Surveillance

Open Access

Intense interseasonal influenza outbreaks, Australia, 2018/19

Ian G Barr[1,2], Yi Mo Deng[1], Miguel L Grau[3], Alvin X Han[4,5], Robin Gilmour[6], Melissa Irwin[7], Peter Markey[8], Kevin Freeman[9], Geoff Higgins[10], Mark Turra[10], Naomi Komadina[1], Heidi Peck[1], Robert Booy[11,12], Sebastian Maurer-Stroh[4,5,13], Vijaykrishna Dhanasekaran[1,3], Sheena Sullivan[1,2]

View Affiliations

View Citation

« Previous Article | Table of Contents | Next Article » | « Back to Search Results

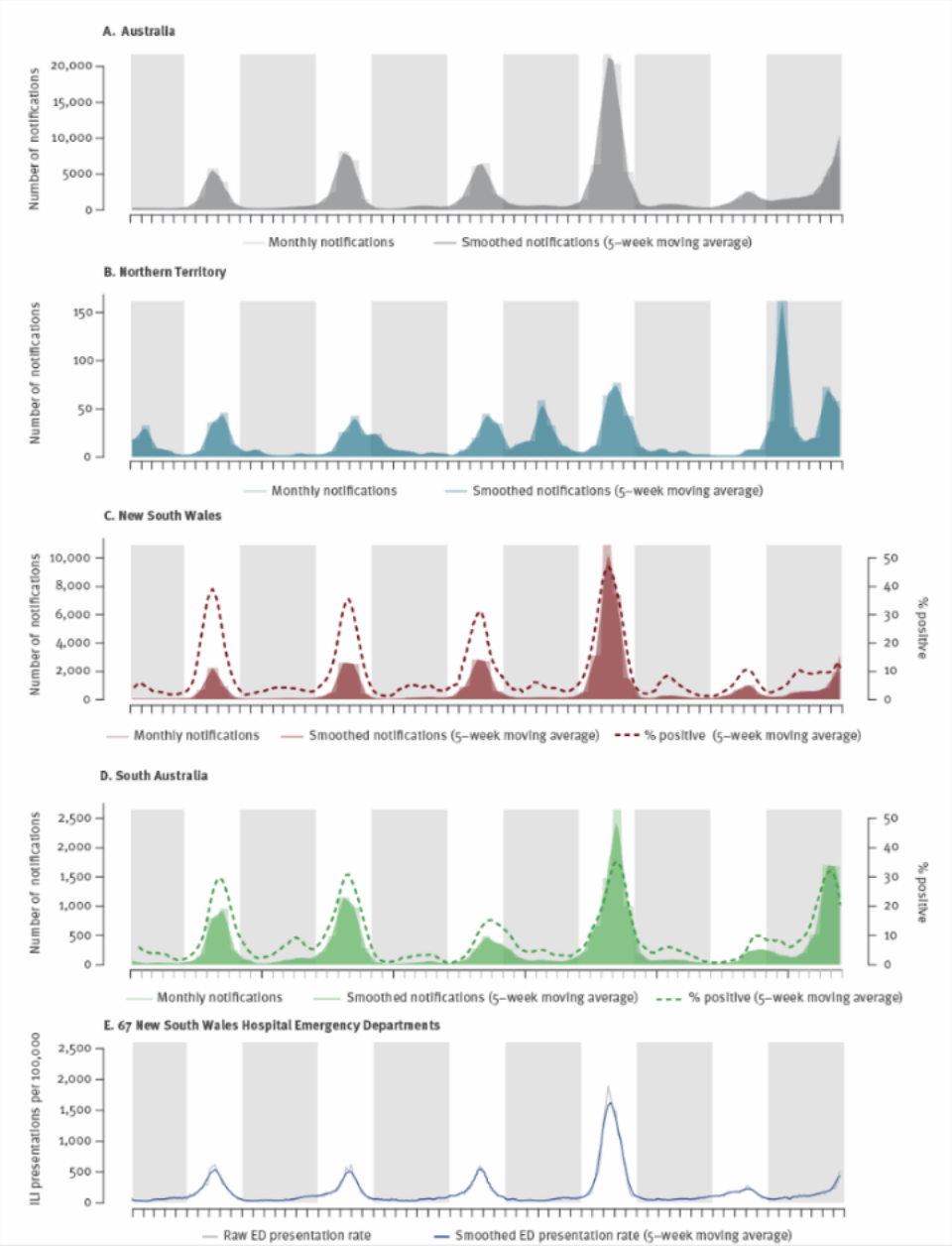
Abstract | Full-Text | Figures & Tables | References (32) | Supplementary Material (2) | Metrics/Cited By | Related Content

