_ISL_435699|2020-03-18

Spike D614G

Key to alternative position numbering:

614	hCoV-19 numbering
600	SARS numbering
Chosen reference:	Spike_hCoV-19_Human_2019_WuhanWIV04
Position in reference:	614
AA in reference:	D
AA in query:	G

Mutation Spike D614G already occurred 6317 times (58.42% of all samples with Spike sequence) in 63 countries. The first strain with this mutation, collected in 2020, was hCoV-19/England/CAMB-7537E/2020. The mutation most recently occurred in strain hCoV-19/Turkey/GLAB-CoV012/2020, collected in April 2020. (see map)

See detailed global statistics for this position

PubMed search for this mutation

NEW: Phylogenetic context for this mutation at NEXTSTRAIN

Alternate numberings, Occurrence statistics, Literature links

and view in phylogenetic tree

Genomic epidemiology of novel coronavirus - Global subsa

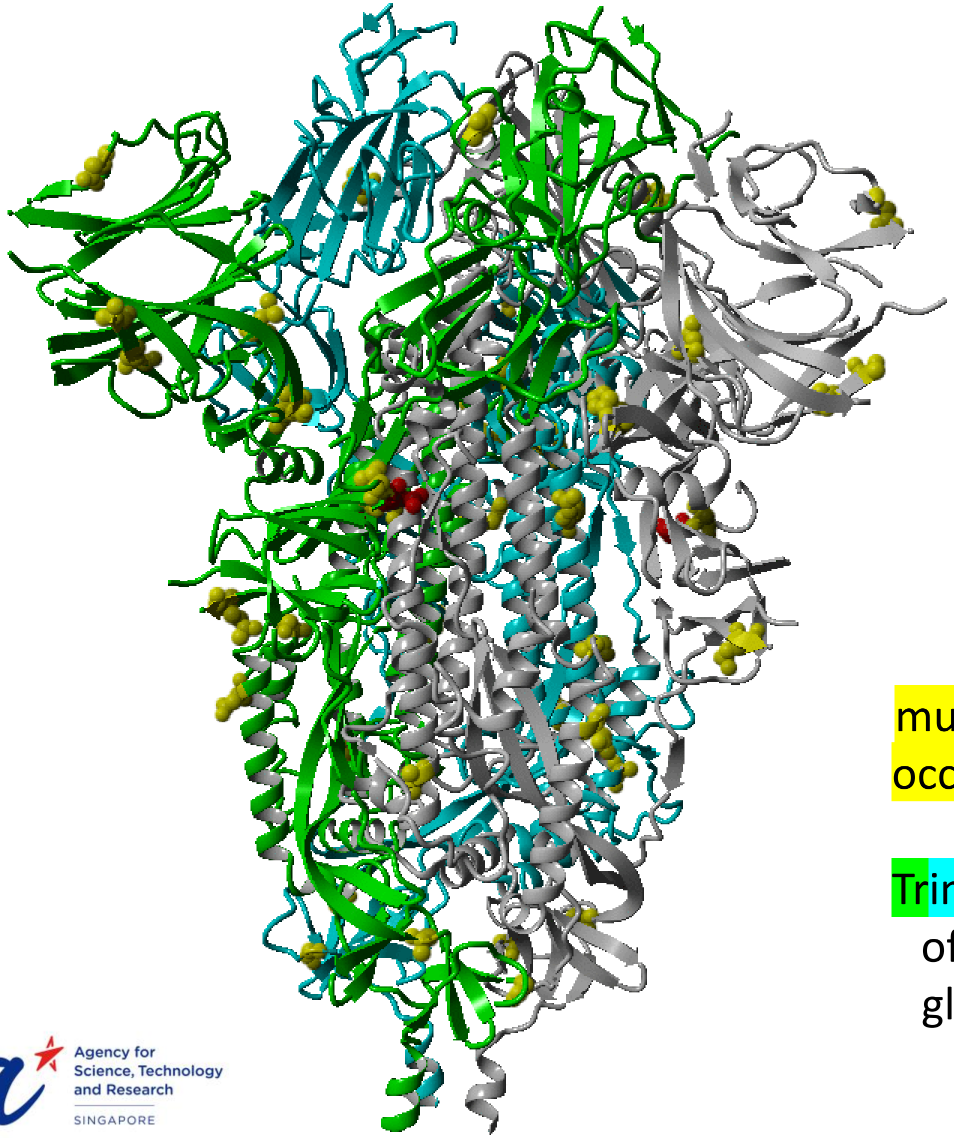
Maintained by the Nextstrain team. Enabled by data from GISAID

Showing 4690 of 4690 genomes sampled between Dec 2019 and Apr 2020.

Example D614G:

- No prior history of site for phenotypic relevance in related viruses
- Structural position not near receptor binding site, not in classical RBD antigenic sites, **at oligomer interface (can indirectly affect stability of complex)**
- Phylogenetic distribution points to founder-like effect and is accompanied with multiple other mutations

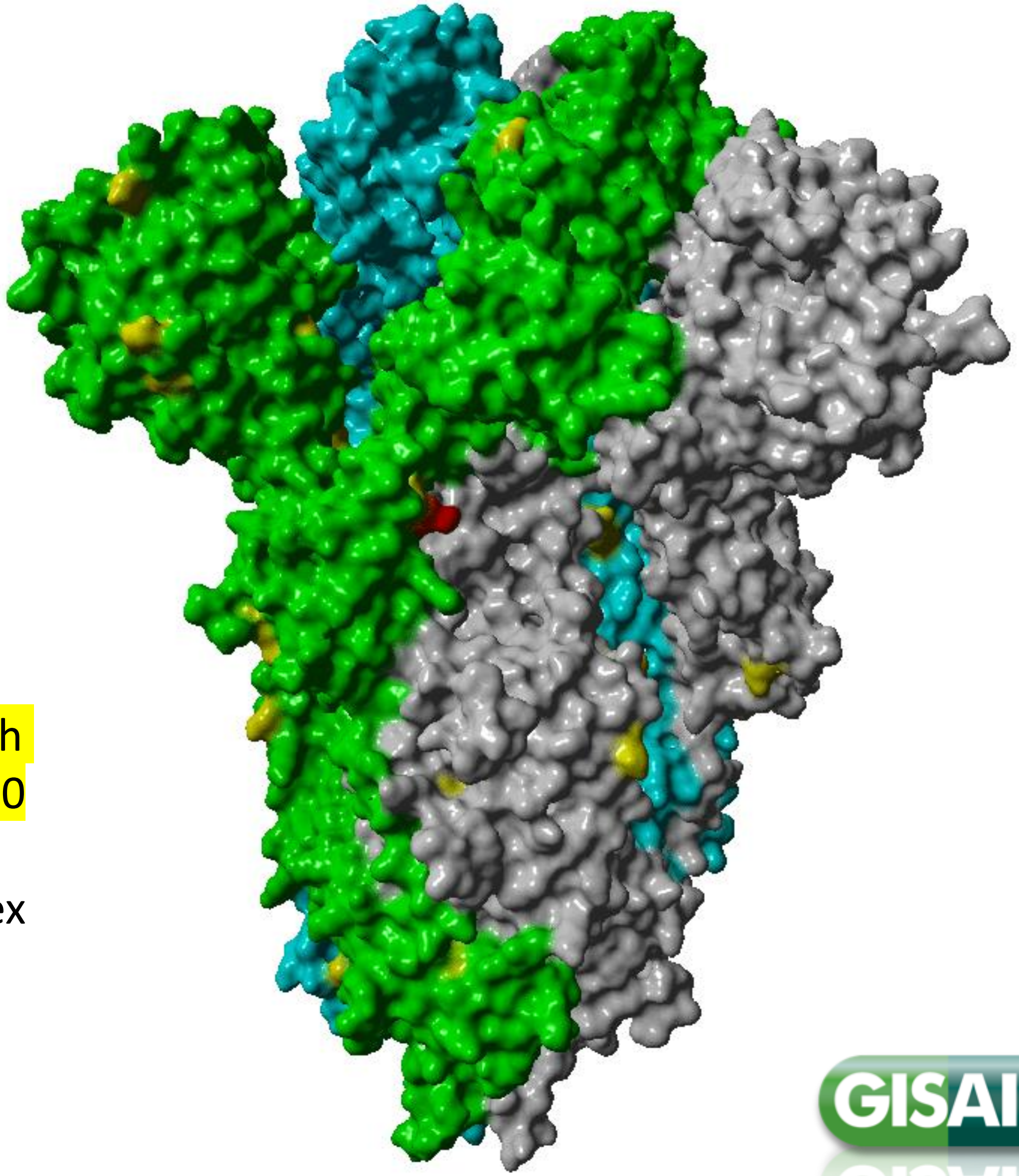
Common spike mutations within the outbreak – May 5 2020



