

Resource Summary Report

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Global Initiative on Sharing All Influenza Data

RRID:SCR_018251

Type: Tool

Proper Citation

Global Initiative on Sharing All Influenza Data (RRID:SCR_018251)

Resource Information

URL: <https://www.gisaid.org/>

Proper Citation: Global Initiative on Sharing All Influenza Data (RRID:SCR_018251)

Description: Portal to share hCoV-19 genome sequences. Collection of genome sequences and related clinical and epidemiological data associated with coronavirus hCoV-19. Global repository of SARS-CoV-2 genomes. Initiative involves public-private-partnerships between Freunde of GISAID and governments of Federal Republic of Germany, Singapore and United States of America, with support from private and corporate philanthropy. International database of hCoV-19 genome sequences and related clinical and epidemiological data. Resource for influenza and hCoV-19 data.

Abbreviations: GISAID

Resource Type: disease-related portal, portal, topical portal, data or information resource, database

Defining Citation: [PMID:28382917](#)

Keywords: hCoV19, hCoV-19 genome sequence, data, coronavirus, SARS coronavirus, Coronavirus, genome, genome database, influenza, SARS-CoV infection, SARS-CoV-2, COVID-19

Related Condition: CoV19, COVID19, COVID-19

Availability: Restricted

Resource Name: Global Initiative on Sharing All Influenza Data

Resource ID: SCR_018251

Alternate IDs: SCR_018279, r3d100010126, SCR_018318

Alternate URLs: <https://doi.org/10.17616/R3Q59F>

License URLs: <https://www.gisaid.org/registration/terms-of-use/>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260731T043020+0000

Ratings and Alerts

No rating or validation information has been found for Global Initiative on Sharing All Influenza Data.

No alerts have been found for Global Initiative on Sharing All Influenza Data.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1964 mentions in open access literature.

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

Wu J, et al. (2026) Emerging adaptation of BJ/94 lineage H9N2 viruses to waterfowl: insights into enhanced replication and immune activation in the host cells. Poultry science, 105(1), 106182.

Shichinohe S, et al. (2026) Characterization of H5N1 high pathogenicity avian influenza virus belonging to clade 2.3.4.4b isolated from Ezo red fox in Japan in a mouse model. Microbiology spectrum, 14(1), e0109725.

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.

Vernuccio R, et al. (2025) Structural insights into tecovirimat antiviral activity and poxvirus resistance. Nature microbiology, 10(3), 734.

Española-Cueto S, et al. (2025) Plasma exchange therapy for the post COVID-19 condition: a phase II, double-blind, placebo-controlled, randomized trial. Nature communications, 16(1), 1929.

Rubin IMC, et al. (2025) Zika Virus Infection in Pregnant Traveler Returning to Denmark from Phuket, Thailand, 2024. Emerging infectious diseases, 31(2), 382.

Yang J, et al. (2025) The haemagglutinin gene of bovine-origin H5N1 influenza viruses currently retains receptor-binding and pH-fusion characteristics of avian host phenotype. Emerging microbes & infections, 14(1), 2451052.

Molina Molina E, et al. (2025) Targeting eEF1A reprograms translation and uncovers broad-spectrum antivirals against cap or m6A protein synthesis routes. *Nature communications*, 16(1), 1087.

Zayou L, et al. (2025) Dynamics of spike-specific neutralizing antibodies across five-year emerging SARS-CoV-2 variants of concern reveal conserved epitopes that protect against severe COVID-19. *Frontiers in immunology*, 16, 1503954.

Zhang C, et al. (2025) Emergence of a novel reassortant H3N3 avian influenza virus with enhanced pathogenicity and transmissibility in chickens in China. *Veterinary research*, 56(1), 56.

Pascua PNQ, et al. (2025) Antiviral Susceptibility of Influenza A(H5N1) Clade 2.3.2.1c and 2.3.4.4b Viruses from Humans, 2023-2024. *Emerging infectious diseases*, 31(4), 751.

Frei L, et al. (2025) Deep mutational learning for the selection of therapeutic antibodies resistant to the evolution of Omicron variants of SARS-CoV-2. *Nature biomedical engineering*, 9(4), 552.

van der Ende J, et al. (2025) Cocirculation of 4 Dengue Virus Serotypes, Putumayo Amazon Basin, 2023-2024. *Emerging infectious diseases*, 31(1), 202.

Lyu L, et al. (2025) Characterizing spatial epidemiology in a heterogeneous transmission landscape using the spatial transmission count statistic. *Communications medicine*, 5(1), 165.

Xu T, et al. (2025) Leveraging viral genome sequences and machine learning models for identification of potentially selective antiviral agents. *Communications chemistry*, 8(1), 189.

Li H, et al. (2025) Assessment of the public health risk of novel reassortant H3N3 avian influenza viruses that emerged in chickens. *mBio*, 16(7), e0067725.

Chan JCM, et al. (2025) Evaluation of pandemic potential of the genotype 4 (G4) swine influenza virus using ex vivo and in vitro cultures of the human respiratory tract. *The Journal of general virology*, 106(7).

Jo G, et al. (2025) Structural basis of broad protection against influenza virus by human antibodies targeting the neuraminidase active site via a recurring motif in CDR H3. *Nature communications*, 16(1), 7067.

Satheshkumar PS, et al. (2025) Emergence of Clade Ib Monkeypox Virus-Current State of Evidence. *Emerging infectious diseases*, 31(8), 1516.

Takashita E, et al. (2025) Influenza A(H1N1)pdm09 Virus with Reduced Susceptibility to Baloxavir, Japan, 2024. *Emerging infectious diseases*, 31(5), 1019.