


Surveillance

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Intense interseasonal influenza outbreaks, Australia, 2018/19

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Ian G Barr^{1,2}, Yi Mo Deng¹, Miguel L Grau³, Alvin X Han^{4,5}, Robin Gilmour⁶, Melissa Irwin⁷, Peter Markey⁸, Kevin Freeman⁹, Geoff Higgins¹⁰, Mark Turra¹⁰, Naomi Komadina¹, Heidi Peck¹, Robert Booy^{11,12}, Sebastian Maurer-Stroh^{4,5,13}, Vijaykrishna Dhanasekaran^{1,3}, Sheena Sullivan^{1,2}

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Abstract



Full-Text



Figures & Tables



References (32)



Supplementary Material (2)



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Introduction

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In 2018, the Australian influenza season was late and progressed with such minimal activity that it barely registered as a season by several surveillance indicators [1]. This was in stark contrast to the 2017 season, when Australia's highest levels of influenza activity were recorded [2]. However, several surveillance indicators suggested that the influenza activity seen in 2018, while low, never really stopped, as it was expected to, at the end of the southern hemisphere spring (November). Instead, Australia experienced an upsurge in influenza cases with a large wet-season outbreak in the tropical north (see [Figure 1](#)), while southern Australia saw record numbers of laboratory-confirmed influenza notifications, increased hospitalisations and dozens of influenza-related deaths in late summer and early autumn, resulting in an early start to the 2019 influenza season throughout the country. Here we summarise the available epidemiological surveillance indicators along with a virological analysis of the influenza viruses collected during these 2018/19 interseasonal influenza outbreaks.

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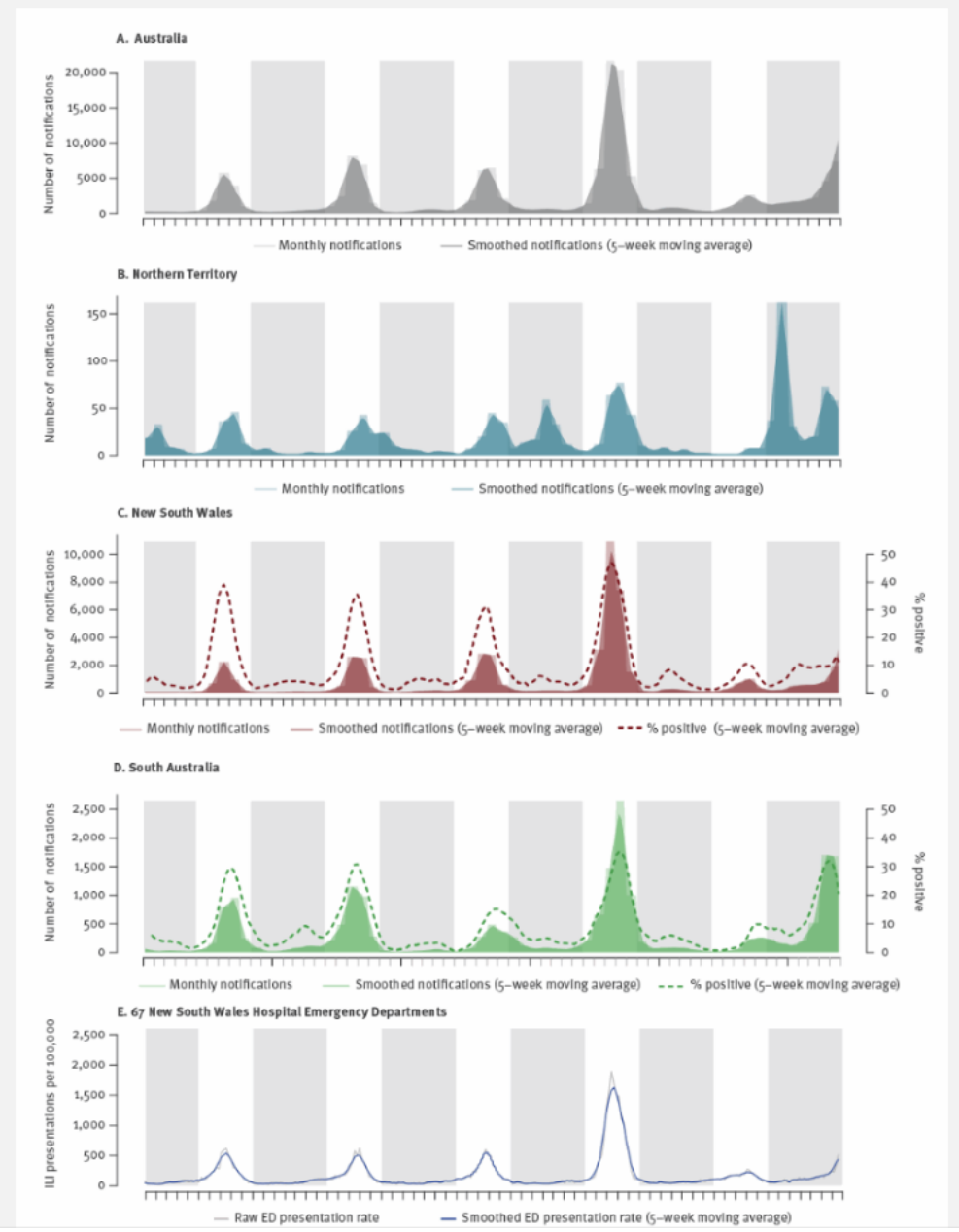
Tools

