



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL



FluSurver and CoVsurver

—
Clyde Dapat, PhD

WHO Collaborating Centre for Reference
and Research on Influenza



**CENTRE FOR
PATHOGEN
GENOMICS**



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





CENTRE FOR
PATHOGEN
GENOMICS



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

Objective

- To identify mutations using FluSurver and CoVsurver

flusurver.bii.a-star.edu.sg



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



Important usage notes:

The main application scenario for FluSurver 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. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the **usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu (including H5N1, H5N6, H5N8 and H7N9) and novel reassortant swine flu H3N2v.**

Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. You could also look at this [NA drug susceptibility example analysis walkthrough starting from GISAID](#) and the [GISAID access summary poster](#)

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequences: 2009 H1N1 NA and HA](#))

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen



To screen for mutations associated with drug resistance

Important usage notes:

The main application scenario for FluSurver 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. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the **usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu (including H5N1, H5N6, H5N8 and H7N9) and novel reassortant swine flu H3N2v.**

Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. You could also look at this [NA drug susceptibility example analysis walkthrough](#) starting from [GISAID](#) and the [GISAID access summary poster](#).

Paste your protein or nucleotide FASTA sequence(s) into the text area below. (Sample FASTA sequences: 2009 H1N1 NA and HA)

>A/Victoria/3035/2023/NA
atgaaltccaaaccaaaaagataataaccattggtgttatgtatgacaattggaaaggctacttaataattacaatgg
aaacataatctcaatatgggttagccactcaattcaaattggaaatcaaaaggccagttgaacatgcataaaaaggcgtca
ttacttatgaaaaacacacttggtaatcagacatttgttaacatcagcaacactaactctgtctgagacaatcagtg
gcttcgttggaaatttagccgggcaattctctctgtccctgttagtggatggctatatacgtagaaagcaacagttag
aatcgggttccaagggggggtgttgttgcataagggaaccattcatatcgtctccctggaaatgcagaacccttc
tgactcaaggggcttgcataaaatgcataaccatccatgtggaaacataaaaggacagaacggccatatgcacccatgt
tgccattatggtaagttcccttcatacaactcaagattgtactcgtcgctgtcagcaagtgctgtcatgtgg
caccataatggctacaacatggaaattctggcccagacaatggggcgtgtgtttaaaatacaatggcataataacag

OR upload your protein or nucleotide sequences in a FASTA file

Choose file No file chosen

The server can automatically determine the type of input (either protein or nucleotide) and the closest reference sequence among current vaccine strains to compare. Also mixtures of genes/proteins (e.g. HA and NA or all genes of the same patient) can be provided as input. To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequences: 2009 H1N1 NA and HA](#))

```
>A/Victoria/3035/2023|NA
atgaatccaaacaaaaagataataaccattggtttatctgtatgacaattggAACGGCTAACTTAATTACAAATTGG
AACACATAATCTCAATATGGGTTAGCCACTCAATTGGAAATCAAAGGCCAGATTGAAACATGCAATAAAAGCGTCA
TTACTTATGAAAACAACACTGGGTAAATCAGACATTGTTAACATCAGCAACACTACTGCTGCTAGACAACTGAG
GCTTCGTTGAAATTAGCGGGCAATTCTCTCTGCCCTGTTAGTGGATGGCTATAACAGTAAAGACAACAGTGTAAG
AAATCGGTTCCAAGGGGGATGTGTTGTATAAGGGAAACCATTATCATGCTCTCCCTGGAATGCGAGAACCTCTCT
TGACTCAAGGGGCTTGCTAAATGACAACATTCAATGAAACAATTAAAGACAAGGCCATATCGAACCCATAATGAGC
TGTCTATTGGTGAAGTCCCTCTCCATAACTCAAGATTGAGTCAGTCGCTGGTCAGCAAGTGCTTGTATGATGG
CACCAATTGGCTAACATTGAAATTCTGCCAGACAATGGGCAGTGCTGTGTTAAACATAATTGGCATAATAACAG
```

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current vaccine strains to compare. Also mixtures of genes/proteins (e.g. HA and NA or all genes of the same patient) can be provided as input. To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Compare with:

Additional settings:

ignore low quality bases for nucleotide input (indicated by lower case, except for all lower case sequences)

(estimated time needed: ~2 seconds per sequence in automatic mode)



Bioinformatics
Institute

Developed by A*STAR Bioinformatics Institute ([BII](#)), Singapore
Copyright © 2024 BII. All Rights Reserved.



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

and The Royal Melbourne Hospital

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	100.000	7	V7A , V36I , N111D , A233T , R240Q , E422D , I435V show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	100.000	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	94.845	4	M2 drug sensitivity positions: 17 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	99.787	3	NA drug sensitivity positions: 35 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	100.000	6	E14D , T22A , I33V , I136L , V217I , V425I show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	100.000	1	V84I show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	93.388	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	100.000	8	I30V , L63I , I226L , R262K , I330V , A343S , I438V , K626R show in structure
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	K757R show in structure
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	L475M show in structure

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)



Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HAA/Sydney/5/2021(H1N1)	98.763	<u>100.000</u>	7	V7A , V36I , N111D , A233T , R240Q , E422D , I435V show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<u>100.000</u>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<u>94.845</u>	4	E6K , V7I , E8Y , T9R show in structure M2 drug sensitivity positions: 17 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NAA/Sydney/5/2021(H1N1)	99.359	<u>99.787</u>	3	S200N , H275Y , N434S show in structure NA drug sensitivity positions: 35 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<u>100.000</u>	6	E14D , T22A , I33V , I136L , V217I , V425I show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<u>100.000</u>	1	V84I show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<u>93.388</u>	0	no mutations

black – not significant

green – common subtype marker

blue – interaction site mutation

orange – mild drug resistance

red – virulence, strong drug resistance

1)	98.883	<u>100.000</u>	8	I30V, L63I, I226L, R262K, I330V, A343S, I438V, K626R show in structure
1N1)	99.868	<u>100.000</u>	1	K757R show in structure
1N1)	99.868	<u>100.000</u>	1	L475M show in structure

[Download report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)

report table for archiving or import to Excel (Comma-separated, one query per line)

[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

and The Royal Melbourne Hospital

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	100.000	7	V7A , V36I , N111D , A233T , R240Q , E422D , I435V show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	100.000	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	94.845	4	M2 drug sensitivity positions: 17.0.1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	99.787	3	NA drug sensitivity positions: 35.0.1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	100.000	6	E14D , T22A , I33V , I136L , V217I , V425I show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	100.000	1	V84I show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	93.388	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	100.000	8	I30V , L63I , I226L , R262K , I330V , A343S , I438V , K626R show in structure
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	K757R show in structure
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	L475M show in structure

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)

flusurver.bii.a-star.edu.sg/tmp/tmpblastout.15517_aln.html#1

flusurver.bii.a-star.edu.sg/tmp/tmpblastout.15517_aln.html#1

Query= A/Victoria/3035/2023|HA

between The University of Melbourne and The Royal Melbourne Hospital

>HA_H1N1_Human_2021_Sydney5
HA|A/Sydney/5/2021|2021-10-16|EPI_ISL_12109632|E3/E1|A /
H1N1|WHO Collaborating Centre for Reference and Research
on Influenza|Centers for Disease Control and
Prevention|DaSilva Juliana
|A/SYDNEY/5/2021|3000822336|EPI2020621
Length = 566

Score = 1162 bits (3006), Expect = 0.0
Identities = 559/566 (98%), Positives = 564/566 (99%)
Frame = +1

Query: 1 MKAILVAMLYTFTTANADTLCIGYHANNSTDVTILEKNVTVHSVNLLLEDKHNGKLCK 180
MKAILV MLYTFTTANADTLCIGYHANNSTDVT+LEKNVTVHSVNLLLEDKHNGKLCK
Sbjct: 1 MKAILVAMLYTFTTANADTLCIGYHANNSTDVTILEKNVTVHSVNLLLEDKHNGKLCK 60

Query: 181 LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPGDFINYEELRE 360
LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPG+FINYEELRE
Sbjct: 61 LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPGNFINYEELRE 120

Query: 361 QLSSVSSFERFEIIPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ 540
QLSSVSSFERFEIIPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ
Sbjct: 121 QLSSVSSFERFEIIPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ 180

Query: 541 TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTTSRYSKKFKPEIATRPKVRDQ 720
TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTTSRYSKKFKPEIA RPKVRD+
Sbjct: 181 TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTTSRYSKKFKPEIAARPKVRDR 240

Query: 721 AGRMNYYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE 900
AGRMNYYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE
Sbjct: 241 AGRMNYYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE 300

Query: 901 GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG 1080
GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG
Sbjct: 301 GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG 360

Query: 1081 MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR 1260
MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR
Sbjct: 361 MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR 420



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

and The Royal Melbourne Hospital

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	100.000	7	V7A , V36I , N111D , A233T , R240Q , E422D , I435V show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	100.000	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	94.845	4	E6K , V7I , E8Y , T9R show in structure M2 drug sensitivity positions: 17 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	99.787	3	S200N , H275Y , N434S show in structure NA drug sensitivity positions: 35 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	100.000	6	E14D , T22A , I33V , I136L , V217I , V425I show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	100.000	1	V84I show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	93.388	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	100.000	8	I30V , L63I , I226L , R262K , I330V , A343S , I438V , K626R show in structure
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	K757R show in structure
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	L475M show in structure

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)

FluSurver . . .

Result for comparison with reference selection: autorefall [Back to Reference Selection](#)

GISAID

UNIVERSITY OF MELBOURNE
The Royal Melbourne Hospital

me and The Royal Melbourne Hospital

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

X

NA H275Y

Key to alternative position numbering:

275	FluSurver numbering (absolute as in 2009 H1N1 pandemic)
274	Classical H3N2 strain numbering
275	Classical H1N1 strain numbering

Chosen reference: NA_H1N1_Human_2021_Sydney5

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this strain at the moment, please contact flusurver.org if you would like it to be included in future.

A mutation at the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance and mild drug resistance](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#).

