

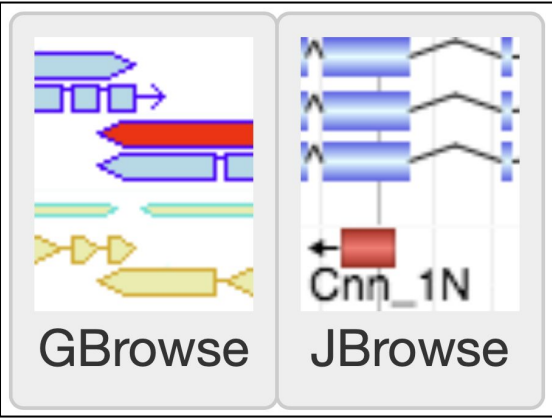
FlyBase updates 2019

Steven Marygold

Overview

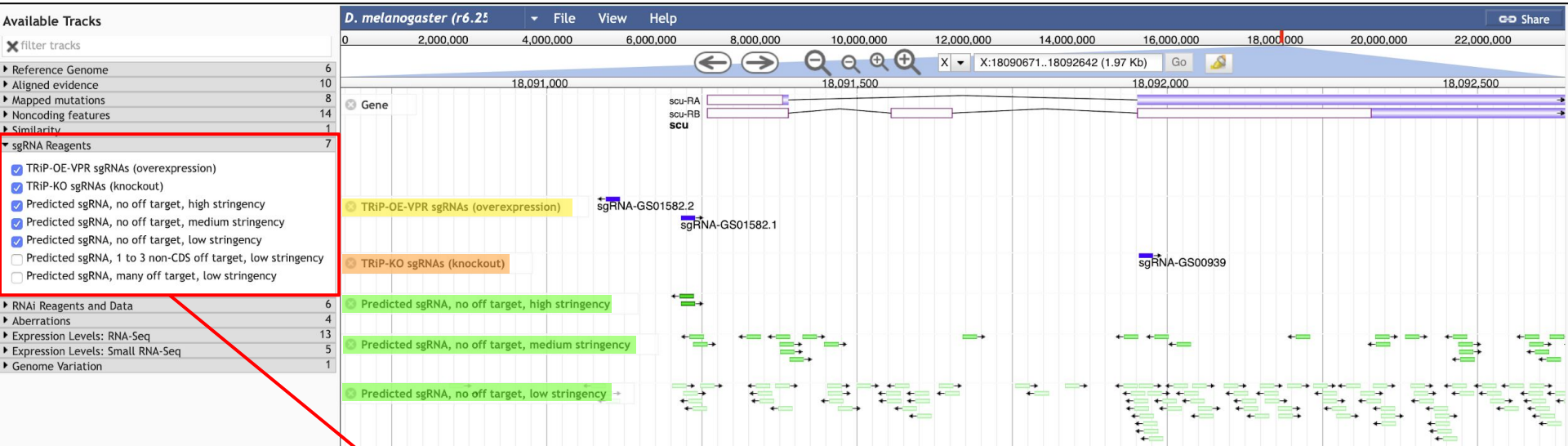
1. New data tracks in JBrowse
 - [sgRNAs, variants, peptides, RNAseq](#)
2. Improved expression data
 - [Summary ribbons & developmental proteome](#)
3. New resources for finding reagents
 - [GAL4 driver table & 'experimental tools'](#)
4. Improvements to functional annotation
 - [Pathways & enzymes](#)
5. FlyBase as a data hub
 - [New links to external resources](#)

JBrowse vs GBrowse



| Genomic Location | | | |
|-------------------|--|-------------------|--|
| Cytogenetic map | 22F1-22F3 | Sequence location | 2L:2,428,372..2,459,823 [+] |
| Recombination map | 2-6 | | |
| Sequence | <input type="text" value="Gene region"/> | | <input type="button" value="Get Decorated FASTA"/> |
| | <input type="button" value="Get Sequence"/> | | |
| Genomic Maps | <div style="border: 1px solid red; padding: 2px; display: inline-block; margin-right: 10px;">GBrowse</div> <div style="border: 1px solid red; padding: 2px; display: inline-block; margin-right: 10px;">JBrowse</div> <div style="border: 1px solid magenta; padding: 2px; display: inline-block; margin-right: 10px;">Help me choose</div> | | |
| | | | |

