Resource Summary Report

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SNPinfo Web Server

RRID:SCR_010589
Type: Tool

Proper Citation

SNPinfo Web Server (RRID:SCR_010589)

Resource Information

URL: http://snpinfo.niehs.nih.gov/

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Description: SNPinfo Web Server is a set of freely available web-based SNP selection tools where investigators can specify genes or linkage regions and select SNPs based on GWAS results, linkage disequilibrium (LD), and predicted functional characteristics of both coding and non-coding SNPs. The algorithm uses GWAS SNP P-value data and finds all SNPs in high LD with GWAS SNPs, so that selection is from a much larger set of SNPs than the GWAS itself. The program can also identify and choose tag SNPs for SNPs not in high LD with any GWAS SNP. We incorporate functional predictions of protein structure, gene regulation, splicing and miRNA binding, and consider whether the alternative alleles of a SNP are likely to have differential effects on function. Users can assign weights for different functional categories of SNPs to further tailor SNP selection. The program accounts for LD structure of different populations so that a GWAS study from one ethnic group can be used to choose SNPs for one or more other ethnic groups. SNP Selection and Functional Information *Candidate Gene SNP Selection (GenePipe):SNP selection for candidate genes based on Genome Wide Association Study (GWAS) results, functional SNP prediction and Linkage Disequilibrium (LD) information. *GWAS Functional SNP Selection (GenomePipe):Functional SNP selection from SNPs that are in high LD with GWAS SNPs *GWAS SNP Selection in Linkage Loci (LinkagePipe):GWAS SNP selection in candidate genomic regions (such as linkage loci) *LD TAG SNP Selection (TagSNP):LD tag SNP selection and visualization for single or multiple populations. Finalization of SNP list from various queries. *SNP Function Prediction (FuncPred): Querying SNP function predictions and ethnic-specific allele frequencies. *SNP Information in DNA Sequence (SNPseq):Visualization of SNP related information in the context of DNA sequence. Preparing DNA Sequence for PCR Primer Design considering SNP information. Detailed information of CpG region.

Resource Type: service resource

Defining Citation: PMID:19417063

Keywords: bio.tools

Resource Name: SNPinfo Web Server

Resource ID: SCR_010589

Alternate IDs: nlx_46274, biotools:snpinfo

Alternate URLs: https://bio.tools/snpinfo

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260815T182357+0000

Ratings and Alerts

No rating or validation information has been found for SNPinfo Web Server.

No alerts have been found for SNPinfo Web Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 254 mentions in open access literature.

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

Chen W, et al. (2026) ADIPOQ rs1063537 polymorphism correlates with diabetic kidney disease severity in southern Chinese Han patients with type 2 diabetes. Medicine, 105(11), e48028.

Timasheva Y, et al. (2026) Integrative Analysis of Oxidative Stress and Cellular Senescence Pathways in Chronic Obstructive Pulmonary Disease. Genes, 17(6).

Koizumi H, et al. (2026) Clinical Details of Low-Frequency Hearing Loss Observed in Autosomal Dominant MYO7A-Associated Hearing Loss Patients. Genes, 17(3).

Küchler EC, et al. (2026) Condylar Bone Quality in Growing Children Is Associated With Genetic Polymorphisms in Genes Involved in Calcium and Phosphate Maintenance. BioMed research international, 2026, 9337029.

Li Z, et al. (2025) The role of CDK8 gene polymorphisms in bladder cancer susceptibility and prognosis: a study in the Chinese Han population. BMC cancer, 25(1), 714.

Yin M, et al. (2025) Development and validation of a risk prediction model for diabetic kidney disease in patients with diabetic retinopathy. Frontiers in endocrinology, 16, 1499866.

Arai Y, et al. (2025) Novel OTOG Variants and Clinical Features of Hearing Loss in a Large Japanese Cohort. Genes, 16(1).

Chang J, et al. (2025) Genetic variants of m1A modification genes and the risk of neuroblastoma: novel insights from a Chinese case-control study. Human genomics, 19(1), 50.

Wang Z, et al. (2025) Association of the YTHDF2 rs3738067 A>G variant with hepatoblastoma risk: a multicenter case-control study in Chinese children. BMC cancer, 26(1), 101.

Xiong J, et al. (2025) Genetic susceptibility to essential hypertension in the Chinese han population: a study on GAB1, GAB2, and GAB3 gene polymorphisms. BMC cardiovascular disorders, 25(1), 223.

Li Y, et al. (2025) New Gene Signature-Based Prognostic Model for Patients With VEGF-Overexpressing Esophageal Squamous Cell Carcinoma. BioMed research international, 2025, 5694628.

Nie L, et al. (2025) Genetic variants in HLA-DQA1/DQB1 genes modulate the risk of gestational diabetes mellitus in a southern Chinese population. Frontiers in endocrinology, 16, 1511561.

Deng C, et al. (2025) Association between NAT10 gene rs8187 G > A polymorphism and Wilms tumor susceptibility in Chinese Han children: a five-center case-control study. BMC cancer, 25(1), 494.

Li M, et al. (2025) Impact of single nucleotide polymorphisms of immunomodulatory factors on treatment response and prognosis in acute myeloid leukemia. Frontiers in immunology, 16, 1571332.

Li M, et al. (2025) Polymorphisms in immunosuppression-related genes are associated with AML. Frontiers in immunology, 16, 1530510.

He X, et al. (2025) Impact of SERPINA3 on the Prognostic Role of KRAS G12R-Mutated Pancreatic Ductal Adenocarcinoma Patients Receiving Gemcitabine-Based Treatment: A Cross-Sectional Study. Health science reports, 8(10), e71332.

Pan T, et al. (2025) Genetic Variants in the NOD-like Receptor Signaling Pathway Are Associated with HIV-1/AIDS in a Northern Chinese Population. International journal of molecular sciences, 26(8).

Lin X, et al. (2025) Lack of association between MALAT1 rs591291 and rs3200401 polymorphisms and venous malformation risk in the Chinese pediatric population. Biochemistry and biophysics reports, 43, 102209.

Mittal P, et al. (2025) Genetic Polymorphisms in MHC Classes I and II Predict Outcomes in Metastatic Colorectal Cancer. International journal of molecular sciences, 26(6).

Hou C, et al. (2025) LINC00461 SNPs rs933647 and rs201864123 modify the risk of adenoid hypertrophy susceptibility for children in South China. Frontiers in genetics, 16, 1509053.