As seen in resolved structures of proteins from related strains, the NA position equivalent to your mutation is involved in:
- [drug binding](#)

[See all interactions for this position](#)

[PubMed search for this mutation \(including alternative numbering\)](#)

PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000 1 L475M
[show in structure](#)

Right-click here to save/download **detailed mutation report** table for archiving or import to Excel (Tab-separated, one mutation per line)
 Right-click here to save/download **query summary report** table for archiving or import to Excel (Comma-separated, one query per line)
 Right-click here to save/download **query clade report** table for archiving or import to Excel (Tab-separated, one query per line)

List of mutations

- [V7A, V36I, N111D, A233T, R240Q, E422D, I435V](#)
[show in structure](#)
- no mutations
- [E6K, V7I, E8Y, T9R](#)
[show in structure](#)
- M2 drug sensitivity positions:
17, 0, 1
Reduced sensitivity or resistance!
- [S200N, H275Y, N434S](#)
[show in structure](#)
- NA drug sensitivity positions:
35, 0, 1
Reduced sensitivity or resistance!
- [E14D, T22A, I33V, I136L, V217I, V425I](#)
[show in structure](#)
- [V84I](#)
[show in structure](#)
- no mutations
- [I0V, L63I, I226L, R262K, I330V, A343S, I438V, K626R](#)
[show in structure](#)
- [K757R](#)
[show in structure](#)
- [L475M](#)
[show in structure](#)

FluSurver

Result for comparison with reference selection: autorefall Back to Reference Selection

NA H275Y

Key to alternative position numbering:
 FluSurver numbering
 (absolute as in 2009 H1N1 pandemic)
 Classical H3N2 strain numbering
 Classical H1N1 strain numbering
 NA_H1N1_Human_2021_Sydney5

Position:	275
Residue:	H
Effect:	Y

Statistics are not available for this strain at the moment, please check back later or contact us if you would like it to be included in future.

Effect equivalent to **NA 275** has been reported in the literature to be to [strong drug resistance and mild drug resistance](#).

Mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#).

This residue is seen in resolved structures of proteins from [H1N1 strains](#), the NA position equivalent to your mutation is involved in: [drug binding](#)

[See all interactions for this position](#)

[Search for this mutation \(including alternative numbering\)](#)

List of mutations

[V7A, V36I, N111D, A233T, R240Q, E422D, I435V](#)
[show in structure](#)

no mutations

[E6K, V7I, E8Y, T9R](#)
[show in structure](#)

M2 drug sensitivity positions:
¹⁷, ₀, ₁
 Reduced sensitivity or resistance!

[S200N, H275Y, N434S](#)
[show in structure](#)

NA drug sensitivity positions:
³⁵, ₀, ₁
 Reduced sensitivity or resistance!

[E14D, T22A, I33V, I136L, V217I, V425I](#)
[show in structure](#)

[V84I](#)
[show in structure](#)

no mutations

[L60V, L63I, I226L, R262K, I330V, A343S, I438V, K626R](#)
[show in structure](#)

[K757R](#)
[show in structure](#)

[L475M](#)
[show in structure](#)

A/Victoria/3035/2023|PB2 - PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000 1

Right-click here to save/download detailed mutation report table for archiving or import to Excel (Tab-separated, one mutation per line)
 Right-click here to save/download query summary report table for archiving or import to Excel (Comma-separated, one query per line)
 Right-click here to save/download query clade report table for archiving or import to Excel (Tab-separated, one query per line)

The Royal Melbourne Hospital
 Melbourne Hospital



> *Antimicrob Agents Chemother.* 2008 Sep;52(9):3284-92. doi: 10.1128/AAC.00555-08.

Epub 2008 Jul 14.

Surveillance for neuraminidase inhibitor resistance among human influenza A and B viruses circulating worldwide from 2004 to 2008

Tiffany G Sheu ¹, Varough M Deyde, Margaret Okomo-Adhiambo, Rebecca J Garten, Xiyan Xu, Rick A Bright, Ebeneé N Butler, Teresa R Wallis, Alexander I Klimov, Larisa V Gubareva

Affiliations + expand

PMID: 18625765 PMCID: PMC2533500 DOI: 10.1128/AAC.00555-08

Abstract

The surveillance of seasonal influenza virus susceptibility to neuraminidase (NA) inhibitors was conducted using an NA inhibition assay. The 50% inhibitory concentration values (IC₅₀s) of 4,570 viruses collected globally from October 2004 to March 2008 were determined. Based on mean IC₅₀s, A(H3N2) viruses (0.44 nM) were more sensitive to oseltamivir than A(H1N1) viruses (0.91 nM). The opposite trend was observed with zanamivir: 1.06 nM for A(H1N1) and 2.54 nM for A(H3N2). Influenza B viruses exhibited the least susceptibility to oseltamivir (3.42 nM) and to zanamivir (3.87 nM). To identify potentially resistant viruses (outliers), a threshold of a mean IC₅₀ value + 3 standard deviations was defined for type/subtype and drug. Sequence analysis of outliers was performed to identify NA changes that might be associated with reduced susceptibility. Molecular markers of oseltamivir resistance were found in six A(H1N1) viruses (H274Y) and one A(H3N2) virus (E119V) collected between 2004 and 2007. Some outliers contained previously

med.ncbi.nlm.nih.gov/18625765/#similar (I222T in the B viruses), while other mutations [e.g., R371K and H274Y in B

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

X

NA H275Y

Key to alternative position numbering:

275 FluSurver numbering
 (absolute as in 2009 H1N1 pandemic)

274 Classical H3N2 strain numbering
 275 Classical H1N1 strain numbering

Chosen reference: NA_H1N1_Human_2021_Sydney5

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this strain at the moment, please contact flusurver.org if you would like it to be included in future.

A mutation at the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#) and [mild drug resistance](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#).

As seen in resolved structures of proteins from related strains, the NA position equivalent to your mutation is involved in:

- [drug binding](#)[See all interactions at this position](#)[PubMed search for this mutation \(including alternative numbering\)](#)

PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000 1

List of mutations

[V7A](#), [V36I](#), [N111D](#), [A233T](#), [R240Q](#), [E422D](#), [I435V](#)
[show in structure](#)

no mutations

[E6K](#), [V7I](#), [E8Y](#), [T9R](#)
[show in structure](#)

M2 drug sensitivity positions:
17, 0, 1
 Reduced sensitivity or resistance!