JBrowse: sgRNA reagents (DRSC)



sgRNA Reagents 7

- TRiP-OE-VPR sgRNAs (overexpression)
- TRiP-KO sgRNAs (knockout)
- Predicted sgRNA, no off target, high stringency
- Predicted sgRNA, no off target, medium stringency
- Predicted sgRNA, no off target, low stringency
- Predicted sgRNA, 1 to 3 non-CDS off target, low stringency
- Predicted sgRNA, many off target, low stringency

JBrowse: proteomic peptides & DGRP variants

Available Tracks

- filter tracks
- Reference Genome 6
- Aligned evidence 10
 - cDNA
 - EST
 - RNA-seq exon junction
 - other aligned sequences
 - proteomic peptides**
 - PeptideAtlas peptides
 - Protein domains (Pfam)
 - Protein domains (SMART)
 - Transcription start sites (modENCODE), embryo
 - Transcription start sites (RAMPAGE), peak calls
- Mapped mutations 8
- Noncoding features 14
- Similarity 1
- sgRNA Reagents 7
- RNAi Reagents and Data 6
- Aberrations 4
- Expression Levels: RNA-Seq 13
- Expression Levels: Small RNA-Seq 5
- Genome Variation 1
 - DGRP variants**

D. melanogaster (r6.25)

0 2,000,000

Gene

proteomic peptides

DGRP variants

proteomic peptides

proteomic peptides

SNV

File View Help

Primary Data

- Type SNV
- Score 999
- Description SNV C -> T
- Position X:18092254..18092254
- Length 1 bp

Attributes

- C5 X
- P5 17986287
- VT SNP
- alternative_alleles T
- description SNV C -> T
- filter PASS
- reference_allele C
- seq_id X

Genotypes (205)

| Category | Count | Percentage |
|--------------------------|------------|-------------|
| non-variant | 203 | 99.02% |
| homozygous for reference | 203 | 99.02% |
| variant | 2 | 0.98% |
| homozygous | 2 | 0.98% |
| T variant | 2 | 0.98% |
| Total | 205 | 100% |

Name **GT**

| | |
|----------|-------------------|
| DGRP-021 | ref (C) / ref (C) |
| DGRP-026 | ref (C) / ref (C) |
| DGRP-028 | ref (C) / ref (C) |
| DGRP-031 | ref (C) / ref (C) |
| DGRP-032 | ref (C) / ref (C) |
| DGRP-038 | ref (C) / ref (C) |
| DGRP-040 | ref (C) / ref (C) |
| DGRP-041 | ref (C) / ref (C) |
| DGRP-042 | ref (C) / ref (C) |
| DGRP-045 | ref (C) / ref (C) |

