Resource Summary Report

Generated by NIF on Apr 25, 2025

GWASdb

RRID:SCR_006015
Type: Tool

Proper Citation

GWASdb (RRID:SCR_006015)

Resource Information

URL: http://jjwanglab.org:8080/gwasdb/

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Description: Combines collections of genetic variants (GVs) from GWAS and their comprehensive functional annotations, as well as disease classifications. Used to maximize utilility of GWAS data to gain biological insights through integrative, multi-dimensional functional annotation portal. In addition to all GVs annotated in NHGRI GWAS Catalog, we manually curate GVs that are marginally significant (P value

Abbreviations: GWASdb

Resource Type: data or information resource, web service, data access protocol, database, software resource

Defining Citation: PMID:22139925

Keywords: genetic variant, genome-wide association study, functional annotation, disease classification, snp, gene, chromosome region, annotation, pathway, protein-protein interaction, bio.tools

Funding: University of Hong Kong Small Project Fund 201007176262;
Research Grants Council of Hong Kong 781511M;
Research Grants Council of Hong Kong 778609M;
Research Grants Council of Hong Kong N_HKU752/10;
Food and Health Bureau of Hong Kong 10091262;
NCI

Resource Name: GWASdb

Resource ID: SCR_006015

Alternate IDs: biotools:gwasdb, nlx_151404

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

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250425T055504+0000

Ratings and Alerts

No rating or validation information has been found for GWASdb.

No alerts have been found for GWASdb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Sadlon A, et al. (2024) Association of Blood MicroRNA Expression and Polymorphisms with Cognitive and Biomarker Changes in Older Adults. The journal of prevention of Alzheimer's disease, 11(1), 230.

Song C, et al. (2024) eRNAbase: a comprehensive database for decoding the regulatory eRNAs in human and mouse. Nucleic acids research, 52(D1), D81.

Iida M, et al. (2024) A network-based trans-omics approach for predicting synergistic drug combinations. Communications medicine, 4(1), 154.

Zhang Y, et al. (2023) CRdb: a comprehensive resource for deciphering chromatin regulators in human. Nucleic acids research, 51(D1), D88.

Kühlwein JK, et al. (2023) ALS is imprinted in the chromatin accessibility of blood cells. Cellular and molecular life sciences : CMLS, 80(5), 131.

Zhou Q, et al. (2023) ChromLoops: a comprehensive database for specific protein-mediated chromatin loops in diverse organisms. Nucleic acids research, 51(D1), D57.

Zhao X, et al. (2022) CircleBase: an integrated resource and analysis platform for human

eccDNAs. Nucleic acids research, 50(D1), D72.

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.

Arandjelovic S, et al. (2021) ELMO1 signaling is a promoter of osteoclast function and bone loss. Nature communications, 12(1), 4974.

Chen X, et al. (2021) Novel lincRNA Discovery and Tissue-Specific Gene Expression across 30 Normal Human Tissues. Genes, 12(5).

Pan Q, et al. (2021) VARAdb: a comprehensive variation annotation database for human. Nucleic acids research, 49(D1), D1431.

Dehghan Z, et al. (2021) Repurposing new drug candidates and identifying crucial molecules underlying PCOS Pathogenesis Based On Bioinformatics Analysis. Daru : journal of Faculty of Pharmacy, Tehran University of Medical Sciences, 29(2), 353.

Singh TP, et al. (2021) Systematic review of genome-wide association studies of abdominal aortic aneurysm. Atherosclerosis, 327, 39.

Mohammadpanah M, et al. (2020) Relationship of hypomethylation CpG islands in interleukin-6 gene promoter with IL-6 mRNA levels in patients with coronary atherosclerosis. Journal of cardiovascular and thoracic research, 12(3), 214.

Zhou J, et al. (2020) CATA: a comprehensive chromatin accessibility database for cancer. Database : the journal of biological databases and curation, 2022.

Luo ZH, et al. (2020) pyMeSHSim: an integrative python package for biomedical named entity recognition, normalization, and comparison of MeSH terms. BMC bioinformatics, 21(1), 252.

Beck T, et al. (2020) GWAS Central: a comprehensive resource for the discovery and comparison of genotype and phenotype data from genome-wide association studies. Nucleic acids research, 48(D1), D933.

Jurisic V, et al. (2020) EGFR Polymorphism and Survival of NSCLC Patients Treated with TKIs: A Systematic Review and Meta-Analysis. Journal of oncology, 2020, 1973241.

Quan Y, et al. (2019) Systems Chemical Genetics-Based Drug Discovery: Prioritizing Agents Targeting Multiple/Reliable Disease-Associated Genes as Drug Candidates. Frontiers in genetics, 10, 474.

Gao M, et al. (2019) PheWAS-Based Systems Genetics Methods for Anti-Breast Cancer Drug Discovery. Genes, 10(2).