D614G

Other mutations with occurrence >10

Trimer complex of viral spike glycoprotein



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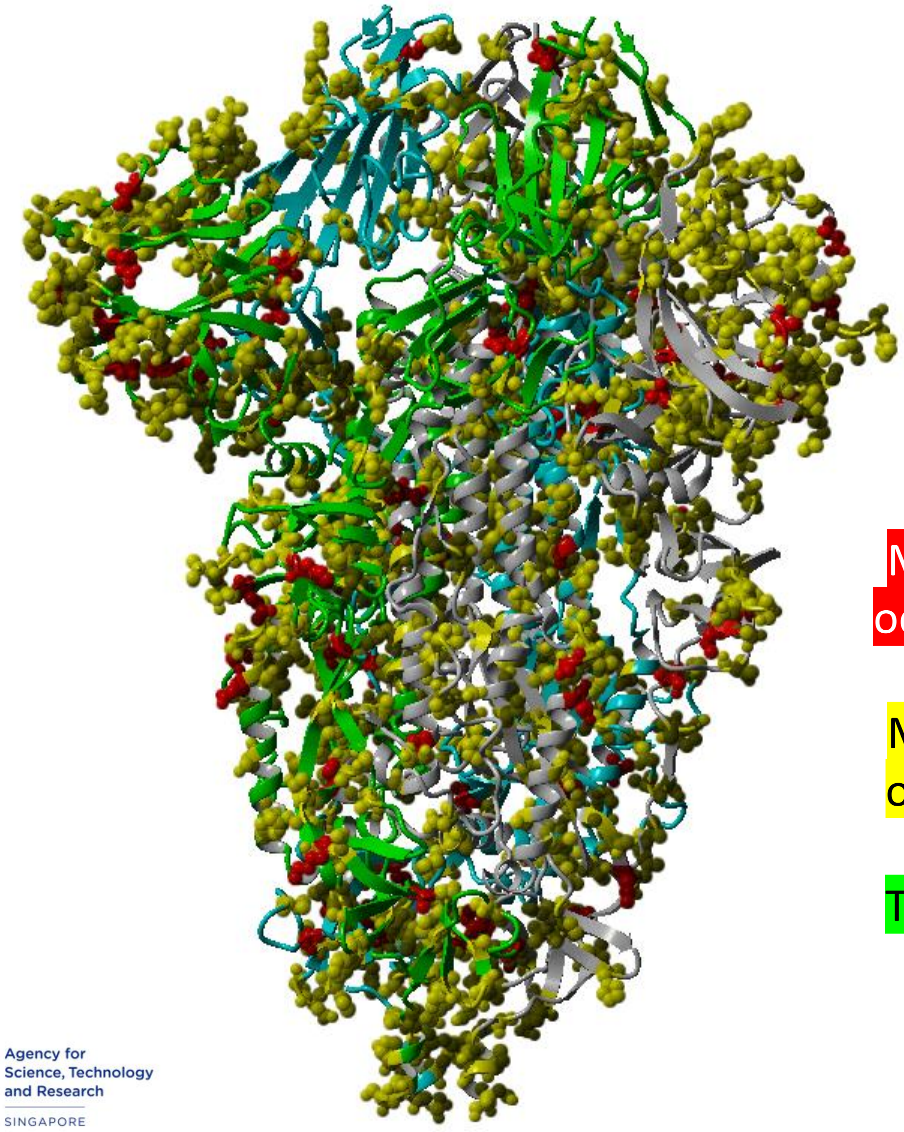
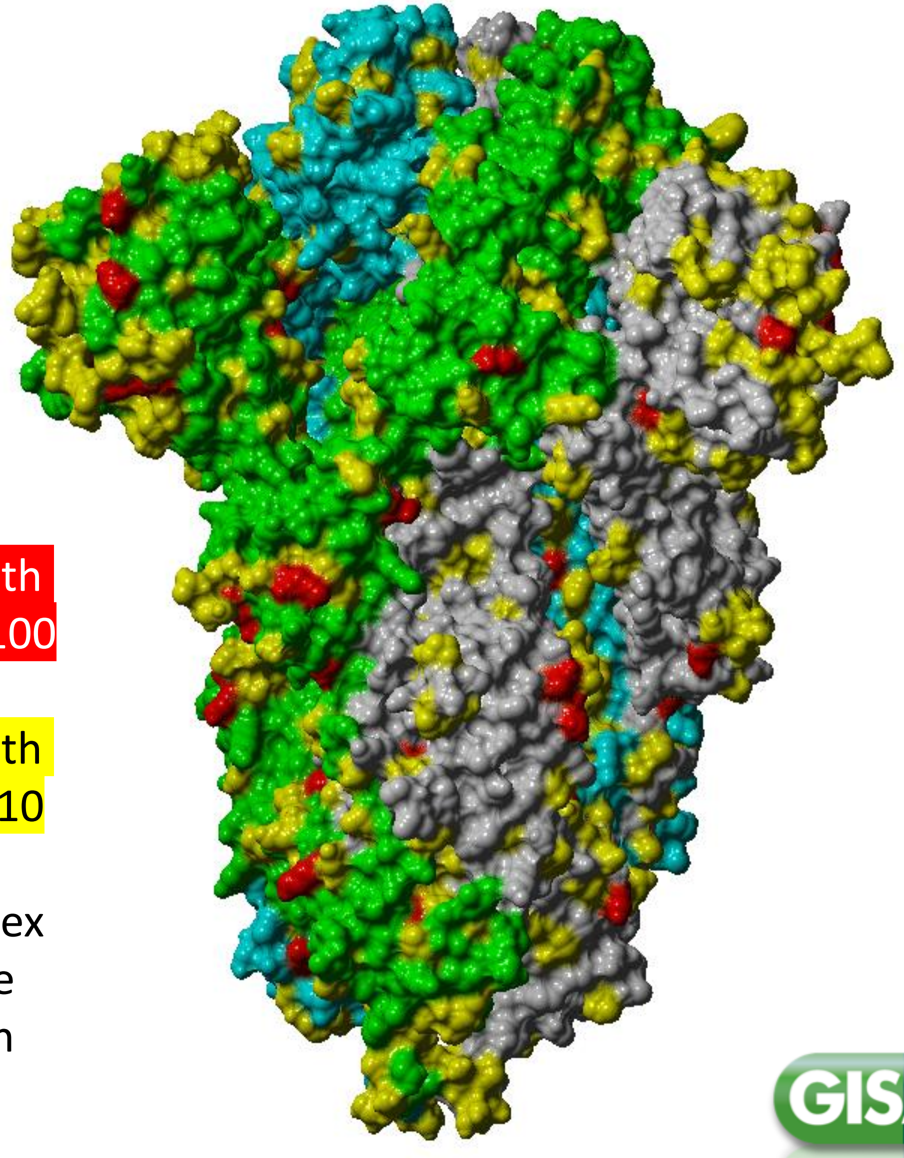
Common spike mutations within the outbreak – Sep 20 2020



