Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

VirVarSeq

RRID:SCR_012116
Type: Tool

Proper Citation

VirVarSeq (RRID:SCR_012116)

Resource Information

URL: http://sourceforge.net/projects/virtools/

Proper Citation: VirVarSeq (RRID:SCR_012116)

Description: Software for a low frequency Virus Variant detection pipeline for Illumina data.

Resource Type: software resource

Defining Citation: PMID:25178459

Keywords: illumina

Resource Name: VirVarSeq

Resource ID: SCR_012116

Alternate IDs: OMICS_05534

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190727+0000

Ratings and Alerts

No rating or validation information has been found for VirVarSeq.

No alerts have been found for VirVarSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

El Khalili O, et al. (2026) Development of a Next-Generation Sequencing Protocol for Assessing Lenacapavir Resistance in HIV-1 Capsid. Journal of medical virology, 98(1), e70773.

Foulkes C, et al. (2025) Assessing bnAb potency in the context of HIV-1 envelope conformational plasticity. PLoS pathogens, 21(1), e1012825.

Álvarez-Rodríguez B, et al. (2024) Mapping mutational fitness effects across the coxsackievirus B3 proteome reveals distinct profiles of mutation tolerability. PLoS biology, 22(7), e3002709.

Piermatteo L, et al. (2023) Unexpected rise in the circulation of complex HBV variants enriched of HBsAg vaccine-escape mutations in HBV genotype-D: potential impact on HBsAg detection/quantification and vaccination strategies. Emerging microbes & infections, 12(1), 2219347.

Gabrielaite M, et al. (2023) Deep-sequencing of viral genomes from a large and diverse cohort of treatment-naive HIV-infected persons shows associations between intrahost genetic diversity and viral load. PLoS computational biology, 19(1), e1010756.

Gratteri C, et al. (2023) Molecular and Structural Aspects of Clinically Relevant Mutations of SARS-CoV-2 RNA-Dependent RNA Polymerase in Remdesivir-Treated Patients. Pharmaceuticals (Basel, Switzerland), 16(8).

Bellocchi MC, et al. (2023) Frequency of Atypical Mutations in the Spike Glycoprotein in SARS-CoV-2 Circulating from July 2020 to July 2022 in Central Italy: A Refined Analysis by Next Generation Sequencing. Viruses, 15(8).

Kelly D, et al. (2021) Complete genome characterization of human noroviruses allows comparison of minor alleles during acute and chronic infections. Access microbiology, 3(3), 000203.

Armero A, et al. (2021) Intra-Host Diversity of SARS-Cov-2 Should Not Be Neglected: Case of the State of Victoria, Australia. Viruses, 13(1).

Mattenberger F, et al. (2021) Globally defining the effects of mutations in a picornavirus capsid. eLife, 10.

Döring M, et al. (2018) geno2pheno[ngs-freq]: a genotypic interpretation system for identifying viral drug resistance using next-generation sequencing data. Nucleic acids research, 46(W1), W271.