Resource Summary Report

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Patterns of Gene Expression in Drosophila Embryogenesis

RRID:SCR_002868
Type: Tool

Proper Citation

Patterns of Gene Expression in Drosophila Embryogenesis (RRID:SCR_002868)

Resource Information

URL: http://insitu.fruitfly.org/cgi-bin/ex/insitu.pl

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Description: Database of embryonic expression patterns using a high throughput RNA in situ hybridization of the protein-coding genes identified in the Drosophila melanogaster genome with images and controlled vocabulary annotations. At the end of production pipeline gene expression patterns are documented by taking a large number of digital images of individual embryos. The quality and identity of the captured image data are verified by independently derived microarray time-course analysis of gene expression using Affymetrix GeneChip technology. Gene expression patterns are annotated with controlled vocabulary for developmental anatomy of Drosophila embryogenesis. Image, microarray and annotation data are stored in a modified version of Gene Ontology database and the entire dataset is available on the web in browsable and searchable form or MySQL dump can be downloaded. So far, they have examined expression of 7507 genes and documented them with 111184 digital photographs.

Abbreviations: BDGP insitu

Synonyms: BDGP Embryonic Expression Patterns

Resource Type: database, data or information resource, software resource, image collection, source code

Defining Citation: PMID:17645804, PMID:12537577

Keywords: embryo, embryogenesis, gene, anatomy, microarray, pattern, protocol, rna, gene expression, expression pattern, embryonic drosophila, in situ hybridization, annotation, est, FASEB list

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Resource Name: Patterns of Gene Expression in Drosophila Embryogenesis

Resource ID: SCR_002868

Alternate IDs: nif-0000-25550

Old URLs: http://www.fruitfly.org/cgi-bin/ex/insitu.pl

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250411T054810+0000

Ratings and Alerts

No rating or validation information has been found for Patterns of Gene Expression in Drosophila Embryogenesis.

No alerts have been found for Patterns of Gene Expression in Drosophila Embryogenesis.

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 RRID.

Gomez JM, et al. (2024) Differential regulation of the proteome and phosphoproteome along the dorso-ventral axis of the early Drosophila embryo. eLife, 13.

Kudron M, et al. (2024) Binding profiles for 954 Drosophila and C. elegans transcription factors reveal tissue specific regulatory relationships. bioRxiv : the preprint server for biology.

de Almeida BP, et al. (2024) Targeted design of synthetic enhancers for selected tissues in the Drosophila embryo. Nature, 626(7997), 207.

Peng D, et al. (2024) Organogenetic transcriptomes of the Drosophila embryo at single cell resolution. Development (Cambridge, England), 151(2).

Sloutskin A, et al. (2024) From promoter motif to cardiac function: a single DPE motif affects transcription regulation and organ function in vivo. Development (Cambridge, England), 151(14).

Sloutskin A, et al. (2023) A single DPE core promoter motif contributes to in vivo transcriptional regulation and affects cardiac function. bioRxiv : the preprint server for biology.

Ashour DJ, et al. (2023) Zasp52 strengthens whole embryo tissue integrity through supracellular actomyosin networks. Development (Cambridge, England), 150(7).

Coleman-Gosser N, et al. (2023) Continuous muscle, glial, epithelial, neuronal, and hemocyte cell lines for Drosophila research. eLife, 12.

Seroka A, et al. (2022) Transcriptional profiling from whole embryos to single neuroblast lineages in Drosophila. Developmental biology, 489, 21.

Panfilio KA, et al. (2022) The extended analogy of extraembryonic development in insects and amniotes. Philosophical transactions of the Royal Society of London. Series B, Biological sciences, 377(1865), 20210268.

Heinen T, et al. (2022) scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation. Genome biology, 23(1), 8.

Yoo B, et al. (2021) 20-hydroxyecdysone (20E) signaling regulates amnioserosa morphogenesis during Drosophila dorsal closure: EcR modulates gene expression in a complex with the AP-1 subunit, Jun. Biology open, 10(8).

Li YR, et al. (2021) Trajectory mapping of the early Drosophila germline reveals controls of zygotic activation and sex differentiation. Genome research, 31(6), 1011.

Atienza-Manuel A, et al. (2021) Endocytosis mediated by an atypical CUBAM complex modulates slit diaphragm dynamics in nephrocytes. Development (Cambridge, England), 148(22).

Bastian FB, et al. (2021) The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. Nucleic acids research, 49(D1), D831.

Dib A, et al. (2021) Pri smORF Peptides Are Wide Mediators of Ecdysone Signaling, Contributing to Shape Spatiotemporal Responses. Frontiers in genetics, 12, 714152.

Ma J, et al. (2021) Kinectin1 depletion promotes EGFR degradation via the ubiquitin-proteosome system in cutaneous squamous cell carcinoma. Cell death & disease, 12(11), 995.

Kim M, et al. (2020) A Functional Analysis of the Drosophila Gene hindsight: Evidence for Positive Regulation of EGFR Signaling. G3 (Bethesda, Md.), 10(1), 117.

Dorogova NV, et al. (2020) Migration of primordial germline cells is negatively regulated by surrounding somatic cells during early embryogenesis in Drosophila melanogaster. Vavilovskii zhurnal genetiki i selektsii, 24(5), 525.

Curt JR, et al. (2019) Anterior CNS expansion driven by brain transcription factors. eLife, 8.