14,000,000 16,000,000 18,000,000 20,000,000 22,000,000

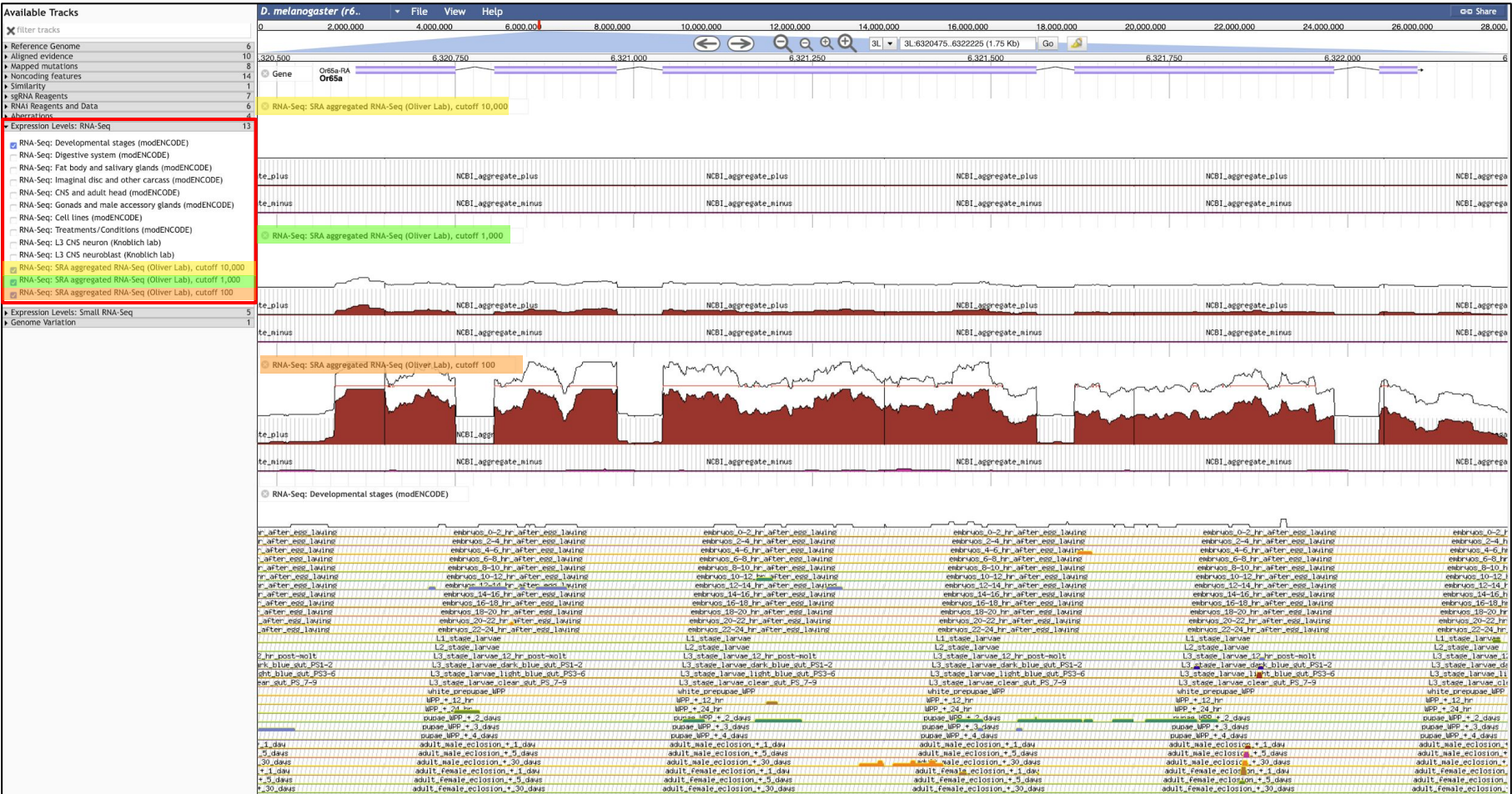
671...18092642 (1.97 Kb) Go

18,092,000 18,092,500

proteomic_peptide_00048298 proteomic_peptide_00051191 proteomic_peptide_00104287 proteomic_peptide_00155912 proteomic_peptide_00028756 proteomic_peptide_00028755 proteomic_peptide_00162718 proteomic_peptide_00162717 proteomic_peptide_00162716

OK

JBrowse: SRA aggregated RNA-Seq (Oliver lab)

