

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

GWASdb

RRID:SCR_006015

Type: Tool

Proper Citation

GWASdb (RRID:SCR_006015)

Resource Information

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

Proper Citation: GWASdb (RRID:SCR_006015)

Description: Combines collections of genetic variants (GVs) from GWAS and their comprehensive functional annotations, as well as disease classifications. Used to maximize utility of GWAS data to gain biological insights through integrative, multi-dimensional functional annotation portal. In addition to all GV's annotated in NHGRI GWAS Catalog, we manually curate GV's that are marginally significant (P value 10⁻³) by looking into supplementary materials of each original publication and provide extensive functional annotations for these GV's. GV's are manually classified by diseases according to Disease Ontology Lite and HPO (Human Phenotype Ontology) for easy access. Database can also conduct gene based pathway enrichment and PPI network association analysis for those diseases with sufficient variants. SOAP services are available. You may Download GWASdb SNP. (This file contains all of the significant SNP in GWASdb. In the pvalue column, 0 means this P-value is not reported in the study but it is significant SNP. In the source column, GWAS:A represents the original data in GWAS catalog, while GWAS:B is our curation data which P-value 10⁻³)

Abbreviations: GWASdb

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

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:gnasdb, nlx_151404

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

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260919T195103+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 [nidm-terms](#).

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).

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

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.

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.

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.

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

Juriscic 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.

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.

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.

Zhao X, et al. (2019) Analysis of Topological Parameters of Complex Disease Genes Reveals the Importance of Location in a Biomolecular Network. *Genes*, 10(2).