

Resource Summary Report

Generated by NIF on Sep 5, 2026

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: data or information resource, database

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: 20260904T000216+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.

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

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.

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.