

Resource Summary Report

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GWAS Atlas

RRID:SCR_027466

Type: Tool

Proper Citation

GWAS Atlas (RRID:SCR_027466)

Resource Information

URL: <https://atlas.ctglab.nl/>

Proper Citation: GWAS Atlas (RRID:SCR_027466)

Description: Updated knowledgebase integrating more curated associations in plants and animals. manually curated resource of genome-wide genotype-to-phenotype associations for a wide range of species. Database of publicly available GWAS summary statistics. Each GWAS can be browsed with the manhattan plot, risk loci, MAGMA (i.e. gene-based) results, SNP heritability and genetic correlations with other GWAS in the database. Full summary statistics can be downloaded from the original source following the provided links.

Resource Type: data or information resource, knowledge base

Defining Citation: [PMID:36263826](#)

Keywords: GWAS summary statistics, manually curated, genome-wide genotype-to-phenotype associations, plants, animals

Availability: Free, Freely available

Resource Name: GWAS Atlas

Resource ID: SCR_027466

Record Creation Time: 20250926T061848+0000

Record Last Update: 20260808T190809+0000

Ratings and Alerts

No rating or validation information has been found for GWAS Atlas.

No alerts have been found for GWAS Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Zhang J, et al. (2026) Mutual learning for joint disease detection and severity prediction reveals multimodal pathogenesis for neurodegenerative disorders. *Bioinformatics* (Oxford, England), 42(1).

Sharew NT, et al. (2026) Using multi-trait polygenic scores to predict lithium responsiveness in patients with bipolar disorder. *medRxiv : the preprint server for health sciences*.

Henechowicz TL, et al. (2026) Polygenic Associations Between Motor Behavior, Neuromotor Traits, and Active Music Engagement in Four Cohorts. *Annals of the New York Academy of Sciences*, 1556(1), e70191.

Hu M, et al. (2025) Investigating the visceral adiposity-major depressive disorder link: a cross-sectional NHANES 2011-2014 analysis and Mendelian randomization study. *Eating and weight disorders : EWD*, 30(1), 82.

McArthur E, et al. (2025) Reconstructing the 3D genome organization of Neanderthals reveals that chromatin folding shaped phenotypic and sequence divergence. *bioRxiv : the preprint server for biology*.

Alex E, et al. (2025) GWAS for behavioral traits in golden retrievers identifies genes implicated in human temperament, mental health, and cognition. *Proceedings of the National Academy of Sciences of the United States of America*, 122(48), e2421757122.

Brongo SE, et al. (2025) Genetic and functional evidence implicates a CRIP3 non-synonymous variant in age-related hearing loss. *medRxiv : the preprint server for health sciences*.

Salih AM, et al. (2025) Bone mineral density and cardiovascular diseases: a two-sample Mendelian randomization study. *JBMR plus*, 9(5), ziaf037.

Zhang Y, et al. (2025) Exploring the classification and treatment of osteoporosis from the perspectives of natural medicines, molecular targets, and symptom clusters. *Scientific reports*, 15(1), 10218.

Zhan H, et al. (2025) Biomarker identification for Alzheimer's disease through integration of comprehensive Mendelian randomization and proteomics data. *Journal of translational medicine*, 23(1), 278.

Zhu D, et al. (2025) Egg-laying ChickenGTEx resource deciphers context-specific regulatory effects on fertility traits. *Nature communications*, 17(1), 553.

Zhang T, et al. (2025) Multi-omics dissection of the genetic regulation underlying fatty acid composition in cattle. *Genome biology*, 26(1), 432.

Shin YW, et al. (2025) Causal Relationship Between Epilepsy, Status Epilepticus and Sleep-Related Traits: A Bidirectional Mendelian Randomization Study. *Brain sciences*, 15(7).

Chowdhury T, et al. (2025) Evaluation of Choline Metabolic Genes in the Liver of the Dam as Candidates for Mediating Choline's Efficacy in Mitigating Ethanol-Induced Cell Death in the Neural Tube: A Preliminary Analysis. *Genes*, 17(1).

Xi Y, et al. (2025) Mapping multitissue regulatory variants reveals a liver-centric coexpression network associated with duck egg-laying performance. *Genome research*, 35(10), 2211.

Enduru N, et al. (2025) Genetic, Transcriptomic, and Epigenomic Insights into Sjögren's Disease: An Integrative Network Investigation and Immune Diseases Comparison. *International journal of molecular sciences*, 26(10).

Martone A, et al. (2025) Genetic factors and symptom dimensions associated with antidepressant treatment outcomes: clues for new potential therapeutic targets? *European archives of psychiatry and clinical neuroscience*, 275(6), 1637.

Yan S, et al. (2024) Gene co-expression network and differential expression analyses reveal key genes for weaning weight in Simmental-Holstein crossbred cattle. *Animal biotechnology*, 35(1), 2404042.

Choi E, et al. (2024) Prioritizing susceptibility genes for the prognosis of male-pattern baldness with transcriptome-wide association study. *Human genomics*, 18(1), 34.

Yang J, et al. (2024) Pathogen stimulations and immune cells synergistically affect the gene expression profile characteristics of porcine peripheral blood mononuclear cells. *BMC genomics*, 25(1), 719.