Resource Summary Report

Generated by <u>dkNET</u> on May 11, 2025

Gene Atlas

RRID:SCR_008089 Type: Tool

Proper Citation

Gene Atlas (RRID:SCR_008089)

Resource Information

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

Proper Citation: Gene Atlas (RRID:SCR_008089)

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: data or information resource, database, atlas

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: 20250509T055903+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 41 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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.

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.

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.

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.

Tu LN, et al. (2021) Shear stress associated with cardiopulmonary bypass induces expression of inflammatory cytokines and necroptosis in monocytes. JCI insight, 6(1).

Ali HS, et al. (2020) IncRNA- RP11-156p1.3, novel diagnostic and therapeutic targeting via CRISPR/Cas9 editing in hepatocellular carcinoma. Genomics, 112(5), 3306.

Salah SMM, et al. (2020) Dysregulation in the expression of (IncRNA-TSIX, TP53INP2 mRNA, miRNA-1283) in spinal cord injury. Genomics, 112(5), 3315.

Alpern D, et al. (2019) BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. Genome biology, 20(1), 71.

Shadrina AS, et al. (2019) Varicose veins of lower extremities: Insights from the first largescale genetic study. PLoS genetics, 15(4), e1008110.

Li J, et al. (2019) A Stress-Associated Protein, PtSAP13, From Populus trichocarpa Provides Tolerance to Salt Stress. International journal of molecular sciences, 20(22).

Endo C, et al. (2018) Genome-wide association study in Japanese females identifies fifteen novel skin-related trait associations. Scientific reports, 8(1), 8974.

Korostynski M, et al. (2018) Cell-type-specific gene expression patterns in the knee cartilage in an osteoarthritis rat model. Functional & integrative genomics, 18(1), 79.