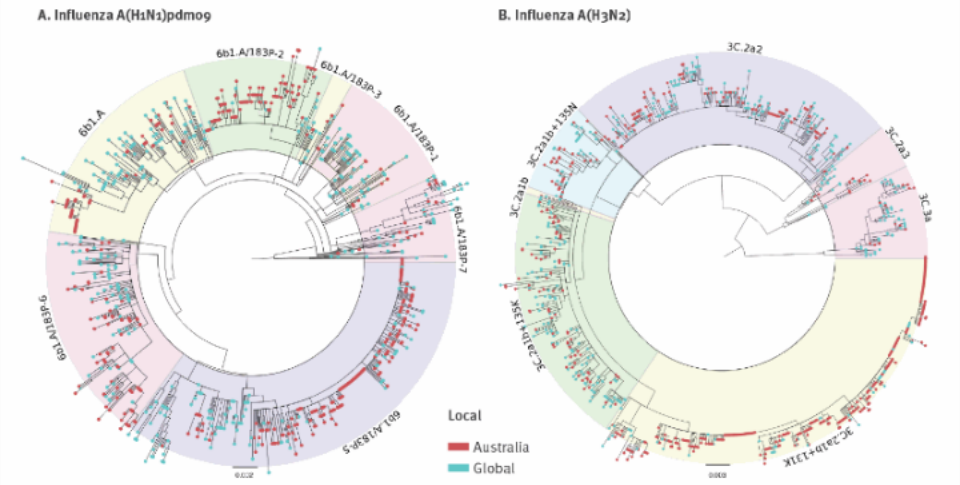
Introduction

Go to section...

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.

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

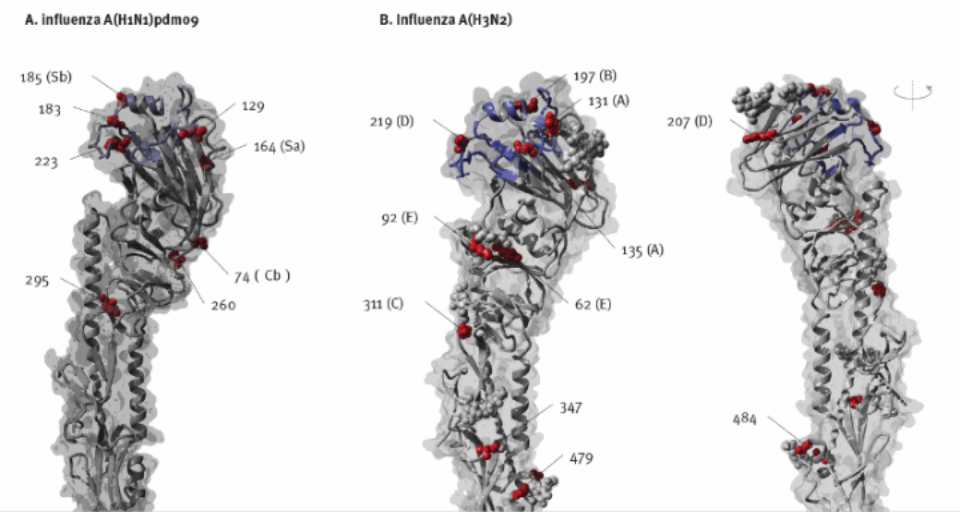




Click to view

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



GISAID

You are logged in as **Sebastian Maurer-Stroh** - logout

Registered Users | **EpiFlu™** | My profile

Browse | Back to results | **Worksets** | **Upload** | **Batch Upload** | **Settings** | **Analysis**

