

Resource Summary Report

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Gene Atlas

RRID:SCR_008089

Type: Tool

Proper Citation

Gene Atlas (RRID:SCR_008089)

Resource Information

URL: <http://www.geneatlas.org/gene/main.jsp>

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Description: This website allows visitors to search for genes of interest based on their spatial expression patterns in the Postnatal Day 7 mouse brain. Geneatlas provides two searching tools: A graphical interface for customized spatial queries; A textual interface for querying annotated structures. Geneatlas is the product of a collaboration between researchers at Baylor College of Medicine, Rice University, and University of Houston.

Abbreviations: Geneatlas

Resource Type: atlas, data or information resource, database

Keywords: gene, brain, mouse, protein, spatial expression, molecular neuroanatomy resource, FASEB list

Funding: Burroughs Wellcome Fund ;
NLM 5T15LM07093;
NCRR P41RR02250

Resource Name: Gene Atlas

Resource ID: SCR_008089

Alternate IDs: nif-0000-10987

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260821T193834+0000

Ratings and Alerts

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

No alerts have been found for Gene Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Li J, et al. (2025) Comprehensive Proteomic Profiling of Exfoliation Glaucoma Via Mass Spectrometry Reveals SVEP1 as a Potential Biomarker. Investigative ophthalmology & visual science, 66(3), 19.

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).

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.

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.

Wang HY, et al. (2025) scDIFF: automatic cell type annotation using scATAC-seq data by incorporating bulk-level genomic and epigenomic information in a deep diffusive transformer. Briefings in bioinformatics, 26(6).

Maehr T, et al. (2025) A safe, T cell-inducing heterologous vaccine against elephant endotheliotropic herpesvirus in a proof-of-concept study. Nature communications, 16(1), 8374.

E C, et al. (2024) Single-Cell Sequencing Combined with Transcriptome Sequencing to Explore the Molecular Mechanisms Related to Psoriasis. Clinical, cosmetic and investigational dermatology, 17, 2197.

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.

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.

- Zeidan AM, et al. (2024) Integrated genetic, epigenetic, and immune landscape of TP53 mutant AML and higher risk MDS treated with azacitidine. *Therapeutic advances in hematology*, 15, 20406207241257904.
- 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.
- 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.
- Efanova E, et al. (2023) Polymorphisms of the GCLC Gene Are Novel Genetic Markers for Susceptibility to Psoriasis Associated with Alcohol Abuse and Cigarette Smoking. *Life (Basel, Switzerland)*, 13(6).
- Salah N, et al. (2023) Evaluation of the role of kefir in management of non-alcoholic steatohepatitis rat model via modulation of NASH linked mRNA-miRNA panel. *Scientific reports*, 13(1), 236.
- Choquet H, et al. (2022) Ancestry- and sex-specific effects underlying inguinal hernia susceptibility identified in a multiethnic genome-wide association study meta-analysis. *Human molecular genetics*, 31(13), 2279.
- Tu LN, et al. (2021) Shear stress associated with cardiopulmonary bypass induces expression of inflammatory cytokines and necroptosis in monocytes. *JCI insight*, 6(1).
- Dong SS, et al. (2021) Phenome-wide investigation of the causal associations between childhood BMI and adult trait outcomes: a two-sample Mendelian randomization study. *Genome medicine*, 13(1), 48.
- Kim SS, et al. (2021) A Compendium of Age-Related PheWAS and GWAS Traits for Human Genetic Association Studies, Their Networks and Genetic Correlations. *Frontiers in genetics*, 12, 680560.
- Choquet H, et al. (2021) A large multiethnic GWAS meta-analysis of cataract identifies new risk loci and sex-specific effects. *Nature communications*, 12(1), 3595.
- Ali HS, et al. (2020) lncRNA- RP11-156p1.3, novel diagnostic and therapeutic targeting via CRISPR/Cas9 editing in hepatocellular carcinoma. *Genomics*, 112(5), 3306.