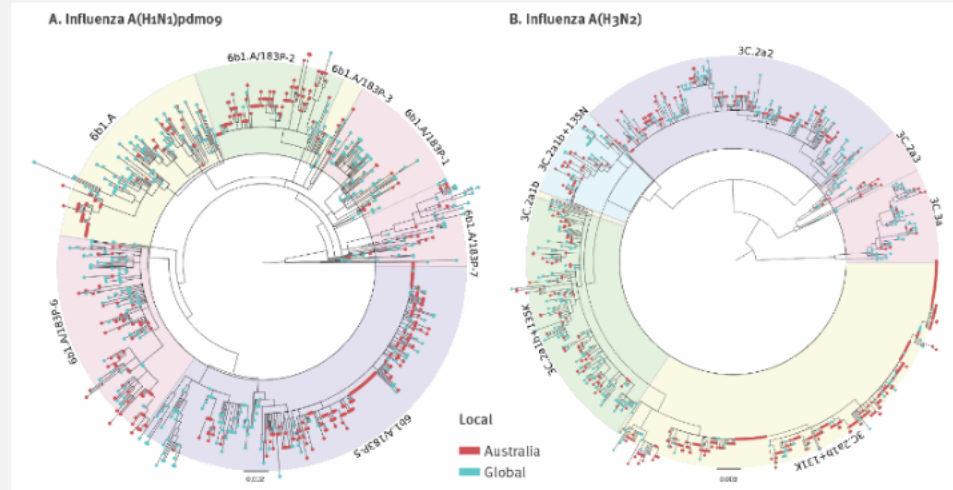
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News/announcements

Candidates interested in applying for the EU-track 2020 cohort of the ECDC Fellowship Programme