[S200N](#), [H275Y](#), [N434S](#)
[show in structure](#)

NA drug sensitivity positions:
35, 0, 1
 Reduced sensitivity or resistance!

[E14D](#), [T22A](#), [I33V](#), [I136L](#), [V217I](#), [V425I](#)
[show in structure](#)

[V84I](#)
[show in structure](#)

no mutations

[I0V](#), [L63I](#), [I226L](#), [R262K](#), [I330V](#), [A343S](#), [I438V](#), [K626R](#)
[show in structure](#)

[K757R](#)
[show in structure](#)

[L475M](#)
[show in structure](#)

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)

[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)

[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)

FluSurver

Result for comparison with reference selection: autorefall

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

PB2 A/Victoria/2570/2019(H1N1) 99.868

[Right-click here to save/download detailed mutation report table for archiving or sharing](#)

[Right-click here to save/download query summary report table for archiving or sharing](#)

[Right-click here to save/download query clade report table for archiving or sharing](#)

X

NA H275Y

Key to alternative position numbers:

- 275 FluSurver number (absolute as in 2009)
- 274 Classical H3N2 strain
- 275 Classical H1N1 strain
- NA_H1N1_Human Chosen reference:

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this structure. Contact flusurver.org if you would like it to be included.

A mutation at the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance and mild drug binding](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance and drug binding](#).

As seen in resolved structures of protein chains from related strains, the NA position equivalent to your mutation is located near [drug binding](#).

[See all interactions for this position](#)

[PubMed search for this mutation \(including alternative positions\)](#)

NA_275_1B9V_A_273

flusurver.bii.a-star.edu.sg/INTERACTIONS/NA/275/NA_275_1B9V_A_2...

JSmol

Spin ON Spin OFF Save IMAGE

Description:
The mutation position (**red atoms**) corresponds to position 273 on viral chain A (**yellow backbone**) and is within 5 Å from drug RA2 (**pink atoms**).

[See all 18 interactions for this position](#)



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	100.000	7	V7A , V36I , N111D , A233T , R240Q , E422D , I435V show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	100.000	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	94.845	4	M2 drug sensitivity positions: 17 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	99.787	3	NA drug sensitivity positions: 35 , 0 , 1 Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	100.000	6	E14D , T22A , I33V , I136L , V217I , V425I show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	100.000	1	V84I show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	93.388	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	100.000	8	I30V , L63I , I226L , R262K , I330V , A343S , I438V , K626R show in structure
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	K757R show in structure
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	100.000	1	L475M show in structure

Right-click here to save/download **detailed mutation report** table for archiving or import to Excel (Tab-separated, one mutation per line)Right-click here to save/download **query summary report** table for archiving or import to Excel (Comma-separated, one query per line)Right-click here to save/download **query clade report** table for archiving or import to Excel (Tab-separated, one query per line)

flusurver_result15517

Search Sheet

Home Insert Page Layout Formulas Data Review View

Paste **B** *I* **A** Wrap Text General Conditional Formatting **Insert** **Format as Table** Cell Styles **Delete** **Format** **Sort & Filter**

S29 fx

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Reference	Query	% AA identity	% length cove	HA vacc.	eff.	total # mutat	Mutation	Interestlevel	Subtype mark	# global occ	# country occ	Prev. reporte	Multiple posit	Structural int	Effect on glycosylation
2	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	V7A	0	-	0	0	-	-	-	-
3	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	V36I	1	-	0	0	-	-	viral oligomer	
4	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	N111D	0	-	0	0	host specificit	-	viral oligomer	
5	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	A233T	1	-	0	0	-	-	viral oligomer	
6	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	R240Q	0	-	0	0	host specificit	host specificit	host cell rece	-
7	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	E422D	1	-	0	0	-	-	viral oligomer	
8	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	I435V	1	-	0	0	-	-	viral oligomer	
9	M1_H1N1_HtA/Victoria/30		100	100	-		252	no mutations	0	-	-	-	-	-	-	-
10	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	E6K	0	-	0	0	-	-	-	-
11	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	V7I	2	-	0	0	host specificit	-	-	-
12	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	E8Y	0	-	0	0	-	-	-	-
13	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	T9R	0	-	0	0	-	-	-	-
14	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	S200N	2	-	0	0	antigenic drift	antigenic drift	binding small	-
15	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	H275Y	3	-	0	0	strong drug r	strong drug r	drug binding	-
16	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	N434S	1	-	0	0	-	-	viral oligomer	
17	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	E14D	0	-	121	4	-	-	-	-
18	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	T22A	0	-	236	12	-	-	-	-
19	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	I33V	0	-	13	1	host specificit	-	-	-
20	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	I136L	0	-	8	2	-	-	-	-
21	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	V217I	1	-	46	5	-	-	viral oligomer	
22	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	V425I	1	-	1042	18	-	-	viral oligomer	
23	NS1_H1N1_HtA/Victoria/30		99.543	100	-		219	V84I	1	-	0	0	-	-	viral oligomer	
24	NS2_H1N1_HtA/Victoria/30		100	93.388	-		113	no mutations	0	-	-	-	-	-	-	-
25	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	I30V	1	-	0	0	-	-	viral oligomer	
26	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	L63I	1	-	0	0	-	-	viral oligomer	
27	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	I226L	1	-	0	0	-	-	a T-cell epitop	-
28	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	I226K	0	-	0	0	-	-	-	-

corona.bii.a-star.edu.sg



CENTRE FOR
PATHOGEN
GENOMICS



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

Enabled by



CoVsurer

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequence: Example hCoV-19 genome](#))

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current strains to compare.

