

# EpiFlu<sup>TM</sup> Database v1.1 www.gisaid.org

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# **BACKGROUND**

The Global Initiative on Sharing All Influenza Data (GISAID) provides a sharing mechanism for its publicly accessible EpiFlu™ database that incentivizes the rapid exchange of influenza virus data, by providing open-access to researchers and the development of medical interventions in a transparent manner, while protecting inherent rights of data submitters.

GISAID fosters benefit sharing and collaboration between submitters and users of data. Scientists' reticence to share data prior to publication via public-domain archives e.g. GenBank, where use of data takes place anonymously and void of any enforceable conditions to safeguard contributors' rights, prompted the creation of GISAID in 2008.

## **OVERVIEW**

The EpiFlu<sup>™</sup> database application, developed by the Max-Planck-Institute for Informatics, enables the analysis of the world's most complete collection of the latest seasonal to new animal influenza viruses. The application is based on a proprietary software code and Oracle software. Extensive metadata are also collected for most isolates. EpiFlu<sup>™</sup> also provides features for searching, filtering specific datasets for download and upload functionality.

All users of EpiFlu<sup>™</sup> have agreed to positively identify themselves. While access is free of charge, all users also agreed that they will not attach any restrictions on the data, but will acknowledge both the originator of the specimen and the submitter of the data, and seek to collaborate with the Originating Laboratory.

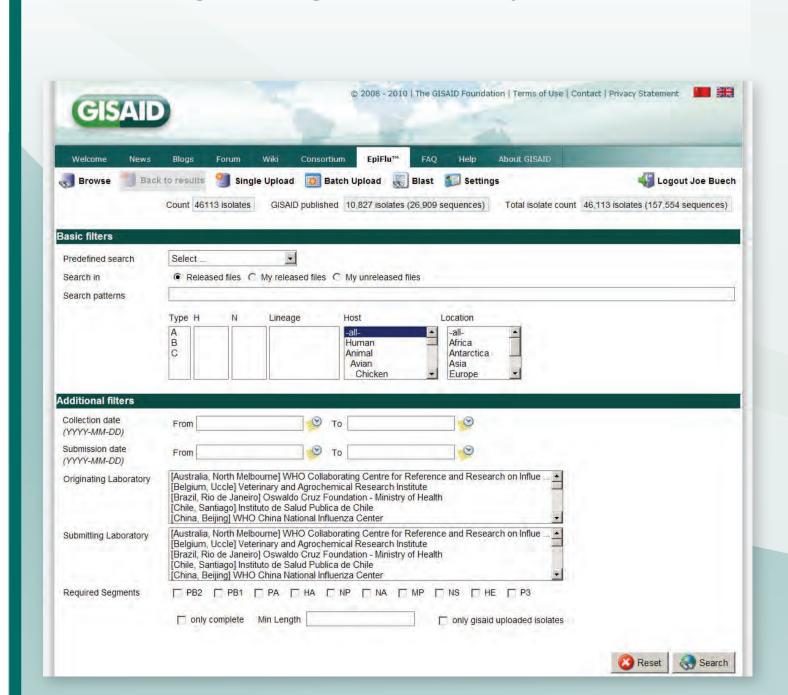


Figure 1. The browser menu

### FEATURES IN DETAIL

- Contains influenza sequences and associated meta data with each isolate
- Genetic, clinical, epidemiological
  & geographical data for human isolates plus species specific data associated with non-human isolates
- Batch and single upload functions
- Ability of submitter to edit data submitted to the platform
- Each isolate accompanied by an audit trail with a history of edits
- Submitted data available for view to other users immediately
- Download facility of meta data associated with isolates in an Excel format
- Sequence download in FASTA format with user defined headers
- BLAST, alignment tool, FluSurver, nextflu phylogenetic trees (Figure 3)

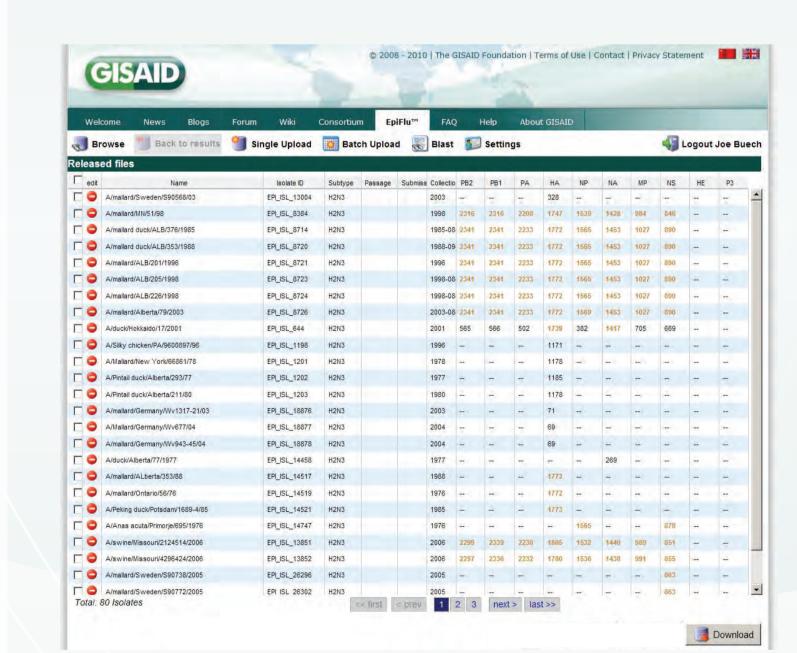
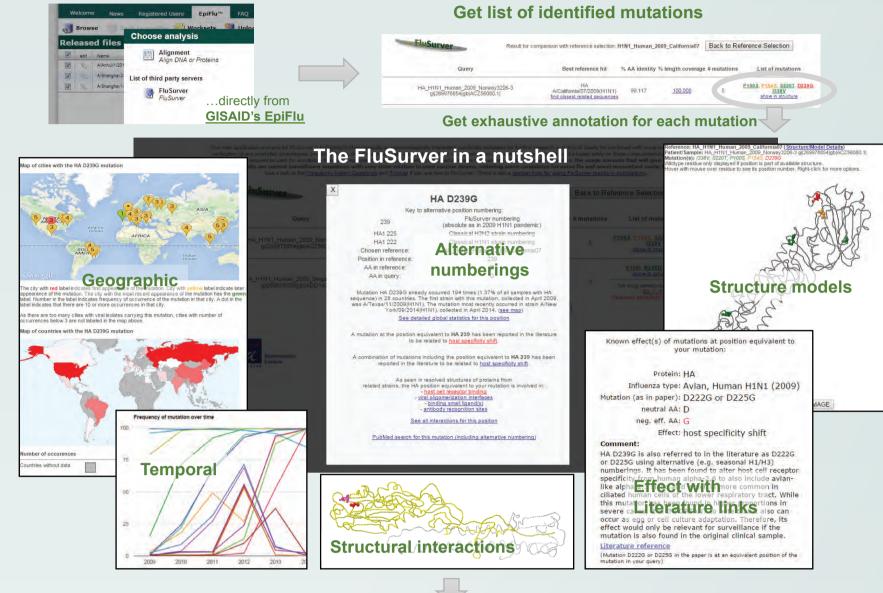


