Resource Summary Report

Generated by <u>dkNET</u> on Apr 22, 2025

Flannotator

RRID:SCR_001608 Type: Tool

Proper Citation

Flannotator (RRID:SCR_001608)

Resource Information

URL: http://www.flyprot.org/

Proper Citation: Flannotator (RRID:SCR_001608)

Description: Allows annotation of gene expression at all stages of development and tissue types (including sub cellular location) using standard Drosophila anatomy ontology. All methods of input use a controlled vocabulary to ensure data integrity.

Abbreviations: Flannotator

Resource Type: data or information resource, database

Keywords: annotation, gene expression, development stage, tissue type, subcellular, stock, gene, protein interaction, embryo

Funding:

Resource Name: Flannotator

Resource ID: SCR_001608

Alternate IDs: nlx_153872

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250422T054951+0000

Ratings and Alerts

No rating or validation information has been found for Flannotator.

No alerts have been found for Flannotator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Shu Z, et al. (2017) Differential Regulation of Cyclin E by Yorkie-Scalloped Signaling in Organ Development. G3 (Bethesda, Md.), 7(3), 1049.

Zacharioudaki E, et al. (2014) Tools and methods for studying Notch signaling in Drosophila melanogaster. Methods (San Diego, Calif.), 68(1), 173.

Lowe N, et al. (2014) Analysis of the expression patterns, subcellular localisations and interaction partners of Drosophila proteins using a pigP protein trap library. Development (Cambridge, England), 141(20), 3994.

Dong B, et al. (2014) Balance between apical membrane growth and luminal matrix resistance determines epithelial tubule shape. Cell reports, 7(4), 941.

Lye CM, et al. (2014) Subcellular localisations of the CPTI collection of YFP-tagged proteins in Drosophila embryos. Development (Cambridge, England), 141(20), 4006.

Rugjee KN, et al. (2013) Fluorescent protein tagging confirms the presence of ribosomal proteins at Drosophila polytene chromosomes. PeerJ, 1, e15.

Costa M, et al. (2013) The Drosophila anatomy ontology. Journal of biomedical semantics, 4(1), 32.

Rees JS, et al. (2011) Method for suppressing non-specific protein interactions observed with affinity resins. Methods (San Diego, Calif.), 54(4), 407.

Hijazi A, et al. (2011) The Ly6 protein coiled is required for septate junction and blood brain barrier organisation in Drosophila. PloS one, 6(3), e17763.

Rees JS, et al. (2011) In vivo analysis of proteomes and interactomes using Parallel Affinity Capture (iPAC) coupled to mass spectrometry. Molecular & cellular proteomics : MCP, 10(6), M110.002386.

Choo SW, et al. (2011) Genome-wide analysis of the binding of the Hox protein Ultrabithorax

and the Hox cofactor Homothorax in Drosophila. PloS one, 6(4), e14778.

Zhao J, et al. (2010) FlyTED: the Drosophila Testis Gene Expression Database. Nucleic acids research, 38(Database issue), D710.

Knowles-Barley S, et al. (2010) BrainTrap: a database of 3D protein expression patterns in the Drosophila brain. Database : the journal of biological databases and curation, 2010, baq005.