

Resource Summary Report

Generated by SPARC SAWG on Aug 5, 2026

Influenza Research Database (IRD)

RRID:SCR_006641

Type: Tool

Proper Citation

Influenza Research Database (IRD) (RRID:SCR_006641)

Resource Information

URL: <https://www.fludb.org/brc/home.spg?decorator=influenza>

Proper Citation: Influenza Research Database (IRD) (RRID:SCR_006641)

Description: The Influenza Research Database (IRD) serves as a public repository and analysis platform for flu sequence, experiment, surveillance and related data.

Abbreviations: IRD

Synonyms: , Influenza Research Database, IRD

Resource Type: data analysis service, analysis service resource, storage service resource, data repository, production service resource, service resource, database, data or information resource

Defining Citation: [PMID:17965094](#)

Keywords: avian, clinical, genomic, host, influenza, isolate, mammalian, nonhuman, phenotypic, preventive, proteomic, repository, strain, epitope, surveillance, treatment, virus, protein sequence, immune, 3d protein structure, align, blast, short peptide, flu protein, sequence variation, snp, phylogenetic tree, human, 3d spacial image, image, clinical data, clinical, genomic, proteomic, phenotype

Related Condition: Influenza virus, Influenza

Funding: NIAID

Availability: Acknowledgement requested, The community can contribute to this resource

Resource Name: Influenza Research Database (IRD)

Resource ID: SCR_006641

Alternate IDs: DOI:10.25504/FAIRsharing.ws7cgw, nif-0000-21222, DOI:10.35094, DOI:10.17616/R3S634, r3d100011558

Alternate URLs: <https://www.fludb.org/>, <https://doi.org/10.17616/R3S634>, <https://doi.org/10.17616/r3s634>, <https://doi.org/10.35094/>, <https://dx.doi.org/10.35094/>, <https://fairsharing.org/10.25504/FAIRsharing.ws7cgw>, <https://doi.org/10.17616/R3S634>

Old URLs: <http://www.fludb.org/brc/home.do?decorator=influenza>

License URLs:

<http://www.fludb.org/brc/staticContent.do?decorator=influenza&type=FluInfo&subtype=FAQ#register>
http://www.fludb.org/brc/submission_landing.do?decorator=influenza

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260805T044138+0000

Ratings and Alerts

No rating or validation information has been found for Influenza Research Database (IRD).

No alerts have been found for Influenza Research Database (IRD).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Jones JE, et al. (2025) Host origin is a determinant of coevolution between gene segments of avian H9 influenza viruses. *Journal of virology*, 99(7), e0151824.

Gonzales JE, et al. (2025) Evolutionary rewiring of the dynamic network underpinning allosteric epistasis in NS1 of the influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America*, 122(8), e2410813122.

Xie T, et al. (2025) ARTreeFormer: A faster attention-based autoregressive model for phylogenetic inference. *PLoS computational biology*, 21(12), e1013768.

González-Domínguez I, et al. (2024) Preclinical evaluation of a universal inactivated influenza B vaccine based on the mosaic hemagglutinin-approach. *NPJ vaccines*, 9(1), 222.

Liang Z, et al. (2024) A(H2N2) and A(H3N2) influenza pandemics elicited durable cross-reactive and protective antibodies against avian N2 neuraminidases. *Nature communications*, 15(1), 5593.

Guan M, et al. (2024) Neu5Gc binding loss of subtype H7 influenza A virus facilitates adaptation to gallinaceous poultry following transmission from waterbirds but restricts spillback. *bioRxiv : the preprint server for biology*.

Wu Y, et al. (2024) Flu-CED: A comparative transcriptomics database of influenza virus-infected human and animal models. *Animal models and experimental medicine*, 7(6), 881.

Phan T, et al. (2024) Synthetic Cell Lines for Inducible Packaging of Influenza A Virus. *ACS synthetic biology*, 13(2), 546.

Kuchinski KS, et al. (2024) Targeted genomic sequencing of avian influenza viruses in wetland sediment from wild bird habitats. *Applied and environmental microbiology*, 90(2), e0084223.

Jang SG, et al. (2024) HA N193D substitution in the HPAI H5N1 virus alters receptor binding affinity and enhances virulence in mammalian hosts. *Emerging microbes & infections*, 13(1), 2302854.

Thieulent CJ, et al. (2024) Development and validation of multiplex one-step qPCR/RT-qPCR assays for simultaneous detection of SARS-CoV-2 and pathogens associated with feline respiratory disease complex. *PloS one*, 19(3), e0297796.

Rabalski L, et al. (2023) Genetic Diversity of Type A Influenza Viruses Found in Swine Herds in Northwestern Poland from 2017 to 2019: The One Health Perspective. *Viruses*, 15(9).

Naguib MM, et al. (2023) A Comparison of Host Responses to Infection with Wild-Type Avian Influenza Viruses in Chickens and Tufted Ducks. *Microbiology spectrum*, 11(4), e0258622.

Jitobaom K, et al. (2023) Human Schlafen 11 inhibits influenza A virus production. *Virus research*, 334, 199162.

McCraw DM, et al. (2023) Designed nanoparticles elicit cross-reactive antibody responses to conserved influenza virus hemagglutinin stem epitopes. *PLoS pathogens*, 19(8), e1011514.

Thieulent CJ, et al. (2023) Development and Validation of a Panel of One-Step Four-Plex qPCR/RT-qPCR Assays for Simultaneous Detection of SARS-CoV-2 and Other Pathogens Associated with Canine Infectious Respiratory Disease Complex. *Viruses*, 15(9).

Xu C, et al. (2022) Immune Escape Adaptive Mutations in Hemagglutinin Are Responsible for the Antigenic Drift of Eurasian Avian-Like H1N1 Swine Influenza Viruses. *Journal of virology*, 96(16), e0097122.

Phyu WW, et al. (2022) Evolutionary Dynamics of Whole-Genome Influenza A/H3N2 Viruses Isolated in Myanmar from 2015 to 2019. *Viruses*, 14(11).

Swaminathan S, et al. (2022) Limited Recognition of Highly Conserved Regions of SARS-CoV-2. *Microbiology spectrum*, 10(1), e0278021.

Lineburg KE, et al. (2021) CD8+ T cells specific for an immunodominant SARS-CoV-2 nucleocapsid epitope cross-react with selective seasonal coronaviruses. *Immunity*, 54(5), 1055.