

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 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 5640 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Hayward MK, et al. (2026) Tissue tension fosters macrophage-driven lipid peroxidation-induced DNA damage. *Cancer cell*, 44(6), 1255.

Monti M, et al. (2026) Integrating interferon gamma receptor pathways, antigenicity, and immune contexture as predictors of immunotherapeutic strategies for mucosal melanomas. *Journal for immunotherapy of cancer*, 14(3).

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).

Kawazu M, et al. (2026) Genomic and Transcriptomic Analysis of High-Grade Endometrial Carcinoma Reveals Biological Heterogeneity and Molecular Classification Challenges. *Cancer research communications*, 6(4), 961.

Tang C, et al. (2026) Investigating the determinants of immunotherapy response in the primary tumour of clear cell renal cell carcinoma (RCC). *BMJ oncology*, 5(2), e001031.

Salazar YEAR, et al. (2026) MalDeepSeq panel: A targeted ultra-deep sequencing approach to trace drug resistance markers in *Plasmodium falciparum*. *Cell reports methods*, 101509.

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

Vemulamanda S, et al. (2026) Development of a Clinical Assay to Guide Patient Therapy in HPV-Associated Head and Neck Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2681.

Takahashi J, et al. (2026) Spatial Multiomic Analyses Reveal Carcinogenic Pathways in End-Stage Renal Disease. *Cancer discovery*, 16(3), 478.

van der Elst A, et al. (2026) Molecular and Immune Landscape of Recurrent and/or Distant Metastatic Squamous Cell Carcinoma of the Head and Neck: An EORTC/IMMUCAN Project. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2732.

Lehmann AE, et al. (2026) Aneuploidy promotes transient stress adaptation and metabolic flexibility in the human fungal pathogen *Aspergillus fumigatus*. *Current biology : CB*, 36(13), 3258.

López-Girona E, et al. (2026) Fine-mapping, candidate gene identification, and marker development for the apple scab resistance gene *Rvi2*. *Journal of experimental botany*, 77(6), 1647.

Wang Z, et al. (2026) Haplotype-Resolved Genome Assembly and Population Genomics Reveal Evolutionary History and Agronomic Traits of Mulberry. *Plant biotechnology journal*, 24(4), 2105.

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.

Blanco-Berdugo L, et al. (2026) Modest increase in the de novo single-nucleotide mutation rate in house mice born by assisted reproduction. *Genome research*, 36(1), 50.

Puccetti G, et al. (2026) A large European diversity panel reveals complex azole fungicide resistance gains of a major wheat pathogen. *mBio*, 17(1), e0276625.

Sigal W, et al. (2026) Congenital Hyperinsulinism and Long QT Syndrome Attributable to a Variant in *KCNE1*. *Hormone research in paediatrics*, 99(4), 518.

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.

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

Chen CJ, et al. (2026) Resolving sampling and population-size biases in domestication genomics supports a South Asian origin of walnuts. *Genome biology*, 27(1).