

# Resource Summary Report

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## [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:** topical portal, data or information resource, 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:** 20260804T043714+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

## Usage and Citation Metrics

We found 113 mentions in open access literature.

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

Berkell M, et al. (2025) Quasi-species prevalence and clinical impact of evolving SARS-CoV-2 lineages in European COVID-19 cohorts, January 2020 to February 2022. Euro surveillance : bulletin Européen sur les maladies transmissibles = European communicable disease bulletin, 30(10).

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.

de Ávila AI, et al. (2025) SARS-CoV-2 biological clones are genetically heterogeneous and include clade-discordant residues. Journal of virology, 99(5), e0225024.

Wu J, et al. (2025) SGV-caller: SARS-CoV-2 genome variation caller. Heliyon, 11(4), e42613.

Liu X, et al. (2025) Generative prediction of real-world prevalent SARS-CoV-2 mutation with in silico virus evolution. Briefings in bioinformatics, 26(3).

Carrier A, et al. (2025) Gut microbiota: a new factor modulating the immunizing potential of viral and cancer vaccines. Research square.

Daroch N, et al. (2025) Respiratory virus infection dynamics and genomic surveillance to detect seasonal influenza subtypes in wastewater: A longitudinal study in Bengaluru, India. PLOS global public health, 5(9), e0004640.

Giombini E, et al. (2025) JN.1 variants circulating in Italy from October 2023 to April 2024: genetic diversity and immune recognition. BMC infectious diseases, 25(1), 291.

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

Spagnolo F, et al. (2025) Dataset of SARS-CoV-2 spike protein receptor binding domain variants in complex with antigen-binding fragments targeting COVID-19 vaccine-referenced variants. Data in brief, 58, 111291.

Ma Y, et al. (2025) A cocktail of SARS-CoV-2 spike stem helix domain and receptor binding domain human monoclonal antibodies prevent the emerge of viral escape mutants. bioRxiv : the preprint server for biology.

Jin Q, et al. (2025) Increased pathogenicity and transmission of SARS-CoV-2 Omicron XBB.1.9 subvariants, including HK.3 and EG.5.1, relative to BA.2. Journal of virology, 99(12), e0134225.

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.

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).

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.

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.

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

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).

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).