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	-all-
B	2	2		Human	Asia	American Samoa
C	3	3		Animal	Europe	Australia
	4	4		Avian	North America	Cook Islands
	5	5		Chicken	Oceania	Fiji

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)

New features | Help | Reset | Search

GISAID

You are logged in as **Sebastian Maurer-Stroh** - logout

Registered Users | EpiFlu™ | My profile

Browse | Back to results | Worksets | Upload | Batch Upload | Settings | Analysis

Released files

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

Total: 7 isolates

<< first | < prev | 1 | next > | last >>

Search in results

Go back | Help | Copy to... | Add to analysis | Download

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
MKTIIALSYILCLIFAQKIPGNDNSTATLCLGHHAVPNGTIVKTITNDRIEVTNATELVQNSSIGEICDSPHQILDGGNCTLIDALLGDPQCDGFQNKKWDLFVERSRAYSN
CYPYDVPDYASLRSLVASSGTLEFKNESFNWTGVKQNGTSSACIRGSSSSFFSRLNWLTHLNYTYPALNVTMPNKEQFDKLYIWGVHHPGTDKDQIFLYARSSGRITVSTRR
SQQAVIPNIGFRPRIRDIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCKSECITPNGSIPNDKPFQNVNRITYGACPRYVKQSTLKLATGM
RNVPEKQTRGIFGAIAGFIENGWEGMMDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRVQDLEKYVEDTKIDLWSYNAELLVALE
NQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHNVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCIALLGFIMWACQKGNI
RCNICI
>HA_A/Victoria/2515/2019_365263
