

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T132720+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 13 mentions in open access literature.

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

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.

Chen R, et al. (2026) Analysis of temporal virus evolution and intra-host diversity in long-term non-progressors by bulk next-generation sequencing. *Microbiology spectrum*, 14(5), e0222725.

Stabell AC, et al. (2026) Diverse paths to broadly neutralizing antibody escape among HIV-1 strains. *Nature microbiology*, 11(6), 1573.

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-naïve 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).

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).

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.

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.