Mutations with occurrence >100

Mutations with occurrence >10

Trimer complex of viral spike glycoprotein



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103720 sequences were compared to reference sequence EPI_ISL_402124.

Spike mutations summary (9 months, >100k genomes)

- Spike similarity to other Coronaviruses
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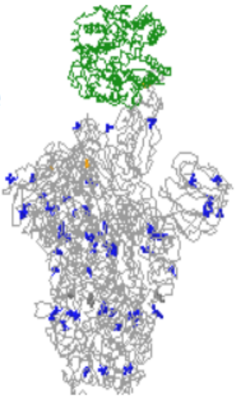
Receptor binding surveillance for complete genomes 2020-09-22

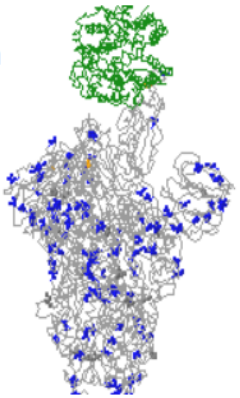
New occurrence of receptor binding mutations 25x S477N in Switzerland, 3x S477N in Germany, 1x S477N in Australia/NSW, 4x S477I in England, 2x N439K in Switzerland, 1x N439K in Germany, 1x E484A in Spain

Total: 37 different rare variants near the binding interface not known to be linked to severity with >1x occurrence. 4157x **S477N** (3709 Australia/VIC, 235 Australia/NSW, 106 England, 27 Switzerland, 21 Australia/QLD, 13 Scotland, 11 Northern Ireland, 8 Sweden, 8 Australia/SAP, 5 Australia/ACT, 4 USA/FL, 3 Germany, 2 Australia/NT, 1 Lebanon, 1 USA/MA, 1 Australia/TAS, 1 USA/WA, 1 Australia/WA), 737x **N439K** (548 Scotland, 95 Ireland, 38 England, 26 Northern Ireland, 12 Wales, 10 Switzerland, 3 USA/IL, 2 Norway, 1 Germany, 1 Romania, 1 USA/WI), 108x **T478I** (107 England, 1 Spain), 40x **N501Y** (36 Australia/VIC, 1 USA/OR, 1 Wales, 1 Brazil, 1 USA/NY), 38x **G485R** (37 Australia/VIC, 1 Anhui), 30x **S494P** (17 England, 3 USA/MI, 2 Sweden, 2 Scotland, 2 India, 1 Singapore, 1 Wales, 1 Nigeria, 1 Spain), 20x **G476S** (9 USA/WA, 4 England, 1 USA/OR, 1 Singapore, 1 India, 1 Suriname, 1 USA/WI, 1 Belgium, 1 United Arab Emirates), 19x **E484Q** (12 Wales, 3 India, 2 Spain, 1 South Africa, 1 USA/CA), 18x **G446V** (3 England, 3 Australia/VIC, 2 USA/VA, 2 South Korea, 1 USA/MN, 1 Wales, 1 USA/CA, 1 Scotland, 1 USA/WA, 1 Finland, 1 Israel, 1 Portugal), 15x **S477I** (7 England, 2 Scotland, 1 Singapore, 1 Indonesia, 1 USA/SC, 1 Colombia, 1 Luxembourg, 1 Australia/VIC), 14x **L455F** (5 England, 2 South Africa, 2 South Korea, 1 Italy, 1 USA/CA, 1 Scotland, 1 USA/MO, 1 Australia/VIC), 13x **R403K** (11 USA/VA, 2 Australia/VIC), 13x **A475V** (3 USA/OR, 2 England, 2 USA/AZ, 2 Australia/VIC, 1 Italy, 1 USA/NY, 1 USA/FL, 1 Australia/NSW), 11x **E484K** (3 England, 2 Sweden, 2 Spain, 1 Wales, 1 Switzerland, 1 USA/IL, 1 USA/CA), 10x **Y453F** (5 Netherlands, 3 Switzerland, 2 South Africa), 8x **F490S** (8 England), 6x **Q493L** (3 USA/WI, 3 USA/MD), 5x **F490L** (2 Singapore, 1 USA/LA, 1 Australia/VIC, 1 USA/CA), 5x **K417N** (2 Germany, 1 Scotland, 1 England, 1 Northern Ireland), 4x **S494L** (2 England, 1 Australia/VIC, 1 Switzerland), 4x **S477R** (2 Switzerland, 1 Egypt, 1 England), 3x **V503F** (1 Switzerland, 1 Netherlands, 1 USA/NY), 3x **E484A** (2 Spain, 1 Northern Ireland), 3x **V445A** (1 Israel, 1 Australia/VIC, 1 Mexico), 3x **T478K** (2 Scotland, 1 England), 3x **S477G** (1 Austria, 1 Spain, 1 Japan), 2x **S477T** (1 England, 1 USA/UT), 2x **Y505W** (1 USA/WA, 1 USA/UN), 2x **G504D** (1 Australia/VIC, 1 Spain), 2x **V503I** (1 England, 1 Scotland), 2x **G446S** (2 England), 2x **N501S** (2 England), 2x **F456L** (1 USA/TX, 1 South Korea), 2x **F486L** (2 Netherlands), 2x **V445I** (2 England), 2x **E484D** (1 Germany, 1 Thailand), 2x **G476A** (1 England, 1 USA/MI)

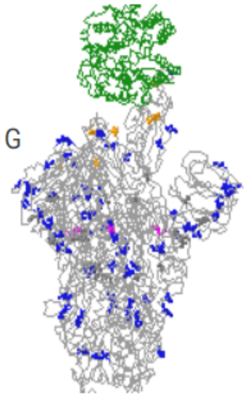
S477N in GH clade



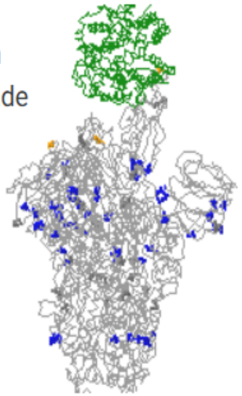
S477N in GR clade



N439K S477N S477I in G clade



E484A in nonG clade



Mutations in the spike glycoprotein for the 1519 new complete genomes.