MKTIIALSYILCLVFAQKIPGNDNSTATLCLGHHAVPNGTIVKTITNDRIEVTNATELVQNSSIGEICDSPHQILDGGNCTLIDALLGDPQCDGFQNKKWDLFVERSRAYSN
CYPYDVPDYASLRSLVASSGTLEFKNESFNWTGVKQNGTSSACIRGSSSSFFSRLNWLTHLNYTYPALNVTMPNKEQFDKLYIWGVHHPGTDKDQIFLYTQSSGRITVSTKR
```

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

Automatic detection of closest reference (larger selection of strains, not always full genomes, NOT SUITED to judge reassortment)

Analyze with FluSurver

Go back

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.

FluSurver

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

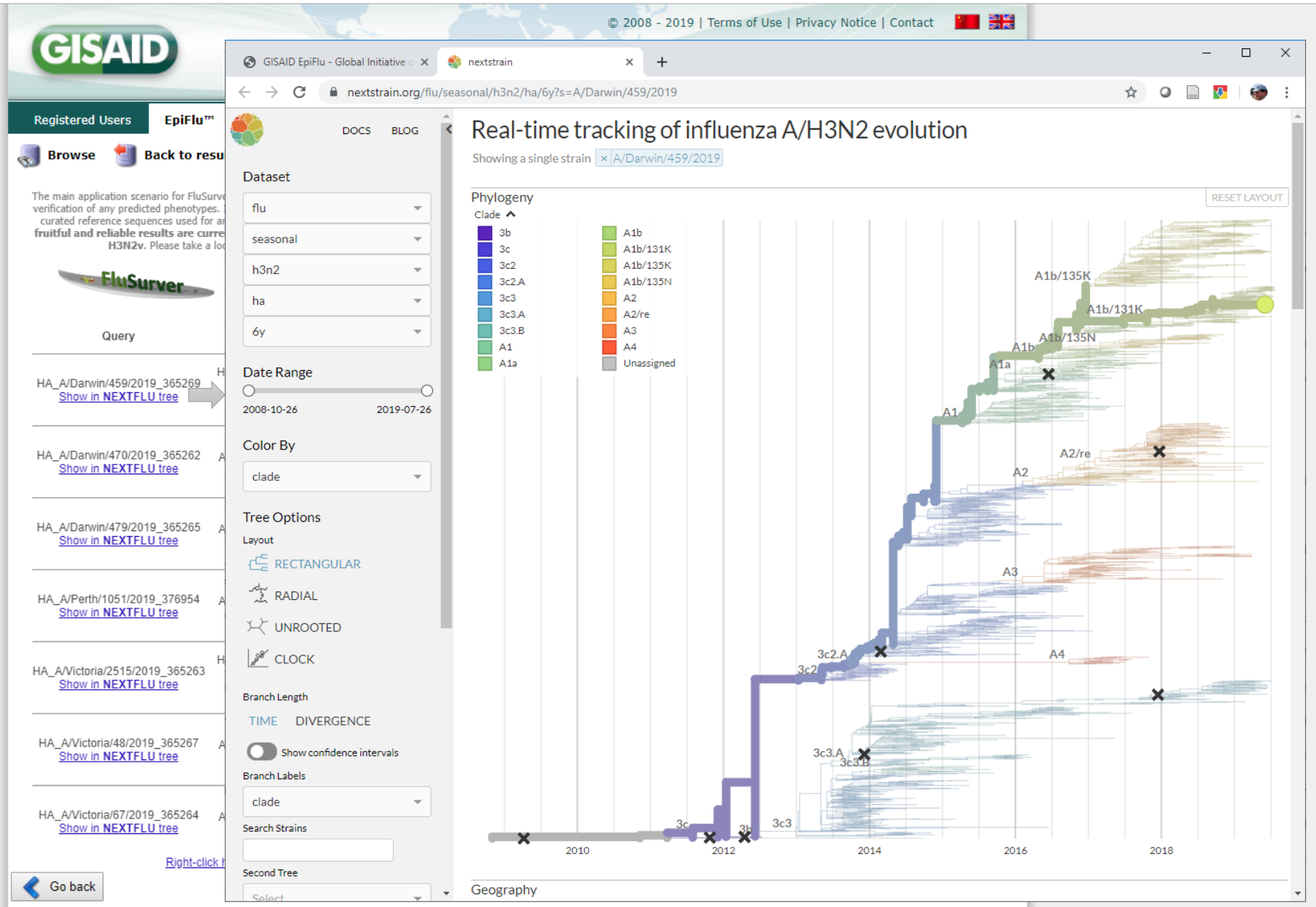
Query	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