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequence: Example hCoV-19 genome](#))

```
>hCoV-19_example_genome
ATTAAGGTTTACCTCCCAGGTAAACAAACCAACCAACTTCGATCTCTGTAGATCTGTTCTCTAAACGAACTTAAAATCTGTG
TGGCTGTCACTCGGCTGCATGCTTAGTCAGTCACGCAGTATAATTAACTAATTACTGTCGTTGACAGGACACGAGTAACCTCG
TCTATCTTCTGCAGGCTGCTTACGGTTCGCCGTGTTGAGCCGATCATCAGCACATCTAGGTTCGCTGGGTGTGACCGAAA
GGTAAGATGGAGAGCCTGTCCTGGTTCAACGAGAAAACACACGTCACACTCAGTTGCCTGTTTACAGGTTCGCGACGTGC
TCGTACGTGGCTTGGAGACTCCGTGGAGGGTCTTATCAGAGGCACGTCAACATCTAAAGATGGCAGTTGTGGCTTAGTAGA
AGTTGAAAAGGCCTTGCCTCAACTTGAACAGCCCTATGTGTTCATCAAACGTTGGATGCTCGAACACTGCACCTCATGGTCATG
TTATGGTTGAGCTGGTAGCAGAACCTGAAGGCATTCACTGAGTGGTGTAGTGGTGAGACACTTGGTGTCCCTCATGTGGG
CCAAATACCAACTCCCTTACCCCAACCTCTCTTACAAACCTCTCTTACAAACCTCTCTTACAAACCTCTCTTACAAACCTCT
```



OR upload your protein or nucleotide sequences in a FASTA file

No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current strains to compare.

To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Compare with:

(Sequence Quality Checker. Estimated time needed: <1 seconds per sequence)

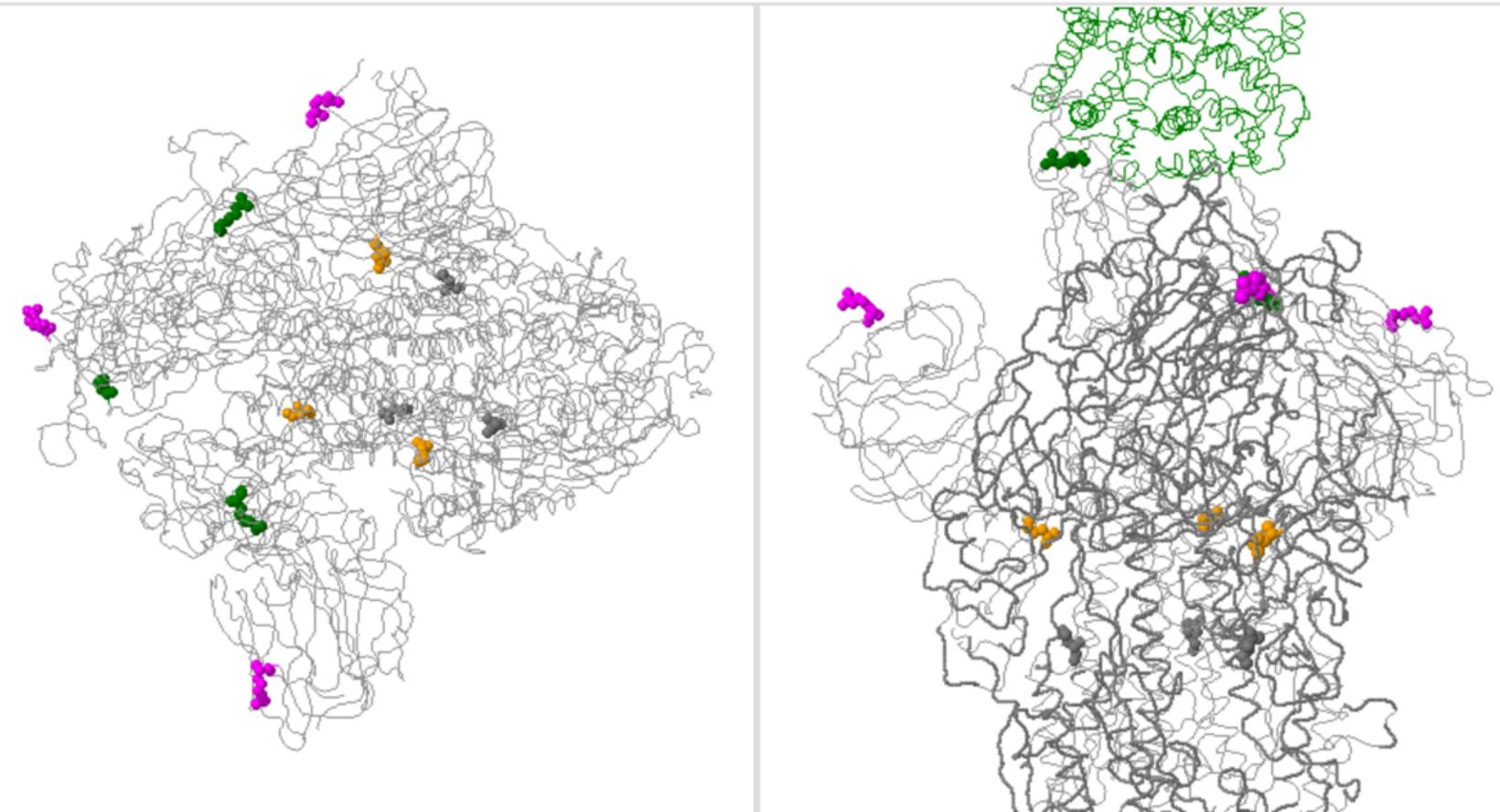
(Complete Analysis. Estimated time needed: ~10 seconds per sequence)



Developed by A*STAR Bioinformatics Institute ([BII](#)), Singapore.