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

Green … ACE2 human host receptor

Gray … CoV spike glycoprotein trimer

Gray balls … Spike glycoprotein variation occurring once (in EpiCoV)

Blue balls … Spike glycoprotein variation occurring more than once (in EpiCoV)

Red balls … Spike glycoprotein variation near host receptor with effect history

Orange balls … Spike glycoprotein variation near host receptor, or other functional annotation

Cyan … Insertion/deletion

Magenta balls … Spike glycoprotein variation altering potential N-glycosylation sites

Spike mutations summary (9 months, >100k genomes)

- Spike similarity to other Coronaviruses
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  - Frequency and trends of most common spike mutations
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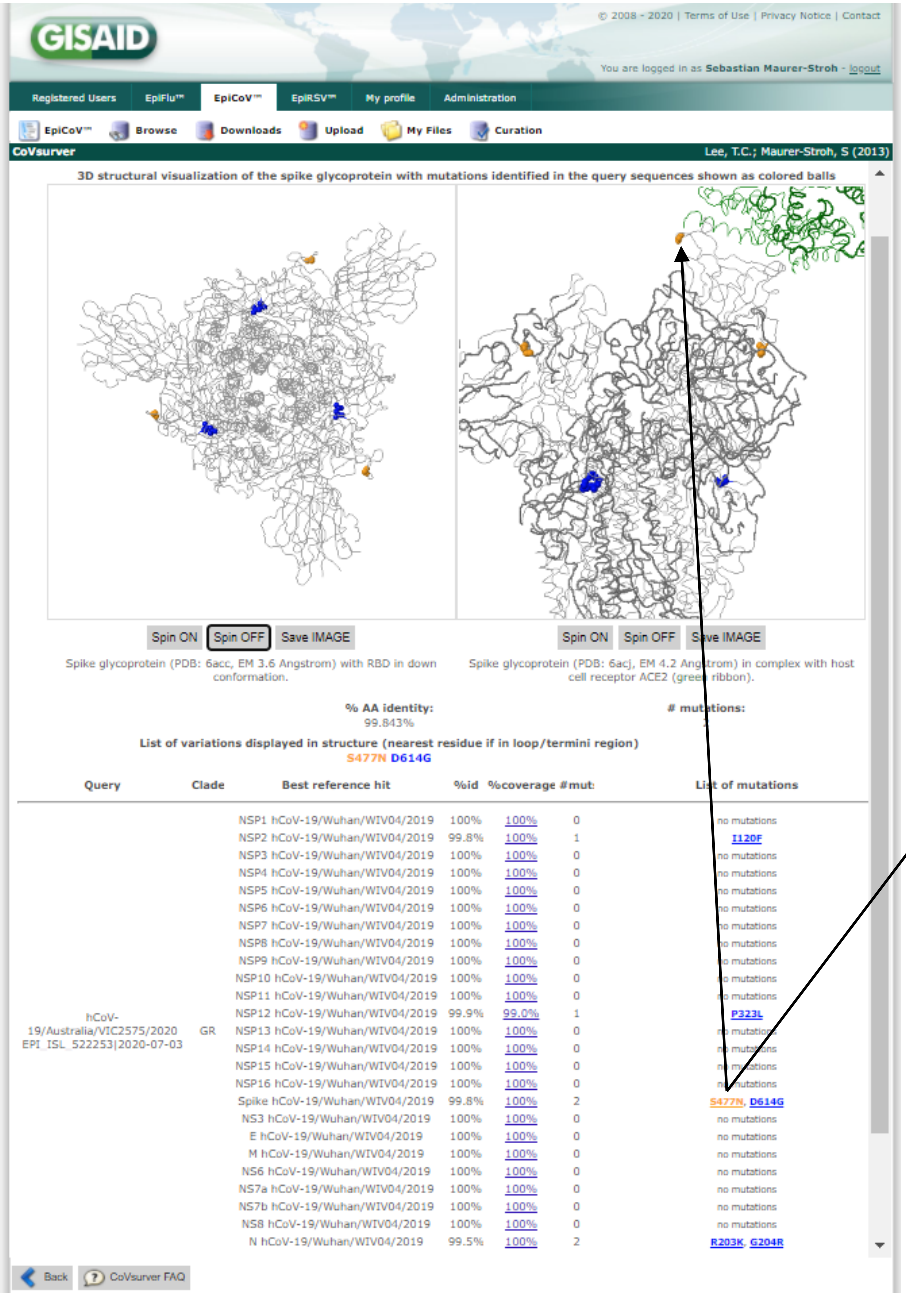
CoVsurver tool to analyse mutations – example Spike S477N



CoVsurver Lee, T.C.; Maurer-Stroh, S (2013)

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

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

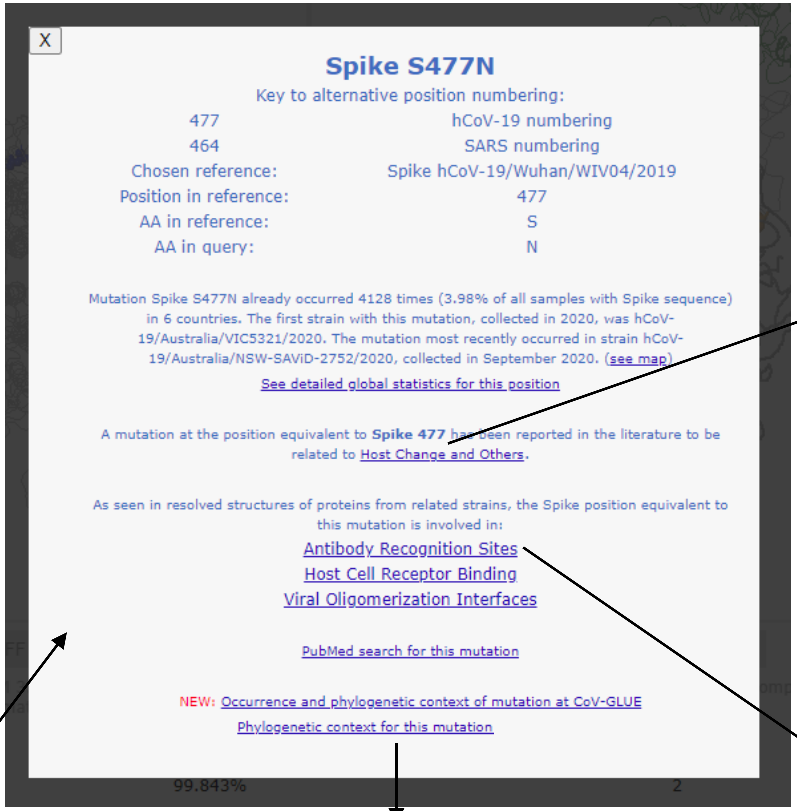
Spike glycoprotein (PDB: 6acj, EM 4.2 Angstrom) in complex with host cell receptor ACE2 (green ribbon).

