Resource Summary Report

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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

Funding:

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

Record Last Update: 20250410T065234+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 4512 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Battilani D, et al. (2025) Beyond population size: Whole-genome data reveal bottleneck legacies in the peninsular Italian wolf. The Journal of heredity, 116(1), 10.

Luo Y, et al. (2025) Experimental validation of genome-environment associations in Arabidopsis. bioRxiv : the preprint server for biology.

Shan M, et al. (2025) Significance of KLK7 expression, polymorphisms, and function in sheep horn growth. BMC genomics, 26(1), 78.

Acford-Palmer H, et al. (2025) Application of a targeted amplicon sequencing panel to screen for insecticide resistance mutations in Anopheles darlingi populations from Brazil. Scientific reports, 15(1), 731.

Matsushita K, et al. (2025) Importance of EQA/PT for the detection of genetic variants in comprehensive cancer genome testing. Scientific reports, 15(1), 1036.

Opmeer Y, et al. (2025) Polymyositis in Kooiker dogs is associated with a 39 kb deletion upstream of the canine IL21/IL2 locus. PLoS genetics, 21(1), e1011538.

Higashino A, et al. (2025) Population Genomics of Japanese Macaques (Macaca fuscata): Insights Into Deep Population Divergence and Multiple Merging Histories. Genome biology and evolution, 17(1).

Jago MJ, et al. (2025) High-throughput method characterizes hundreds of previously unknown antibiotic resistance mutations. Nature communications, 16(1), 780.

Anglero-Rodriguez YI, et al. (2025) High resistance barrier and prophylactic protection in preclinical models of SARS-CoV-2 with two siRNA combination. Nucleic acids research, 53(1).

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.

Blanco E, et al. (2025) Dominant negative variants in ITPR3 impair T cell Ca2+ dynamics causing combined immunodeficiency. The Journal of experimental medicine, 222(1).

Zhang L, et al. (2025) Linkage Mapping and Identification of Candidate Genes for Cold Tolerance in Rice (Oryza Sativa L.) at the Bud Bursting Stage. Rice (New York, N.Y.), 18(1), 1.

Paz LN, et al. (2025) Insights into host-pathogen interaction based on the comparison of genomes of leptospira interrogans isolated from dogs, humans, and a rodent in the same epidemiological context: A one health approach. Heliyon, 11(1), e41531.

Tian Y, et al. (2025) Population Genomics Reveals Elevated Inbreeding and Accumulation of Deleterious Mutations in White Raccoon Dogs. Biology, 14(1).

Suzuki S, et al. (2025) Comparison of actionable alterations in cancers with kinase fusion, mutation, and copy number alteration. PloS one, 20(1), e0305025.

Zhang X, et al. (2025) Genomic variation responding to artificial selection on different lines of Pekin duck. Poultry science, 104(2), 104785.

Kim JW, et al. (2025) Clinical implementation of next-generation sequencing testing and genomically-matched therapy: a real-world data in a tertiary hospital. Scientific reports, 15(1), 2171.

Negatu DA, et al. (2025) Durlobactam to boost the clinical utility of standard of care ?-lactams against Mycobacterium abscessus lung disease. Antimicrobial agents and chemotherapy, 69(1), e0104624.

Liu Z, et al. (2025) Genome architecture of the allotetraploid wild grass Aegilops ventricosa reveals its evolutionary history and contributions to wheat improvement. Plant communications, 6(1), 101131.

Kokuryo T, et al. (2025) Whole-genome Sequencing Analysis of Bile Tract Cancer Reveals Mutation Characteristics and Potential Biomarkers. Cancer genomics & proteomics, 22(1),

34.