Figure 2. Selected influenza surveillance data, Australia, 2014–2019

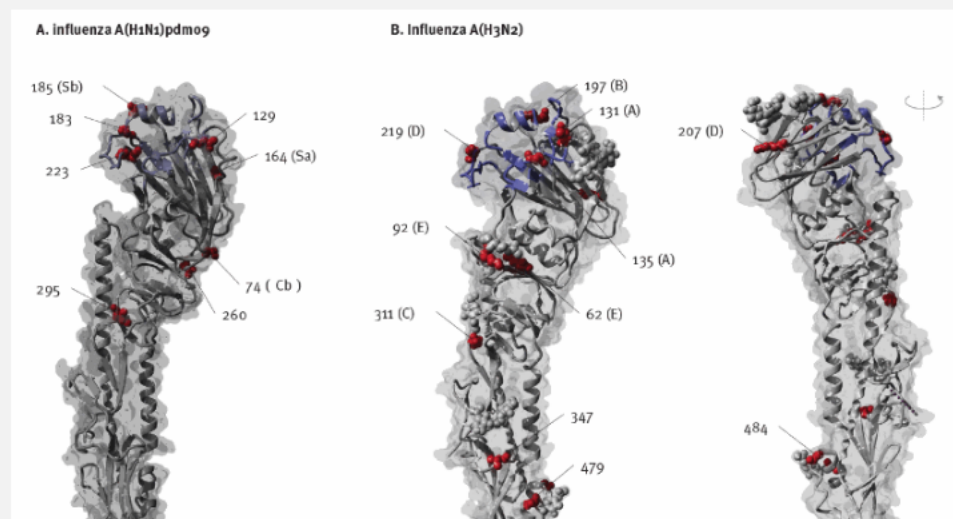




Click to view

Tip branches representing individual viruses collected since September 2018 in Australia are shown in red and those from overseas locations are shown in green. Clade designations are indicated on the circumference and separated by the coloured sections. For a full list of sequences used to generate these trees see the Global Initiative on Sharing All Influenza Data (GISAID) listing in [Supplementary Table 1](#).

Figure 5. Structural images of influenza A(H1N1)pdm09 and A(H3N2) haemagglutinin molecules showing changes in the most commonly circulating clades in Australia, 2018/19





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Count **7 isolates** GISAID published **151,421 isolates (673,285 sequences)** Total isolate count **286,670 isolates (1,199,258 sequences)**

Basic filters

Predefined search: Select ...
Search in: Released files Worksets
Search patterns:

Type	H	N	Lineage	Host	Location
A	1	1		-all-	Antarctica
B	2	2		Human	Asia
C	3	3		Animal	Europe
	4	4		Avian	North America
	5	5		Chicken	Oceania

Additional filters

Collection date (YYYY-MM-DD) From: 2019-06-01 To: 2019-06-08

Submission date (YYYY-MM-DD) From: To:

Originating Laboratory: [Afghanistan, Kabul] National Public Health Laboratory
[Albania, Tirana] Institute of Public Health
[Algeria, Algiers] Institut Pasteur d'Algerie
[Argentina, Buenos Aires] CEMIC University Hospital
[Argentina, Buenos Aires] Instituto Nacional Enfermedades Infecciosas C.G.Malbran

Submitting Laboratory: [Argentina, Buenos Aires] Instituto Nacional Enfermedades Infecciosas C.G.Malbran
[Argentina, Buenos Aires] Instituto Nacional de Tecnología Agropecuaria (INTA)
[Argentina, Mar del Plata] Instituto Nacional de Epidemiología Juan Hector Jara
[Australia, Casuarina] Royal Darwin Hospital
[Australia, Geelong] CSIRO Australian Animal Health Laboratory

Required Segments: PB2 PB1 PA HA NP NA MP NS HE P3
 only complete Min Length:
 Direct submissions to GISAID Import from public-domain (INSDC)



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Released files

<input checked="" type="checkbox"/>	edit	Name	Isolate ID	Subtype	Host	Collection date	Passage	PB2	PB1	PA	HA	NP	NA	MP	NS
<input checked="" type="checkbox"/>		A/Perth/1051/2019	EPI_ISL_376954	H3N2	Human	2019-06-07	SIAT1	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Darwin/459/2019	EPI_ISL_365269	H3N2	Human	2019-06-02	SIAT1	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Victoria/48/2019	EPI_ISL_365267	H3N2	Human	2019-06-05	SIAT2	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Darwin/479/2019	EPI_ISL_365265	H3N2	Human	2019-06-08	SIAT1	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Victoria/67/2019	EPI_ISL_365264	H3N2	Human	2019-06-03	SIAT1	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Victoria/2515/2019	EPI_ISL_365263	H3N2	Human	2019-06-02	SIAT1	---	---	---	1733	---	1467	1027	---
<input checked="" type="checkbox"/>		A/Darwin/470/2019	EPI_ISL_365262	H3N2	Human	2019-06-05	SIAT1	---	---	---	1733	---	1467	1027	---

< | >

Total: 7 isolates << first < prev **1** next > last >>

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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 the recent H7N9 and avian H5N8/H5N6, for GISAID users only!) 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 example analysis walkthrough](#) and the [GISAID access preview poster](#).

Note for H7N9 analysis: A tutorial with example analysis and interpretation is available [here](#).

