Resource Summary Report

Generated by RRID on Aug 12, 2026

Open Targets Genetics Portal

RRID:SCR_021701
Type: Tool

Proper Citation

Open Targets Genetics Portal (RRID:SCR_021701)

Resource Information

URL: https://genetics.opentargets.org/

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Description: Portal offers features to help discover associations between genes, variants, and traits including Browse and rank gene and variant associations identified by Locus-to-Gene (L2G) scoring pipeline, Uncover credible sets for variant and trait associations based on mapping analyses pipeline, Explore and compare studies from UK Biobank, FinnGen, and GWAS Catalog using multi-trait comparison tool eQTL Catalogue.

Resource Type: data or information resource, portal

Defining Citation: DOI:10.1093/nar/gkaa840

Keywords: Discover associations, associations between genes, variants, traits, rank gene and variant associations,

Availability: Free, Freely available

Resource Name: Open Targets Genetics Portal

Resource ID: SCR_021701

Alternate URLs: https://github.com/opentargets

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260811T043654+0000

Ratings and Alerts

No rating or validation information has been found for Open Targets Genetics Portal.

No alerts have been found for Open Targets Genetics Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 171 mentions in open access literature.

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

Holen B, et al. (2026) Shared genetic variants across substance use disorders implicate common neurobiological pathways, a genome-wide mixed methods study. General psychiatry, 39(2), e70017.

Moreno E, et al. (2026) Genome-wide association meta-analyses over one million individuals identify 54 loci associated with urinary incontinence and its subtypes. medRxiv : the preprint server for health sciences.

Huang K, et al. (2026) Exploring a genetic basis for the metabolic perturbations in ME/CFS using UK biobank. iScience, 29(1), 114316.

Aarts EM, et al. (2026) Network-based framework for studying etiology and phenotypic diversity in primary ciliopathies. Genome biology, 27(1).

Blew CO, et al. (2026) Plasma GDF15 affects long-term dementia risk and alters neuroimmune signaling. Science advances, 12(26), eaec7614.

Rentsch CT, et al. (2026) Bridging Genomics and Pharmacoepidemiology to Expand Treatment Options for Alcohol Use Disorder. medRxiv : the preprint server for health sciences.

Moazzam-Jazi M, et al. (2026) Interplay between obesity-associated insulin resistance and immune system through the lens of evolutionary medicine. Molecular metabolism, 106, 102335.

Rødevand L, et al. (2026) Evidence for overlapping genetic architecture between lifestyle factors and severe mental disorders with different patterns across diagnoses. EBioMedicine, 128, 106304.

Kafita D, et al. (2026) Decoding the dark genome reveals its organisation into modular disease networks. Scientific reports, 16(1).

Geller F, et al. (2026) Central role of glycosylation processes in human genetic susceptibility to SARS-CoV-2 infections with Omicron variants. Nature genetics, 58(2), 299.

Buniello A, et al. (2025) Open Targets Platform: facilitating therapeutic hypotheses building in drug discovery. Nucleic acids research, 53(D1), D1467.

Wiström ED, et al. (2025) The genetic overlap between major depressive disorder, white blood cell counts and interleukin 6. Journal of affective disorders reports, 20.

Jordà P, et al. (2025) Genetic analyses across cardiovascular traits: leveraging genetic correlations to empower locus discovery and prediction in common cardiovascular diseases. NPJ genomic medicine, 10(1), 65.

Jia Y, et al. (2025) Stratified shared genetic architecture of IBD and RA: an integrated analysis from polygenic overlap to directional heterogeneity. Frontiers in immunology, 16, 1711302.

Lu T, et al. (2025) Estimating effects of serum vitamin B12 levels on psychiatric disorders and cognitive impairment: a Mendelian randomization study. Communications medicine, 5(1), 316.

Dang C, et al. (2025) Polycystic ovary syndrome and risk of pregnancy-induced hypertension, gestational diabetes mellitus, and preeclampsia: a Bayesian Mendelian randomization study. Diabetology & metabolic syndrome, 17(1), 204.

Zhang X, et al. (2025) Multi-ancestry whole genome sequencing analysis of lean body mass. Genome biology, 26(1), 106.

Hu S, et al. (2025) Fine-scale population structure and widespread conservation of genetic effect sizes between human groups across traits. Nature genetics, 57(2), 379.

Yoshiji S, et al. (2025) Integrative proteogenomic analysis identifies COL6A3-derived endotrophin as a mediator of the effect of obesity on coronary artery disease. Nature genetics, 57(2), 345.

El Rouby N, et al. (2025) Genome Wide Association Study (GWAS) Identifies Novel Genetic Loci for Second-Generation Antipsychotics (SGA)-Induced Metabolic Syndrome (MetS). Clinical and translational science, 18(4), e70216.