© 2024 A*STAR Bioinformatics Institute (BII).

CoVsurer

3D structural visualization of the spike glycoprotein with aa changes identified in the query sequences shown as colored balls[Spin ON](#)[Spin OFF](#)[Save IMAGE](#)[Spin ON](#)[Spin OFF](#)[Save IMAGE](#)

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:

99.686%

aa changes:

4

List of variations displayed in structure (nearest residue if in loop/termini region)
T19K(20) N317V R454A D775Y

Query	Clade	VariantInf	Best reference hit	%id	%coveraç	#Δs	List of aa changes
hCoV-19_example_genome	L	rare	NSP1 WIV04	100%	100%	0	no aa changes
			NSP2 WIV04	100%	100%	0	no aa changes
			NSP3 WIV04	100%	100%	0	no aa changes
			NSP4 WIV04	100%	100%	0	no aa changes
			NSP5 WIV04	98.7%	100%	4	T26Q\$, H64Q , N65P\$, S301G\$
			NSP6 WIV04	100%	100%	0	no aa changes
			NSP7 WIV04	100%	100%	0	no aa changes
			NSP8 WIV04	100%	100%	0	no aa changes
			NSP9 WIV04	100%	100%	0	no aa changes
			NSP10 WIV04	100%	100%	0	no aa changes
			NSP11 WIV04	100%	100%	0	no aa changes
			NSP12 WIV04	100%	99.0%	0	no aa changes
			NSP13 WIV04	100%	100%	0	no aa changes
			NSP14 WIV04	99.1%	100%	5	F89L , D90F\$, N238H\$, H330Q , D331N\$
			NSP15 WIV04	100%	100%	0	no aa changes
			NSP16 WIV04	100%	100%	0	no aa changes
			Spike WIV04	99.7%	100%	4	T19K , N317V\$, R454A\$, D775Y\$
			NS3 WIV04	100%	100%	0	no aa changes
			E WIV04	98.7%	100%	1	R61N\$
			M WIV04	99.5%	100%	1	Y204A\$
			NS6 WIV04	100%	100%	0	no aa changes
			NS7a WIV04	100%	100%	0	no aa changes
			NS7b WIV04	100%	100%	0	no aa changes
			NS8 WIV04	100%	100%	0	no aa changes
			N WIV04	100%	100%	0	no aa changes

[Right-click here to save/download query summary report table for archiving or import to Excel \(Tab-separated, one query per line\) \(protseqs\)](#)

% AA identity:

99.686%

aa changes:

4

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

T19K(20) N317V R454A D775Y



All Melbourne Hospitals

Query	Clade	VariantInf	Best reference hit	%id	%coverage	#Δs	List of aa changes
			NSP1 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP2 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP3 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP4 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP5 WIV04	98.7%	<u>100%</u>	4	<u>T26Q\$</u> , <u>H64Q</u> , <u>N65P\$</u> , <u>S301G\$</u>
			NSP6 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP7 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP8 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP9 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP10 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP11 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP12 WIV04	100%	<u>99.0%</u>	0	no aa changes
			NSP13 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP14 WIV04	99.1%	<u>100%</u>	5	<u>F89L</u> , <u>D90F\$</u> , <u>N238H\$</u> , <u>H330Q</u> , <u>D331N\$</u>
				100%	<u>100%</u>	0	no aa changes
				100%	<u>100%</u>	0	no aa changes
				99.7%	<u>100%</u>	4	<u>T19K</u> , <u>N317V\$</u> , <u>R454A\$</u> , <u>D775Y\$</u>
				100%	<u>100%</u>	0	no aa changes
				98.7%	<u>100%</u>	1	<u>R61N\$</u>
				99.5%	<u>100%</u>	1	<u>Y204A\$</u>
				100%	<u>100%</u>	0	no aa changes
				100%	<u>100%</u>	0	no aa changes
				100%	<u>100%</u>	0	no aa changes
				100%	<u>100%</u>	0	no aa changes
				100%	<u>100%</u>	0	no aa changes

black – no known effects

blue – occurring >100x

orange – receptor binding site, antigenicity

magenta – glycosylation site

cyan – insertion/deletion

green – reported phenotype change

red – predicted enhancing effect

for archiving or import to Excel (Tab-separated, one query per line) (protseqs)

% AA identity:

99.686%

aa changes:

4

List of variations displayed in structure (nearest residue if in loop/termini region)
T19K(20) N317V R454A D775Y