Loaded protein sequences of your selected isolates for FluSurver analysis:

```
>HA_A/Victoria/48/2019_365267
MKTIIALSYILCLIFFAQKIPGNDNSTATLCLGHHAVPNGTIVKTIITNDRIEVTNATELVQNSSIGEICDSPHQILDGGNCTLIDALLGDPQCDGFQNKKWDLFVERSRAYSN
CYPYDVPDYASLRSLVASSGTLEFKNESFNWTGKQNGTSSACIRGSSSSFFSRLNWLTHLNYTPALNVTMPNKEQFDKLYIWGVHHPGTDKQDIFLYARSSGRITVSTRR
SQQAVIPNIGFRPRIRDIPSRISIIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAIPGCKSECITPNGSIPNDKPFQNVNRTYGACPRYVKQSTLKLATGM
RNVPEKQTRGIFGAIAGFIENGWEGMMDGWYGFHRQNSEGRQAADLKTQAAIDQINGKLNRLIGKTNKHFHQIEKEFSEVEGRVQDLEKYVEDTKIDLWSYNAELLVALE
NQHTIDLTDSEMKNLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHNVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCIALLGFIMWACQKGNIR
CNICII
>HA_A/Victoria/2515/2019_365263
MKTIIALSYILCLVFAQKIPGNDNSTATLCLGHHAVPNGTIVKTIITNDRIEVTNATELVQNSSIGEICDSPHQILDGGNCTLIDALLGDPQCDGFQNKKWDLFVERSRAYSN
CYPYDVPDYASLRSLVASSGTLEFKNESFNWTGKQNGTSSACIRGSSSSFFSRLNWLTHLNYTPALNVTMPNKEQFDKLYIWGVHHPGTDKQDIFLYTQSSGRITVSTR
```

Please select the reference strain(s) to compare to:

Analyze with FluSurver



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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 and novel reassortant swine flu H3N2v.** Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. There is also a [special note for using FluSurver results in publications](#).



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

Query	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
HA_A/Darwin/459/2019_365269 Show in NEXTFLU tree	HA A/Singapore/NFIMH-16-0019//2016(H3N2) find closest related sequences	98.233	100.000	10	E78G , K108R , T147K , K176T , P210L , S235F , H327Q , V363M , E495G , V545I show in structure
HA_A/Darwin/470/2019_365262 Show in NEXTFLU tree	HA A/Texas/50/2012(H3N2) find closest related sequences	96.113	100.000	22	V14I , L19I , E78G , K108R , N137K , N144T , T147K , R158G , N160S , N161S , F175Y , K176T , N187K , V202G , Q213R , P214S , K223R , N241D , V363M , I422V , D505N , V545I show in structure
HA_A/Darwin/479/2019_365265 Show in NEXTFLU tree	HA A/Texas/50/2012(H3N2) find closest related sequences	96.113	100.000	22	V14I , L19I , E78G , K108R , N137K , N144T , T147K , R158G , N160S , N161S , F175Y , K176T , N187K , V202G , Q213R , P214S , K223R , N241D , V363M , I422V , D505N , V545I show in structure
HA_A/Perth/1051/2019_376954 Show in NEXTFLU tree	HA A/Texas/50/2012(H3N2) find closest related sequences	96.113	100.000	22	V14I , L19I , E78G , K108R , N137K , N144T , T147K , R158G , N160S , N161S , F175Y , K176T , N187K , V202G , Q213R , P214S , K223R , N241D , V363M , I422V , D505N , V545I show in structure
HA_A/Victoria/2515/2019_365263 Show in NEXTFLU tree	HA A/Singapore/NFIMH-16-0019//2016(H3N2) find closest related sequences	98.057	100.000	11	E78G , K108R , T147K , K176T , P210L , A212I , S235F , H327Q , V363M , E495G , V545I show in structure
HA_A/Victoria/48/2019_365267 Show in NEXTFLU tree	HA A/Texas/50/2012(H3N2) find closest related sequences	96.113	100.000	22	V14I , L19I , E78G , K108R , N137K , N144T , T147K , R158G , N160S , N161S , F175Y , K176T , N187K , V202G , Q213R , P214S , K223R , N241D , V363M , I422V , D505N , V545I show in structure
HA_A/Victoria/67/2019_365264 Show in NEXTFLU tree	HA A/Texas/50/2012(H3N2) find closest related sequences	96.290	100.000	21	K2M , L19I , E78G , K108R , N137K , N144T , T147K , R158G , N160S , N161S , F175Y , K176T , N187K , V202G , Q213R , P214S , N241D , V363M , I422V , D505N , V545I show in structure

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

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The main application scenario for FluSurver is the verification of any predicted phenotypes. The curated reference sequences used for all fruitful and reliable results are currently H3N2v. Please take a look at the FluSurver application.

