

Virus Families



Arenaviridae



Bunyavirales



Caliciviridae



Coronaviridae



Filoviridae



Flaviviridae



Hepeviridae



Herpesviridae



Paramyxoviridae



Picornaviridae



Poxviridae



Reoviridae



Rhabdoviridae



Togaviridae

Featured Viruses



Dengue



Ebolavirus



Enterovirus



Hepatitis C Virus



Influenza Virus



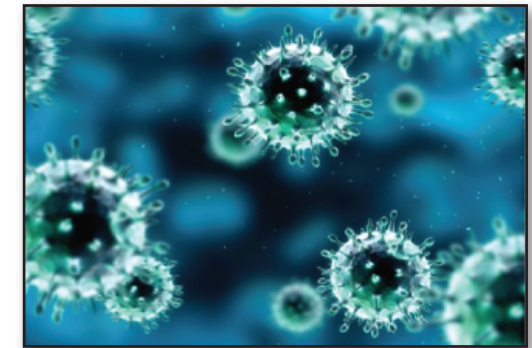
Lassa Virus



Zika Virus

What they are & what they do...

The Influenza Research Database (IRD) and Virus Pathogen Resource (ViPR) are freely available, NIAID-funded resources that support the research of viral pathogens in the NIAID Category A-C Priority Pathogen lists and those causing (re)emerging infectious diseases. IRD and ViPR integrate data from external sources (GenBank, UniProt, Immune Epitope Database, Protein Data Bank, etc.), direct submissions, and internal curation and analysis pipelines, and provide a suite of bioinformatics analysis and visualization tools to expedite virology research.



www.fludb.org
www.viprbrc.org

***Expect More
from Your Database***

Search and Retrieve Data

- Genomes, genes, proteins and annotations
- Mature peptide predictions from polyproteins
- Genotypes, subtypes and clades
- Influenza consensus sequences & polymorphism scores
- Protein ortholog groups
- Immune epitopes
- Sequence Features (SFs) including phenotype markers
- Surveillance, clinical and serology data
- 3D protein structures
- Host factor data
- Antiviral drug data
- Commonly-used PCR primers
- Computationally-derived data
- Sequence search API

Analyze and Visualize

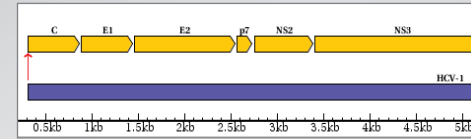
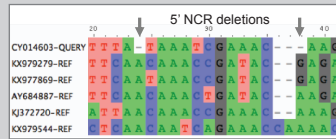
- BLAST sequence similarity search
- Short peptide search
- Genome annotation including SF annotation
- Flavivirus & Rotavirus genotype/subtype prediction
- Influenza H1 and H5 clade classification
- Influenza HA subtype numbering conversion
- Multiple sequence alignment
- Computationally intensive phylogenetics
- Metadata-driven Comparative Analysis Tool
- Sequence Variation (SNP) analysis
- Sequence Feature Variant Type (SFVT) analysis
- 3D protein structure visualization
- Host factor enrichment & network analysis
- PCR primer design

Save to Workbench

- Save and share private data and analysis results
- Share data and analysis results with collaborators
- Analyze your own data/metadata using IRD/ViPR tools

Sequence Submission

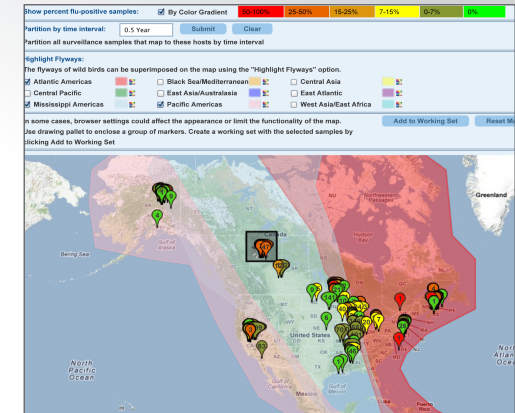
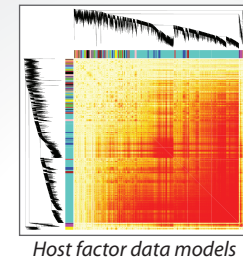
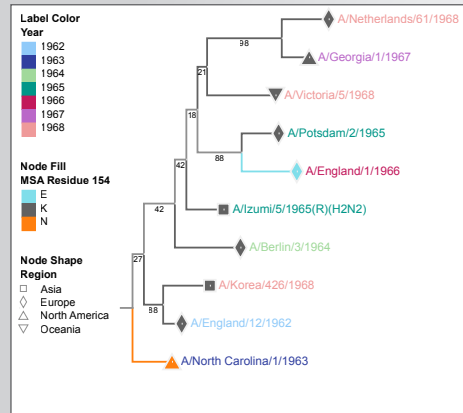
- Process sequence data for GenBank submission



Ortholog Group Search Result

Ortholog Group Number	Ortholog Group Name	Ortholog Classifier	Total # of Proteins	Pfam Domain / Domain Architecture
2768	Glycoprotein_L_A_S	SOG	9	Herpes_UL1-Gly_C
2769	Transactivating segment protein VP16_A_S	SOG	9	Alpha_TIF-HSV_VP16_C

Comparative evolutionary genomics based on orthology and protein domain architecture



SEQUENCE FEATURE DEFINITION	
Protein Name	HA
Sequence Feature Name	Influenza_A_H5_species-adaptation_110(1)
Sequence Feature ID	Influenza_A_H5_SF423
Reference Strain	A/Viet Nam/1203/2004(H5N1)
Reference Sequence Accession	AY818135
Reference Position	110(G4 HA1)

SOURCE STRAIN(S)						
Source Strain	VT Number	Source Position	Source Accession	3D Protein Structure	Publication	Evidence Codes
A/chicken/Fujian/1042/2005	VT-1	110	DQ320876	4BH2, 4BH3, 4BH4, 4N5Z	PubMed: 19020946	CDC H5N1

VARIANT TYPES				
Strain Count	Variant Type	Phenotypic Variant Type	Sequence Variation 110	Total Variation
1906	VT-1	No	D	0
4537	VT-2	Yes	N	1
613	VT-3	No	S	1

Phenotypic marker curated as a Sequence Feature

Metadata-driven Comparative Analysis Report

Download Input | Generate Phylogenetic Tree | Visualize Aligned Sequences | Download

Reference Coordinate
Select from the drop-down list to convert the existing position numbers to a different numbering (coordinate) scheme using a Reference Sequence

4:H7N3 A/Turkey/Istanbul/220158/02/H7N3

Chi-square Test of Independence Result
There are 26 positions that have a significant non-random distribution between the specified groups.
Group1: <=2014
Group2: >=2015

Position	Ref Coordinate	Chi-square Value	P-value	Degree Freedom	Residue Diversity	Sequence Feature
136	118	78.782	6.935E-19	1	group1(75 S) group2(12 N)	View SF
143*	125	78.683	5.881E-17	3	group1(71 A, 2 S, 2 T) group2(1 A, 11 V)	View SF
400*	378	60.25	8.353E-15	1	group1(3 A, 72 E) group2(12 A)	N/A
503*	481	60.25	8.353E-15	1	group1(3 R, 72 S) group2(12 R)	N/A
186	168	51.529	7.053E-13	1	group1(5 I, 70 L) group2(12 I)	View SF

Meta-CATS reports positions significantly different between groups of sequences