Resource Summary Report

Generated by NIF on Apr 18, 2025

EMBRYS

RRID:SCR_006689
Type: Tool

Proper Citation

EMBRYS (RRID:SCR_006689)

Resource Information

URL: https://www.embrys.jp/embrys/html/About.html

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Description: Data collection of gene expression patterns mapped in whole-mount mouse embryo (ICR strain) of mid-gestational stages (Embryonic Day 9.5, 10.5, 11.5), in which most striking dynamics in pattern formation and organogenesis is observed. Collection of gene expression patterns of transcription factors (TFs) and TF-related factors such as transcription cofactors. Genes were extracted from databases including RIKEN Transcription Factor Database and Panther Classification System.

Abbreviations: EMBRYS

Synonyms: Embryonic Gene Expression Database for Biomedical Research Source, Embryonic gene expression Database as a Biomedical Research Source

Resource Type: database, data or information resource

Keywords: Gene, expression, pattern, mapped, whole mount, mouse, embryo, ICR strain, mid gestational stage, transcription, factor, cofactor, data

Funding: Japanese Ministry of Education Culture Sports Science and Technology MEXT ; Japanese Ministry of Health Labor and Welfare

Availability: Free, Freely available

Resource Name: EMBRYS

Resource ID: SCR_006689

Alternate IDs: nlx_153839

Old URLs: http://embrys.jp/embrys/html/MainMenu.html

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250412T055118+0000

Ratings and Alerts

No rating or validation information has been found for EMBRYS.

No alerts have been found for EMBRYS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Gamart J, et al. (2021) SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. Development (Cambridge, England), 148(23).

Yokoyama S, et al. (2017) Analysis of transcription factors expressed at the anterior mouse limb bud. PloS one, 12(5), e0175673.

Motohashi T, et al. (2016) Gene array analysis of neural crest cells identifies transcription factors necessary for direct conversion of embryonic fibroblasts into neural crest cells. Biology open, 5(3), 311.

Clarkson MD, et al. (2016) Representation of anatomy in online atlases and databases: a survey and collection of patterns for interface design. BMC developmental biology, 16(1), 18.

Bhat R, et al. (2016) Deep phylogenomics of a tandem-repeat galectin regulating appendicular skeletal pattern formation. BMC evolutionary biology, 16(1), 162.

Ogura Y, et al. (2015) Identification of HOXD4 Mutations in Spinal Extradural Arachnoid Cyst. PloS one, 10(11), e0142126.

Shimizu H, et al. (2013) The AERO system: a 3D-like approach for recording gene expression patterns in the whole mouse embryo. PloS one, 8(10), e75754.

Ito Y, et al. (2012) A systems approach and skeletal myogenesis. Comparative and functional genomics, 2012, 759407.