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

Funding:

Availability: Restricted

Resource Name: Global Initiative on Sharing All Influenza Data

Resource ID: SCR_018251

Alternate IDs: SCR_018279, SCR_018318

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

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250509T060255+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 1852 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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.

Souza UJB, et al. (2025) Two Years of SARS-CoV-2 Omicron Genomic Evolution in Brazil (2022-2024): Subvariant Tracking and Assessment of Regional Sequencing Efforts. Viruses, 17(1).

Chen Z, et al. (2025) Disruption of seasonal influenza circulation and evolution during the 2009 H1N1 and COVID-19 pandemics in Southeastern Asia. Nature communications, 16(1), 475.

Deng YM, et al. (2025) Influenza A(H5N1) Virus Clade 2.3.2.1a in Traveler Returning to Australia from India, 2024. Emerging infectious diseases, 31(1), 135.

Lee B, et al. (2025) Inferring effects of mutations on SARS-CoV-2 transmission from genomic surveillance data. Nature communications, 16(1), 441.

Brcko IC, et al. (2025) Comprehensive molecular epidemiology of influenza viruses in Brazil: insights from a nationwide analysis. Virus evolution, 11(1), veae102.

Tort LFL, et al. (2025) SARS-CoV-2 Omicron XBB infections boost cross-variant neutralizing antibodies, potentially explaining the observed delay of the JN.1 wave in some Brazilian regions. IJID regions, 14, 100503.

Khemiri H, et al. (2025) SARS-CoV-2 excretion and genetic evolution in nasopharyngeal and stool samples from primary immunodeficiency and immunocompetent pediatric patients. Virology journal, 22(1), 9.

Chen ZS, et al. (2025) Influenza A Virus H7 nanobody recognizes a conserved immunodominant epitope on hemagglutinin head and confers heterosubtypic protection. Nature communications, 16(1), 432.

Bbosa N, et al. (2025) Case Reports of Human Monkeypox Virus Infections, Uganda, 2024. Emerging infectious diseases, 31(1), 144.

Cavalli M, et al. (2025) Next generation sequencing of multiple SARS-CoV-2 infections in the Omicron Era. Scientific reports, 15(1), 3372.

Schafers J, et al. (2025) Pasteurisation temperatures effectively inactivate influenza A viruses in milk. Nature communications, 16(1), 1173.

Adelusi TI, et al. (2025) Designing of an innovative conserved multiepitope subunit vaccine targeting SARS-CoV-2 glycoprotein and nucleoprotein through immunoinformatic. Scientific reports, 15(1), 2563.

Marques AD, et al. (2025) Evolution of SARS-CoV-2 in white-tailed deer in Pennsylvania 2021-2024. PLoS pathogens, 21(1), e1012883.

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.

Rosas-Murrieta NH, et al. (2024) Comparative Review of the State of the Art in Research on the Porcine Epidemic Diarrhea Virus and SARS-CoV-2, Scope of Knowledge between Coronaviruses. Viruses, 16(2).

Prakash S, et al. (2024) Cross-protection induced by highly conserved human B, CD4+, and CD8+ T-cell epitopes-based vaccine against severe infection, disease, and death caused by multiple SARS-CoV-2 variants of concern. Frontiers in immunology, 15, 1328905.

Champredon D, et al. (2024) Emergence and spread of SARS-CoV-2 variants of concern in Canada: a retrospective analysis from clinical and wastewater data. BMC infectious diseases, 24(1), 139.

Wu C, et al. (2024) Rapid identification of full-length genome and tracing variations of monkeypox virus in clinical specimens based on mNGS and amplicon sequencing. Virologica Sinica, 39(1), 134.