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: 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 repository, data or information resource, database, storage service resource, 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: 20260804T043139+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 8619 mentions in open access literature.

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

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.

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

Park J, et al. (2026) A robust pleiotropy method with applications to lipid traits and to inflammatory bowel disease subtypes with sample overlap. HGG advances, 7(1), 100501.

Hsu HC, et al. (2026) Expression of Bacillus in colorectal tissues is associated with improved cetuximab therapy for patients with metastatic colorectal cancer. Translational oncology, 63, 102575.

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.

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.

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. Cancer discovery, 15(2), 286.

Jiang A, et al. (2025) Assessing MC1R Variants in Lentigo Maligna Melanoma within the Utah Population. Cancer research communications, 5(7), 1228.

Gou M, et al. (2025) Exploration of the benefits and resistance mechanisms of immunotherapy based on PD-L1 expression, circulating tumor DNA and T-cell receptor profiles in advanced gastric cancer. Cancer immunology, immunotherapy : CII, 75(1), 12.

Stanciu A, et al. (2025) Personalized ctDNA detection and genomic profiling in the NeoRHEA Study. NPJ breast cancer, 11(1), 137.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. Cancer discovery, 15(8), 1630.

Wisniewski DJ, et al. (2025) Dual inhibition of EGFR and PI3Kinase signaling in EGFR amplified triple negative breast cancer cells induces apoptosis and reduces tumor growth. bioRxiv : the preprint server for biology.

Zhong Y, et al. (2025) ABO exon polymorphisms are related to ischemic stroke in a Chinese Han population. BMC medical genomics, 18(1), 102.

Wang H, et al. (2025) CD5 and p53 immunohistochemistry: valuable prediction method in molecular typing of CD5-positive diffuse large B-cell lymphoma. BMC cancer, 25(1), 726.

He M, et al. (2025) Case Report: Identification of a novel hemizygous CFAP47 variant in a primary ciliary dyskinesia patient with dual ciliary and flagellar defects. Frontiers in medicine, 12, 1574684.

Xu M, et al. (2025) Environmental carcinogens often exacerbate endogenous mutagenic processes to enhance tumor promotion. Cell reports, 44(7), 115978.

Chenyue Z, et al. (2025) Genetic etiology of ventriculomegaly in 73 fetuses identified by High-Throughput sequencing. Scientific reports, 15(1), 23622.

Wang M, et al. (2025) Diagnosis and recombinant human growth hormone treatment of Wiedemann-Steiner syndrome: discovery of novel KMT2A variants and review of existing literature. BMC pediatrics, 25(1), 523.

Baba H, et al. (2025) Functional and structural analysis of missense variants in the human PDCD1 Gene. Journal of public health in Africa, 16(4), 1348.

Zeng R, et al. (2025) Analysis of gene polymorphisms in patients with pulmonary infections based on next-generation sequencing technology and their prognostic predictive value. Frontiers in medicine, 12, 1599791.