

Resource Summary Report

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SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation

RRID:SCR_018759

Type: Tool

Proper Citation

SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation (RRID:SCR_018759)

Resource Information

URL: <https://marks.hms.harvard.edu/sars-cov-2/>

Proper Citation: SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation (RRID:SCR_018759)

Description: Portal for quantitative models using virus sequence variation to predict mutation effects for SARS-CoV-2 proteins, alignments to homologs in other viruses, 3D structures, evolutionarily coupled residues and structure predictions.

Resource Type: data or information resource, disease-related portal, portal, topical portal

Keywords: SARS-CoV-2, in silico mutation scan, 3D contact prediction, COVID-19, virus sequence variation, mutation prediction, SARS-CoV-2 protein, alignment, 3D structure, structure prediction

Related Condition: COVID-19

Availability: Free, Available for download, Freely available

Resource Name: SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation

Resource ID: SCR_018759

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260821T194151+0000

Ratings and Alerts

No rating or validation information has been found for SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation.

No alerts have been found for SARS-CoV-2 mutation effects and 3D structure prediction from sequence covariation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 99 mentions in open access literature.

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

Nazario-Toole AE, et al. (2022) Whole-genome Sequencing of SARS-CoV-2: Using Phylogeny and Structural Modeling to Contextualize Local Viral Evolution. *Military medicine*, 187(1-2), e130.

Martischang R, et al. (2022) Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) seroconversion and occupational exposure of employees at a Swiss university hospital: A large longitudinal cohort study. *Infection control and hospital epidemiology*, 43(3), 326.

Dai W, et al. (2022) Design, Synthesis, and Biological Evaluation of Peptidomimetic Aldehydes as Broad-Spectrum Inhibitors against Enterovirus and SARS-CoV-2. *Journal of medicinal chemistry*, 65(4), 2794.

Alagu Lakshmi S, et al. (2021) Ethnomedicines of Indian origin for combating COVID-19 infection by hampering the viral replication: using structure-based drug discovery approach. *Journal of biomolecular structure & dynamics*, 39(13), 4594.

Le Bert N, et al. (2021) Highly functional virus-specific cellular immune response in asymptomatic SARS-CoV-2 infection. *The Journal of experimental medicine*, 218(5).

Cotugno N, et al. (2021) Virological and immunological features of SARS-CoV-2-infected children who develop neutralizing antibodies. *Cell reports*, 34(11), 108852.

Cione E, et al. (2021) Neuron-specific enolase serum levels in COVID-19 are related to the severity of lung injury. *PloS one*, 16(5), e0251819.

Vassilopoulou E, et al. (2021) Breastfeeding and COVID-19: From Nutrition to Immunity. *Frontiers in immunology*, 12, 661806.

Schubert G, et al. (2021) The African Network for Improved Diagnostics, Epidemiology and Management of common infectious Agents. *BMC infectious diseases*, 21(1), 539.

Cheemarla NR, et al. (2021) Dynamic innate immune response determines susceptibility to SARS-CoV-2 infection and early replication kinetics. *The Journal of experimental medicine*, 218(8).

Yapici-Eser H, et al. (2021) Neuropsychiatric Symptoms of COVID-19 Explained by SARS-CoV-2 Proteins' Mimicry of Human Protein Interactions. *Frontiers in human neuroscience*, 15, 656313.

Neches RY, et al. (2021) Atypical Divergence of SARS-CoV-2 Orf8 from Orf7a within the Coronavirus Lineage Suggests Potential Stealthy Viral Strategies in Immune Evasion. *mBio*, 12(1).

Malik YS, et al. (2021) Evolutionary and codon usage preference insights into spike glycoprotein of SARS-CoV-2. *Briefings in bioinformatics*, 22(2), 1006.

Sommer AP, et al. (2021) Tutankhamun's Antimalarial Drug for Covid-19. *Drug research*, 71(1), 4.

Tanaka Y, et al. (2021) Dynamic changes in gene-to-gene regulatory networks in response to SARS-CoV-2 infection. *Scientific reports*, 11(1), 11241.

Chen Y, et al. (2021) Proteomic Analysis Identifies Prolonged Disturbances in Pathways Related to Cholesterol Metabolism and Myocardium Function in the COVID-19 Recovery Stage. *Journal of proteome research*, 20(7), 3463.

Rian K, et al. (2021) Mechanistic modeling of the SARS-CoV-2 disease map. *BioData mining*, 14(1), 5.

Singh DK, et al. (2021) Responses to acute infection with SARS-CoV-2 in the lungs of rhesus macaques, baboons and marmosets. *Nature microbiology*, 6(1), 73.

Ioannou GN, et al. (2021) Development of COVIDVax Model to Estimate the Risk of SARS-CoV-2-Related Death Among 7.6 Million US Veterans for Use in Vaccination Prioritization. *JAMA network open*, 4(4), e214347.

Song J, et al. (2021) The comprehensive study on the therapeutic effects of baicalein for the treatment of COVID-19 in vivo and in vitro. *Biochemical pharmacology*, 183, 114302.