Resource Summary Report

Generated by NIF on May 20, 2025

outbreak.info

RRID:SCR_018282
Type: Tool

Proper Citation

outbreak.info (RRID:SCR_018282)

Resource Information

URL: https://outbreak.info/

Proper Citation: outbreak.info (RRID:SCR_018282)

Description: Resource to aggregate all outbreak information into single location during outbreaks of emerging diseases, such as COVID-19.

Resource Type: data or information resource, topical portal, portal

Keywords: COVID-19 data collection, single location, outbreak information, emerging disease

Related Condition: COVID-19

Funding: NIAID

Availability: Free, Freely available

Resource Name: outbreak.info

Resource ID: SCR_018282

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250519T204025+0000

Ratings and Alerts

No rating or validation information has been found for outbreak.info.

No alerts have been found for outbreak.info.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 102 mentions in open access literature.

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

Suntronwong N, et al. (2025) Neutralization of omicron subvariants and antigenic cartography following multiple COVID 19 vaccinations and repeated omicron non JN.1 or JN.1 infections. Scientific reports, 15(1), 1454.

Yuan M, et al. (2025) Structural Immunology of SARS-CoV-2. Immunological reviews, 329(1), e13431.

Merrett JE, et al. (2024) Highly sensitive wastewater surveillance of SARS-CoV-2 variants by targeted next-generation amplicon sequencing provides early warning of incursion in Victoria, Australia. Applied and environmental microbiology, 90(8), e0149723.

Li K, et al. (2024) Genome-wide association study between SARS-CoV-2 single nucleotide polymorphisms and virus copies during infections. PLoS computational biology, 20(9), e1012469.

Walmsley S, et al. (2024) Declining Levels of Neutralizing Antibodies to SARS-CoV-2 Omicron Variants Are Enhanced by Hybrid Immunity and Original/Omicron Bivalent Vaccination. Vaccines, 12(6).

de Campos-Mata L, et al. (2024) A monoclonal antibody targeting a large surface of the receptor binding motif shows pan-neutralizing SARS-CoV-2 activity. Nature communications, 15(1), 1051.

Aßmann E, et al. (2024) Impact of reference design on estimating SARS-CoV-2 lineage abundances from wastewater sequencing data. GigaScience, 13.

Sohail MS, et al. (2024) Cross-Reactivity Assessment of Vaccine-Derived SARS-CoV-2 T Cell Responses against BA.2.86 and JN.1. Viruses, 16(3).

Luo L, et al. (2024) An evolutionary theory on virus mutation in COVID-19. Virus research, 344, 199358.

Deng J, et al. (2024) Natural evidence of coronaviral 2'-O-methyltransferase activity affecting viral pathogenesis via improved substrate RNA binding. Signal transduction and targeted therapy, 9(1), 140.

Van Dusen J, et al. (2024) Identification of SARS-CoV-2 variants in indoor dust. PloS one, 19(2), e0297172.

Aguilar-Martinez SL, et al. (2024) Genomic and Phylogenetic Characterisation of SARS-CoV-2 Genomes Isolated in Patients from Lambayeque Region, Peru. Tropical medicine and infectious disease, 9(2).

Sharma S, et al. (2024) In-silico evaluation of the T-cell based immune response against SARS-CoV-2 omicron variants. Scientific reports, 14(1), 25413.

Ma E, et al. (2024) A predictive language model for SARS-CoV-2 evolution. Signal transduction and targeted therapy, 9(1), 353.

Choga WT, et al. (2024) Rapid dynamic changes of FL.2 variant: A case report of COVID-19 breakthrough infection. International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases, 138, 91.

Moreno Rojas AF, et al. (2024) SARS-CoV-2 variants are associated with different clinical courses in children with MIS-C. World journal of pediatrics : WJP, 20(2), 143.

Ip JD, et al. (2024) The significance of recurrent de novo amino acid substitutions that emerged during chronic SARS-CoV-2 infection: an observational study. EBioMedicine, 107, 105273.

Yang Q, et al. (2024) Conserved role of spike S2 domain N-glycosylation across beta-coronavirus family. bioRxiv : the preprint server for biology.

Park J, et al. (2024) Accurate predictions of SARS-CoV-2 infectivity from comprehensive analysis. eLife, 13.

Trigo-Tasende N, et al. (2023) Wastewater early warning system for SARS-CoV-2 outbreaks and variants in a Coruña, Spain. Environmental science and pollution research international, 30(32), 79315.