Figure 2. The search results page

#### **Browse Functions**

- Can choose to browse all isolates in the database, user submitted isolates, or isolates not available on other databases (Figure 1)
- Can browse using one or more filters for:
  - Type, subtype, isolate name, genes, species, region, country of origin
  - Lineage swl or seasonal for H1N1, Yamagata or Victoria for Type B influenza viruses
  - Isolate Originating laboratory
  - Isolate sequence Submitting laboratory
  - Isolate specimen date
  - Isolate submission date
  - Can define fields to be displayed



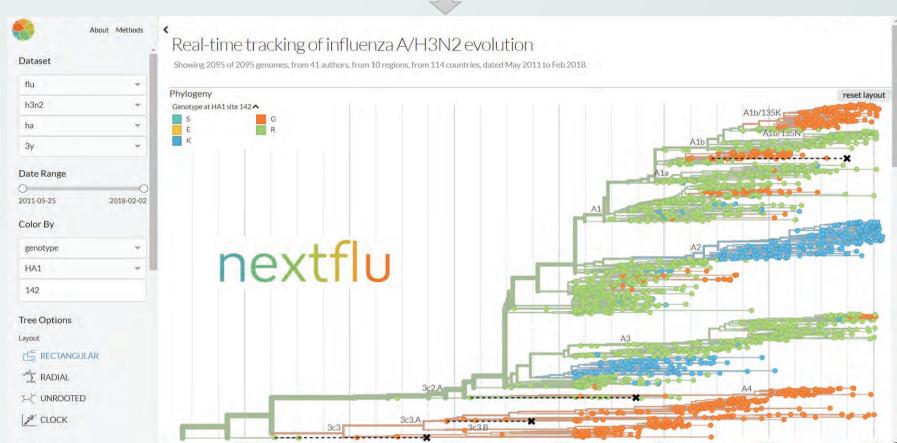


Figure 3. FluSurver mutation analysis connected to nextflu phylogenetic trees

# **Upload Functions**

- Can upload data via single upload function or batch upload sheet (Figure 4) for multiple isolates
- Metadata only needs to be entered once for each isolate
- Once isolates uploaded, extra gene sequences can be added via the edit function
- For isolates added via the batch upload sheet multiple extra gene sequences can be added by reusing the initial batch upload sheet
- Batch upload occurs in real time, with an immediate response
- Error messages are displayed for isolates
  & sequences not uploaded
- Duplicate sequences & isolates are flagged and not added
- Successful uploads are flagged and isolate accession and segment accession numbers are added to the return batch upload sheet

# **RESULTS**

As of August 2019, 9,000 participants rely on data from 1,200 laboratories entrusted to GISAID from 198 nations.

EpiFlu<sup>™</sup> database remains essential for the Global Influenza Surveillance and Response System (GISRS) and WHO biannual vaccine strain selection. Data in EpiFlu<sup>™</sup> is comprised of 1,2 million nucleotide sequences from nearly 300,000 influenza virus strains.

Among GISAID's contributors are OIE and FAO Reference Laboratories for Avian Influenza, as well as all WHO National Influenza Centers and WHO Collaborating Centers for Surveillance, Epidemiology and Control of Influenza. To provide a complete picture of circulating influenza strains, data from public-domain archives are routinely imported.

# OUTLOOK & CONCLUSION

Since in 2010, the Federal Republic of Germany constitutes an important pillar for the sustainability of GISAID through its ongoing commitment to host the EpiFlu™ database. GISAID is in the process of developing a new and advanced database application software (v3.0) to address the needs of the user community for advanced bioinformatics capabilities.

This development will also extend the spectrum of data analysis tools. The functionality of the database will also be expanded to include more data types.

GISAID EpiFlu<sup>™</sup> has not only become a trusted, but indispensable resource for the global scientific community of influenza researchers in addition to public and veterinary health officials.



Figure 4: The batch upload facility, successfully uploaded isolates