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
- 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

Sequence curation pipeline
flags potential sequence artifacts

Mature peptide annotations for viruses that generate polyproteins

Phylogenetic tree inference and visualization

3D protein structure with epitopes & sequence conservation highlighted

Avian influenza surveillance data mapping

Metadata-driven Comparative Analysis Report
Select from the drop-down list to convert the existing position numbers to a different numbering (coordinate) scheme using a Reference Sequence

Ortholog Group Search Result
Comparative evolutionary genomics based on orthology and protein domain architecture

SeqFeature

<table>
<thead>
<tr>
<th>Source Strain</th>
<th>VT Marker</th>
<th>Source Position</th>
<th>Source Annotation</th>
<th>Protein Structure</th>
<th>Evidence Code</th>
<th>Comment</th>
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</thead>
</table>
| VT-1          | 110       | EG300876        | -                  | M2                | CDC-MHC      | Introduction of M2A/M2B (from influenza Hemagglutinin) and A/England/12/1962 vaccine. This sequence is the consensus sequence of M2A and M2B strains isolated between 2003 and 2006.

VARIANT TYPES

- Source Incremental
- MAFs Incremental
- ViPR Phylogeny Tree
- Find a VT

Strain Count | Variant Type | Phenotypic Variant Type | Sequence Variation | Total Variation |
<table>
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Phenotype marker curated as a Sequence Feature