HA_A/Darwin/459/2019_365269 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019//2016(H3N2) find closest related sequences	98.233	100.000	10	E78G, K108R, T147K, K176T, P210L, S235F, H327Q, V363M, E495G, V545I show in structure
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/SingaporeINFIMH-16-0019//2016(H3N2) find closest related sequences	98.057	100.000	11	E78G, K108R, T147K, K176T, P210L, A212T, 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)

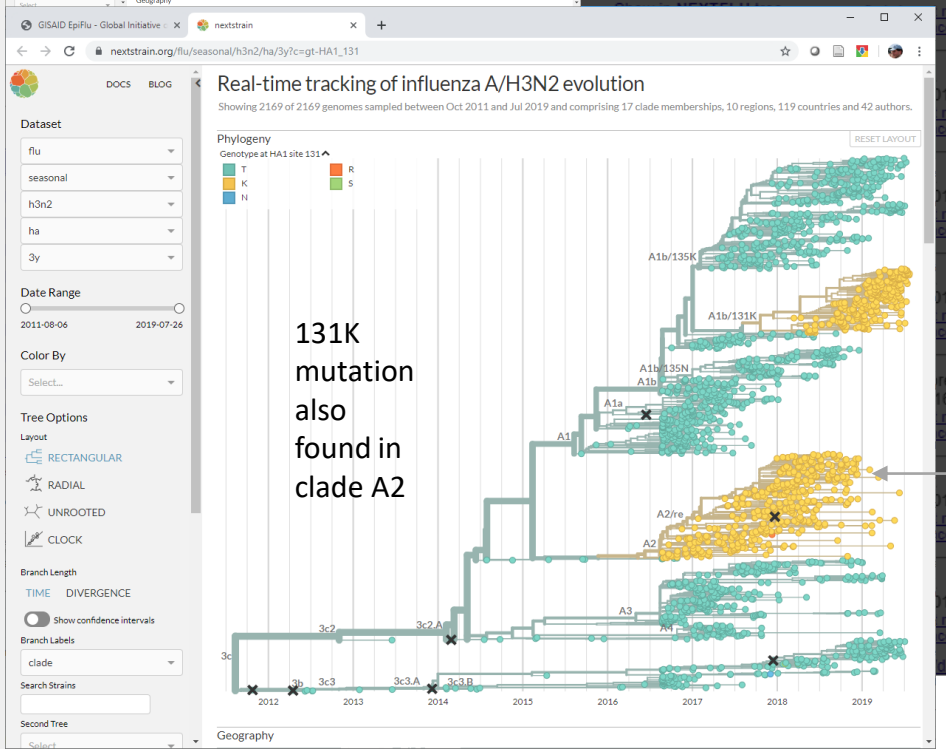
Go back

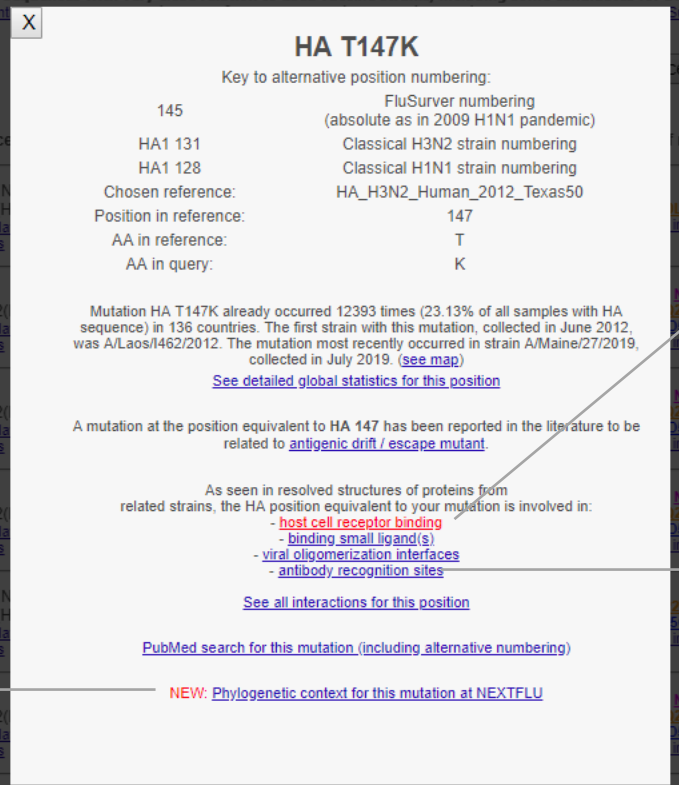
New strain belongs to clade A1b/131K

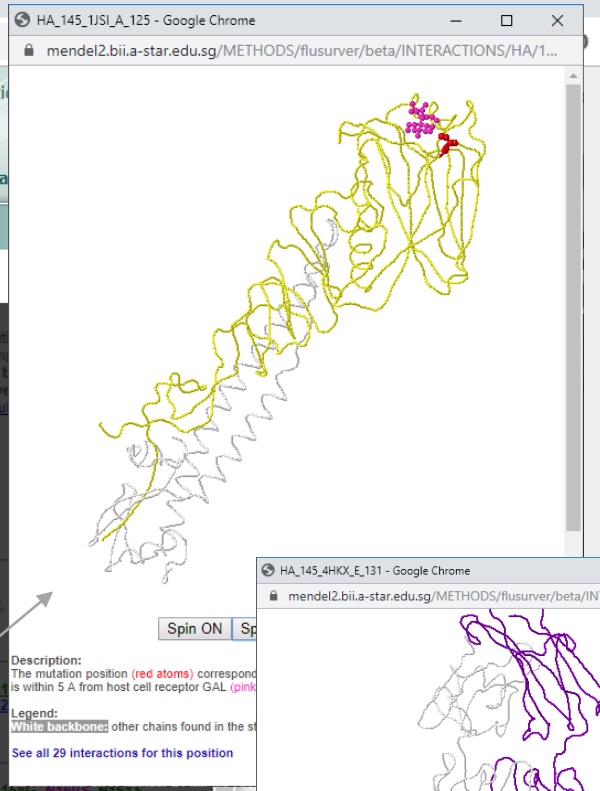
Closest to earlier Singapore/2016 vaccine reference