% AA identity: 99.843%

 # mutations: 2

List of variations displayed in structure (nearest residue if in loop/termini region)
S477N D614G

Query	Clade	Best reference hit	%id	%coverage	#mut	List of mutations
hCoV-19/Australia/VIC2575/2020 EPI_ISL_522253|2020-07-03	GR	NSP1 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP2 hCoV-19/Wuhan/WIV04/2019	99.8%	100%	1	I120F
		NSP3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP4 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP5 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP7 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP9 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP10 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP11 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP12 hCoV-19/Wuhan/WIV04/2019	99.9%	99.0%	1	P323L
		NSP13 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP14 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP15 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP16 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		Spike hCoV-19/Wuhan/WIV04/2019	99.8%	100%	2	S477N, D614G
		NS3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		E hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		M hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS7a hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS7b hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		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

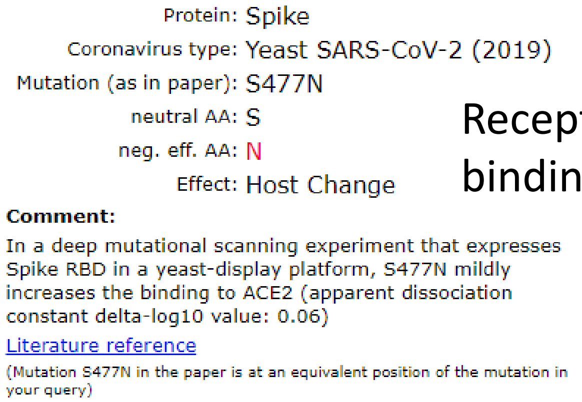
A mutation at the position equivalent to **Spike 477** has been reported in the literature to be related to Host Change and Others.

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



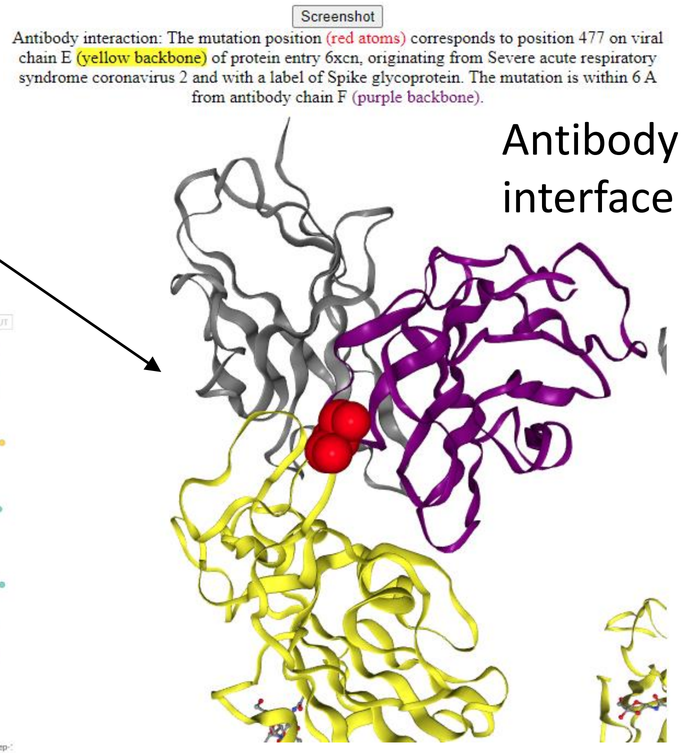
Protein: Spike
Coronavirus type: Yeast SARS-CoV-2 (2019)
Mutation (as in paper): S477N
neutral AA: S
neg. eff. AA: N
Effect: Host Change

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

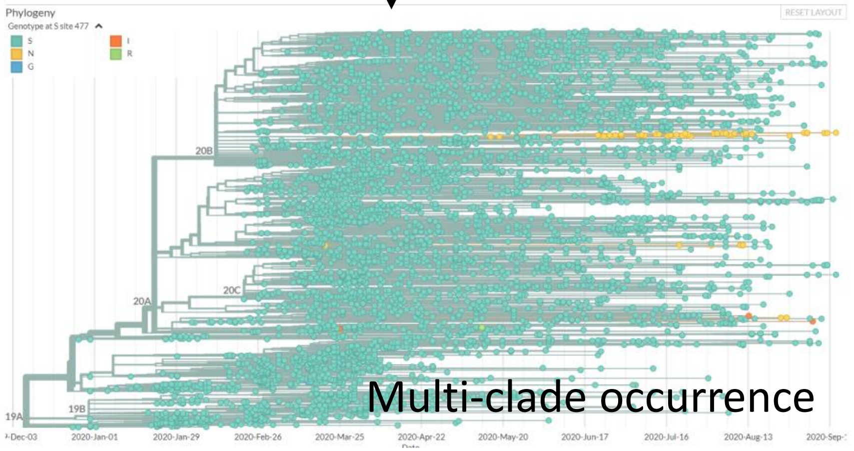
(Mutation S477N in the paper is at an equivalent position of the mutation in your query)

Receptor binding



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 A from antibody chain F (purple backbone).

Antibody interface



Multi-clade occurrence

Spike mutations summary (9 months, >100k genomes)

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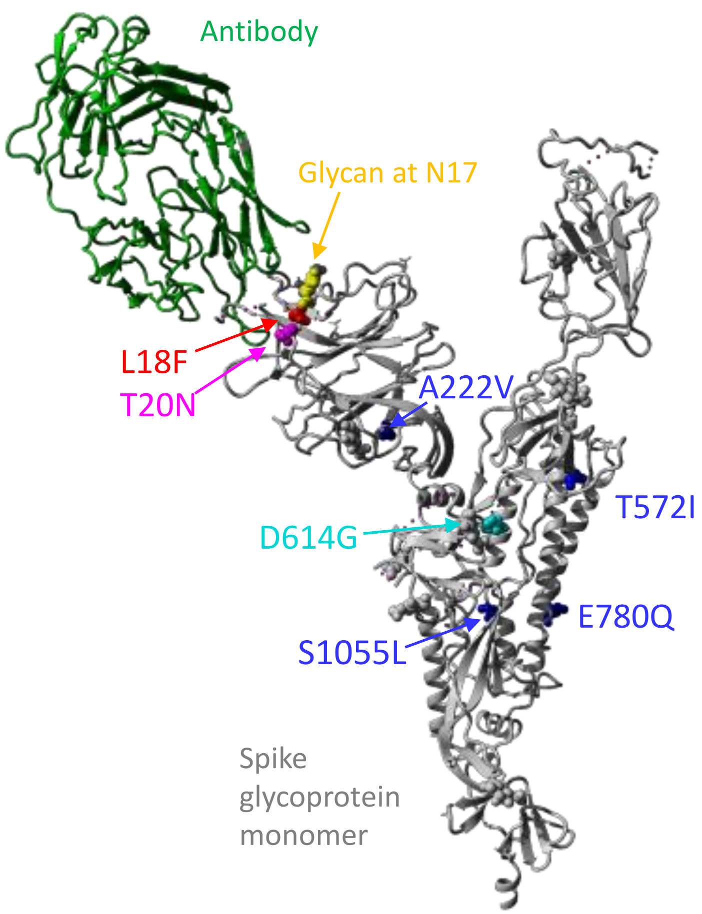
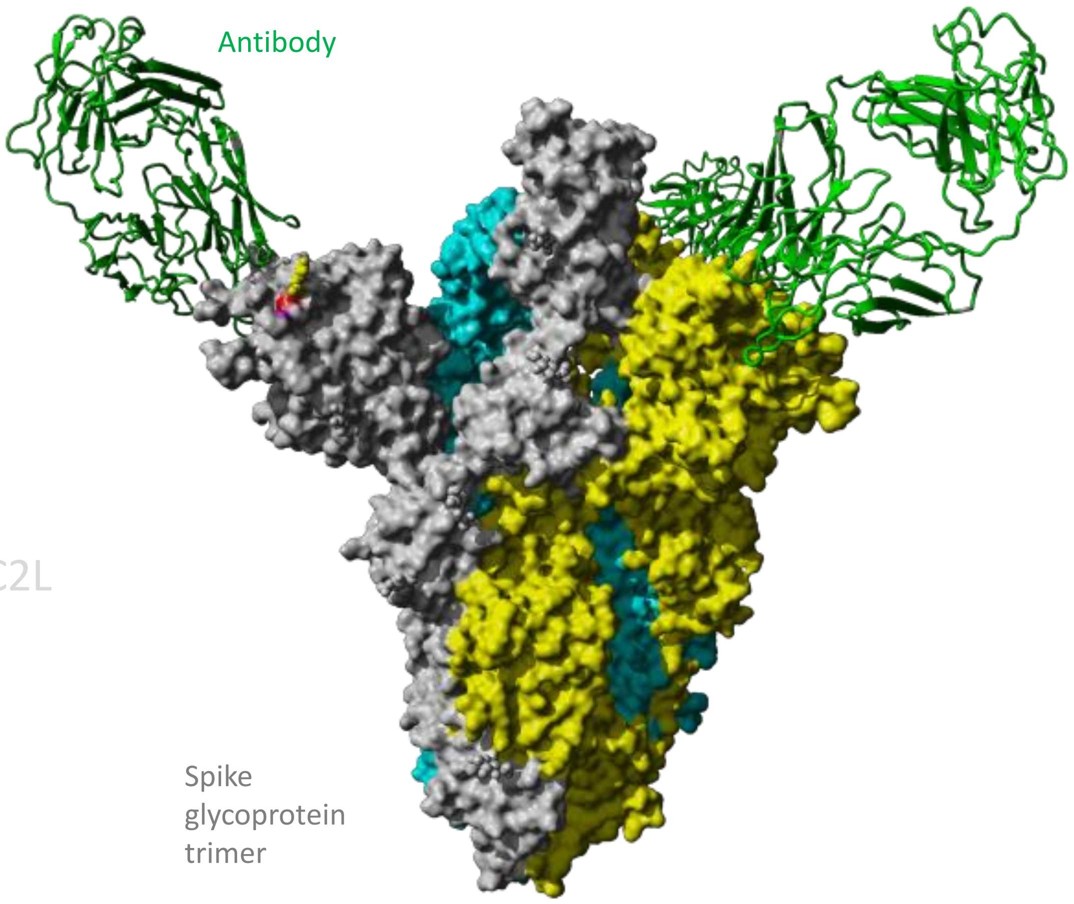
Summary of AA differences in 4 reinfection cases

