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: 20260725T190702+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 211 mentions in open access literature.

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

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.

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.

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

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.

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.

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

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 R, et al. (2025) GC vitamin D-binding protein gene functional genetic variants and gestational diabetes mellitus risk and prediction. Scientific reports, 15(1), 27807.

Jiang S, et al. (2025) Association of genetic variants in m1A modification core genes and neuroblastoma risk. BMC cancer, 25(1), 1606.

Ma L, et al. (2024) Identification of hepatoblastoma susceptibility loci in the TRMT6 gene from a seven-center case-control study. Journal of cellular and molecular medicine, 28(1), e18006.

Shilenok I, et al. (2024) C11orf58 (Hero20) Gene Polymorphism: Contribution to Ischemic Stroke Risk and Interactions with Other Heat-Resistant Obscure Chaperones. Biomedicines, 12(11).

Liu L, et al. (2024) Polymorphisms in myeloperoxidase and tissue inhibitor of metalloproteinase-1 genes and their association with preeclampsia in the Chinese Han population. Heliyon, 10(17), e36685.

Chen Y, et al. (2024) Identification of common genetic variants in KCNQ family genes associated with gastric cancer survival in a Chinese population. Journal of biomedical research, 39(1), 76.

Fang J, et al. (2024) Development and validation of a nomogram model based on blood-based genomic mutation signature for predicting the risk of brain metastases in non-small cell lung cancer. BMC pulmonary medicine, 24(1), 633.

Liu J, et al. (2024) Genetic variants of m7G modification genes influence neuroblastoma susceptibility. Heliyon, 10(1), e23658.

Lin Q, et al. (2024) Association of RAN and RANBP2 Gene Polymorphisms With Glioma Susceptibility in Chinese Children. Cancer reports (Hoboken, N.J.), 7(7), e2136.

Gholami M, et al. (2023) Haplotypic variants of COVID-19 related genes are associated with blood pressure and metabolites levels. Journal of medical virology, 95(1), e28355.

Zeng D, et al. (2023) TRMT61B rs4563180 G>C variant reduces hepatoblastoma risk: a case-control study of seven medical centers. Aging, 15(15), 7583.

Fukasaku H, et al. (2023) Association of PDGFRA polymorphisms with the risk of corneal astigmatism in a Japanese population. Scientific reports, 13(1), 16075.