

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## GeneATLAS

RRID:SCR\_017577

Type: Tool

### Proper Citation

GeneATLAS (RRID:SCR\_017577)

### Resource Information

**URL:** <http://geneatlas.roslin.ed.ac.uk>

**Proper Citation:** GeneATLAS (RRID:SCR\_017577)

**Description:** Database of associations between traits and variants using UK Biobank cohort. Searchable atlas of genetic associations. Assists researchers to query UK Biobank. Provides unbiased view of phenotype and genotype associations across of traits.

**Synonyms:** Gene ATLAS, Gene Atlas

**Resource Type:** data analysis service, data or information resource, database, service resource, atlas, production service resource, analysis service resource

**Keywords:** Association, trait, variant, UK Biobank, cohort, atlas, genetic, phenotype, genotype, FASEB list

**Availability:** Free, Available for download, Freely available

**Resource Name:** GeneATLAS

**Resource ID:** SCR\_017577

**Record Creation Time:** 20220129T080335+0000

**Record Last Update:** 20260801T190607+0000

### Ratings and Alerts

No rating or validation information has been found for GeneATLAS.

No alerts have been found for GeneATLAS.

### Data and Source Information

## Usage and Citation Metrics

We found 132 mentions in open access literature.

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

Gao K, et al. (2025) Machine learning analysis of FOSL2 and RHoBTB1 as central immunological regulators in knee osteoarthritis synovium. The Journal of international medical research, 53(4), 3000605251333646.

Walker GJ, et al. (2025) Assessment of the Influence of UVR in Cutaneous Melanoma. Photodermatology, photoimmunology & photomedicine, 41(3), e70024.

Saranyuk R, et al. (2025) Genetic Interactions of Phase II Xenobiotic-Metabolizing Enzymes GSTO1 and GCLC in Relation to Alcohol Abuse and Psoriasis Risk. Journal of xenobiotics, 15(2).

Garcia-Salinas OI, et al. (2025) The impact of ancestral, genetic, and environmental influences on germline de novo mutation rates and spectra. Nature communications, 16(1), 4527.

He H, et al. (2025) Integrated multi-omics and machine learning reveals immune-metabolic signatures in osteoarthritis: from bulk RNA-seq to single-cell resolution. Frontiers in immunology, 16, 1599930.

Zhou H, et al. (2025) Exploring the Interaction Mechanisms of Antibody-Mediated Immune Responses with Gout and Rheumatoid Arthritis Through a Bidirectional Two-Sample Mendelian Randomization Study. Journal of pain research, 18, 2707.

Ye ZN, et al. (2025) Risk factors for non-responsiveness to 5-aminosalicylic acid in patients with ulcerative colitis identified using retrospective clinical study and Mendelian randomization. Scientific reports, 15(1), 9182.

Kleist AB, et al. (2025) Encoding and decoding selectivity and promiscuity in the human chemokine-GPCR interaction network. Cell, 188(13), 3603.

Du Y, et al. (2024) Multi-omics technologies and molecular biomarkers in brain tumor-related epilepsy. CNS neuroscience & therapeutics, 30(4), e14717.

Cao J, et al. (2024) Mechanistic study of pre-eclampsia and macrophage-associated molecular networks: bioinformatics insights from multiple datasets. Frontiers in genetics, 15, 1376971.

Xie Z, et al. (2024) iGWAS: Image-based genome-wide association of self-supervised deep phenotyping of retina fundus images. PLoS genetics, 20(5), e1011273.

Aierken A, et al. (2024) No bidirectional relationship between constipation and colorectal cancer in European and Asian populations: A Mendelian randomization study. Medicine, 103(43), e40206.

Wu T, et al. (2024) MutL homolog 1 participates in interference-sensitive meiotic crossover formation in soybean. *Plant physiology*, 195(4), 2579.

Guo J, et al. (2024) Phenome-wide association study in 25,639 pregnant Chinese women reveals loci associated with maternal comorbidities and child health. *Cell genomics*, 4(10), 100632.

Guo R, et al. (2024) Genetic correlation and Mendelian randomization analyses support causal relationships between dietary habits and age at menarche. *Scientific reports*, 14(1), 8425.

Wang Y, et al. (2024) Identifying hub genes for chemo-radiotherapy sensitivity in cervical cancer: a bi-dataset in silico analysis. *Discover oncology*, 15(1), 434.

Vilor-Tejedor N, et al. (2024) Genetic characterization of the ALFA study: Uncovering genetic profiles in the Alzheimer's continuum. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 20(3), 1703.

Wang T, et al. (2024) Characterizing hedgehog pathway features in senescence associated osteoarthritis through Integrative multi-omics and machine learning analysis. *Frontiers in genetics*, 15, 1255455.

Wu Y, et al. (2024) Characterizing mitochondrial features in osteoarthritis through integrative multi-omics and machine learning analysis. *Frontiers in immunology*, 15, 1414301.

Cui Y, et al. (2024) Identification of key genes to predict response to chemoradiotherapy and prognosis in esophageal squamous cell carcinoma. *Frontiers in molecular biosciences*, 11, 1512715.