

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## [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, portal, topical 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:** 20260821T194130+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 155 mentions in open access literature.

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

Zhang Y, et al. (2026) A Viral Mutation Profiling and Discovery Strategy for Sensitive Multiplex Detection of Viruses and Variants in Saliva by Proteomics. *bioRxiv : the preprint server for biology*.

Sutta A, et al. (2026) Collectin-11, a complement pattern recognition molecule, mediates pulmonary SARS-CoV-2 neutralization and protection. *PLoS pathogens*, 22(5), e1014216.

Ma Y, et al. (2026) A cocktail of SARS-CoV-2 S stem helix domain and receptor binding domain human monoclonal antibodies prevents the emergence of viral escape mutants. *Microbiology spectrum*, 14(6), e0000626.

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.

Ma Y, et al. (2025) Analysis of the Relationship Between the Charge Increment of the SARS-CoV-2 Spike Protein and Evolution. *Viruses*, 17(11).

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 Europeen sur les maladies transmissibles = European communicable disease bulletin*, 30(10).

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*.

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

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.

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.

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.

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.

Zhang X, et al. (2024) CovEpiAb: a comprehensive database and analysis resource for immune epitopes and antibodies of human coronaviruses. *Briefings in bioinformatics*, 25(3).

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).

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