

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

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: 20260829T182603+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 2596 mentions in open access literature.

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

Jena AB, et al. (2026) Halved but Potent: Exploring the Inhibitory Property of Curcumin Derivatives Against Evolving SARS-CoV-2 Strains. The protein journal, 45(2), 384.

Komoyo GF, et al. (2026) Influenza Surveillance in the Central African Republic From 2015 to 2018 to Inform Vaccination and Treatment Strategies. Influenza and other respiratory viruses, 20(1), e70221.

Dor G, et al. (2026) Identification and genomic characterization of BA.3.2: a highly divergent BA.3-related SARS-CoV-2 lineage from southern Africa. Virus evolution, 12(1), veag016.

Ogrzewalska M, et al. (2026) Genomic analysis of high pathogenicity avian influenza viruses from Antarctica reveals multiple introductions from South America. Nature communications, 17(1).

Rizwan MA, et al. (2026) Genomic Evolution of Influenza A(H1N1)pdm09 and A/H3N2 Viruses Among Children in Wuhan, China, Spanning the COVID-19 Pandemic (2020-2023). Viruses, 18(2).

Flagg M, et al. (2026) Replication Efficiency of Contemporary Highly Pathogenic Avian Influenza A(H5N1) Virus Isolates in Human Nasal Epithelium Model. Emerging infectious diseases, 32(5), 794.

Silva-Caso W, et al. (2026) Genetic diversity and molecular characterization of HRSV-A on the coast of Peru, 2009-2020. Frontiers in microbiology, 17, 1704867.

G??zel I, et al. (2026) Genomic and Phylogenetic Dissection of SARS-CoV-2 Transmission Networks in Healthcare Workers. *International journal of microbiology*, 2026, 6610060.

Crespo-Bellido A, et al. (2026) Emergence of D1.1 reassortant H5N1 avian influenza viruses in North America. *bioRxiv : the preprint server for biology*.

Ndiaye NA, et al. (2026) Genomic Surveillance of SARS-CoV-2 in Senegal (2020-2024): Variant Turnover, Omicron Introductions, and Interregional Spread. *Influenza and other respiratory viruses*, 20(6), e70273.

Guo Y, et al. (2026) Broad cross-T cell immunity between emerging SARS-CoV-2 serotypes waved by spike-signature mutations. *Emerging microbes & infections*, 15(1), 2610856.

Falchieri M, et al. (2026) Detection of Two High Pathogenicity Avian Influenza Virus (HPAIV) Subtypes, H5N1 and H5N5, in a Mass Mortality Event in Wild Seabirds and Co-Location With Dead Seals. *Transboundary and emerging diseases*, 2026, 4680980.

Carranza C, et al. (2026) Diversity and clinical correlations of SARS-CoV-2 variant during the introduction of the Delta variant in Guatemala. *Access microbiology*, 8(3).

Ali MZ, et al. (2026) Two decades (2005 to 2025) of avian influenza research trends, knowledge gaps and distribution of emerging H5N1 2.3.4.4b clade in South Asia. *One health outlook*, 8(1).

Zhao Z, et al. (2026) Evolutionary and Modification Features of Two Monkeypox Virus Strains: Insights from Integrated Genomic and Epigenomic Analyses. *Viruses*, 18(2).

Li J, et al. (2026) Syrian hamster is a valuable animal model for evaluating the transmissibility of emerging influenza viruses. *Emerging microbes & infections*, 15(1), 2629629.

Jin L, et al. (2026) A predictive model for rapid assessment of protective efficacy against emerging SARS-CoV-2 variants. *Infectious Disease Modelling*, 11(3), 1022.

Usama M, et al. (2026) Computational prediction of binding affinity and structural impact of three Pakistani SARS-CoV-2 spike RBD variants on human ACE2 interaction. *PLoS one*, 21(4), e0346242.

Bay P, et al. (2026) Prospective multicentre study of upper respiratory mucosal transcriptomics reveals two major endotypes of critically ill COVID-19 patients. *Communications medicine*, 6(1).

Yang Z, et al. (2026) Deciphering 6-mer Spectra Distribution Rules in Coronavirus Genomes: Application to Comparative Genomic Analysis. *International journal of molecular sciences*, 27(8).