FluSurver

Query

HA_A/Darwin/459/2019_365269 [Show in NEXTFLU tree](#)

HA_A/Darwin/470/2019_365262 [Show in NEXTFLU tree](#)

HA_A/Darwin/479/2019_365265 [Show in NEXTFLU tree](#)

HA_A/Perth/1051/2019_376954 [Show in NEXTFLU tree](#)

HA_A/Victoria/2515/2019_365263 [Show in NEXTFLU tree](#)

HA_A/Victoria/48/2019_365267 [Show in NEXTFLU tree](#)

HA_A/Victoria/67/2019_365264 [Show in NEXTFLU tree](#)

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nextstrain

nextstrain.org/flu/seasonal/h3n2/ha/6y?s=A/Darwin/459/2019

DOCS BLOG

Real-time tracking of influenza A/H3N2 evolution

Showing a single strain [x A/Darwin/459/2019](#)

Phylogeny

Clade

- 3b
- 3c
- 3c2
- 3c2.A
- 3c3
- 3c3.A
- 3c3.B
- A1
- A1a
- A1b
- A1b/131K
- A1b/135K
- A1b/135N
- A2
- A2/re
- A3
- A4
- Unassigned

Tree Options

Layout

- RECTANGULAR
- RADIAL
- UNROOTED
- CLOCK

Branch Length

- TIME
- DIVERGENCE

Show confidence intervals

Branch Labels

- clade

Search Strains

Second Tree

Geography

New strain belongs to clade A1b/131K

Closest to earlier Singapore/2016 vaccine reference

A1b/131K



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The main application scenario for FluSurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with verification of any predicted phenotypes. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computer-accurated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the usage scenario for FluSurver is to provide fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu and novel H3N2v. Please take a look at the [Frequency](#)

FluSurver

Query Best reference

HA_A/Singapore/05/2015
HA_A/Darwin/459/2019_365269

HA T147K

Key to alternative position numbering:

145	FluSurver numbering (absolute as in 2009 H1N1 pandemic)
HA1 131	Classical H3N2 strain numbering
HA1 128	Classical H1N1 strain numbering
Chosen reference:	HA_H3N2_Human_2012_Texas50
Position in reference:	147
AA in reference:	T
AA in query:	K

Mutation HA T147K already occurred 12393 times (23.13% of all samples with HA sequence) in 136 countries. The first strain with this mutation, collected in June 2012, was A/Laos/1462/2012. The mutation most recently occurred in strain A/Maine/27/2019, collected in July 2019. ([see map](#))

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

A mutation at the position equivalent to HA 147 has been reported in the literature to be related to [antigenic drift / escape mutant](#).

