Resource Summary Report

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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: 20260905T132447+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 Kravitz .

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.

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).

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

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.

Saghir H, et al. (2026) Dynamic assessment of proliferation to guide response-adapted therapy in the setting of neoadjuvant chemotherapy in ER+/HER2- breast cancer. Translational oncology, 63, 102597.

Lettera E, et al. (2026) Molecular and phenotypic blueprint of human hematopoiesis links proliferation stress to stem cell aging. The Journal of experimental medicine, 223(2).

Subardjo YP, et al. (2026) Weight-loss effects of macronutrient-based diets modified by genetic variants: a protocol for systematic review of randomised controlled trials. BMJ open, 16(1), e110935.

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.

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).

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.

Leban T, et al. (2026) Multiomics Data Synthesis of FAM83H in Amelogenesis Imperfecta. International dental journal, 76(1), 109293.

Ncir WB, et al. (2026) First LDLRAP1 and Recurrent LDLR Mutations in Tunisian Families With Familial Hypercholesterolemia. Journal of cellular and molecular medicine, 30(1), e70997.

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).