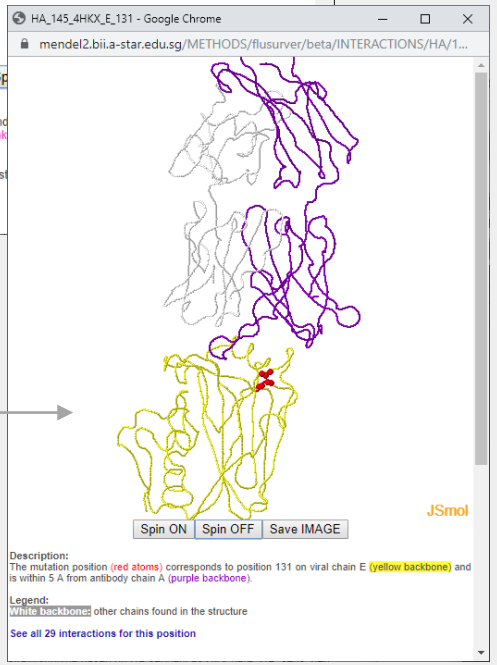


A1b/131K





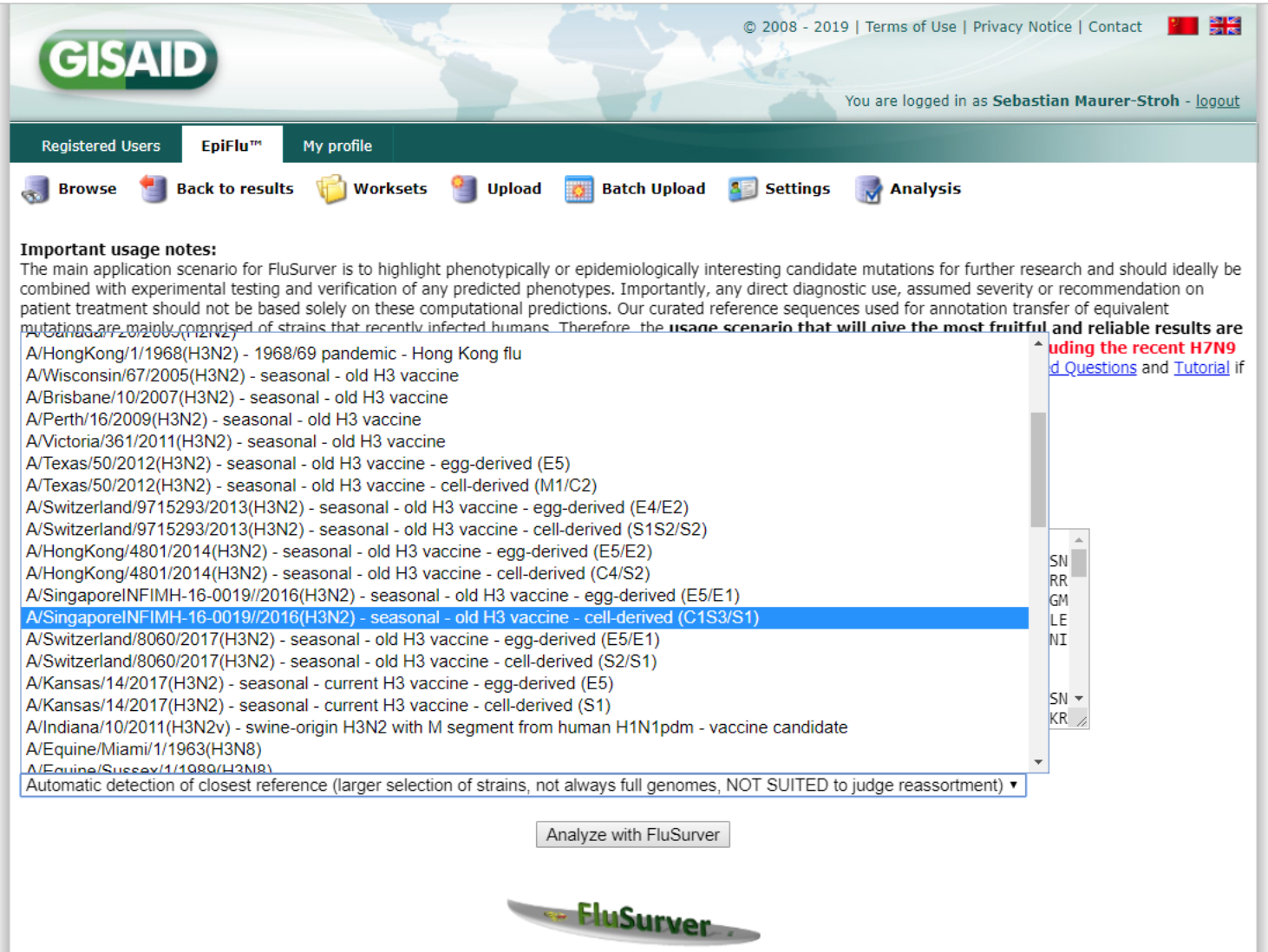




131K = T147K is in receptor binding and antigenic region

Could 131K/T147K be an egg adaptation mutation?

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



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.

FluSurver

Result for comparison with reference selection: **H3N2_Human_2016_SingaporeINFIMH-16-0019_cell** Back to Reference Selection

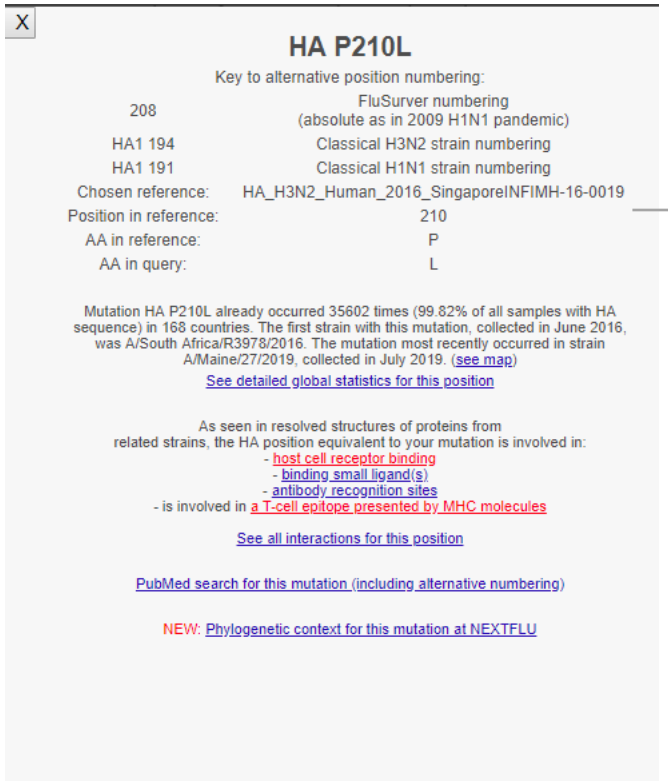
Query	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
HA_A/Darwin/459/2019_365269 Show in NEXTFLU tree	HA A/SingaporeINFIMH-16-0019_cell//2016(H3N2) find closest related sequences	98.587	100.000	8	E78G, K108R, T147K, S235F, H327Q, V363M, E495G, V545I show in structure
