

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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 toolkit, software resource, source code

Defining Citation: [PMID:22728672](https://pubmed.ncbi.nlm.nih.gov/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: 20260731T042954+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 [kravitz2](#).

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- κ B-driven transcription. *Nature communications*, 16(1), 10953.