Resource Summary Report

Generated by NIF on May 11, 2025

FlyAtlas: the Drosophila gene expression atlas

RRID:SCR_005032
Type: Tool

Proper Citation

FlyAtlas: the Drosophila gene expression atlas (RRID:SCR_005032)

Resource Information

URL: http://www.flyatlas.org/

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Description: FlyAtlas gives you a quick answer to the question: where is my gene of interest expressed/enriched in the adult fly? For each gene and tissue, you''re given the mRNA SIGNAL (how abundant the mRNA is), the mRNA ENRICHMENT (compared to whole flies), and the Affymetrix PRESENT CALL (out of 4 arrays, how many times it was detectably expressed). The dataset so far comprises 44 Affymetrix Dros2 expression arrays, each mapping the expression of 18770 transcripts - corresponding to the vast majority of known Drosophila genes. The dataset thus contains over 822800 separate datapoints. This website is intended to make the data easily accessible and comprehensible to mere mortals. FlyAtlas provides the most comprehensive view yet of expression in multiple tissues of Drosophila melanogaster. Meta-analysis of the data shows that a significant fraction of the genome is expressed with great tissue specificity in the adult, demonstrating the need for the functional genomic community to embrace a wide range of functional phenotypes. Well-known developmental genes are often reused in surprising tissues in the adult, suggesting new functions. The homologs of many human genetic disease loci show selective expression in the Drosophila tissues analogous to the affected human tissues, providing a useful filter for potential candidate genes. Additionally, the contributions of each tissue to the whole-fly array signal can be calculated, demonstrating the limitations of whole-organism approaches to functional genomics and allowing modeling of a simple tissue fractionation procedure that should improve detection of weak or tissue-specific signals.

Abbreviations: FlyAtlas

Resource Type: data or information resource, expression atlas, atlas

Defining Citation: PMID:17534367

Keywords: adult, wild-type, canton s, brain, head, eye, thoracicoabdominal ganglion, salivary gland, crop, midgut, hindgut, heart, ovary, fat body, testis, male accessory glands, virgin spermatheca, mated spermatheca spermatheca, carcass, cns, salivary gland, tubule, larval, s2 cells, whole fly

Funding: BBSRC

Resource Name: FlyAtlas: the Drosophila gene expression atlas

Resource ID: SCR_005032

Alternate IDs: nlx_98284

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250509T055718+0000

Ratings and Alerts

No rating or validation information has been found for FlyAtlas: the Drosophila gene expression atlas.

No alerts have been found for FlyAtlas: the Drosophila gene expression atlas.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

Noyes NC, et al. (2023) Innate and learned odor-guided behaviors utilize distinct molecular signaling pathways in a shared dopaminergic circuit. Cell reports, 42(2), 112026.

Sun Y, et al. (2022) Loss of Bicra impairs Drosophila learning and choice abilities. Neuroscience letters, 769, 136432.

Stanek TJ, et al. (2022) Sex-specific variation in R-loop formation in Drosophila melanogaster. PLoS genetics, 18(6), e1010268.

Houle D, et al. (2021) Predicting the Evolution of Sexual Dimorphism in Gene Expression.

Molecular biology and evolution, 38(5), 1847.

Kanoh H, et al. (2021) cGMP signaling pathway that modulates NF-?B activation in innate immune responses. iScience, 24(12), 103473.

Poupault C, et al. (2021) A combinatorial cis-regulatory logic restricts color-sensing Rhodopsins to specific photoreceptor subsets in Drosophila. PLoS genetics, 17(6), e1009613.

Meng FW, et al. (2020) Sox100B Regulates Progenitor-Specific Gene Expression and Cell Differentiation in the Adult Drosophila Intestine. Stem cell reports, 14(2), 226.

Ruzicka F, et al. (2019) Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. PLoS biology, 17(4), e3000244.

Lo Piccolo L, et al. (2019) The lncRNA hsr? regulates arginine dimethylation of human FUS to cause its proteasomal degradation in Drosophila. Journal of cell science, 132(20).

Payne BL, et al. (2019) Codon Usage Differences among Genes Expressed in Different Tissues of Drosophila melanogaster. Genome biology and evolution, 11(4), 1054.

Miyamoto T, et al. (2019) Neuronal Gluconeogenesis Regulates Systemic Glucose Homeostasis in Drosophila melanogaster. Current biology : CB, 29(8), 1263.

Sita LV, et al. (2019) Nomenclature and Comparative Morphology of the Teneurin/TCAP/ADGRL Protein Families. Frontiers in neuroscience, 13, 425.

Tas D, et al. (2018) Parallel roles of transcription factors dFOXO and FER2 in the development and maintenance of dopaminergic neurons. PLoS genetics, 14(3), e1007271.

Laktionov PP, et al. (2018) Genome-wide analysis of gene regulation mechanisms during Drosophila spermatogenesis. Epigenetics & chromatin, 11(1), 14.

Zandawala M, et al. (2018) Modulation of Drosophila post-feeding physiology and behavior by the neuropeptide leucokinin. PLoS genetics, 14(11), e1007767.

Coux RX, et al. (2018) L(3)mbt and the LINT complex safeguard cellular identity in the Drosophila ovary. Development (Cambridge, England), 145(7).

Wang X, et al. (2018) Drosophila multicopper oxidase 3 is a potential ferroxidase involved in iron homeostasis. Biochimica et biophysica acta. General subjects, 1862(8), 1826.

Smolko AE, et al. (2018) The H3K9 methyltransferase SETDB1 maintains female identity in Drosophila germ cells. Nature communications, 9(1), 4155.

Jagla T, et al. (2018) Developmental Expression and Functions of the Small Heat Shock Proteins in Drosophila. International journal of molecular sciences, 19(11).

Tikhonov M, et al. (2018) Conserved sequences in the Drosophila mod(mdg4) intron promote poly(A)-independent transcription termination and trans-splicing. Nucleic acids research, 46(20), 10608.