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

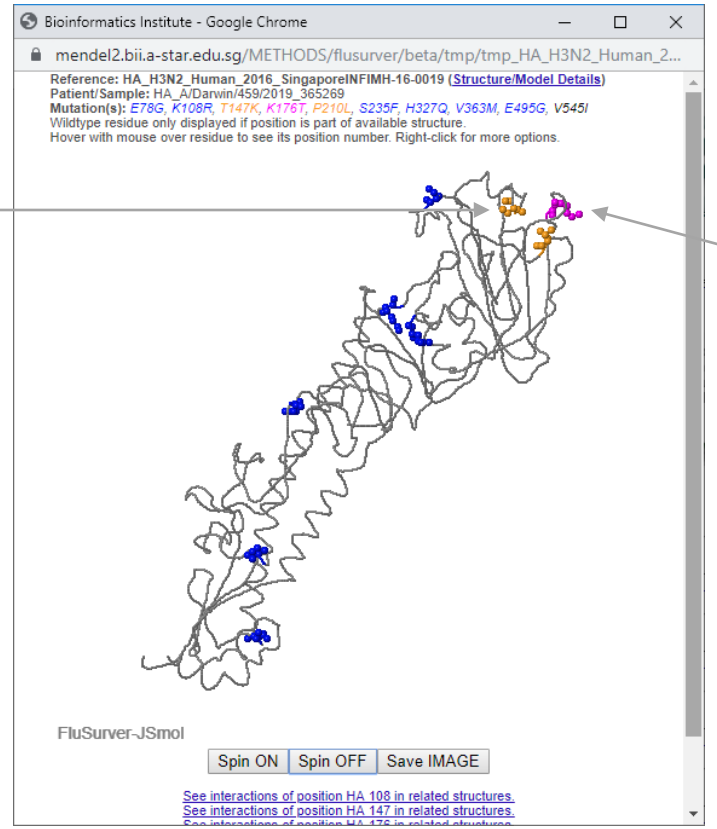
Right-click here to save/download **detailed mutation report** table for archiving or import to Excel (Tab-separated, one mutation per line)
Right-click here to save/download **query summary report** table for archiving or import to Excel (Comma-separated, one query per line)

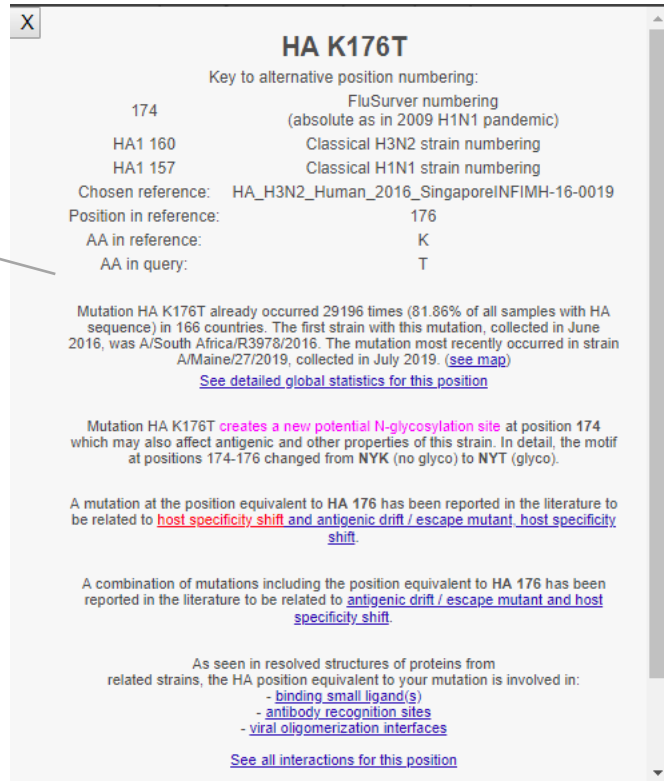
Back to Reference Selection

Go back

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







New Glyco site!

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