

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[SnpSift](#)

RRID:SCR_015624

Type: Tool

Proper Citation

SnpSift (RRID:SCR_015624)

Resource Information

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

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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: 20260905T133212+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 631 mentions in open access literature.

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

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple?negative breast cancer. *Genome medicine*, 18(1).

Moreno-Rodriguez T, et al. (2026) Convergent evolution of complex structural variants drives therapy resistance in metastatic prostate cancer. *Genome biology*, 27(1).

Pe?nerová P, et al. (2026) The genomic impact of population connectivity and decline in Africa's elephants. *Nature communications*, 17(1).

Wagner M, et al. (2026) The Genomics of Convergent Adaptation to Intertidal Gravel Beaches in Mediterranean Clingfishes. *Genome biology and evolution*, 18(3).

Buenconsejo GY, et al. (2026) Genomic heterogeneity of NAD(P)H dehydrogenase predisposes *Cryptosporidium* to clofazimine resistance. *Nature microbiology*, 11(6), 1559.

Al Smadi MA, et al. (2026) Genetic alterations in poor-quality individually selected sperm highlight candidate biomarkers for male subfertility. *Scientific reports*, 16(1).

Wang W, et al. (2026) Isolation of novel phages from a resistant *Dorea longicatena* strain reveals genes associated with phage resistance. *Npj viruses*, 4(1).

Guðjónsdóttir SM, et al. (2026) Genome Shows no Recent Inbreeding in Near-Extinction Woolly Rhinoceros Sample Found in Ancient Wolf's Stomach. *Genome biology and evolution*, 18(1).

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.

Donner J, et al. (2026) Association of the Disheveled 2 (DVL2) Gene c.2044delC Variant with Increased Risk of Canine Cleft Palate. *Animal genetics*, 57(3), e70101.

Mazza F, et al. (2026) HapScoreDB: a database of protein language model functional scores for haplotype-resolved protein sequences. *Nucleic acids research*, 54(D1), D1087.

Castro E Silva MA, et al. (2026) The evolutionary history and unique genetic diversity of Indigenous Americans. *Nature*, 653(8113), 134.

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

Sun D, et al. (2026) Analysis of familial exudative vitreoretinopathy (FEVR) cases in the UK 100 000 genomes project increases diagnostic rate and implicates heterozygous CTNND1 mutations in FEVR. *Journal of medical genetics*, 63(3), 187.

Li J, et al. (2026) Chromosome-level genome and population resequencing reveal genetic diversity, demographic history, and climate risk in the East Asian relict tree *Perkinsiodendron macgregorii*. *Plant diversity*, 48(3), 487.

Perret M, et al. (2026) A comprehensive genome-wide scan for parent-of-origin expressed genes in the pig clarifies the conservation landscape of genomic imprinting. *Genetics, selection, evolution : GSE*, 58(1).

Lim FS, et al. (2026) No longer uncertain: the validation of tenebrionid insects as hosts of *Blattambidensovirus incertum*1 isolates by phylogeny and infection studies. *The Journal of general virology*, 107(2).

Rivera MG, et al. (2026) Genome assembly and annotation of a deep-diving pinniped, the northern elephant seal (*Mirounga angustirostris*). *The Journal of heredity*, 117(3), 512.

Baltayev N, et al. (2026) Germline pathogenic variant spectrum and prevalence among colorectal cancer patients undergoing multigene panel testing in Kazakhstan. *Scientific reports*, 16(1).

Thambiraja M, et al. (2026) Genetic basis of immunity in Indian cattle as revealed by comparative analysis of *Bos* genome. *Scientific reports*, 16(1).