Resource Summary Report

Generated by dkNET on Apr 15, 2025

VirHostNet: Virus-Host Network

RRID:SCR_005978
Type: Tool

Proper Citation

VirHostNet: Virus-Host Network (RRID:SCR_005978)

Resource Information

URL: http://pbildb1.univ-lyon1.fr/virhostnet/

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Description: Public knowledge base specialized in the management and analysis of integrated virus-virus, virus-host and host-host interaction networks coupled to their functional annotations. It contains high quality and up-to-date information gathered and curated from public databases (VirusMint, Intact, HIV-1 database). It allows users to search by host gene, host/viral protein, gene ontology function, KEGG pathway, Interpro domain, and publication information. It also allows users to browse viral taxonomy.

Abbreviations: VirHostNet

Synonyms: Virus-Host Network

Resource Type: database, data or information resource

Defining Citation: PMID:18984613

Keywords: interaction, protein, virus, protein-protein interaction, protein interaction, infectious disease, antiviral drug design, proteome, interactome, molecular function, cellular pathway, protein domain, virus-virus, virus-host, bio.tools

Funding:

Availability: Acknowledgement requested, Public

Resource Name: VirHostNet: Virus-Host Network

Resource ID: SCR_005978

Alternate IDs: nif-0000-03634, OMICS_01910, biotools:virhostnet

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

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250412T055016+0000

Ratings and Alerts

No rating or validation information has been found for VirHostNet: Virus-Host Network.

No alerts have been found for VirHostNet: Virus-Host Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Ignatieva EV, et al. (2017) A database of human genes and a gene network involved in response to tick-borne encephalitis virus infection. BMC evolutionary biology, 17(Suppl 2), 259.

Billing AM, et al. (2014) Proteome profiling of virus-host interactions of wild type and attenuated measles virus strains. Journal of proteomics, 108, 325.

Simonis N, et al. (2012) Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. Retrovirology, 9, 26.

Le Breton M, et al. (2011) Flavivirus NS3 and NS5 proteins interaction network: a high-throughput yeast two-hybrid screen. BMC microbiology, 11, 234.

Navratil V, et al. (2011) When the human viral infectome and diseasome networks collide: towards a systems biology platform for the aetiology of human diseases. BMC systems biology, 5, 13.

Fumagalli M, et al. (2010) Genome-wide identification of susceptibility alleles for viral infections through a population genetics approach. PLoS genetics, 6(2), e1000849.