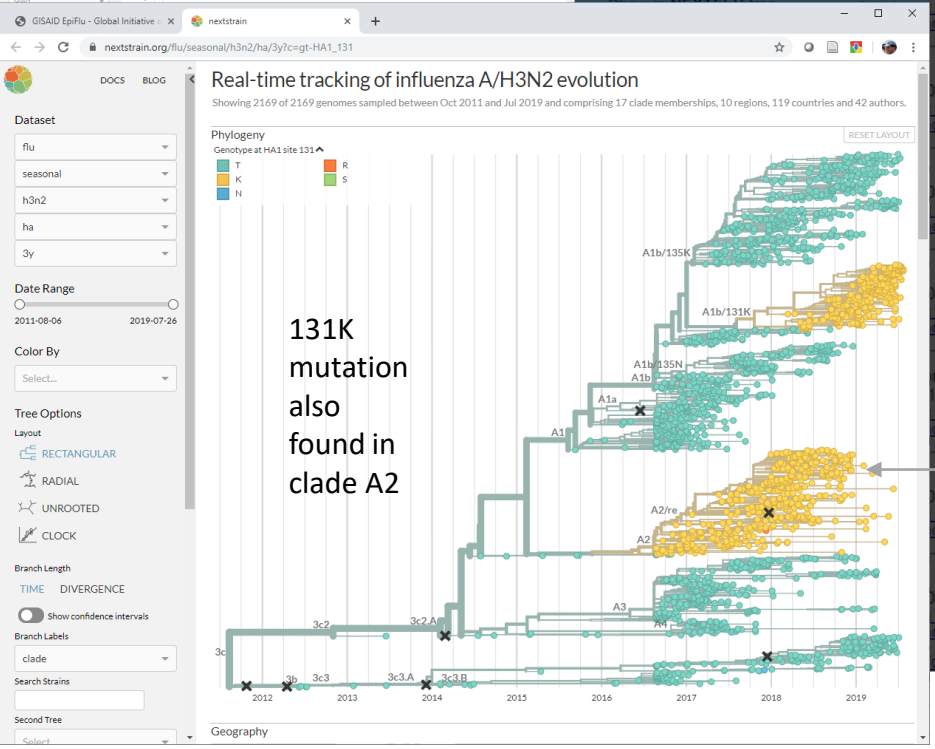
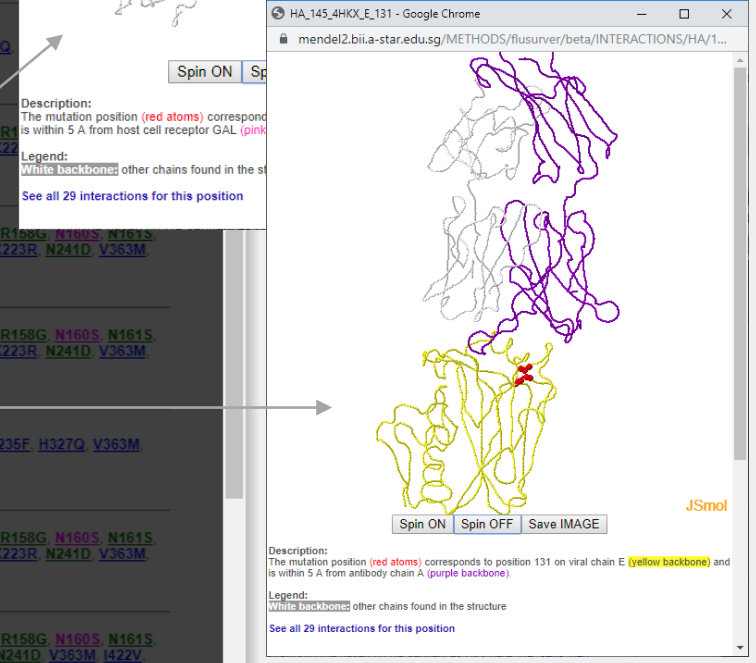
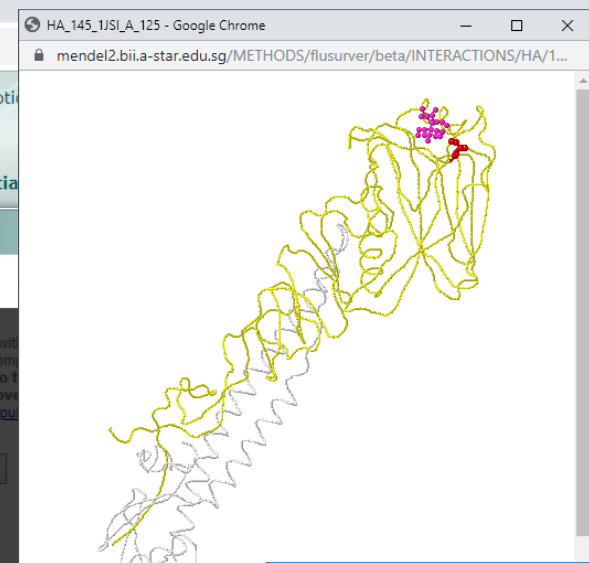
As seen in resolved structures of proteins from related strains, the HA position equivalent to your mutation is involved in:

- [host cell receptor binding](#)
- [binding small ligand\(s\)](#)
- [viral oligomerization interfaces](#)
- [antibody recognition sites](#)

