Resource Summary Report

Generated by NIF on Apr 29, 2025

VBRC

RRID:SCR_005971
Type: Tool

Proper Citation

VBRC (RRID:SCR_005971)

Resource Information

URL: http://vbrc.org/index.asp

Proper Citation: VBRC (RRID:SCR_005971)

Description: One of eight Bioinformatics Resource Centers nationwide providing comprehensive web-based genomics resources including a relational database and web application supporting data storage, annotation, analysis, and information exchange to support scientific research directed at viruses belonging to the Arenaviridae, Bunyaviridae, Filoviridae, Flaviviridae, Paramyxoviridae, Poxviridae, and Togaviridae families. These centers serve the scientific community and conduct basic and applied research on microorganisms selected from the NIH/NIAID Category A, B, and C priority pathogens that are regarded as possible bioterrorist threats or as emerging or re-emerging infectious diseases. The VBRC provides a variety of analytical and visualization tools to aid in the understanding of the available data, including tools for genome annotation, comparative analysis, whole genome alignments, and phylogenetic analysis. Each data release contains the complete genomic sequences for all viral pathogens and related strains that are available for species in the above-named families. In addition to sequence data, the VBRC provides a curation for each virus species, resulting in a searchable, comprehensive mini-review of gene function relating genotype to biological phenotype, with special emphasis on pathogenesis.

Abbreviations: VBRC

Synonyms: Viral Bioinformatics Resource Center

Resource Type: database, service resource, data or information resource, storage service resource, data repository, production service resource, data analysis service, analysis service resource

Keywords: virus, arenaviridae, bunyaviridae, filoviridae, flaviviridae, paramyxoviridae, poxviridae, togaviridae, blast, ortholog, variation, sequence analysis, genome, gene, epidemiology, bioinformatics resource center, phenotype, pathogenesis, pathogen, annotation, genomics

Funding: NIAID contract HHSN266200400036C

Resource Name: VBRC

Resource ID: SCR_005971

Alternate IDs: nif-0000-03632

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250429T055023+0000

Ratings and Alerts

No rating or validation information has been found for VBRC.

No alerts have been found for VBRC.

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 NIF.

Han SY, et al. (2024) Elucidating the callus-to-shoot-forming mechanism in Capsicum annuum 'Dempsey' through comparative transcriptome analyses. BMC plant biology, 24(1), 367.

Ludi AB, et al. (2024) Epidemiological investigation of foot-and-mouth disease outbreaks in a Vietnamese bear rescue centre. Frontiers in veterinary science, 11, 1389029.

Ceberio N, et al. (2024) Virtual BUILD Research Collaboratory: A biomedical data science training using innovative pedagogy to address structures of racism and inequitable stress for undergraduates of color. PloS one, 19(2), e0294307.

Chen FL, et al. (2023) Evaluating instruments for assessing healthspan: a multi-center cross-sectional study on health-related quality of life (HRQL) and frailty in the companion dog.

GeroScience, 45(4), 2089.

Hunter-Ishikawa M, et al. (2023) Modification of Domestic Animal Lameness Scales for Use in Asiatic Black Bears (Ursus thibetanus). Animals : an open access journal from MDPI, 13(21).

Shubitz LF, et al. (2021) ?cps1 vaccine protects dogs against experimentally induced coccidioidomycosis. Vaccine, 39(47), 6894.

Satyam R, et al. (2021) COVIDium: a COVID-19 resource compendium. Database : the journal of biological databases and curation, 2021.

Park SI, et al. (2021) Agrobacterium-Mediated Capsicum annuum Gene Editing in Two Cultivars, Hot Pepper CM334 and Bell Pepper Dempsey. International journal of molecular sciences, 22(8).

Baruch J, et al. (2021) Assessment of bovine respiratory disease progression in calves challenged with bovine herpesvirus 1 and Mannheimia haemolytica using point-of-care and laboratory-based blood leukocyte differential assays. Translational animal science, 5(4), txab200.

Dewsbury DMA, et al. (2019) A complete cross-over design evaluating canine acceptance of Carprieve® and Rimadyl® carprofen chewable tablets in healthy dogs. BMC veterinary research, 15(1), 394.

Toenshoff ER, et al. (2018) The End of a 60-year Riddle: Identification and Genomic Characterization of an Iridovirus, the Causative Agent of White Fat Cell Disease in Zooplankton. G3 (Bethesda, Md.), 8(4), 1259.

Tu SL, et al. (2018) Base-By-Base Version 3: New Comparative Tools for Large Virus Genomes. Viruses, 10(11).

Amgarten D, et al. (2017) Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. BMC genomics, 18(1), 346.

Nettles JH, et al. (2014) Asymmetric binding to NS5A by daclatasvir (BMS-790052) and analogs suggests two novel modes of HCV inhibition. Journal of medicinal chemistry, 57(23), 10031.

Odom MR, et al. (2009) Poxvirus protein evolution: family wide assessment of possible horizontal gene transfer events. Virus research, 144(1-2), 233.