

How-To

Abstract

This is a short manual on how to navigate the web interface accompanied with the manuscript "The developmental proteome of *Drosophila melanogaster*".

Contents

- 1 Data sets
 - 1.1 Whole life cycle
 - 1.2 Embryogenesis
- 2 Web interface structure
 - 2.1 Search
 - 2.2 Selected proteins
 - 2.3 Data analysis
 - 2.3.1 Proteomics
 - 2.3.2 Proteomics/RNA
 - 2.3.3 Similar protein profiles
 - 2.3.4 Scatter plots
 - 2.3.5 Clusters
- 3 Advanced settings

The developmental proteome of *Drosophila melanogaster* Welcome Whole Life Cycle 1 Embryogenesis

Search: Show 5 entries

flybasecgid_gene	transcript	description
CG9565	Nep3-[RC,RB,RA]	Nepriysin 3
CG9572	CG9572-[RB,RA,RD]	
CG9577	CG9577-[RA]	
CG9578	CG9578-[RA]	
CG9581	CG9581-[RA]	

Showing 1 to 5 of 7,952 entries Previous 1 2 3 4 5 ... 1591 Next

Selected proteins: CG9577-[RA] 4

Update selection 5

Proteomics 6 Proteomics/RNA Similar protein profiles Scatter plots Clusters

Links to flybase.org

CG9577

Download Plot

Advanced settings

y-axis range to display

selected manual

18 21 40 42

Value types to display

measured missing imputed

dropped

Show calculated mean

CG9577 (FBtr0070007)

log₂(LFO intensity)

timepoint

replicate

- 1
- 2
- 3
- 4

and mean of measured values

- 1
- 2
- 3
- 4

value type

- measured
- missing
- ▲ imputed
- × dropped

percentile of measured values

- 1%
- 99%

1 Data sets

In the top menu [1], you can select the dataset to work with: “Whole Life Cycle” or “embryogenesis”.

1.1 Whole life cycle

The dataset contains the following 15 time points (measured in quadruplicates):

- E02: 0-2 hours old embryos
- E06: 4-6 hours old embryos
- E12: 10-12 hours old embryos
- E20: 18-20 hours old embryos
- L1: 40-44 hours after egg laying
- L2: 66-68 hours after egg laying
- eL3: 83-85 hours after egg laying
- L3c: crawling larvae
- P1: white pupae
- P2-P5: every 24 hours after pupation (white pupae)
- Aym/Ayf: adult young male/female flies 4 hours after hatching
- Am/Af: 1 week old adult male/female flies

1.2 Embryogenesis

Embryos were collected in quadruplicates with a 30 min laying window for the following time points: 0h, 1h, 2h, 3h, 4h, 5h, 6h, 8h, 10h, 12h, 14h, 16h, 18h, 20h.

2 Web interface structure

2.1 Search

After selecting one of the data sets, a table with all detected proteins will appear. The protein of interest can be queried in the “Search” bar [2] and selected from the table by clicking [3]. After selecting one entry, the protein will be saved in the “update selection” window on the upper right site.

2.2 Selected proteins

This feature allows keeping information about previous searches. For a completely new search, please delete the entry in the upper right window [4] and click the update selection button [5].

2.3 Data analysis

After selecting the protein of interest, the data can be chosen from a second menu [6] with the following tabs:

- Proteomics
- Proteomics/RNA
- Similar protein profiles
- Scatter plots
- Clusters

All the graphical representations are navigable by hovering over the dots/lines. Additionally, it is possible to download any graphical representation via the “download” button.

2.3.1 Proteomics

Bar plots representing protein abundance (y-axis) throughout the collected time points of the selected dataset (x-axis). Colored dots indicate the different replicates. The grey scale of the bars represents the number of replicates in which the protein was measured (grey=1, black=4). The value type legend specifies the origin of the data (for detailed information, please check supplemental methods). In each plot two thresholds are presented: 1% (continuous line) and 99% (dashed line) of the LFQ intensities found in the complete dataset. The orange line indicates the tendency of protein expression based on measured and imputed values.

2.3.2 Proteomics/RNA

Protein and RNA profiles of the selected protein are shown. The RNA data is retrieved from the modENCODE project (Graveley et al., 2011). All transcripts for each protein are color-coded and by hovering over the lines, their gene names are displayed.

2.3.3 Similar protein profiles

This feature allows searching for proteins with similar expression profiles to the protein of interest. The 100 most similar proteins are listed in the table on the left (scored by similarity) and can be searched in the search tab. By selecting proteins, expression profiles of protein and RNA will be added to the graphical output in a different color.

2.3.4 Scatter plots

Different scatter plots from the manuscript are available for interactive searches (see left menu for selection). The selected proteins from the search (if available in the scatter plot) are highlighted.

2.3.5 Clusters

Significantly changing whole life cycle protein profiles were clustered and are shown by stage (embryo, larva, pupa, adult). The cluster of interest can be selected and respective protein profiles will be visualized. The clusters that contain information about the selected proteins will be displayed (lower right).

Embryogenesis data was complemented with tissue-specific expression data. Therefore, a second tab “tissue” allows the selection of tissue and cluster number showing the respective protein expression profiles.

3 Advanced settings

This tab allows modifying different aspects of the graphical output:

- y-axis: the ordinate range can be defined [7]
- Value types [8]:
 - **measured**: calculated LFQ intensities
 - **missing**: no LFQ intensity calculated, but measured intensity
 - **imputed**: calculated by imputation (see supplemental methods)
 - **dropped**: a single measured replicate value without intensities in neighboring time points was dropped and replaced by an imputed value
- Show/hide calculated mean (orange line)