Strainname	Accession	Collection Date	Clade (Lineage)	Spike AA mutations	Other AA mutations
hCoV-19/Hong Kong/HKU-200823-001/2020	EPI_ISL_516798	2020-03-26	V (B.1.79)	E780Q	NSP3_L1304F, NSP3_P1103L, NSP5_K61R, NSP6_L37F, NS3_G251V, NS8_E64stop
hCoV-19/Hong Kong/HKU-200823-002/2020	EPI_ISL_516799	2020-08-17	G (B.2)	L18F, A222V, D614G	NSP6_L142F, NSP12_P323L, N_A220V
hCoV-19/Belgium/rega-0309752/2020	EPI_ISL_522349	2020-03-09	GR (B.1.1)	D614G	NSP6_F228L, NSP12_P323L, NS8_L84S, N_G204R, N_R203K
hCoV-19/Belgium/rega-0710751/2020	EPI_ISL_522350	2020-06-10	S (A)	S1055L	NS8_L84S
hCoV-19/USA/NV-NSPHL-A0110/2020	EPI_ISL_514673	2020-04-18	GH (B.1)	D614G	NSP1_L92F, NSP2_T85I, NSP3_A465V, NSP12_P323L, NSP13_V169F, NS3_Q57H
hCoV-19/USA/NV-NSPHL-A0207/2020	EPI_ISL_514674	2020-06-05	GH (B.1)	D614G	NSP2_T85I, NSP6_P44S, NSP12_P323F, NS3_Q57H, N_A398V
hCoV-19/Netherlands/un-EMC-751/2020	EPI_ISL_523507	2020-04-06	L (B)		NSP2_D268del, NSP13_R392C
hCoV-19/Netherlands/un-EMC-754/2020	EPI_ISL_523510	2020-06-08	L (B)	T20N, T572I	NSP2_D268del, NSP3_S100P, NSP12_T806A, NSP3_T1288I, NSP3_D821N, NSP4_H313Y, NSP13_R392C, M_S4F

4 reinfection cases spike glycoprotein comparison



PDB:7C2L



2 of 4 reinfection cases have mutations possibly interfering with the structural conformation of glycosylation sites in a region that is also broadly recognized by antibodies which would provide a hypothetical mechanism for immune escape potentially contributing to permitting second infection. However, this doesn’t apply to all cases and many other factors could play a role too. Importantly, these mutations are rare and occur sporadically without causing large clusters so far.

GISAID provisions for analysing Spike mutations

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- Enabling all registered users through dedicated download of all current Spike proteins as well as complete genome alignment
- Spike protein mutation annotation for all entries, common ones in drop down
- Integrated mutation analysis tool CoVsurver:
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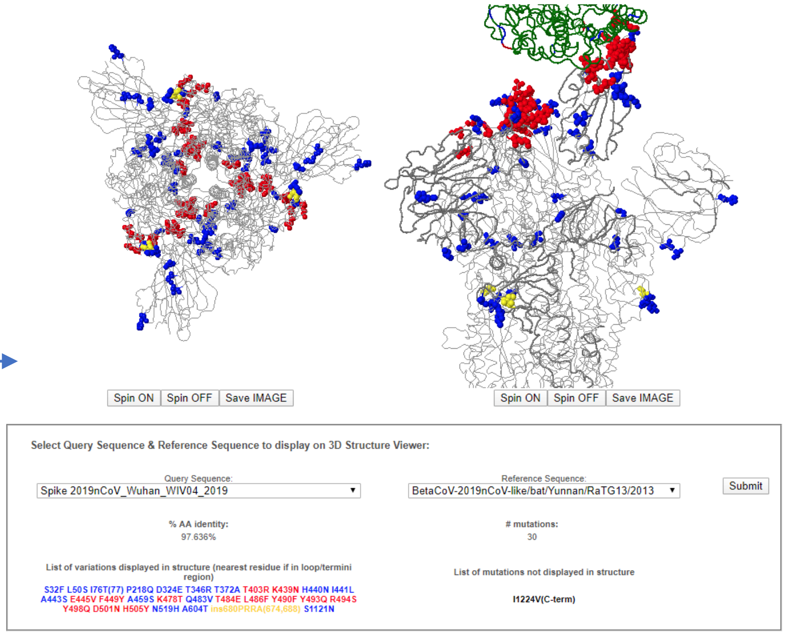
- Upcoming: live dashboard for spike mutations
- **Needed in near future: serological panel data linked to sequences**

Annex

Spike host receptor changes for nearest bat and nearest pangolin sequences

Strain 1	Strain 2	Spike overall identity	Interface mutations
Human Wuhan	Bat Yunnan	98%	13
Pangolin Guangdong	Bat Yunnan	90%	13
Pangolin Guangdong	Human Wuhan	91%	1



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: Spike 2019nCoV_Wuhan_WIV04_2019