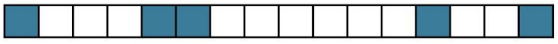


Expression Summary ribbons on Gene Reports

Expression Data

Expression Summary Ribbons

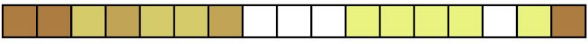
egg/oocyte
stem cell
imaginal tissue
anlage/primordium
sensory system
nervous system
circulatory system
tracheal system
digestive system
adipose system
endocrine system
excretory system
reproductive system
integumentary system
muscle system
other anatomical entity



anatomy - manually curated

Colored tiles in ribbon indicate that expression data has been curated by FlyBase for that anatomical location. Colorless tiles indicate that there is no curated data for that location.

embryo 0-2h
embryo 2-4h
embryo 4-8h
embryo 8-12h
embryo 12-16h
embryo 16-20h
embryo 20-24h
larva L1
larva L2
larva L3 12h
larva L3
white prepupa
late prepupa
pupa 2-3d
pupa 4d
adult male
adult female



stages - modENCODE RNA-seq

Expression legend: low high
For complete stage-specific expression data, view the **modENCODE Development RNA-Seq** section under **High-Throughput Expression** below.

Developmental proteome (Casas-Vila et al, 2017)

Developmental Proteome: Life Cycle

Developmental Proteome: Egrf Life Cycle Data (Casas-Vila Proteome Life Cycle)

Styles

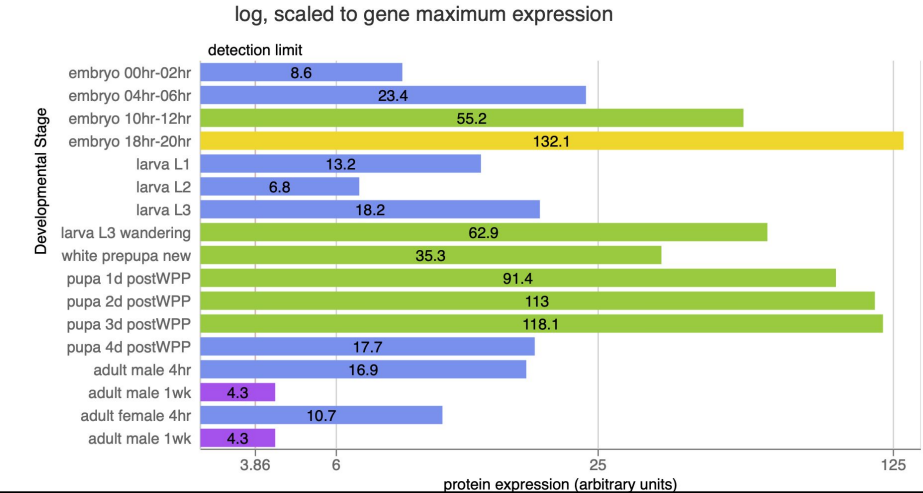
- linear
- log

Scales

- gene maximum expression
- low expression bin max
- moderate expression bin max

Guide to proteome expression level colors

- at/below limit of detection (≤ 3.86)
- no/extremely low expression (< 6)
- very low expression (6 - 25)
- low expression (25 - 125)
- moderate expression (125 - 375)
- high expression (375 - 1500)
- very high expression (> 1500)



Developmental Proteome: Embryogenesis

Developmental Proteome: Egrf Embryogenesis Data (Casas-Vila Proteome Embryogenesis)