Query	Clade	VariantInf	Best reference hit	%id	%coveraç	#Δs	List of aa changes
hCoV-19_example_genome	L	rare	NSP1 WIV04	100%	100%	0	no aa changes
			NSP2 WIV04	100%	100%	0	no aa changes
			NSP3 WIV04	100%	100%	0	no aa changes
			NSP4 WIV04	100%	100%	0	no aa changes
			NSP5 WIV04	98.7%	100%	4	T26Q\$, H64Q , N65P\$, S301G\$
			NSP6 WIV04	100%	100%	0	no aa changes
			NSP7 WIV04	100%	100%	0	no aa changes
			NSP8 WIV04	100%	100%	0	no aa changes
			NSP9 WIV04	100%	100%	0	no aa changes
			NSP10 WIV04	100%	100%	0	no aa changes
			NSP11 WIV04	100%	100%	0	no aa changes
			NSP12 WIV04	100%	99.0%	0	no aa changes
			NSP13 WIV04	100%	100%	0	no aa changes
			NSP14 WIV04	99.1%	100%	5	F89L , D90F\$, N238H\$, H330Q , D331N\$
			NSP15 WIV04	100%	100%	0	no aa changes
			NSP16 WIV04	100%	100%	0	no aa changes
			Spike WIV04	99.7%	100%	4	T19K , N317V\$, R454A\$, D775Y\$
			NS3 WIV04	100%	100%	0	no aa changes
			E WIV04	98.7%	100%	1	
			M WIV04	99.5%	100%	1	
			NS6 WIV04	100%	100%	0	no aa changes
			NS7a WIV04	100%	100%	0	no aa changes
			NS7b WIV04	100%	100%	0	no aa changes
			NS8 WIV04	100%	100%	0	no aa changes
			N WIV04	100%	100%	0	no aa changes

[Right-click here to save/download query summary report table for archiving or import to Excel \(Tab-separated, one query per line\) \(protseqs\)](#)

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

T19K(20) N317V R454A D775Y



Query

Clade V X

Spike T19K

Key to alternative position numbering:

19 hCoV-19 numbering

23 SARS numbering

Chosen reference:

Position in reference: 19

AA in reference: T

AA in query: K

AA change Spike T19K already occurred 375 times (0.01% of all samples with Spike sequence) in 39 countries. The first strain with this aa change, collected in June 2020, was hCoV-19/England/QEUH-5E8537/2020. The aa change most recently occurred in strain hCoV-19/Hubei/HCDC-WH4293/2024, collected in March 2024. ([see map](#))

[See detailed global statistics for this position](#)



Mutation Spike T19K removes a potential N-glycosylation site at position 17 which may also affect antigenic and other properties of this strain. In detail, the motif at positions 17-19 changed from NLT (glyco) to NLK (no glyco).

[PubMed search for this aa change](#)

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

[Phylogenetic context for this mutation at Nextstrain](#)

hCoV-19_example_genome L

[Right-click here to save/download](#)

aa changes

aa changes

aa changes

aa changes

Q, N65P\$, S301G\$

aa changes

I38H\$, H330Q, D331N\$

aa changes

aa changes

R454A\$, D775Y\$

aa changes

R61N\$

Y204A\$

aa changes

aa changes

aa changes

aa changes

[try_per_line\) \(protseqs\)](#)

[Back to Reference Selection](#)

● ● ● mendel.bii.a-star.edu.sg/METHODS/corona/current/MUTATIONS/hCoV-19_Human_2019_WuhanWIV04/geo/S...

⌚ mendel.bii.a-star.edu.sg/METHODS/corona/current/MUTATIONS/hCoV-19_Human_2019_WuhanWIV04/geo/...

Map of cities with the Spike T19K mutation



The city with **red** label indicates first appearance of the mutation. City with **blue** label indicate later appearance of the mutation. The city with the most recent appearance of the mutation has the **green** label. Number in the label indicates frequency of occurrence of the mutation in that city. Click on the city marker to show the frequency of mutations found in the city.

Number of occurrences

Countries without data



1



Region	# Occ.	Date_of_collection(YYYYMMDD)	Most_Recent_Accession
England	74	20220208	EPI_ISL_9890362
Auvergne-Rhone-Alpes	12	20220214	EPI_ISL_10365718
Tennessee	9	20220130	EPI_ISL_10215705
Tamil Nadu	9	20211125	EPI_ISL_14679882
California	9	20220210	EPI_ISL_10323321
San Salvador	8	20210802	EPI_ISL_5158233
Ile-de-France	7	20210731	EPI_ISL_11445510
Maharashtra	5	20211225	EPI_ISL_9678177
Saxony	5	20211214	EPI_ISL_8224551
Bretagne	5	20210405	EPI_ISL_1675080
Baden-Wurttemberg	4	20210306	EPI_ISL_1356542
Connecticut	4	20211126	EPI_ISL_7018945
Lazio	4	20211206	EPI_ISL_14932721
Kerman	4	20220112	EPI_ISL_10195264
Syddanmark	4	20220107	EPI_ISL_8655959
Midtjylland	4	20220130	EPI_ISL_9739569
Scotland	3	20211123	EPI_ISL_6923877
Catalunya	3	20220213	EPI_ISL_10227020
Goa	3	20211216	EPI_ISL_15292768
Sicily	3	20210903	EPI_ISL_4849121
Minnesota	3	20220202	EPI_ISL_10044460
Para	3	20210911	EPI_ISL_11495515
Centre-Val de Loire	3	20211105	EPI_ISL_11633258
Lambarene	2	20210221	EPI_ISL_11522626
Missouri	2	20211231	EPI_ISL_12060271
Grand Est	2	20220207	EPI_ISL_9979046
Lombardy	2	20211116	EPI_ISL_6808924
New York	2	20220119	EPI_ISL_9659336
Andhra Pradesh	2	20220105	EPI_ISL_10205032
Aisen	2	20220512	EPI_ISL_12982127
Hawaii	2	20220513	EPI_ISL_13375035

