Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

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, software toolkit, source code

Defining Citation: PMID:22728672

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

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: 20260801T042750+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 591 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of Candida glabrata (Nakaseomyces glabratus) from across Canada, 2013-2020. Microbiology spectrum, 14(1), e0180325.

Alemán S, et al. (2026) Unraveling Cytomegalovirus Drug Resistance in Transplant Patients by Targeting Deep Sequencing. Journal of medical virology, 98(1), e70768.

Miglierina E, et al. (2026) DIS3 licenses B cells for plasma cell differentiation in humans. Cellular & molecular immunology, 23(1), 31.

Chen Y, et al. (2026) Whole-genome sequencing reveals novel ryanodine receptor mutations P4568L and Y4701D conferring high-level chlorantraniliprole resistance in Spodoptera litura (Lepidoptera: Noctuidae). Pest management science, 82(1), 815.

Sawant A, et al. (2025) Immune Checkpoint Blockade Delays Cancer Development and Extends Survival in DNA Polymerase Mutator Syndromes. Cancer research, 85(6), 1130.

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.

Dols-Icardo O, et al. (2025) Identification of a pathogenic mutation in ARPP21 in patients with amyotrophic lateral sclerosis. Journal of neurology, neurosurgery, and psychiatry, 96(2), 132.

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.

Black GS, et al. (2025) Long-read single-cell RNA sequencing enables the study of cancer subclone-specific genotypes and phenotypes in chronic lymphocytic leukemia. Genome research, 35(4), 686.

Siles L, et al. (2025) Rescue of the disease-associated phenotype in CRISPR-corrected hiPSCs as a therapeutic approach for inherited retinal dystrophies. Molecular therapy. Nucleic acids, 36(1), 102482.

Varano G, et al. (2025) B-cell Receptor Silencing Reveals the Origin and Dependencies of High-Grade B-cell Lymphomas with MYC and BCL2 Rearrangements. Blood cancer discovery, 6(4), 364.

Sadamitsu K, et al. (2025) Establishment and genetic characterization of zebrafish RW line. Scientific reports, 15(1), 14512.

Bauer R, et al. (2025) Pathogenic variation in insulin resistance genes is common in polycystic ovary syndrome (PCOS): a strategy for causal gene discovery using whole-exome sequencing (WES) in complex traits. medRxiv : the preprint server for health sciences.

Ding J, et al. (2025) Integrative multi-omics analysis deciphers the regulatory mechanisms of egg weight traits in chickens. Poultry science, 104(11), 105813.

Li ES, et al. (2025) Molecular subtyping of endometrial carcinoma cell lines uncovers subtype-specific targetable vulnerabilities. NPJ precision oncology, 9(1), 254.

Maruzani R, et al. (2025) Predicting high confidence ctDNA somatic variants with ensemble machine learning models. Scientific reports, 15(1), 18384.

Tsang J, et al. (2025) Identification of novel genetic mutations for the treatment prognostication of canine lymphoma. NPJ precision oncology, 9(1), 174.

Ramasamy R, et al. (2025) Genome-wide allele-specific expression in multi-tissue samples from healthy male baboons reveals the transcriptional complexity of mammals. Cell genomics, 5(5), 100823.

Breitkreuz C, et al. (2025) Differentiation of European yellow rust subraces within the 'Warrior(-)' genetic group. PloS one, 20(5), e0323046.

Minello A, et al. (2025) A recurrent pathogenic BRCA2 truncating variant reveals a role for BRCA2-PCAF complex in modulating NF-?B-driven transcription. Nature communications, 16(1), 10953.