

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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:** 20260905T132644+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 60 mentions in open access literature.

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

Hauner A, et al. (2026) Development and validation of a sample-to-result real time multiplex RT-PCR test for human African trypanosomiasis and arboviral febrile illnesses in the Democratic Republic of the Congo. BMC infectious diseases, 26(1).

Hauner A, et al. (2026) Technical validation and implementation of a multiplex real-time PCR for differential diagnostic detection of Zika virus, yellow fever virus, dengue virus and chikungunya virus (ZYDC-PCR). BMC infectious diseases, 26(1).

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.

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.

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.

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).

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).

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.

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

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.