[See all interactions for this position](#)

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

NEW: [Phylogenetic context for this mutation at NEXTFLU](#)



131K = T147K is in receptor binding and antigenic region



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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 using the recent H7N9

- A/HongKong/1/1968(H3N2) - 1968/69 pandemic - Hong Kong flu
 - A/Wisconsin/67/2005(H3N2) - seasonal - old H3 vaccine
 - A/Brisbane/10/2007(H3N2) - seasonal - old H3 vaccine
 - A/Perth/16/2009(H3N2) - seasonal - old H3 vaccine
 - A/Victoria/361/2011(H3N2) - seasonal - old H3 vaccine
 - A/Texas/50/2012(H3N2) - seasonal - old H3 vaccine - egg-derived (E5)
 - A/Texas/50/2012(H3N2) - seasonal - old H3 vaccine - cell-derived (M1/C2)
 - A/Switzerland/9715293/2013(H3N2) - seasonal - old H3 vaccine - egg-derived (E4/E2)
 - A/Switzerland/9715293/2013(H3N2) - seasonal - old H3 vaccine - cell-derived (S1S2/S2)
 - A/HongKong/4801/2014(H3N2) - seasonal - old H3 vaccine - egg-derived (E5/E2)
 - A/HongKong/4801/2014(H3N2) - seasonal - old H3 vaccine - cell-derived (C4/S2)
 - A/SingaporeINFIMH-16-0019//2016(H3N2) - seasonal - old H3 vaccine - egg-derived (E5/E1)
 - A/SingaporeINFIMH-16-0019//2016(H3N2) - seasonal - old H3 vaccine - cell-derived (C1S3/S1)
 - A/Switzerland/8060/2017(H3N2) - seasonal - old H3 vaccine - egg-derived (E5/E1)
 - A/Switzerland/8060/2017(H3N2) - seasonal - old H3 vaccine - cell-derived (S2/S1)
 - A/Kansas/14/2017(H3N2) - seasonal - current H3 vaccine - egg-derived (E5)
 - A/Kansas/14/2017(H3N2) - seasonal - current H3 vaccine - cell-derived (S1)
 - A/Indiana/10/2011(H3N2v) - swine-origin H3N2 with M segment from human H1N1pdm - vaccine candidate
 - A/Equine/Miami/1/1963(H3N8)
 - A/Equine/Sussex/1/1989(H3N8)
- Automatic detection of closest reference (larger selection of strains, not always full genomes, NOT SUITED to judge reassortment) ▾

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Could 131K/T147K be an egg adaptation mutation?

Check against cell-derived reference and compare to egg-derived version



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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 and novel reassortant swine flu H3N2v.** Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. There is also a [special note for using FluSurver results in publications](#).



Result for comparison with reference selection: H3N2_Human_2016_SingaporeINFIMH-16-0019_cell

[Back to Reference Selection](#)

Query	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
HA_A/Darwin/459/2019_365269 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	98.587	100.000	8	E78G , K108R , T147K , S235F , H327Q , V363M , E495G , V545I show in structure
HA_A/Darwin/470/2019_365262 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	97.880	100.000	12	V14I , E78G , K108R , T147K , Q213R , K223R , S235F , H327Q , V363M , E495G , E500G , V545I show in structure
HA_A/Darwin/479/2019_365265 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	97.880	100.000	12	V14I , E78G , K108R , T147K , Q213R , K223R , S235F , H327Q , V363M , E495G , E500G , V545I show in structure
HA_A/Perth/1051/2019_376954 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	97.880	100.000	12	V14I , E78G , K108R , T147K , Q213R , K223R , S235F , H327Q , V363M , E495G , E500G , V545I show in structure
HA_A/Victoria/2515/2019_365263 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	98.410	100.000	9	E78G , K108R , T147K , A212T , S235F , H327Q , V363M , E495G , V545I show in structure
HA_A/Victoria/48/2019_365267 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	97.880	100.000	12	V14I , E78G , K108R , T147K , Q213R , K223R , S235F , H327Q , V363M , E495G , E500G , V545I show in structure
HA_A/Victoria/67/2019_365264 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	98.057	100.000	11	K2M , E78G , K108R , T147K , Q213R , S235F , H327Q , V363M , E495G , E500G , V545I 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 \(Comma-separated, one query per line\)](#)

