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

Funding:

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: 20250420T014504+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 201 mentions in open access literature.

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

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

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.

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.

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 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.

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.

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.

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.

Zumaraga MP, et al. (2023) The Interindividual Variability of Phytofluene Bioavailability is Associated with a Combination of Single Nucleotide Polymorphisms. Molecular nutrition & food research, 67(2), e2200580.

Lee S, et al. (2023) Genetic variants of NEUROD1 target genes are associated with clinical outcomes of small-cell lung cancer patients. Thoracic cancer, 14(13), 1145.

Lee YH, et al. (2023) Genetic Variants in Histone Modification Regions Predict Clinical Outcomes of Pemetrexed Chemotherapy in Lung Adenocarcinoma. Oncology, 101(2), 96.

Seo JI, et al. (2023) Whole Exome Sequencing of a Patient with a Milder Phenotype of Xeroderma Pigmentosum Group C. Medicina (Kaunas, Lithuania), 59(4).

Lee JH, et al. (2023) Genetic variants in key necroptosis regulators predict prognosis of non-small cell lung cancer after surgical resection. Thoracic cancer, 14(26), 2678.

Hebbar P, et al. (2023) Linkage analysis using whole exome sequencing data implicates SLC17A1, SLC17A3, TATDN2 and TMEM131L in type 1 diabetes in Kuwaiti families. Scientific reports, 13(1), 14978.

Chen S, et al. (2023) Genetic variants in RNA m5 C modification genes associated with

survival and chemotherapy efficacy of colorectal cancer. Cancer medicine, 12(2), 1376.

Ramirez I, et al. (2023) The investigation of WNT6 and WNT10A single nucleotide polymorphisms as potential biomarkers for dental pulp calcification in orthodontic patients. PloS one, 18(8), e0288782.

Kristof Z, et al. (2023) Variation along P2RX7 interacts with early traumas on severity of anxiety suggesting a role for neuroinflammation. Scientific reports, 13(1), 7757.

Graczyk MM, et al. (2023) Genotype-by-diagnosis interaction influences self-control in human cocaine addiction. Translational psychiatry, 13(1), 51.