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 analysis software, data processing software, software application, software resource

Defining Citation: PMID:21813454

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

Funding:

Availability: Open source, Available for download

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/

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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 50 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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

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 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.

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.

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

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.

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

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

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.

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.

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).

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.

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.

Hawliczek A, et al. (2020) Deep sampling and pooled amplicon sequencing reveals hidden genic variation in heterogeneous rye accessions. BMC genomics, 21(1), 845.