

Resource Summary Report

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Influenza Virus Resource

RRID:SCR_002984

Type: Tool

Proper Citation

Influenza Virus Resource (RRID:SCR_002984)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/genomes/FLU/>

Proper Citation: Influenza Virus Resource (RRID:SCR_002984)

Description: Database of data obtained from the NIAID Influenza Genome Sequencing Project as well as from GenBank, combined with tools for flu sequence analysis and annotation. In addition, it provides links to other resources that contain flu sequences, publications and general information about flu viruses. Users can search the Flu database, build queries, retrieve sequences, and apply analysis tools. This includes selecting influenza sequences by virus, subtype, host, and other criteria, finding complete genome sets, aligning sequence and others in the database (up to 1000 sequences), viewing clustering and phylogenetic trees, BLAST searching a flu sequence against the database, and more.

Abbreviations: Influenza Virus Resource

Synonyms: NCBI Influenza Virus Resource

Resource Type: database, data or information resource

Defining Citation: [PMID:17942553](#)

Keywords: genomics, genome, flu, variation, annotation, blast, cluster, phylogenetic tree, align, data analysis service

Related Condition: Influenza virus

Availability: Free, Available for download, Freely available

Resource Name: Influenza Virus Resource

Resource ID: SCR_002984

Alternate IDs: nif-0000-03023, r3d100011004

Alternate URLs: <https://doi.org/10.17616/R3S61C>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260808T190355+0000

Ratings and Alerts

No rating or validation information has been found for Influenza Virus Resource.

No alerts have been found for Influenza Virus Resource.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).

Wang X, et al. (2025) The novel H10N3 avian influenza virus acquired airborne transmission among chickens: an increasing threat to public health. mBio, 16(2), e0236324.

Lin S, et al. (2024) Cross-Species Transmission Potential of H4 Avian Influenza Viruses in China: Epidemiological and Evolutionary Study. Viruses, 16(3).

Menon T, et al. (2024) CD8+ T-cell responses towards conserved influenza B virus epitopes across anatomical sites and age. Nature communications, 15(1), 3387.

Moeini S, et al. (2023) Phylogenetic analysis and docking study of neuraminidase gene of influenza A/H1N1 viruses circulating in Iran from 2010 to 2019. Virus research, 334, 199182.

Yang F, et al. (2022) A multiplex real-time RT-PCR method for detecting H5, H7 and H9 subtype avian influenza viruses in field and clinical samples. Virus research, 309, 198669.

Guo F, et al. (2021) Host Adaptive Evolution of Avian-Origin H3N2 Canine Influenza Virus. Frontiers in microbiology, 12, 655228.

Guo F, et al. (2020) Origin and Evolution of H1N1/pdm2009: A Codon Usage Perspective. Frontiers in microbiology, 11, 1615.

van de Sandt CE, et al. (2019) Challenging immunodominance of influenza-specific CD8+ T cell responses restricted by the risk-associated HLA-A*68:01 allomorph. Nature

communications, 10(1), 5579.

Htwe KTZ, et al. (2019) Phylogeographic analysis of human influenza A and B viruses in Myanmar, 2010-2015. PloS one, 14(1), e0210550.

Guo F, et al. (2019) Adaptive Evolution of Human-Isolated H5Nx Avian Influenza A Viruses. Frontiers in microbiology, 10, 1328.

Mohebbi A, et al. (2019) Molecular epidemiology of the hemagglutinin gene of prevalent influenza virus A/H1N1/pdm09 among patient in Iran. Virus research, 259, 38.

Arai Y, et al. (2018) Multiple polymerase gene mutations for human adaptation occurring in Asian H5N1 influenza virus clinical isolates. Scientific reports, 8(1), 13066.

Lackenby A, et al. (2018) Global update on the susceptibility of human influenza viruses to neuraminidase inhibitors and status of novel antivirals, 2016-2017. Antiviral research, 157, 38.

Wang D, et al. (2018) Characterization of avian influenza H9N2 viruses isolated from ostriches (*Struthio camelus*). Scientific reports, 8(1), 2273.

Hyoung KJ, et al. (2017) A consensus-hemagglutinin-based vaccine delivered by an attenuated *Salmonella* mutant protects chickens against heterologous H7N1 influenza virus. Oncotarget, 8(24), 38780.

Li Y, et al. (2017) Construction of Multilevel Structure for Avian Influenza Virus System Based on Granular Computing. BioMed research international, 2017, 5404180.

Huang ZZ, et al. (2017) Charged amino acid variability related to N-glyco -sylation and epitopes in A/H3N2 influenza: Hem -agglutinin and neuraminidase. PloS one, 12(7), e0178231.

Li C, et al. (2017) Genetic evolution of influenza H9N2 viruses isolated from various hosts in China from 1994 to 2013. Emerging microbes & infections, 6(11), e106.

Wang C, et al. (2017) A Multiplex RT-PCR Assay for Detection and Differentiation of Avian-Origin Canine H3N2, Equine-Origin H3N8, Human-Origin H3N2, and H1N1/2009 Canine Influenza Viruses. PloS one, 12(1), e0170374.