Styles

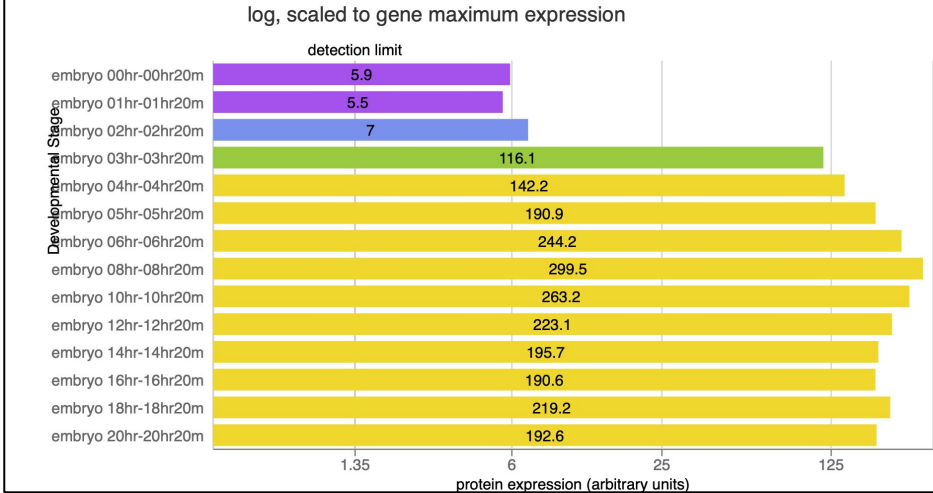
- linear
- log

Scales

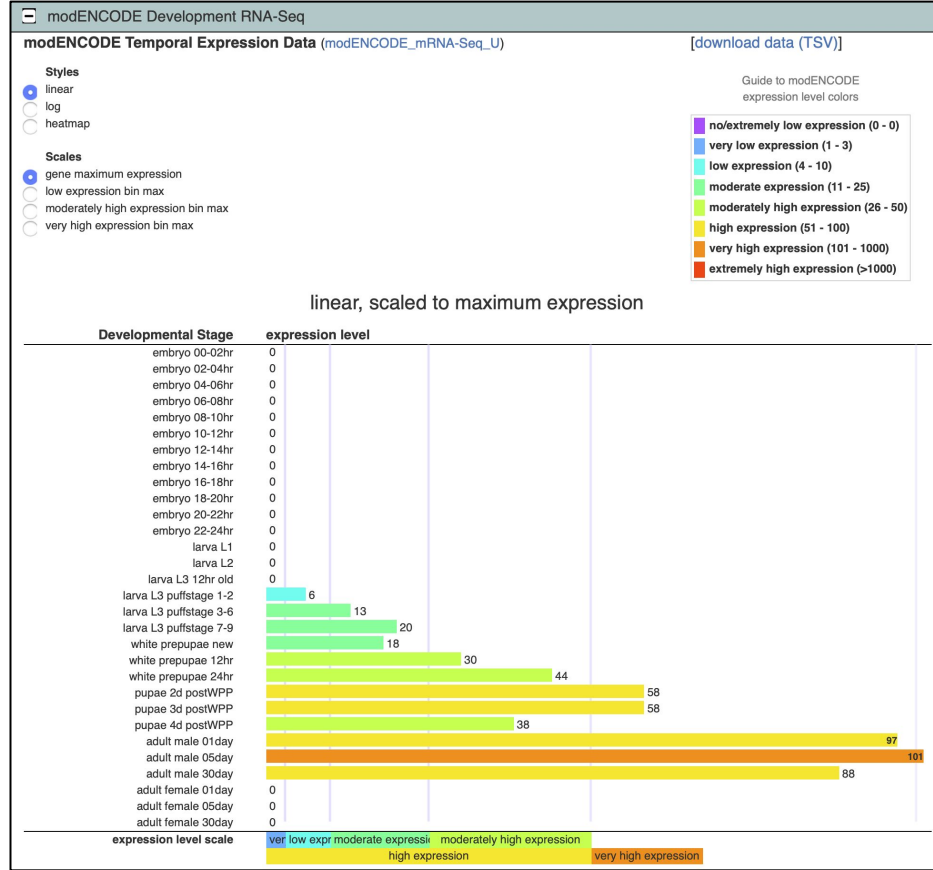
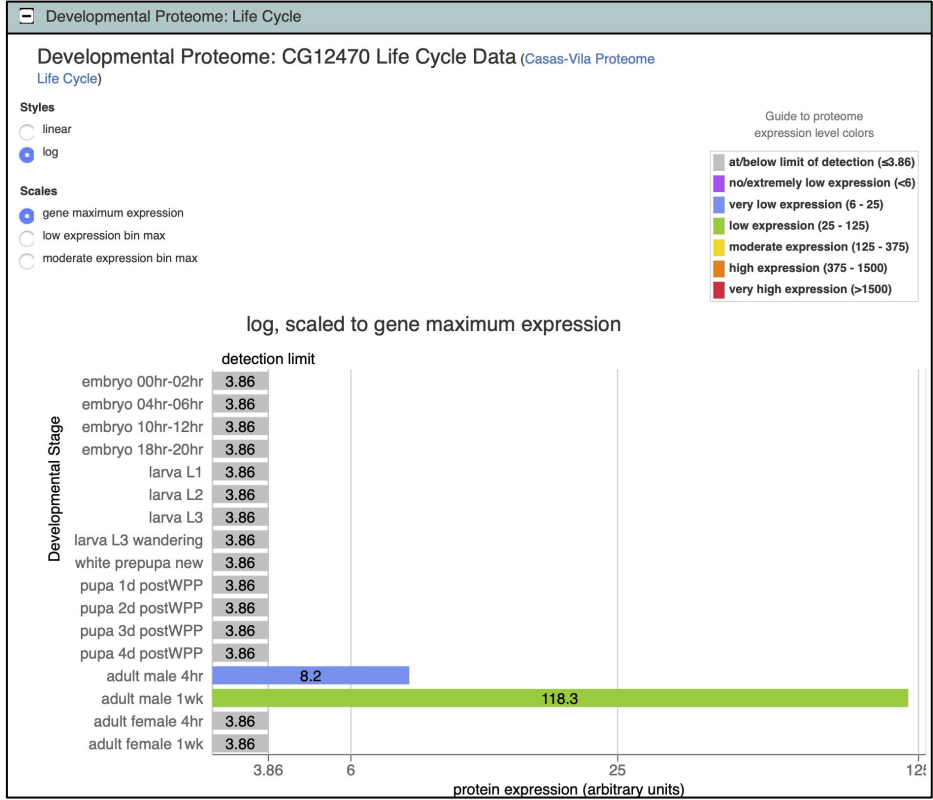
- gene maximum expression
- low expression bin max
- moderate expression bin max

