

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, data or information resource, database, topical portal, portal

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: 20260729T044439+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 [kravitz2](#) .

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.

Xue X, et al. (2025) Epidemiological investigation and fiber gene genetic analysis of fowl adenovirus serotype 4 from 2017 to 2021 in Yunnan Province, China. Journal of veterinary science, 26(3), e27.

Coggon A, et al. (2025) Quantifying the zoonotic risk profile of European influenza A viruses in swine from 2010 to 2020 inclusive. Journal of virology, 99(7), e0030625.

Chen D, et al. (2025) Drug Resistance Predictions Based on a Directed Flag Transformer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(36), e02756.

Guinat C, et al. (2025) Poultry farm density and proximity drive highly pathogenic avian influenza spread. Communications biology, 8(1), 1306.

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).

Lan R, et al. (2025) Continuous evolution of Eurasian avian-like H1N1 swine influenza viruses with pdm/09-derived internal genes enhances pathogenicity in mice. Journal of

virology, 99(10), e0043025.

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

Fuchs J, et al. (2025) SARS-CoV-2 infection dynamics in a MHCI-mismatched lung transplant recipient. *Nature communications*, 16(1), 8292.

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

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.

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.

Mat Yassim AS, et al. (2025) A 22 month prospective assessment of neutralizing and IgG antibody levels against SARS-CoV-2 variants following homologous and heterologous BNT162b2 boosting. *Scientific reports*, 15(1), 21175.

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.

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.

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.

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

España-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.