

Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

[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

Resource Name: vipR

Resource ID: SCR_010685

Alternate IDs: OMICS_00081

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190701+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 58 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hauner A, et al. (2025) Technical validation of a multiplex real-time PCR for combined detection of Rift Valley fever, chikungunya, Zika and dengue viruses. *Journal of virological methods*, 337, 115174.

Pereira Neto TA, et al. (2025) Highly conserved Betacoronavirus sequences are broadly recognized by human T cells. *Cell*.

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

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*.

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.

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.

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.

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.

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

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.

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.

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).

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*.