Guide to proteome expression level colors

- at/below limit of detection (≤ 1.35)
- no/extremely low expression (< 6)
- very low expression (6 - 25)
- low expression (25 - 125)
- moderate expression (125 - 375)
- high expression (375 - 1500)
- very high expression (> 1500)



Developmental proteome vs RNAseq



Frequently Used GAL4 Table - with images!

QuickSearch

Human Disease **GAL4 etc** Expression Phenotype References

Search FlyBase Orthologs Protein Domains Gene Groups GO Data Class

Search for GAL4 and other drivers and reporters by ex

Driver/Reporter: GAL4 binary driver

Developmental Stage: e.g., third instar larval

Anatomy/Cell Type: e.g., neuron

Cellular Component: e.g., neuromuscular junction

Fill only

Frequently Used GAL4 Drivers table

FlyBase Frequently Used GAL4 Drivers

Home Tools Downloads Links Community Species About Help Archives


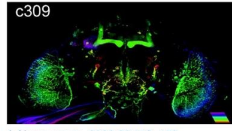
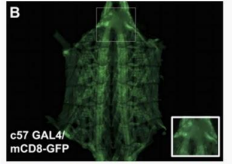
J2G Jump to Gene Go

Please note: This table does not describe the entire expression pattern of each GAL4 driver. You can find the complete curated pattern on the allele, insertion or construct report of each driver.

Do you have a contribution that could help FlyBase to improve this list? Please contact FlyBase if you have comments about the expression pattern of one of these drivers, know of a driver that should be added, or if you would like to contribute a representative expression pattern image.

