Resource Summary Report

Generated by dkNET on May 19, 2025

SnpSift

RRID:SCR_015624
Type: Tool

Proper Citation

SnpSift (RRID:SCR_015624)

Resource Information

URL: http://snpeff.sourceforge.net/SnpSift.html

Proper Citation: SnpSift (RRID:SCR_015624)

Description: Software toolkit for filtering and manipulating annotated files. After annotation, the software's filter function can find relevant genomic variants in large data files.

Synonyms: SnpEff

Resource Type: software resource, source code, software toolkit

Defining Citation: PMID:22728672

Keywords: annotation, filtering, genomic variant, single nucleotide polymorphism, bio.tools

Funding:

Availability: Open Source, Free, Available for download

Resource Name: SnpSift

Resource ID: SCR_015624

Alternate IDs: biotools:snpsift

Alternate URLs: https://bio.tools/snpsift

License: LGPLv3

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250519T204827+0000

Ratings and Alerts

No rating or validation information has been found for SnpSift.

No alerts have been found for SnpSift.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 504 mentions in open access literature.

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

Opmeer Y, et al. (2025) Polymyositis in Kooiker dogs is associated with a 39 kb deletion upstream of the canine IL21/IL2 locus. PLoS genetics, 21(1), e1011538.

Kerle IA, et al. (2025) Translational and clinical comparison of whole genome and transcriptome to panel sequencing in precision oncology. NPJ precision oncology, 9(1), 9.

Tejedor JR, et al. (2025) Integration of multi-omics layers empowers precision diagnosis through unveiling pathogenic mechanisms on maple syrup urine disease. Journal of inherited metabolic disease, 48(1), e12829.

Ishiguro T, et al. (2025) Immune Stress-induced Tumor Mutation Burden and Neoantigen Expression in 4T1 Mammary Cancer Cells: A Potential Mechanism for Long-term Survival in Patients Treated With Immune Checkpoint Inhibitors. Cancer genomics & proteomics, 22(1), 1.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite Platynothrus peltifer. Science advances, 11(4), eadn0817.

Negatu DA, et al. (2025) Durlobactam to boost the clinical utility of standard of care ?-lactams against Mycobacterium abscessus lung disease. Antimicrobial agents and chemotherapy, 69(1), e0104624.

Kokuryo T, et al. (2025) Whole-genome Sequencing Analysis of Bile Tract Cancer Reveals Mutation Characteristics and Potential Biomarkers. Cancer genomics & proteomics, 22(1),

34.

Oldrieve GR, et al. (2024) Mechanisms of life cycle simplification in African trypanosomes. Nature communications, 15(1), 10485.

von Beck T, et al. (2024) Analysis of rare genetic variants in All of Us cohort patients with common variable immunodeficiency. Frontiers in genetics, 15, 1409754.

Mead A, et al. (2024) Comparison of Conservation Strategies for California Channel Island Oak (Quercus tomentella) Using Climate Suitability Predicted From Genomic Data. Evolutionary applications, 17(12), e70057.

Pallotti S, et al. (2024) Whole genome sequencing analysis of alpaca suggests TRPV3 as a candidate gene for the suri phenotype. BMC genomics, 25(1), 185.

Fanning NC, et al. (2024) Association of rare and common genetic variants in MOCOS with inadequate response to allopurinol. Rheumatology (Oxford, England), 63(11), 3025.

Saballos AI, et al. (2024) Mapping of flumioxazin tolerance in a snap bean diversity panel leads to the discovery of a master genomic region controlling multiple stress resistance genes. Frontiers in plant science, 15, 1404889.

Sigeman H, et al. (2024) The rate of W chromosome degeneration across multiple avian neo-sex chromosomes. Scientific reports, 14(1), 16548.

Bristol JA, et al. (2024) Latent Epstein-Barr virus infection collaborates with Myc over-expression in normal human B cells to induce Burkitt-like Lymphomas in mice. PLoS pathogens, 20(4), e1012132.

Ralli S, et al. (2024) Variant ranking pipeline for complex familial disorders. Scientific reports, 14(1), 13599.

Fulton JE, et al. (2024) The RHCE gene encodes the chicken blood system I. Genetics, selection, evolution : GSE, 56(1), 47.

Sadamitsu K, et al. (2024) Establishment of a zebrafish inbred strain, M-AB, capable of regular breeding and genetic manipulation. Scientific reports, 14(1), 7455.

Niciura SCM, et al. (2024) Multi-omics data elucidate parasite-host-microbiota interactions and resistance to Haemonchus contortus in sheep. Parasites & vectors, 17(1), 102.