Resource Summary Report

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GWAS Central

RRID:SCR_006170
Type: Tool

Proper Citation

GWAS Central (RRID:SCR_006170)

Resource Information

URL: http://www.gwascentral.org/

Proper Citation: GWAS Central (RRID:SCR_006170)

Description: Publicly available database of summary level findings from genetic association studies in humans, including genome wide association studies (GWAS). Previously named HGBASE, HGVbase and HGVbaseG2P.

Synonyms: Genome Wide Association Studies Central, Human Genome Variation database of Genotype to Phenotype information, HGVbaseG2P

Resource Type: service resource, data or information resource, data repository, database, storage service resource

Defining Citation: PMID:18948288

Keywords: Human Genome Variation database of Genotype-to-Phenotype information, genetic association study, genotype, phenotype, gene, genome region, disease, frequency data, region, genome, marker, single nucleotide polymorphism, genetic variant, allele, genome wide association study, human genome, chromosome, genetics

Funding: European Union GEN2PHEN project ;
University of Leicester; Leicester; United Kingdom ;
GlaxoSmithKline

Resource Name: GWAS Central

Resource ID: SCR_006170

Alternate IDs: nlx_151672, nif-0000-02958, SCR_007709, r3d100010565

Alternate URLs: http://www.hgvbaseg2p.org, https://doi.org/10.17616/R34G8W

License URLs: http://www.gwascentral.org/info/data/data-sharing-statement

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260729T044128+0000

Ratings and Alerts

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

No alerts have been found for GWAS Central.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 105 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Kiruba B, et al. (2025) Mapping integral cell-type-specific interferon-induced gene regulatory networks (GRNs) involved in systemic lupus erythematosus using systems and computational analysis. Heliyon, 11(1), e41342.

Zhou C, et al. (2025) Paradoxical regulation of IGF2 in promoting lipid metabolism in adipose tissues. Communications biology, 8(1), 1026.

Xu F, et al. (2024) Diagnostic implications of ubiquitination-related gene signatures in Alzheimer's disease. Scientific reports, 14(1), 10728.

Kot A, et al. (2024) Clinical Potential of Misshapen/NIKs-Related Kinase (MINK) 1-A Many-Sided Element of Cell Physiology and Pathology. Current issues in molecular biology, 46(12), 13811.

Guillet S, et al. (2024) ACK1 and BRK non-receptor tyrosine kinase deficiencies are associated with familial systemic lupus and involved in efferocytosis. eLife, 13.

Wang Y, et al. (2024) ApoL6 associates with lipid droplets and disrupts Perilipin1-HSL interaction to inhibit lipolysis. Nature communications, 15(1), 186.

Guillet S, et al. (2024) ACK1 and BRK non-receptor tyrosine kinase deficiencies are associated with familial systemic lupus and involved in efferocytosis. medRxiv : the preprint server for health sciences.

Wei S, et al. (2024) SMEK1 ablation promotes glucose uptake and improves obesity-related metabolic dysfunction via AMPK signaling pathway. American journal of physiology. Endocrinology and metabolism, 326(6), E776.

Price TR, et al. (2023) Identification of genetic drivers of plasma lipoprotein size in the Diversity Outbred mouse population. Journal of lipid research, 64(12), 100471.

Kour B, et al. (2023) Identification of Plausible Candidates in Prostate Cancer Using Integrated Machine Learning Approaches. Current genomics, 24(5), 287.

Sollis E, et al. (2023) The NHGRI-EBI GWAS Catalog: knowledgebase and deposition resource. Nucleic acids research, 51(D1), D977.

Lu Q, et al. (2023) Sema7A protects against high-fat diet-induced obesity and hepatic steatosis by regulating adipo/lipogenesis. Molecular metabolism, 70, 101698.

Hughes LA, et al. (2023) Copy number variation in tRNA isodecoder genes impairs mammalian development and balanced translation. Nature communications, 14(1), 2210.

Beck T, et al. (2023) GWAS Central: an expanding resource for finding and visualising genotype and phenotype data from genome-wide association studies. Nucleic acids research, 51(D1), D986.

Mallick I, et al. (2023) In-silico identification and prioritization of therapeutic targets of asthma. Scientific reports, 13(1), 15706.

Günes Günsel G, et al. (2022) The arginine methyltransferase PRMT7 promotes extravasation of monocytes resulting in tissue injury in COPD. Nature communications, 13(1), 1303.

Dong C, et al. (2021) INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome biology, 22(1), 241.

Forgacova N, et al. (2021) Repurposing non-invasive prenatal testing data: Population study of single nucleotide variants associated with colorectal cancer and Lynch syndrome. Oncology letters, 22(5), 779.

Gupta R, et al. (2021) Artificial intelligence to deep learning: machine intelligence approach for drug discovery. Molecular diversity, 25(3), 1315.

Hameed BMZ, et al. (2021) Big Data Analytics in urology: the story so far and the road ahead. Therapeutic advances in urology, 13, 1756287221998134.