Reference Sequence: BetaCoV-2019nCoV-like/bat/Yunnan/RaTG13/2013

% AA identity: 97.636%

mutations: 30

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

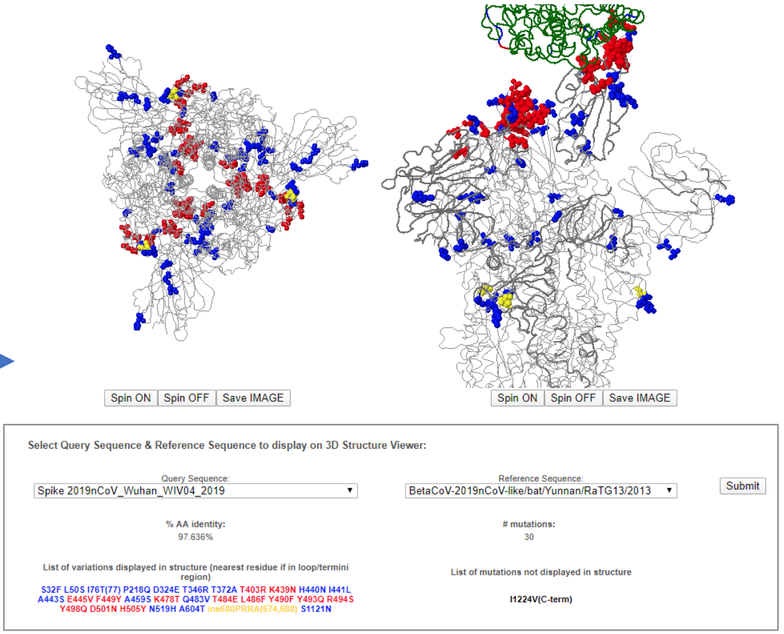
S32F L50S I76T(77) P218Q D324E T346R T372A T403R K439N H440N I441L A443S E445V F449Y A459S K478T Q483V T484E L486F Y490F Y493Q R494S Y498Q D501N H505Y N519H A604T ins680PRRA(674,688) S1121N

List of mutations not displayed in structure

I1224V(C-term)

Spike host receptor changes for nearest bat and nearest pangolin sequences

Strain 1	Strain 2	Spike overall identity	Interface mutations
Human Wuhan	Bat Yunnan	98%	13
Pangolin Guangdong	Bat Yunnan	90%	13
Pangolin Guangdong	Human Wuhan	91%	1



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: Spike 2019nCoV_Wuhan_WIV04_2019 ▼

Reference Sequence: BetaCoV-2019nCoV-like/bat/Yunnan/RaTG13/2013 ▼

% AA identity: 97.636%

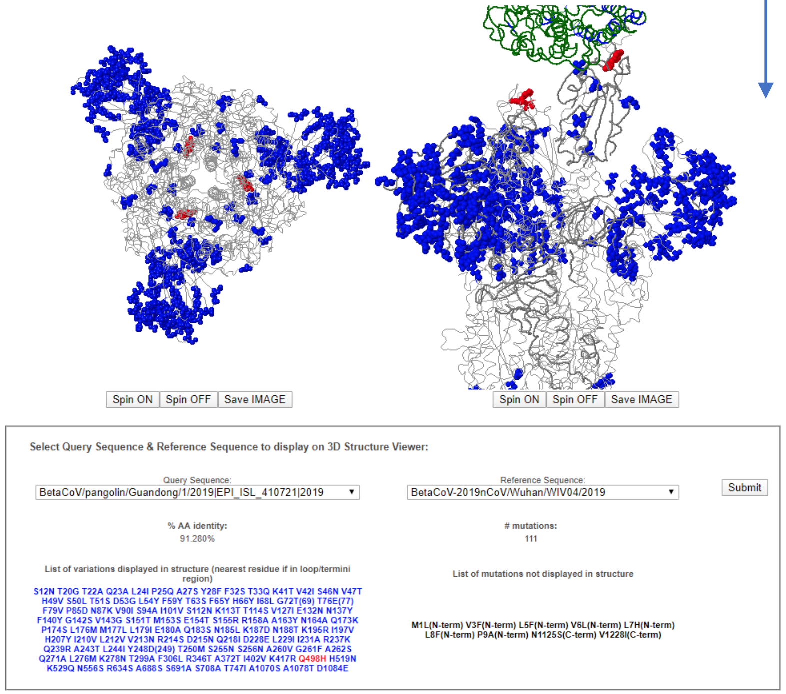
mutations: 30

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

S32F L50S I76T(77) P218Q D324E T346R T372A T403R K439N H440N I441L A443S E445V F449Y A459S K478T Q483V T484E L486F Y490F Y493Q R494S Y498Q D501N H505Y N519H A604T ins680PRRA(674,688) S1121N

List of mutations not displayed in structure

I1224V(C-term)



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: BetaCoV/pangolin/Guandong/1/2019|EPI_ISL_410721|2019 ▼

Reference Sequence: BetaCoV-2019nCoV/Wuhan/WIV04/2019 ▼

% AA identity: 91.280%

mutations: 111

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

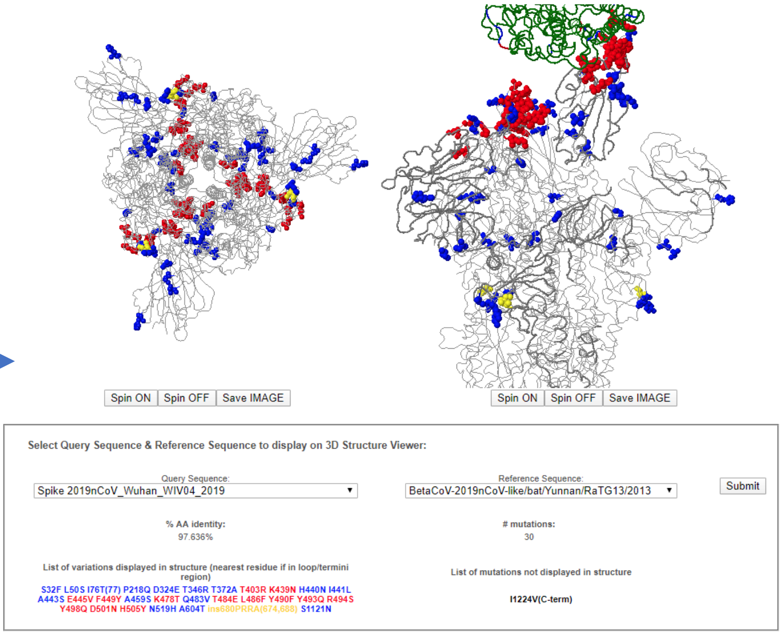
S12N T20G T22A Q23A L24I P25Q A27S Y28F F32S T33Q K41T V42I S46N V47T H49V S50L T51S D53G L54Y F59Y T63S F65Y H66Y I68L G72T(69) T76E(77) F79V P85D N87K V90I S94A I101V S112N K113T T114S V127I E132N N137Y F140Y G142S V143G S151T M153S E154T S155R R158A A163Y N164A Q173K P174S L176M M177L L179I E180A Q183S N185L K187D N188T K195R I197V H207Y I210V L212V V213N R214S D215N Q218I D228E L229I I231A R237K Q239R A243T L244I Y248D(249) T250M S255N S256N A260V G261F A262S Q271A L276M K278N T299A F306L R346T A372T I402V K417R Q498H H519N K529Q N556S R634S A688S S691A S708A T747I A1070S A1078T D1084E

List of mutations not displayed in structure

M1L(N-term) V3F(N-term) L5F(N-term) V6L(N-term) L7H(N-term) L8F(N-term) P9A(N-term) N1125S(C-term) V1228I(C-term)

