Resource Summary Report

Generated by RRID on Apr 11, 2025

VirusMINT

RRID:SCR_005987
Type: Tool

Proper Citation

VirusMINT (RRID:SCR_005987)

Resource Information

URL: http://mint.bio.uniroma2.it/virusmint/

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Description: A virus protein interactions database that collects and annotates all the interactions between human and viral proteins and integrates this information in the human protein interaction network. It uses the PSI-MI standard and is fully integrated with the MINT database. You can search for any viral or human protein by entering either common names or database identifiers or display a complete viral interactome.

Abbreviations: VirusMINT

Resource Type: data or information resource, database

Defining Citation: PMID:18974184

Keywords: protein interaction, virus, protein, bio.tools

Related Condition: Papilloma virus, Human immunodeficiency virus, Epstein-Barr virus, Hepatitis B virus, Hepatitis C virus, Herpes virus, Simian virus 40

Funding:

Resource Name: VirusMINT

Resource ID: SCR_005987

Alternate IDs: nif-0000-03636, OMICS_01909, biotools:virusmint

Alternate URLs: https://bio.tools/virusmint

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250410T065357+0000

Ratings and Alerts

No rating or validation information has been found for VirusMINT.

No alerts have been found for VirusMINT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Rezatofighi SE, et al. (2024) Exogenous interactome analysis of bovine viral diarrhea virus-host using network based-approach and identification of hub genes and important pathways involved in virus pathogenesis. Biochemistry and biophysics reports, 40, 101825.

Ismail MMF, et al. (2023) Potential role of PIM1 inhibition in the treatment of SARS-CoV-2 infection. Journal, genetic engineering & biotechnology, 21(1), 65.

Singh N, et al. (2021) Network analysis of host-pathogen protein interactions in microbe induced cardiovascular diseases. In silico biology, 14(3-4), 115.

Song G, et al. (2021) An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. Genomics, proteomics & bioinformatics, 19(1), 108.

Natesh J, et al. (2021) Promising phytochemicals of traditional Himalayan medicinal plants against putative replication and transmission targets of SARS-CoV-2 by computational investigation. Computers in biology and medicine, 133, 104383.

Khorsand B, et al. (2020) Comprehensive host-pathogen protein-protein interaction network analysis. BMC bioinformatics, 21(1), 400.

Parida PK, et al. (2020) The natural way forward: Molecular dynamics simulation analysis of phytochemicals from Indian medicinal plants as potential inhibitors of SARS-CoV-2 targets. Phytotherapy research : PTR, 34(12), 3420.

Farooq QUA, et al. (2020) A systems biology-driven approach to construct a comprehensive protein interaction network of influenza A virus with its host. BMC infectious diseases, 20(1), 480.

Corona E, et al. (2018) Systematic detection of positive selection in the human-pathogen interactome and lasting effects on infectious disease susceptibility. PloS one, 13(5), e0196676.

Mei S, et al. (2016) Computational discovery of Epstein-Barr virus targeted human genes and signalling pathways. Scientific reports, 6, 30612.

Han Y, et al. (2016) Hepatitis C Virus Protein Interaction Network Analysis Based on Hepatocellular Carcinoma. PloS one, 11(4), e0153882.

van der Lee R, et al. (2015) Integrative Genomics-Based Discovery of Novel Regulators of the Innate Antiviral Response. PLoS computational biology, 11(10), e1004553.

Mei S, et al. (2015) A novel one-class SVM based negative data sampling method for reconstructing proteome-wide HTLV-human protein interaction networks. Scientific reports, 5, 8034.

Barman RK, et al. (2014) Prediction of interactions between viral and host proteins using supervised machine learning methods. PloS one, 9(11), e112034.

Bartha I, et al. (2014) GuavaH: a compendium of host genomic data in HIV biology and disease. Retrovirology, 11, 6.