Resource Summary Report

Generated by NIF on Apr 17, 2025

vipR

RRID:SCR_010685
Type: Tool

Proper Citation

vipR (RRID:SCR_010685)

Resource Information

URL: http://htsvipr.sourceforge.net/

Proper Citation: vipR (RRID:SCR_010685)

Description: A software program to screen for sequence variants (SNPs, deletions) in sequence data generated by high-throughput-sequencing platforms.

Abbreviations: vipR

Resource Type: software resource

Funding:

Resource Name: vipR

Resource ID: SCR_010685

Alternate IDs: OMICS_00081

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250410T070014+0000

Ratings and Alerts

No rating or validation information has been found for vipR.

No alerts have been found for vipR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Nakatani Y, et al. (2024) Long axial-range double-helix point spread functions for 3D volumetric super-resolution imaging. bioRxiv : the preprint server for biology.

Xiao D, et al. (2024) Large-FOV 3D localization microscopy by spatially variant point spread function generation. Science advances, 10(10), eadj3656.

Wang H, et al. (2023) In silico epitope prediction and evolutionary analysis reveals capsid mutation patterns for enterovirus B. PloS one, 18(8), e0290584.

Zhao Q, et al. (2023) Margin-Based Modal Adaptive Learning for Visible-Infrared Person Re-Identification. Sensors (Basel, Switzerland), 23(3).

Tarke A, et al. (2023) Targets and cross-reactivity of human T cell recognition of common cold coronaviruses. Cell reports. Medicine, 4(6), 101088.

Gupta S, et al. (2022) Genome-wide mutational analysis of Chikungunya strains from 2016 to 2017 outbreak of central India: An attempt to elucidate the immunological basis for outbreak. Heliyon, 8(11), e11400.

Grifoni A, et al. (2022) Defining antigen targets to dissect vaccinia virus and monkeypox virus-specific T cell responses in humans. Cell host & microbe, 30(12), 1662.

Mhango C, et al. (2022) Rotavirus Genotypes in Hospitalized Children With Acute Gastroenteritis Before and After Rotavirus Vaccine Introduction in Blantyre, Malawi, 1997-2019. The Journal of infectious diseases, 225(12), 2127.

Chen H, et al. (2022) Expression of the Bacillus thuringiensis vip3A Insecticidal Toxin Gene Is Activated at the Onset of Stationary Phase by VipR, an Autoregulated Transcription Factor. Microbiology spectrum, 10(4), e0120522.

Simmonds P, et al. (2021) Extensive C->U transition biases in the genomes of a wide range of mammalian RNA viruses; potential associations with transcriptional mutations, damage- or host-mediated editing of viral RNA. PLoS pathogens, 17(6), e1009596.

Shastri J, et al. (2021) Clinical, Serological, Whole Genome Sequence Analyses to Confirm SARS-CoV-2 Reinfection in Patients From Mumbai, India. Frontiers in medicine, 8, 631769.

Öhrman C, et al. (2021) Reorganized Genomic Taxonomy of Francisellaceae Enables

Design of Robust Environmental PCR Assays for Detection of Francisella tularensis. Microorganisms, 9(1).

Abou-Hamdan M, et al. (2021) Variant analysis of the first Lebanese SARS-CoV-2 isolates. Genomics, 113(1 Pt 2), 892.

Nicolas Calderon K, et al. (2021) Evaluation of Conserved RNA Secondary Structures within and between Geographic Lineages of Zika Virus. Life (Basel, Switzerland), 11(4).

Fadaka AO, et al. (2021) Immunoinformatics design of a novel epitope-based vaccine candidate against dengue virus. Scientific reports, 11(1), 19707.

Kar T, et al. (2020) A candidate multi-epitope vaccine against SARS-CoV-2. Scientific reports, 10(1), 10895.

Lhomme S, et al. (2020) Insertions and Duplications in the Polyproline Region of the Hepatitis E Virus. Frontiers in microbiology, 11, 1.

Cleemput S, et al. (2020) Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. bioRxiv : the preprint server for biology.

Anand P, et al. (2020) SARS-CoV-2 strategically mimics proteolytic activation of human ENaC. eLife, 9.

Kamaraj US, et al. (2019) Application of a targeted-enrichment methodology for full-genome sequencing of Dengue 1-4, Chikungunya and Zika viruses directly from patient samples. PLoS neglected tropical diseases, 13(4), e0007184.