Spike host receptor changes for nearest bat and nearest pangolin sequences

Strain 1	Strain 2	Spike overall identity	Interface mutations
Human Wuhan	Bat Yunnan	98%	13
Pangolin Guangdong	Bat Yunnan	90%	13
Pangolin Guangdong	Human Wuhan	91%	1



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: Spike 2019nCoV_Wuhan_WIV04_2019 ▾

Reference Sequence: BetaCoV-2019nCoV-like/bat/Yunnan/RaTG13/2013 ▾

% AA identity: 97.636%

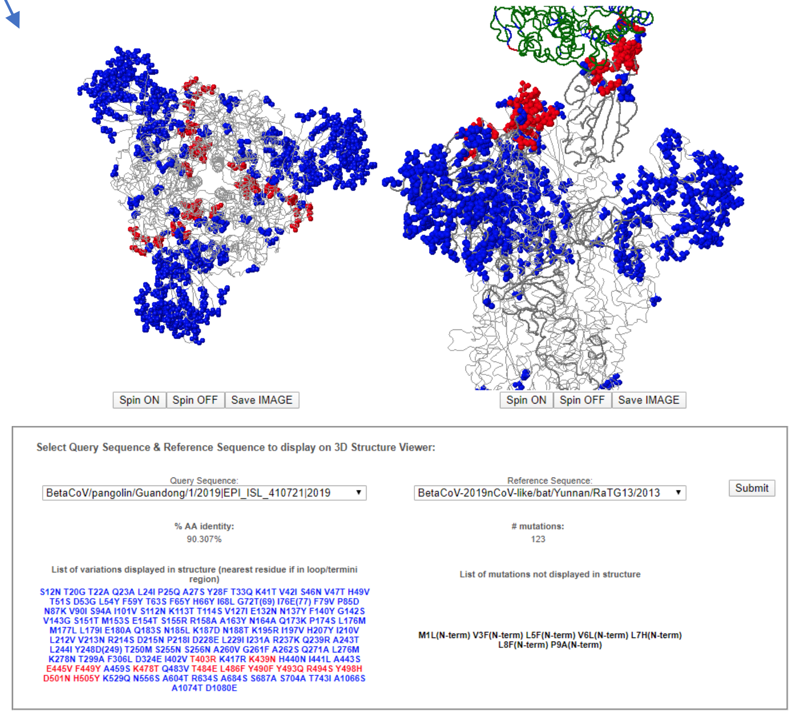
mutations: 30

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

S32F L50S I76T(77) P218Q D324E T346R T372A T403R K439N H440N I441L A443S E445V F449Y A459S K478T Q483V T484E L486F Y490F Y493Q R494S Y498Q D501N H505Y N519H A604T ins680PRRA(674,688) S1121N

List of mutations not displayed in structure

I1224V(C-term)



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: BetaCoV/pangolin/Guandong/1/2019|EPI_ISL_410721|2019 ▾

Reference Sequence: BetaCoV-2019nCoV-like/bat/Yunnan/RaTG13/2013 ▾

% AA identity: 90.307%

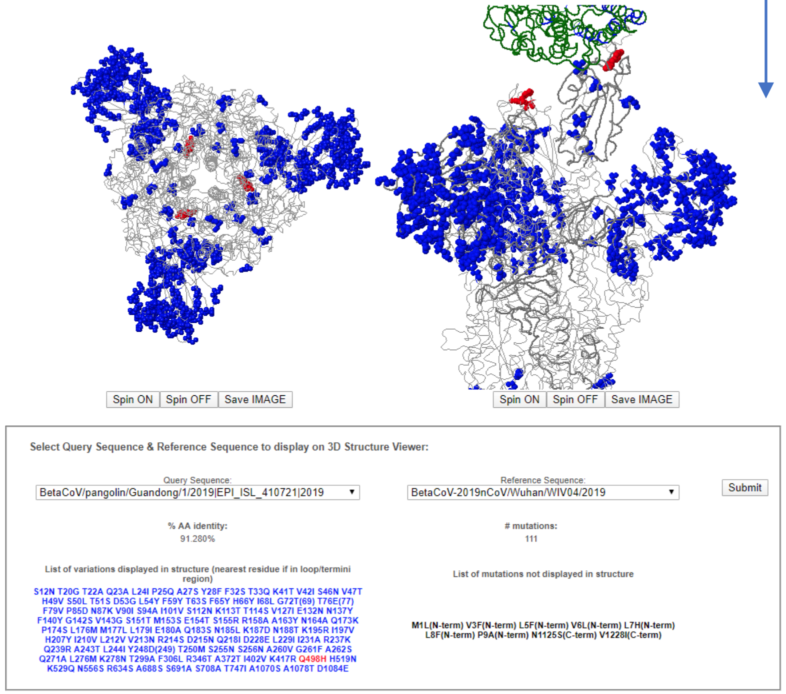
mutations: 123

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

S12N T20G T22A Q23A L24I P25Q A27S Y28F T33Q K41T V42I S46N V47T H49V T51S D53G L54Y F59Y T63S F65Y H66Y I68L G72T(69) I76E(77) F79V P85D N87K V90I S94A I101V S112N K113T T114S V127I E132N N137Y F140Y G142S V143G S151T M153S E154T S155R R158A A163Y N164A Q173K P174S L176M M177L L179I E180A Q183S N185L K187D N188T K195R I197V H207Y I210V L212V V213N R214S D215N P218I D228E L229I I231A R237K Q239R A243T L244I Y248D(249) T250M S255N S256N A260V G261F A262S Q271A L276M K278N T299A F306L D324E I402V T403R K417R K439N H440N I441L A443S E445V F449Y A459S K478T Q483V T484E L486F Y490F Y493Q R494S Y498H D501N H505Y K529Q N556S A604T R634S A684S S687A S704A T743I A1066S A1074T D1080E

List of mutations not displayed in structure

M1L(N-term) V3F(N-term) L5F(N-term) V6L(N-term) L7H(N-term) L8F(N-term) P9A(N-term)



Select Query Sequence & Reference Sequence to display on 3D Structure Viewer:

Query Sequence: BetaCoV/pangolin/Guandong/1/2019|EPI_ISL_410721|2019 ▾

Reference Sequence: BetaCoV-2019nCoV/Wuhan/WIV04/2019 ▾

% AA identity: 91.280%

mutations: 111

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

S12N T20G T22A Q23A L24I P25Q A27S Y28F F32S T33Q K41T V42I S46N V47T H49V S50L T51S D53G L54Y F59Y T63S F65Y H66Y I68L G72T(69) T76E(77) F79V P85D N87K V90I S94A I101V S112N K113T T114S V127I E132N N137Y F140Y G142S V143G S151T M153S E154T S155R R158A A163Y N164A Q173K P174S L176M M177L L179I E180A Q183S N185L K187D N188T K195R I197V H207Y I210V L212V V213N R214S D215N Q218I D228E L229I I231A R237K Q239R A243T L244I Y248D(249) T250M S255N S256N A260V G261F A262S Q271A L276M K278N T299A F306L R346T A372T I402V K417R Q498H H519N K529Q N556S R634S A688S S691A S708A T747I A1070S A1078T D1084E

List of mutations not displayed in structure

M1L(N-term) V3F(N-term) L5F(N-term) V6L(N-term) L7H(N-term) L8F(N-term) P9A(N-term) N1125S(C-term) V1228I(C-term)