Resource Summary Report

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rSNPBase

RRID:SCR_001947
Type: Tool

Proper Citation

rSNPBase (RRID:SCR_001947)

Resource Information

URL: http://rsnp.psych.ac.cn/

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Description: Database for curated regulatory single nucleotide polymorphisms (SNPs) to assist researchers in selecting candidate SNPs for further genetic studies (especially for QTL studies), identifying causal variants of certain phenotypes, and exploring in-depth molecular mechanisms. It is characterized by several unique features: (i) To improve reliability, all SNPs in rSNPBase are annotated with reference to experimentally supported regulatory elements. (ii) rSNPBase focuses on rSNPs involved in a wide range of regulation types, including proximal and distal transcriptional regulation and post-transcriptional regulation, and identifies their potentially regulated genes. (iii) Linkage disequilibrium (LD) correlations between SNPs were analysed so that the regulatory feature is annotated to SNP-set rather than a single SNP. (iv) rSNPBase provides the spatio-temporal labels and experimental eQTL labels for SNPs.

Abbreviations: rSNPBase

Synonyms: rSNPBase - A database for curated regulatory SNPs

Resource Type: data or information resource, database

Defining Citation: PMID:24285297

Keywords: single nucleotide polymorphism, linkage disequibrilium, regulatory annotation, regulatory single nucleotide polymorphism, regulatory element, FASEB list

Funding:

Availability: Free, Public

Resource Name: rSNPBase

Resource ID: SCR_001947

Alternate IDs: OMICS_01929

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250502T055310+0000

Ratings and Alerts

No rating or validation information has been found for rSNPBase.

No alerts have been found for rSNPBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Wang S, et al. (2025) Interpretation of molecular autopsy findings in 45 sudden unexplained death cases: from coding region to untranslated region. International journal of legal medicine, 139(1), 15.

Bruncsics B, et al. (2023) Genetic risk of depression is different in subgroups of dietary ratio of tryptophan to large neutral amino acids. Scientific reports, 13(1), 4976.

Sengupta D, et al. (2023) Identifying polymorphic cis-regulatory variants as risk markers for lung carcinogenesis and chemotherapy responses in tobacco smokers from eastern India. Scientific reports, 13(1), 4019.

Zhong Y, et al. (2023) RBFOX1 and Working Memory: From Genome to Transcriptome Revealed Posttranscriptional Mechanism Separate From Attention-Deficit/Hyperactivity Disorder. Biological psychiatry global open science, 3(4), 1042.

Silva MJ, et al. (2023) Genetic variants associated with SARS-CoV-2 infection also affect lung function and asthma severity. Heliyon, 9(9), e19235.

Lee JH, et al. (2022) Epigenetic readers and lung cancer: the rs2427964C>T variant of the bromodomain and extraterminal domain gene BRD3 is associated with poorer survival outcome in NSCLC. Molecular oncology, 16(3), 750.

Das AP, et al. (2022) Prioritization and Meta-analysis of regulatory SNPs identified IL6, TGFB1, TLR9 and MMP7 as significantly associated with cervical cancer. Cytokine, 157, 155954.

Sadhukhan S, et al. (2022) Analysis of DNMT1 gene variants in progression of neural tube defects-an in silico to in vitro approach. Bioscience reports, 42(12).

Shoily SS, et al. (2021) Disparities in COVID-19 severities and casualties across ethnic groups around the globe and patterns of ACE2 and PIR variants. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 92, 104888.

Díaz-Ordóñez L, et al. (2021) Evaluation of CYP2C19 Gene Polymorphisms in Patients with Acid Peptic Disorders Treated with Esomeprazole. Pharmacogenomics and personalized medicine, 14, 509.

Gao Y, et al. (2021) LincSNP 3.0: an updated database for linking functional variants to human long non-coding RNAs, circular RNAs and their regulatory elements. Nucleic acids research, 49(D1), D1244.

Koli? I, et al. (2021) Association study of rs7799039, rs1137101 and rs8192678 gene variants with disease susceptibility/severity and corresponding LEP, LEPR and PGC1A gene expression in multiple sclerosis. Gene, 774, 145422.

Zhu T, et al. (2021) Assessing the Function of the ZFP90 Variant rs1170426 in SLE and the Association Between SLE Drug Target and Susceptibility Genes. Frontiers in immunology, 12, 611515.

Li Y, et al. (2021) Genome-wide prioritization reveals novel gene signatures associated with cardiotoxic effects of tyrosine kinase inhibitors. Oncology letters, 21(2), 94.

Qi X, et al. (2020) An integrative analysis of genome-wide association study and regulatory SNP annotation datasets identified candidate genes for bipolar disorder. International journal of bipolar disorders, 8(1), 6.

Ye J, et al. (2020) A genome-wide multiphenotypic association analysis identified candidate genes and gene ontology shared by four common risky behaviors. Aging, 12(4), 3287.

Jalilvand A, et al. (2020) A case-control study on the SNP309T ? G and 40-bp Del1518 of the MDM2 gene and a systematic review for MDM2 polymorphisms in the patients with breast cancer. Journal of clinical laboratory analysis, 34(12), e23529.

Qi YY, et al. (2020) SCUBE3 Is Likely a Susceptibility Gene for Systemic Lupus Erythematosus for Chinese Populations. Journal of immunology research, 2020, 8897936.

Pirim D, et al. (2020) Hepatic lipase (LIPC) sequencing in individuals with extremely high and low high-density lipoprotein cholesterol levels. PloS one, 15(12), e0243919.

Liang X, et al. (2019) Integrating genome-wide association study with regulatory SNP annotation information identified candidate genes and pathways for schizophrenia. Aging, 11(11), 3704.