Resource Summary Report

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EMAGE Gene Expression Database

RRID:SCR_005391
Type: Tool

Proper Citation

EMAGE Gene Expression Database (RRID:SCR_005391)

Resource Information

URL: http://www.emouseatlas.org/emage

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Description: A database of in situ gene expression data in the developing mouse embryo and an accompanying suite of tools to search and analyze the data. mRNA in situ hybridization, protein immunohistochemistry and transgenic reporter data is included. The data held is spatially annotated to a framework of 3D mouse embryo models produced by EMAP (e-Mouse Atlas Project). These spatial annotations allow users to query EMAGE by spatial pattern as well as by gene name, anatomy term or Gene Ontology (GO) term. The conceptual framework which houses the descriptions of the gene expression patterns in EMAGE is the EMAP Mouse Embryo Anatomy Atlas. This consists of a set of 3D virtual embryos at different stages of development, as well as an accompanying ontology of anatomical terms found at each stage. The raw data images can be conventional 2D photographs (of sections or wholemount specimens) or 3D images of wholemount specimens derived from Optical Projection Tomography (OPT) or confocal microscopy. Users may submit data using a Data submission tool or without.

Abbreviations: EMAGE

Synonyms: Emage (e-Mouse Atlas of Gene Expression), e-Mouse Atlas of Gene Expression

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

Defining Citation: PMID:19767607

Keywords: genetics, 3d model, anatomy, development, mouse morphology, molecular neuroanatomy resource, gene expression, in situ hybridization, immunohistochemistry, embryo, in situ reporter, embryonic mouse, optical projection tomography, confocal microscopy, annotation, pathway, gene association, protein, theiler stage, gene expression, embryology, dna, protein, protein-protein interaction, protein binding, gene, embryology, anatomy, genetics, bio.tools

Funding: MRC

Availability: Except where noted, Creative Commons Attribution License, The community can contribute to this resource

Resource Name: EMAGE Gene Expression Database

Resource ID: SCR_005391

Alternate IDs: biotools:emage, nif-0000-00080

Alternate URLs: https://bio.tools/emage

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250412T054941+0000

Ratings and Alerts

No rating or validation information has been found for EMAGE Gene Expression Database.

No alerts have been found for EMAGE Gene Expression Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Urbanek ME, et al. (2021) Genetic predisposition to tinnitus in the UK Biobank population. Scientific reports, 11(1), 18150.

Beck SV, et al. (2020) Differences among families in craniofacial shape at early life-stages of Arctic charr (Salvelinus alpinus). BMC developmental biology, 20(1), 21.

Li J, et al. (2019) Application of Computational Biology to Decode Brain Transcriptomes. Genomics, proteomics & bioinformatics, 17(4), 367.

Somorjai IML, et al. (2018) Wnt evolution and function shuffling in liberal and conservative chordate genomes. Genome biology, 19(1), 98.

Galperin MY, et al. (2017) The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. Nucleic acids research, 45(D1), D1.

Adutwum-Ofosu KK, et al. (2016) The molecular and cellular signatures of the mouse eminentia thalami support its role as a signalling centre in the developing forebrain. Brain structure & function, 221(7), 3709.

Peng G, et al. (2016) Spatial Transcriptome for the Molecular Annotation of Lineage Fates and Cell Identity in Mid-gastrula Mouse Embryo. Developmental cell, 36(6), 681.

Fongang B, et al. (2016) Comparison between Timelines of Transcriptional Regulation in Mammals, Birds, and Teleost Fish Somitogenesis. PloS one, 11(5), e0155802.

Tadeu AM, et al. (2015) Transcriptional profiling of ectoderm specification to keratinocyte fate in human embryonic stem cells. PloS one, 10(4), e0122493.

Richardson L, et al. (2014) EMAGE mouse embryo spatial gene expression database: 2014 update. Nucleic acids research, 42(Database issue), D835.

Hayamizu TF, et al. (2013) EMAP/EMAPA ontology of mouse developmental anatomy: 2013 update. Journal of biomedical semantics, 4(1), 15.

Armas P, et al. (2013) Beyond the binding site: in vivo identification of tbx2, smarca5 and wnt5b as molecular targets of CNBP during embryonic development. PloS one, 8(5), e63234.

Baines AC, et al. (2013) Disruption of the Sec24d gene results in early embryonic lethality in the mouse. PloS one, 8(4), e61114.

Chacon MA, et al. (2013) MHC class I protein is expressed by neurons and neural progenitors in mid-gestation mouse brain. Molecular and cellular neurosciences, 52, 117.

Swedlow JR, et al. (2012) Innovation in biological microscopy: current status and future directions. BioEssays : news and reviews in molecular, cellular and developmental biology, 34(5), 333.

Armit C, et al. (2012) eMouseAtlas, EMAGE, and the spatial dimension of the transcriptome. Mammalian genome : official journal of the International Mammalian Genome Society, 23(9-10), 514.

Gaudet P, et al. (2011) Towards BioDBcore: a community-defined information specification for biological databases. Database : the journal of biological databases and curation, 2011, baq027.

Guryanova OA, et al. (2011) Nonreceptor tyrosine kinase BMX maintains self-renewal and tumorigenic potential of glioblastoma stem cells by activating STAT3. Cancer cell, 19(4), 498.

Hochheiser H, et al. (2011) The FaceBase Consortium: a comprehensive program to facilitate craniofacial research. Developmental biology, 355(2), 175.

Thessen AE, et al. (2011) Data issues in the life sciences. ZooKeys(150), 15.