Resource Summary Report

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Berkeley Drosophila Transcription Network Project

RRID:SCR_008640
Type: Tool

Proper Citation

Berkeley Drosophila Transcription Network Project (RRID:SCR_008640)

Resource Information

URL: http://bdtnp.lbl.gov/Fly-Net/index.jsp?w=home

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Description: The goal of this project is to decipher the transcriptional information contained in the extensive cis-acting DNA sequences that direct the patterns of gene expression that underlie animal development. Using the early embryo of the fruitfly Drosophila melanogaster as a model, these researchers are developing experimental and computational methods to systematically characterize and dissect the complex expression patterns and regulatory interactions already present prior to gastrulation. They have identified 37 principal regulatory factors within this network for initial analysis together with their target genes. Sponsors: This project is chiefly funded by a grant from NIGMS and NHGRI, R01 GM070444. Additional funding comes from grants to Michael Eisen, Sue Celniker, and Bernd Hamann.

Synonyms: BDTNP

Resource Type: data or information resource, portal, topical portal

Keywords: embryo, experimental, expression, gastrulation, gene, analysis, animal, cis-acting, computational, development, dna, information, interaction, regulatory, target, transcriptional

Resource Name: Berkeley Drosophila Transcription Network Project

Resource ID: SCR_008640

Alternate IDs: nif-0000-32986

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T195706+0000

Ratings and Alerts

No rating or validation information has been found for Berkeley Drosophila Transcription Network Project.

No alerts have been found for Berkeley Drosophila Transcription Network Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Bhattacharya N, et al. (2025) Network based simultaneous embedding of cells and marker genes from scRNA-seq studies. Briefings in bioinformatics, 26(5).

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

Zhao Y, et al. (2023) Spatial Reconstruction of Oligo and Single Cells by De Novo Coalescent Embedding of Transcriptomic Networks. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(20), e2206307.

Sharrock TE, et al. (2022) Different temporal requirements for tartan and wingless in the formation of contractile interfaces at compartmental boundaries. Development (Cambridge, England), 149(21).

Gupta S, et al. (2020) Feature Selection for Topological Proximity Prediction of Single-Cell Transcriptomic Profiles in Drosophila Embryo Using Genetic Algorithm. Genes, 12(1).

Tanevski J, et al. (2020) Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life science alliance, 3(11).

Sen SQ, et al. (2019) Neuroblast-specific open chromatin allows the temporal transcription factor, Hunchback, to bind neuroblast-specific loci. eLife, 8.

Arbel H, et al. (2019) Exploiting regulatory heterogeneity to systematically identify enhancers with high accuracy. Proceedings of the National Academy of Sciences of the United States of America, 116(3), 900.

Sayal R, et al. (2016) Quantitative perturbation-based analysis of gene expression predicts enhancer activity in early Drosophila embryo. eLife, 5.

Blatti C, et al. (2015) Integrating motif, DNA accessibility and gene expression data to build regulatory maps in an organism. Nucleic acids research, 43(8), 3998.

Niu M, et al. (2014) De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. BMC genomics, 15, 1047.