

# Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

## SARS-CoV-2-Sequences

RRID:SCR\_018319

Type: Tool

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### Proper Citation

SARS-CoV-2-Sequences (RRID:SCR\_018319)

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### Resource Information

**URL:** <https://www.ncbi.nlm.nih.gov/genbank/sars-cov-2-seqs/>

**Proper Citation:** SARS-CoV-2-Sequences (RRID:SCR\_018319)

**Description:** Collection of SARS-CoV-2 sequences currently available in GenBank genetic sequence database and Sequence Read Archive. Updated as additional sequences are released.

**Synonyms:** Severe Acute Respiratory Syndrome CoronaVirus 2 Sequences

**Resource Type:** data or information resource, data repository, data set, service resource, storage service resource

**Keywords:** SARS-CoV-2, SARS coronavirus, SARS-CoV infection, Coronavirus, data, SARS-CoV-2 sequence collection, nucleotide, genome, Betacoronavirus, protein

**Related Condition:** COVID-19

**Funding:** The Federal Government

**Availability:** Free, Available for download, Freely available

**Resource Name:** SARS-CoV-2-Sequences

**Resource ID:** SCR\_018319

**License URLs:** <https://www.ncbi.nlm.nih.gov/home/about/policies/>

**Record Creation Time:** 20220129T080339+0000

**Record Last Update:** 20260821T194127+0000

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### Ratings and Alerts

No rating or validation information has been found for SARS-CoV-2-Sequences.

No alerts have been found for SARS-CoV-2-Sequences.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Ferreira da Silva L, et al. (2024) A novel viral RNA detection method based on the combined use of trans-acting ribozymes and HCR-FRET analyses. PloS one, 19(9), e0310171.

Figueiredo-Nunes I, et al. (2023) Exploring new antiviral targets for influenza and COVID-19: Mapping promising hot spots in viral RNA polymerases. Virology, 578, 45.

Karthick K, et al. (2023) Pyridine Derivatives as Potential Inhibitors for Coronavirus SARS-CoV-2: A Molecular Docking Study. Bioinformatics and biology insights, 17, 11779322221146651.

Elssaig EH, et al. (2022) Omicron SARS-CoV-2 Variants in an In Silico Genomic Comparison Study with the Original Wuhan Strain and WHO-Recognized Variants of Concern. Polish journal of microbiology, 71(4), 577.

Martínez-González B, et al. (2022) Vaccine breakthrough infections with SARS-CoV-2 Alpha mirror mutations in Delta Plus, Iota, and Omicron. The Journal of clinical investigation, 132(9).

Ahmed-Abakur EH, et al. (2022) In-silico genomic landscape characterization and evolution of SARS-CoV-2 variants isolated in India shows significant drift with high frequency of mutations. Saudi journal of biological sciences, 29(5), 3494.

Martínez-González B, et al. (2022) SARS-CoV-2 Point Mutation and Deletion Spectra and Their Association with Different Disease Outcomes. Microbiology spectrum, 10(2), e0022122.

Gupta V, et al. (2021) Comparative Genomics and Integrated Network Approach Unveiled Undirected Phylogeny Patterns, Co-mutational Hot Spots, Functional Cross Talk, and Regulatory Interactions in SARS-CoV-2. mSystems, 6(1).

Nallusamy S, et al. (2021) Exploring Phytochemicals of Traditional Medicinal Plants Exhibiting Inhibitory Activity Against Main Protease, Spike Glycoprotein, RNA-dependent RNA Polymerase and Non-Structural Proteins of SARS-CoV-2 Through Virtual Screening. Frontiers in pharmacology, 12, 667704.

Mazzocco G, et al. (2021) AI Aided Design of Epitope-Based Vaccine for the Induction of Cellular Immune Responses Against SARS-CoV-2. *Frontiers in genetics*, 12, 602196.

Pan B, et al. (2021) Identification of Epidemiological Traits by Analysis of SARS-CoV-2 Sequences. *Viruses*, 13(5).

Hossain MG, et al. (2021) SARS-CoV-2 host diversity: An update of natural infections and experimental evidence. *Journal of microbiology, immunology, and infection = Wei mian yu gan ran za zhi*, 54(2), 175.

Lv J, et al. (2021) Detection of Phenotype-Related Mutations of COVID-19 via the Whole Genomic Data. *IEEE/ACM transactions on computational biology and bioinformatics*, 18(4), 1242.

Kumari P, et al. (2021) A computational analysis of molecular evolution for virulence genes of zoonotic novel coronavirus (COVID-19). *Computational biology and chemistry*, 93, 107532.

Banaganapalli B, et al. (2021) Multilevel systems biology analysis of lung transcriptomics data identifies key miRNAs and potential miRNA target genes for SARS-CoV-2 infection. *Computers in biology and medicine*, 135, 104570.

Tarig M S Alnour , et al. (2021) Unique SARS-CoV-2 Variant Exhibiting Plenteous Missense Mutations in Structural and Nonstructural Genes. *Cytology and genetics*, 55(6), 606.

Raimondi MT, et al. (2020) Bioengineering tools to speed up the discovery and preclinical testing of vaccines for SARS-CoV-2 and therapeutic agents for COVID-19. *Theranostics*, 10(16), 7034.

Rouchka EC, et al. (2020) Variant analysis of 1,040 SARS-CoV-2 genomes. *PloS one*, 15(11), e0241535.

Ahmed-Abakur EH, et al. (2020) Genetic variations among SARS-CoV-2 strains isolated in China. *Gene reports*, 21, 100925.

Barreto HG, et al. (2020) Diagnosing the novel SARS-CoV-2 by quantitative RT-PCR: variations and opportunities. *Journal of molecular medicine (Berlin, Germany)*, 98(12), 1727.