Resource Summary Report

Generated by T1D on Sep 5, 2026

dbSNP

RRID:SCR_002338
Type: Tool

Proper Citation

dbSNP (RRID:SCR_002338)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/SNP/

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Description: General database of genetic variations maintained by the NCBI. Database as central repository for both single base nucleotide substitutions and short deletion and insertion polymorphisms. Distinguishes report of how to assay SNP from use of that SNP with individuals and populations. This separation simplifies some issues of data representation. However, these initial reports describing how to assay SNP will often be accompanied by SNP experiments measuring allele occurrence in individuals and populations. Community can contribute to this resource.

Abbreviations: dbSNP

Synonyms: dbSNP: Database for Short Genetic Variations, Entrez SNP - Single Nucleotide Polymorphism, SNV Database, NCBI SNV Database, NCBI Short Genetic Variations Database, NCBI Short Genetic Variations, NCBI Single Nucleotide Polymorphism, Entrez SNP, dbSNP, NCBI Short Genetic Variations (SNV) database

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:21154707

Keywords: insertion, polymorphism, short, deletion, single, nucleotide, genetic, variation, genomics, genotype, disease, allele, microsatellite, marker, multinucleotide, heterozygous, sequence, gold standard, bio.tools

Funding: NLM

Availability: Free, Freely available

Resource Name: dbSNP

Resource ID: SCR_002338

Alternate IDs: nif-0000-02734, biotools:dbsnp, OMICS_00264, r3d100010652

Alternate URLs: http://www.ncbi.nlm.nih.gov/projects/SNP/, https://bio.tools/dbsnp, https://doi.org/10.17616/R3XG81

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260903T234526+0000

Ratings and Alerts

No rating or validation information has been found for dbSNP.

No alerts have been found for dbSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9088 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ma Y, et al. (2026) Gene-culture coevolution shapes olfactory receptor gene diversity in Orang Asli populations. Cell reports, 117181.

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. Cancer research communications, 6(4), 811.

Martín A, et al. (2026) Targeted KRASG12V Degradation in vivo Elicits Lung Adenocarcinoma Regression with Subsequent Relapse from Dysregulated Proteolysis. Cancer research.

Temimi L, et al. (2026) Association of EGFR gene polymorphisms rs2072454 and rs2227983 with lung cancer susceptibility in a Western Algerian population: a case-control study. Journal of the Egyptian National Cancer Institute, 38(1).

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).

Radovich M, et al. (2026) Broader gene representation by whole-exome sequencing improves accuracy of tumor mutational burden assessment for selection of pembrolizumab immunotherapy. Cancer immunology, immunotherapy : CII, 75(6).

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.

Mroczkowska-B?karciak A, et al. (2026) CALR-mutant myeloproliferative neoplasms: insights from next-generation sequencing. Journal of applied genetics, 67(1), 155.

Zhu Y, et al. (2026) Optimization strategies for voriconazole dosing in pediatric populations: integrating therapeutic indications and age-stratified pharmacokinetics. Antimicrobial agents and chemotherapy, 70(3), e0116925.

McClelland P, et al. (2026) A multi-ancestry genetic reference for the Quebec population. Nature communications, 17(1), 1319.

Sakr AA, et al. (2026) Diagnostic and immunological roles of leptin gene rs7799039 polymorphism and cytokines in COVID-19, HCV, and dual infection. Scientific reports, 16(1), 4361.

Betti M, et al. (2026) Biopsy RNA-seq captures TROP-2-linked migration and clonal resistance to forecast aggressiveness in metastatic melanoma. Journal of experimental & clinical cancer research : CR, 45(1).

Xu W, et al. (2026) Variants in the interferon regulatory factor 5 gene confer genetic risk for systemic lupus erythematosus in a Han Chinese population. Annals of medicine, 58(1), 2622737.

Gan H, et al. (2026) Identification and phased de novo mutation of the EPS8L2 gene in a patient with progressive hearing loss: A case report. Medicine, 105(4), e46930.

Chirmade S, et al. (2026) GWAS SVatalog: a visualization tool to aid fine-mapping of GWAS loci with structural variations. Heredity, 135(3), 199.

Jia X, et al. (2026) Effect of telomere length and related gene polymorphism in signaling pathway on semen quality. Scientific reports, 16(1), 6575.

Krebs K, et al. (2026) Pharmacokinetic recall study of Estonian Biobank participants with novel genetic variants in CYP2C19 and CYP2D6. NPJ genomic medicine, 11(1), 10.

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Zeng L, et al. (2026) Identification of a Novel Likely Pathogenic Variant of DIAPH3 Associated With New Phenotype of Sensorineural Hearing Loss. Molecular genetics & genomic medicine, 14(1), e70179.

Huang AY, et al. (2026) Accurate detection of somatic single-nucleotide variants from bulk RNA-seq data using RNA-MosaicHunter. Nucleic acids research, 54(1).