HFI P

SEARCH DATA ANALYZE & VISUALIZE WORKBENCH SUBMIT DATA

Search

Search our comprehensive database for:

Sequences & Strains

Animal Surveillance

Sequence Feature Variant Types

Immune epitope data

3D protein structures

Host Factor Data

Browse All Search Types

Analyze

Analyze data online:

Sequence Alignment

Phylogenetic Tree

Sequence Variation (SNP)

Metadata-driven Comparative Analysis

HPAI H5N1 Clade Classification

BLAST

Browse All Tools

Save to Workbench

Sign up for a workbench to:

Store and share data

Combine working sets

Integrate your data with IRD data

Store and share analyses

Custom search alert

Sign Up!

Sian In

Highlights

IRD Workbench

The IRD Workbench allows users to save 'working sets' of sequences, searches and analysis results between web sessions in their own private workspace. Users can share working sets or analysis results with collaborators.

Key Highlights:

Save and organize working sets of sequences, analysis results and search criteria Visualize saved analysis results Share working sets and analysis results with others Upload personal sequences and combine with existing working sets

Go to Workbench

Video Tutorial Static Tutorial

Announcements

Erasmus University, Rotterdam, Netherlands, part of the Mt. Sinai School of Medicine CEIRS project, submitted 69 influenza sequences to GenBank using the IRD sequence submission tool during month of June 2014.

St.Jude Children's Research Hospital CEIRS submitted 745 influenza sequences to GenBank using the IRD sequence submission tool between March 1 and June 30, 2014.

The Ohio State University, part of the former University of Minnesota CEIRS project, submitted 1,233 influenza sequences to GenBank using the IRD sequence submission tool during month of March 2014.

USDA Swine Influenza Surveillance Consortium submitted a total of 1,223 influenza sequences to GenBank using the IRD sequence submission tool during first six months of 2014.

St.Jude Children's Research Hospital CEIRS deposited 60,650 surveillance samples into IRD during month of March 2014.

Community Spotlight

View Archive

A recent article published in Influenza and Other Respiratory Viruses reported the identification of artifacts in influenza sequence records, including the inclusion of primer sequences, vector sequences, and poly(A) tails as part of the influenza sequence. David Suarez and his co-authors chose to use the Influenza Research Database (IRD) as the primary public database to support their analysis because of its comprehensive influenza sequence data, various sequence filtering options, and private and shared workbenches for data storage and sharing. To avoid these artifacts, IRD also provides a GenBank sequence submission tool that identifies the presence of primer/vector sequences and assists sequence submitters with their removal before submission. (Posted on March 14, 2014)

What's New with Flu

A novel method for improved phylogenetic inferencing has been reported recently in Nature. By allowing the use of host-specific local clock models within the popular BEAST algorithm, the method provides better resolution of evolutionary patterns and has helped decipher the flow of influenza virus genes between different host species. IRD is currently collaborating with the CIPRES resource to provide direct access to BEAST and other advanced phylogenetic algorithm through the IRD portal (coming this summer) (Posted on March 14, 2014).

Previous Scientific Reports

Quick Search

IRD will search in data fields associated with genomic sequence, protein, strain and surveillance data. (Details including wildcard usage)

Keyword:

Ex: CY042246, China, H3N2...

Connect with Us



Influenza Research Database (IRD)

Like 197



IRD videos on youtube

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Data Summary

Updated August 8, 2014

GenBank data downloaded daily.

Data Aggregated by IRD (Source)

Strains (GenBank)	81,404
Sequences (GenBank)	341,509
Proteins (GenBank and UniProt)	459,461
3D Protein Structures (PDB)	503
Experimentally Determined Epitopes (IEDB)	5,968