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

T19K(20) N317V R454A D775Y

Query

Clade V X

Spike T19K

Key to alternative position numbering:

19 hCoV-19 numbering

23 SARS numbering

Chosen reference:

Position in reference: 19

AA in reference: T

AA in query: K

AA change Spike T19K already occurred 375 times (0.01% of all samples with Spike sequence) in 39 countries. The first strain with this aa change, collected in June 2020, was hCoV-19/England/QEUH-5E8537/2020. The aa change most recently occurred in strain hCoV-19/Hubei/HCDC-WH4293/2024, collected in March 2024. ([see map](#))

[See detailed global statistics for this position](#)

Mutation Spike T19K removes a potential N-glycosylation site at position 17 which may also affect antigenic and other properties of this strain. In detail, the motif at positions 17-19 changed from **NLT** (glyco) to **NLK** (no glyco).

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

hCoV-19_example_genome L

[Right-click here to save/download](#)

aa changes

aa changes

aa changes

aa changes

Q, N65P\$, S301G\$

aa changes

I38H\$, H330Q, D331N\$

aa changes

aa changes

R454A\$, D775Y\$

aa changes

R61N\$**Y204A\$**

aa changes

aa changes

aa changes

aa changes

D775Y_per_line) (protseqs)[Back to Reference Selection](#)

Mutation statistics for Spike at position 19

AA	# Occ.	%	Geo_Distribution
Q	13	0.00	
F	263	0.00	(geo)
M	53	0.00	
Y	1	0.00	
G	201	0.00	(geo)
N	62	0.00	
insDLI	1	0.00	
V	467	0.00	(geo)
H	1	0.00	
J	79	0.00	
R	3824216	28.22	(geo)
A	125	0.00	
insNLI	3	0.00	
I	4582506	33.82	(geo)
K	714	0.01	(geo)
P	12	0.00	
stop	6	0.00	
E	7	0.00	
del	541	0.00	(geo)
L	5623	0.04	(geo)
insQKRL	2	0.00	
S	138	0.00	(geo)
T	5135142	37.90	reference aa

13550176 sequences were compared to reference sequence EPI_ISL_402124. Last updated on Apr 01 2024 by Raphael Tze Chuen Lee

Above are the occurrences of all amino acid residues at position 20 in Spike. For statistics of all position in Spike click here: [hCoV-19_Spike_mutations_table](#)

% AA identity:

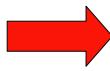
99.686%

aa changes:

4

List of variations displayed in structure (nearest residue if in loop/termini region)
T19K(20) N317V R454A D775Y

Query	Clade	VariantInf	Best reference hit	%id	%coveraç	#Δs	List of aa changes
			NSP1 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP2 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP3 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP4 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP5 WIV04	98.7%	<u>100%</u>	4	T26Q\$, H64Q, N65P\$, S301G\$
			NSP6 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP7 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP8 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP9 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP10 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP11 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP12 WIV04	100%	<u>99.0%</u>	0	no aa changes
hCoV-19_example_genome	L	rare	NSP13 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP14 WIV04	99.1%	<u>100%</u>	5	F89L, D90F\$, N238H\$, H330Q, D331N\$
			NSP15 WIV04	100%	<u>100%</u>	0	no aa changes
			NSP16 WIV04	100%	<u>100%</u>	0	no aa changes
			Spike WIV04	99.7%	<u>100%</u>	4	T19K, N317V\$, R454A\$, D775Y\$
			NS3 WIV04	100%	<u>100%</u>	0	no aa changes
			E WIV04	98.7%	<u>100%</u>	1	R61N\$
			M WIV04	99.5%	<u>100%</u>	1	Y204A\$
			NS6 WIV04	100%	<u>100%</u>	0	no aa changes
			NS7a WIV04	100%	<u>100%</u>	0	no aa changes
			NS7b WIV04	100%	<u>100%</u>	0	no aa changes
			NS8 WIV04	100%	<u>100%</u>	0	no aa changes
			N WIV04	100%	<u>100%</u>	0	no aa changes


[Right-click here to save/download query summary report table for archiving or import to Excel \(Tab-separated, one query per line\) \(protseqs\)](#)

File Search Sheet

Home Insert Page Layout Formulas Data Review View

Paste Insert
Delete
Format
Sort & Filter

Calibri (Body) 12 A A Wrap Text General
B I U Merge & Center \$ % .00 .00 Conditional Formatting Format as Table Cell Styles

O22 X ✓ fx |

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Query	Strand	%N	Length(nt)	Length(aa)	#Muts	%Muts	#UniqueMut	%UniqueMut	#ExistingMut	%ExistingMut	Comment	Symbol	Reference	Unique
2	hCoV-19_expositive		0.00%	29891	9710	15	0.15%	13	0.13%	2	0.02%	%UniqueMuWarning	hCoV19/Wu1(NSP5_		
3															
4															
5															
6															
7															
8															
9															
10															
11															
12															
13															
14															
15															
16															
17															
18															
19															
20															
21															
22															
23															
24															
25															

covsurver_result27461_perquery +

Ready 130%



World Health
Organization
Philippines



CENTRE FOR
PATHOGEN
GENOMICS



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL

THANK YOU

clyde.dapat@influenzacentre.org



KDCA

Korea Disease Control and
Prevention Agency



Doherty
Institute

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