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HA_A/Darwin/459/2019_365269 [Show in NEXTFLU tree](#) HA A/SingaporeINFIMH-16-0019//2016(H3N2) [find closest related sequences](#) 98.233 [100.000](#) 10 [E78G, K108R, T147K, K176T, P210L, S235F, H327Q, V363M, E495G, V545I](#) [show in structure](#) egg

HA_A/Darwin/459/2019_365269 [Show in NEXTFLU tree](#) HA A/SingaporeINFIMH-16-0019 **cell**/2016(H3N2) [find closest related sequences](#) 98.587 [100.000](#) 8 [E78G, K108R, T147K, S235F, H327Q, V363M, E495G, V545I](#) [show in structure](#) cell

HA P210L

Key to alternative position numbering:

208	FluSurver numbering (absolute as in 2009 H1N1 pandemic)
HA1 194	Classical H3N2 strain numbering
HA1 191	Classical H1N1 strain numbering

Chosen reference: HA_H3N2_Human_2016_SingaporeINFIMH-16-0019
 Position in reference: 210
 AA in reference: P
 AA in query: L

Mutation HA P210L already occurred 35602 times (99.82% of all samples with HA sequence) in 168 countries. The first strain with this mutation, collected in June 2016, was A/South Africa/R3978/2016. The mutation most recently occurred in strain A/Maine/27/2019, collected in July 2019. ([see map](#))
[See detailed global statistics for this position](#)

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

- [host cell receptor binding](#)
- [binding small ligand\(s\)](#)
- [antibody recognition sites](#)

- is involved in [a T-cell epitope presented by MHC molecules](#)

[See all interactions for this position](#)

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

NEW: [Phylogenetic context for this mutation at NEXTFLU](#)

Bioinformatics Institute - Google Chrome

mendel2.bii.a-star.edu.sg/METHODS/flusurver/beta/tmp/tmp_HA_H3N2_Human_2...

Reference: HA_H3N2_Human_2016_SingaporeINFIMH-16-0019 ([Structure/Model Details](#))
 Patient/Sample: HA_A/Darwin/459/2019_365269
 Mutation(s): E78G, K108R, T147K, K176T, P210L, S235F, H327Q, V363M, E495G, V545I
 Wildtype residue only displayed if position is part of available structure.
 Hover with mouse over residue to see its position number. Right-click for more options.

FluSurver-JSmol

[Spin ON](#) [Spin OFF](#) [Save IMAGE](#)

[See interactions of position HA 108 in related structures.](#)
[See interactions of position HA 147 in related structures.](#)
[See interactions of position HA 176 in related structures.](#)

HA K176T

Key to alternative position numbering:

174	FluSurver numbering (absolute as in 2009 H1N1 pandemic)
HA1 160	Classical H3N2 strain numbering
HA1 157	Classical H1N1 strain numbering

Chosen reference: HA_H3N2_Human_2016_SingaporeINFIMH-16-0019
 Position in reference: 176
 AA in reference: K
 AA in query: T

Mutation HA K176T already occurred 29196 times (81.86% of all samples with HA sequence) in 166 countries. The first strain with this mutation, collected in June 2016, was A/South Africa/R3978/2016. The mutation most recently occurred in strain A/Maine/27/2019, collected in July 2019. ([see map](#))
[See detailed global statistics for this position](#)

Mutation HA K176T **creates a new potential N-glycosylation site** at position 174 which may also affect antigenic and other properties of this strain. In detail, the motif at positions 174-176 changed from NYK (no glyco) to NYT (glyco).

A mutation at the position equivalent to HA 176 has been reported in the literature to be related to [host specificity shift and antigenic drift / escape mutant, host specificity shift](#).

A combination of mutations including the position equivalent to HA 176 has been reported in the literature to be related to [antigenic drift / escape mutant and host specificity shift](#).

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

- [binding small ligand\(s\)](#)
- [antibody recognition sites](#)
- [viral oligomerization interfaces](#)

[See all interactions for this position](#)

New Glyco site!

2 typical egg passage adaptations in the new A1b/131K clade, but 131/147K is not passage adaptation