

How to request IAV-S Repository Isolates

The repository contains over 5000 viruses and individual IAV-S repository isolates are not listed in the catalog. Customers will need to search for isolates of interest (see below) and provide a list to the diagnostic virology lab before submitting a reagent request. Please note that there have been recent changes to the USDA repository:

- **Viruses with a collection date of July 2022 or later will need to be propagated. There will be a 2-week delay in orders (barring any propagation issues).**
- **Due to virus isolates in the USDA IAV-S Repository no longer being supported by the USDA Surveillance program, the price per isolate will be \$197, effective June 1, 2023.**

Once you have selected your isolates:

1. To confirm isolate availability, email nvsl.dvl.comm@usda.gov the list of isolates (specify 1 or 2 vials) before submitting the request.
2. After the list is finalized, email nvsl_concerns@usda.gov and include your:
 - a. shipping permit
 - b. completed VS Form 4-9 (the reagent code number for repository isolates is SIV-REP and the reagent name is the barcode ID).

Below is the link to the request form and ordering instructions:

[USDA APHIS | Reagents and Proficiency Testing Available from the NVSL](#)

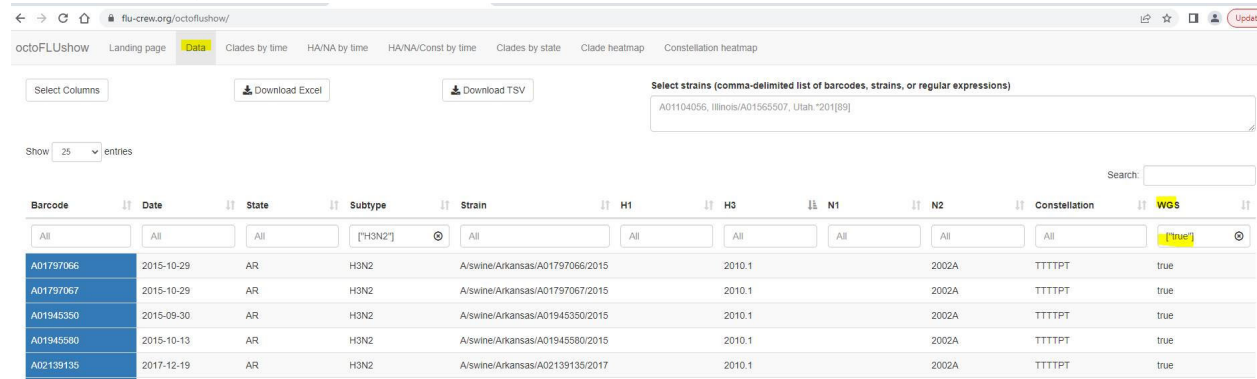
Options to search for repository isolates:

1. Octoflu

<https://flu-crew.org/octoflushow/>

Octoflu is a user-friendly platform to search viruses in the repository/USDA surveillance program. It also breaks down the lineage of the internal genes, if sequenced.

Click on the Data tab and filter for preferred characteristics. There is an option to select viruses that have had WGS (select true).



The screenshot shows the Octoflu web application interface. At the top, there are navigation tabs: octoFLUshow, Landing page, Data (selected), Clades by time, HA/NA by time, HA/NA/Const by time, Clades by state, Clade heatmap, and Constellation heatmap. Below the tabs, there are buttons for 'Select Columns', 'Download Excel', and 'Download TSV'. A search box contains the text 'A01104056, Illinois/A01565507, Utah *201[89]'. Below the search box, there is a 'Show 25 entries' dropdown. The main table displays search results with columns: Barcode, Date, State, Subtype, Strain, H1, H3, N1, N2, Constellation, and WGS. The WGS column has a 'true' filter selected. The table shows five rows of data, all with WGS set to true.

Barcode	Date	State	Subtype	Strain	H1	H3	N1	N2	Constellation	WGS
A01797066	2015-10-29	AR	H3N2	A/swine/Arkansas/A01797066/2015		2010.1		2002A	TTTTPT	true
A01797067	2015-10-29	AR	H3N2	A/swine/Arkansas/A01797067/2015		2010.1		2002A	TTTTPT	true
A01945350	2015-09-30	AR	H3N2	A/swine/Arkansas/A01945350/2015		2010.1		2002A	TTTTPT	true
A01945580	2015-10-13	AR	H3N2	A/swine/Arkansas/A01945580/2015		2010.1		2002A	TTTTPT	true
A02139135	2017-12-19	AR	H3N2	A/swine/Arkansas/A02139135/2017		2010.1		2002A	TTTTPT	true

Manuscript providing examples: <https://pubmed.ncbi.nlm.nih.gov/34913720/>

2. GenBank

USDA Swine Surveillance Influenza A virus isolates can be identified in GenBank by their eight digit barcode designations in the virus name, e.g. A/swine/North Carolina/A02431994/2019(H1N2). The

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information in GenBank will usually list USDA Swine Surveillance, or similar, in the author, journal or Consortium field. Many of the available isolates will have H and N sequenced, but some will have full genome sequencing completed.

3. USDA Surveillance Report “representative viruses”

There are also quarterly reports available to the public under the IAV-S surveillance tab that provide a list of the representative strains in the US (see table 4 in the quarterly report)

<https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/influenza-a-virus>

FY22 Q4 example:

Table 4. IAV-S Surveillance NADC Representative HA genes*

Strain	HA GenBank	Global Clade	US Clade
A/swine/Iowa/A02750864/2022	OP596618	1A.1.1.3	alpha-del
A/swine/Nebraska/A02711851/2022	OP292923	1A.3.3.2	pandemic
A/swine/North_Carolina/A02636642/2022	ON426971	1A.3.3.3-c1	gamma-c1
A/swine/Iowa/A02711806/2022	ON427112	1A.3.3.3-c3	gamma-c3
A/swine/Iowa/A02750859/2022	OP622342	1B.2.1	delta2
A/swine/Oklahoma/A02710705/2022	OP292920	1B.2.2.2	delta1b
A/swine/Iowa/A02750897/2022	OP622360	1990.4.a	IV-A
A/swine/Iowa/A02750686/2022	OP099959	2010.1	2010.1

*6-month HA1 consensus generated and best-matched field strain in the repository was identified.

- April 2022 to September 2022 USDA HA data downloaded (n = 239 H1, n = 126 H3) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (<https://github.com/flu-crew/parnas>).
- The 6 H1 selections cover 88% of observed diversity; the 2 H3 selections cover 67% of observed diversity.
- Clades were required to have a detection rate of at least 2% to be considered for selection (n >= 8).
 - Omitted 1A.4 (n = 4), 1B.2.2.1 (n = 1), 2010.2 (n = 5), 1990.4.b1 (n = 2), and 1990.4 (n = 1)