

Resource Summary Report

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SNVer

RRID:SCR_002061

Type: Tool

Proper Citation

SNVer (RRID:SCR_002061)

Resource Information

URL: <http://snver.sourceforge.net/>

Proper Citation: SNVer (RRID:SCR_002061)

Description: Statistical software tool for calling common and rare variants in analysis of pool or individual next-generation sequencing data. This software is optimized for analysis of whole-exome sequencing data and whole-genome sequencing data.

Resource Type: data processing software, software application, software resource, data analysis software

Defining Citation: [PMID:21813454](#)

Keywords: statistical analysis software, sequencing, dna, whole-exome, whole-genome, variant, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SNVer

Resource ID: SCR_002061

Alternate IDs: OMICS_00076, biotools:snver

Alternate URLs: <https://sourceforge.net/projects/snver/>, <https://bio.tools/snver>

License: GNU General Public License version 3.0

License URLs: <https://sourceforge.net/directory/os:windows/license:gplv3/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260805T044032+0000

Ratings and Alerts

No rating or validation information has been found for SNVer.

No alerts have been found for SNVer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

Lee JK, et al. (2025) Clonal haematopoiesis of indeterminate potential: a risk factor for future exacerbation in patients with COPD. ERJ open research, 11(3).

Lee JK, et al. (2024) Clonal Hematopoiesis of Indeterminate Potential Is Associated with Current Smoking Status and History of Exacerbation in Patients with Chronic Obstructive Pulmonary Disease. Tuberculosis and respiratory diseases, 87(3), 309.

Shin SJ, et al. (2024) Clonal hematopoiesis in LGI1-antibody encephalitis. Annals of clinical and translational neurology, 11(10), 2785.

Sun Y, et al. (2024) Assessing the impact of sequencing platforms and analytical pipelines on whole-exome sequencing. Frontiers in genetics, 15, 1334075.

Lee J, et al. (2024) The DNA repair pathway as a therapeutic target to synergize with trastuzumab deruxtecan in HER2-targeted antibody-drug conjugate-resistant HER2-overexpressing breast cancer. Journal of experimental & clinical cancer research : CR, 43(1), 236.

Lee G, et al. (2024) Prediction of metabolites associated with somatic mutations in cancers by using genome-scale metabolic models and mutation data. Genome biology, 25(1), 66.

Park C, et al. (2024) Combination of acalabrutinib with lenalidomide and rituximab in relapsed/refractory aggressive B-cell non-Hodgkin lymphoma: a single-arm phase II trial. Nature communications, 15(1), 2776.

Lee WJ, et al. (2023) Clonal hematopoiesis with DNMT3A mutation is associated with lower white matter hyperintensity volume. CNS neuroscience & therapeutics, 29(5), 1243.

Qiu D, et al. (2022) A G358S mutation in the Plasmodium falciparum Na⁺ pump PfATP4 confers clinically-relevant resistance to cipargamin. Nature communications, 13(1), 5746.

Yim J, et al. (2022) Clinicopathologic and Genetic Features of Primary T-cell Lymphomas of the Central Nervous System: An Analysis of 11 Cases Using Targeted Gene Sequencing. The American journal of surgical pathology, 46(4), 486.

Pan B, et al. (2022) Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. *Genome biology*, 23(1), 2.

Gil J, et al. (2021) Accurate, Efficient and User-Friendly Mutation Calling and Sample Identification for TILLING Experiments. *Frontiers in genetics*, 12, 624513.

Barbosa C, et al. (2021) The Genomic Basis of Rapid Adaptation to Antibiotic Combination Therapy in *Pseudomonas aeruginosa*. *Molecular biology and evolution*, 38(2), 449.

Maier W, et al. (2021) Freely accessible ready to use global infrastructure for SARS-CoV-2 monitoring. *bioRxiv : the preprint server for biology*.

Bush SJ, et al. (2021) Generalizable characteristics of false-positive bacterial variant calls. *Microbial genomics*, 7(8).

Desai S, et al. (2021) An integrated approach to determine the abundance, mutation rate and phylogeny of the SARS-CoV-2 genome. *Briefings in bioinformatics*, 22(2), 1065.

Middlebrook EA, et al. (2021) Deep Sequencing of MHC-Adapted Viral Lines Reveals Complex Recombinational Exchanges With Endogenous Retroviruses Leading to High-Frequency Variants. *Frontiers in genetics*, 12, 716623.

Schilbert HM, et al. (2020) Comparison of Read Mapping and Variant Calling Tools for the Analysis of Plant NGS Data. *Plants (Basel, Switzerland)*, 9(4).

Kuca T, et al. (2020) Changes Introduced in the Open Reading Frame of Bovine Viral Diarrhea Virus During Serial Infection of Pregnant Swine. *Frontiers in microbiology*, 11, 1138.

Weedall GD, et al. (2020) An Africa-wide genomic evolution of insecticide resistance in the malaria vector *Anopheles funestus* involves selective sweeps, copy number variations, gene conversion and transposons. *PLoS genetics*, 16(6), e1008822.