Resource Summary Report

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GWAS: Catalog of Published Genome-Wide Association Studies

RRID:SCR_012745
Type: Tool

Proper Citation

GWAS: Catalog of Published Genome-Wide Association Studies (RRID:SCR_012745)

Resource Information

URL: http://www.ebi.ac.uk/gwas/

Proper Citation: GWAS: Catalog of Published Genome-Wide Association Studies (RRID:SCR_012745)

Description: Catalog of published genome-wide association studies. Genome-wide set of genetic variants in different individuals to see if any variant is associated with trait and disease. Database of genome-wide association study (GWAS) publications including only those attempting to assay single nucleotide polymorphisms (SNPs). Publications are organized from most to least recent date of publication. Studies are identified through weekly PubMed literature searches, daily NIH-distributed compilations of news and media reports, and occasional comparisons with an existing database of GWAS literature (HuGE Navigator). Works with HANCESTRO ancestry representation.

Abbreviations: GWASC

Synonyms: A Catalog of Published Genome-Wide Association Studies, Catalog of Published GWAS, Catalog of published GWAS studies, NHGRI GWAS Catalog, Catalog of Published Genome-Wide Association Studies, GWAS and PGS Catalogs

Resource Type: data or information resource, catalog, database

Defining Citation: PMID:19474294

Keywords: gene-wide association study, adult, genome, genome-wide association study, single nucleotide polymorphism, publication, literature, phenotype, trait, disease, loci, genetic variant, disorder, snp trait association

Funding: NHGRI U41 HG007823;
BBSRC ;
NHGRI U24 HG012542

Availability: Free, Freely available

Resource Name: GWAS: Catalog of Published Genome-Wide Association Studies

Resource ID: SCR_012745

Alternate IDs: nif-0000-06666

Old URLs: http://www.genome.gov/gwastudies

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250407T220030+0000

Ratings and Alerts

No rating or validation information has been found for GWAS: Catalog of Published Genome-Wide Association Studies.

No alerts have been found for GWAS: Catalog of Published Genome-Wide Association Studies.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 833 mentions in open access literature.

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

Tan X, et al. (2025) Advancing allergic rhinitis research through phenome-wide association studies: Insights from known genetic loci. The World Allergy Organization journal, 18(1), 101014.

Cerezo M, et al. (2025) The NHGRI-EBI GWAS Catalog: standards for reusability, sustainability and diversity. Nucleic acids research, 53(D1), D998.

Wang K, et al. (2024) Interplay between immune cells and metabolites in epilepsy: insights from a Mendelian randomization analysis. Frontiers in aging neuroscience, 16, 1400426.

Xiao F, et al. (2024) Functional dissection of human cardiac enhancers and noncoding de novo variants in congenital heart disease. Nature genetics, 56(3), 420.

Li L, et al. (2024) Genome-wide DNA methylation profiling reveals a novel hypermethylated biomarker PRKCB in gastric cancer. Scientific reports, 14(1), 26605.

Zhu Y, et al. (2024) Mendelian randomization highlights sleep disturbances mediated the effect of depression on chronic pain. Brain and behavior, 14(7), e3596.

Lin F, et al. (2024) Replication of previous autism-GWAS hits suggests the association between NAA1, SORCS3, and GSDME and autism in the Han Chinese population. Heliyon, 10(1), e23677.

Chen C, et al. (2024) PancanQTLv2.0: a comprehensive resource for expression quantitative trait loci across human cancers. Nucleic acids research, 52(D1), D1400.

Wu H, et al. (2024) Identifying the genetic association between severe autoimmune type 2 diabetes and the risk of focal epilepsy. Frontiers in endocrinology, 15, 1396912.

Teixeira SK, et al. (2024) Assessing the predictive efficacy of European-based systolic blood pressure polygenic risk scores in diverse Brazilian cohorts. Scientific reports, 14(1), 28123.

Lichtenstein L, et al. (2024) Endothelial force sensing signals to parenchymal cells to regulate bile and plasma lipids. Science advances, 10(39), eadq3075.

Zhou H, et al. (2024) Reverse causation between multiple sclerosis and psoriasis: a genetic correlation and Mendelian randomization study. Scientific reports, 14(1), 8845.

Wang Q, et al. (2024) Molecular profiling of human substantia nigra identifies diverse neuron types associated with vulnerability in Parkinson's disease. Science advances, 10(2), eadi8287.

Jiang Z, et al. (2024) Association between human blood metabolites and cerebral cortex architecture: evidence from a Mendelian randomization study. Frontiers in neurology, 15, 1386844.

Newsham I, et al. (2024) Early detection and diagnosis of cancer with interpretable machine learning to uncover cancer-specific DNA methylation patterns. Biology methods & protocols, 9(1), bpae028.

Diz-de Almeida S, et al. (2024) Novel risk loci for COVID-19 hospitalization among admixed American populations. eLife, 13.

Tsukamoto M, et al. (2024) GWAS of Folate Metabolism With Gene-environment Interaction Analysis Revealed the Possible Role of Lifestyles in the Control of Blood Folate Metabolites in Japanese: The J-MICC Study. Journal of epidemiology, 34(5), 228.

Yuan C, et al. (2024) Genetic prediction of the relationship between metabolic syndrome and

colorectal cancer risk: a Mendelian randomization study. Diabetology & metabolic syndrome, 16(1), 109.

Cruchaga C, et al. (2024) Novel early-onset Alzheimer-associated genes influence risk through dysregulation of glutamate, immune activation, and intracell signaling pathways. Research square.

Cai YM, et al. (2024) Genome-wide enhancer RNA profiling adds molecular links between genetic variation and human cancers. Military Medical Research, 11(1), 36.