Export TSV

Contact FlyBase

| Allele | Insertions / Constructs | Image | Assoc. gene | Common terms | Major tissue | Major stage | Description | # Stocks | # Refs |
|--------------------------------|-------------------------|--|-------------|------------------|--|-----------------------------|--|----------|--------|
| Scer\GAL4 ^{ase,neuro} | P[ase-GAL4] |  <p>A type I</p> <p>Mira nuclei GFP</p> <p>PLoS ONE. 2013;8:e79588 (FBrf0223411)</p> | ase | | type I neuroblast | larval stage | Drives expression in type I, but not type II, neuroblasts. | 0 | 22 |
| Scer\GAL4 ^{c309} | P[GawB]c309 |  <p>c309</p> <p>J. Neurogenet.. 2009;23:156--172 (FBrf0207600)</p> | | | mushroom body | larval stage adult stage | Drives expression in the alpha, beta, alpha', beta', and gamma lobes of the mushroom body. | 1 | 46 |
| Scer\GAL4 ^{C57} | P[GawB]C57 |  <p>B</p> <p>c57 GAL4/ mCD8-GFP</p> <p>Proc. Natl. Acad. Sci. U.S.A.. 2010;107:742--747 (FBrf0209730)</p> | | body wall muscle | somatic muscle embryonic/larval hypodermal muscle | larval stage | Drives expression in the larval body wall muscles. | 2 | 98 |

Experimental Tools

- Detection tags
 - FLAG
 - EGFP
 - mCherry
- Localization tags
 - NLS
 - Signal peptides
 - Organelle localization
- Binary expression systems
 - GAL4/UAS
 - *lexA/lexAop*
 - tetR/tetO
- Genome engineering
 - FLP/FRT
 - *phiC31/attB/attP*
 - Cas9
- Sensors
 - pH sensor
 - Calcium sensor
 - Redox sensor

| General Information | | | |
|---------------------------------------|--|------------|-------------|
| Symbol | mCherry | FlyBase ID | FBto0000118 |
| Name | monomeric Cherry fluorescent protein | | |
| Description | | | |
| Description | mCherry is a monomeric red fluorescent protein with an excitation peak of 587nm and an emission peak of 610nm in vitro. It is an artificial derivative of the naturally occurring fluorescent protein encoded by the <i>Discosoma</i> drFP583 gene (GenBank:AF168419; AAF03369) (PMID:15558047). | | |
| Uses | red fluorescent protein | | |
| External Crossreferences and Linkouts | <p>FPbase - A database for users of fluorescent proteins. mcherry</p> <p>GenBank Nucleotide - A collection of sequences from several sources, including GenBank, RefSeq, TPA, and PDB. AY678264</p> | | |

| Transgenic Constructs | | | | | | |
|--|--|------------------|--|---|--|--------|
| Encodes tool (63) Export to HitList | | | | | | |
| Transgenic construct(s) | Component allele | Reg. region | Encoded product / tool <small>Show Uses</small> | Tagged with <small>Show Uses</small> | Also carries <small>Show Uses</small> | Stocks |
| P{sChFP} | Disc\RFP ^{mCherry} .sqh | sqh | mCherry | | | 4 |
| P{UAS-mCherry.NLS} | Disc\RFP ^{mCherry.UAS.Tag} .NLS(Unk) | UAS ^t | mCherry | Tag:NLS(Unk) | | 4 |
| P{UAS-mCherry.CAAX.S} | Disc\RFP ^{mCherry.UAS.cSa} .Tag:M(Ras64B) | UAS | mCherry | Tag:M(Ras64B) | | 3 |

| Tagged with the tool (503) Export to HitList | | | | | | |
|---|---|-------------------|--|---|--|--------|
| Transgenic construct(s) | Component allele | Reg. region | Encoded product / tool <small>Show Uses</small> | Tagged with <small>Show Uses</small> | Also carries <small>Show Uses</small> | Stocks |
| M{ <i>lexAop-UAS-morphotrap.ext.mCh</i> } | Zzzz\vhGFP4 ^{<i>lexAop.UAS.morphotrap.ext.mCherry</i>} | <i>lexAop UAS</i> | Zzzz\vhGFP4 | mCherry | <i>loxP lox2272</i> | 2 |
| M{UASp-mCherry.cpb} | cpb ^{UASp.mCherry} | UASp | cpb | mCherry | | 2 |
| M{UASp-mCherry.Eb1.DN} | Eb1 ^{DN.UASp.mCherry} | UASp | Eb1 | mCherry | | 2 |

