

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

SnpEff

RRID:SCR_005191

Type: Tool

Proper Citation

SnpEff (RRID:SCR_005191)

Resource Information

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

Proper Citation: SnpEff (RRID:SCR_005191)

Description: Genetic variant annotation and effect prediction software toolbox that annotates and predicts effects of variants on genes (such as amino acid changes). By using standards, such as VCF, SnpEff makes it easy to integrate with other programs.

Abbreviations: SnpEff

Synonyms: SnpEff - Genetic variant annotation and effect prediction toolbox

Resource Type: software resource

Defining Citation: [PMID:22728672](#)

Keywords: genome, genetic variant, annotation, effect, variant, gene, cancer variant, gatk, hgsv, single nucleotide polymorphisms, genome sequence, java, bio.tools

Related Condition: Cancer

Availability: Free, Freely available

Resource Name: SnpEff

Resource ID: SCR_005191

Alternate IDs: biotools:snpeff, OMICS_00186

Alternate URLs: <https://bio.tools/snpeff>, <https://sources.debian.org/src/snpeff/>

License: GNU Lesser General Public License, v3

Record Creation Time: 20220129T080228+0000

Ratings and Alerts

No rating or validation information has been found for SnpEff.

No alerts have been found for SnpEff.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5186 mentions in open access literature.

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

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. *Journal of virology*, 100(1), e0148725.

Burns R, et al. (2026) Diploid origins and early genome stabilization in the allotetraploid *Arabidopsis suecica*. *The New phytologist*, 249(1), 524.

DiSanza BL, et al. (2026) Bi-allelic variants in BCAT1 impair mitochondrial function and are associated with a candidate neurometabolic disorder. *HGG advances*, 7(1), 100525.

den Hoed J, et al. (2026) Functional characterization of pathogenic SATB2 missense variants identifies distinct effects on chromatin binding and transcriptional activity. *HGG advances*, 7(1), 100537.

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.

Ma WH, et al. (2026) Targeting PTPN13 with 11-amino-acid peptides of C-terminal APC prevents immune evasion of colorectal cancer. *Cell research*, 36(1), 72.

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.

Kim CY, et al. (2026) Integrative multi-omics of matched primary and liver metastatic colorectal cancer organoids identifies putative molecular targets. *Translational oncology*, 63, 102592.

Yu J, et al. (2026) Unraveling the population genetic structure and identifying candidate genes for dorsal plumage color in Liangshan Yanying chickens. *Poultry science*, 105(1), 106180.

Waesche C, et al. (2026) Population-wide single-pollen nuclei genotyping in rye sheds light on the genetic basis and environmental plasticity of meiotic recombination. *The New phytologist*, 249(1), 512.

Bang S, et al. (2026) A Growth-Coupled Evolutionary Strategy Enhances Heme Biosynthesis in *Saccharomyces cerevisiae*. *Biotechnology journal*, 21(1), e70175.

Marques CI, et al. (2025) Physiological plasticity in zebra finch color varieties mitigates DNA damage under oxidative stress. *iScience*, 28(7), 112937.

Guerrero C, et al. (2025) Dynamics of Mutant Hematopoietic Progenitor Cells Are Not Associated with Clinical Outcomes in Multiple Myeloma. *Blood cancer discovery*, 6(3), 203.

Akopyan M, et al. (2025) Reference genome choice compromises population genetic analyses. *Cell*.

Liu Z, et al. (2025) ctDNA detects residual disease after neoadjuvant chemoradiotherapy and guides adjuvant therapy in esophageal squamous cell carcinoma. *Cell reports. Medicine*, 6(9), 102334.

Smith JD, et al. (2025) Genomic Signatures of Poor Prognosis in Merkel Cell Carcinoma: A Single-Institution Prospective Study. *Molecular cancer research : MCR*.

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

Ishino T, et al. (2025) Immunopectidomics combined with full-length transcriptomics uncovers diverse neoantigens. *Cell reports*, 45(1), 116781.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

Chihab LY, et al. (2025) Comparative performance analysis of neoepitope prediction algorithms in head and neck cancer. *Frontiers in immunology*, 16, 1494453.