Signaling Pathways

| General Information | | | |
|----------------------------|--|-------------------|------------------------|
| Name | JAK-STAT Signaling Pathway | Species | <i>D. melanogaster</i> |
| Symbol | JAKSTAT | FlyBase ID | FBgg0000883 |
| Date last reviewed | 2018-04-23 | Number of members | 26 |
| Description | | | |
| Description | The JAK-STAT signaling pathway is initiated by the binding of an extracellular ligand to a cell surface receptor leading to receptor dimerization and the intracellular activation of a Janus kinase (JAK) family member. JAK phosphorylates cytoplasmic STAT family members which dimerize, translocate into the nucleus and regulate target gene expression. In <i>Drosophila</i> , the core pathway is limited to three ligands (the Unpaired family of cytokines), a single receptor (dome), JAK kinase (hop) and STAT (Stat92E). (Adapted from FBfr0225259). | | |
| Notes and selected reviews | Selected publications for background information: The <i>Drosophila</i> JAK-STAT pathway (FBfr0222849), Tools and methods for studying the <i>Drosophila</i> JAK/STAT pathway (FBfr0225259), JAK/STAT pathway dysregulation in tumors: a <i>Drosophila</i> perspective (FBfr0225146), JAK/STAT Pathway in <i>Drosophila</i> Immunity (FBfr0225141). | | |
| Related Gene Groups | | | |
| Component group(s) | JAK-STAT Signaling Pathway Core Components Negative Regulators of JAK-STAT Signaling Pathway Positive Regulators of JAK-STAT Signaling Pathway | | |

| Members (26) | | | |
|------------------|--------------------------------|-----------------------------------|--|
| For all members: | View Orthologs | Export to HitList | Export to Batch Download |

| JAK-STAT Signaling Pathway Core Components | | | | |
|--|---|--|--|--------|
| Gene Symbol | Gene Name | Gene Group Membership | GO Molecular Function (Experimental) | # Refs |
| dome | domeless | | cytokine receptor activity SOCS family protein binding STAT family protein binding protein heterodimerization activity protein tyrosine kinase binding | 5 |
| hop | hopscotch | NON-RECEPTOR TYROSINE KINASES | cytokine receptor binding protein tyrosine kinase activity | 3 |
| Stat92E | Signal-transducer and activator of transcription protein at 92E | OTHER DNA BINDING DOMAIN TRANSCRIPTION FACTORS | DNA-binding transcription activator activity, RNA polymerase II-specific cytokine receptor binding histone binding | 2 |

QuickSearch

[Human Disease](#)
[GAL4 etc](#)
[Expression](#)
[Phenotype](#)
[References](#)

[Search FlyBase](#)
[Orthologs](#)
[Protein Domains](#)
[Gene Groups](#)
[GO](#)
[Data Class](#)

Search using a gene or Gene Group symbol, name, synonym or ID:

Enter text:

Alternatively, browse all [Gene Group reports](#), or just [Pathway reports](#)

Note: Wild cards (*) can be added to your search term

- Epidermal Growth Factor Receptor
- Fibroblast Growth Factor Receptor
- Hedgehog
- Hippo
- Insulin-like Receptor
- JAK-STAT
- Notch
- PDGF/VEGF Receptor-Related
- Sevenless
- Toll
- Torso
- Wnt-TCF

Metabolic Pathways

☰ Pathways

+ Gene Group - Pathway Membership (FlyBase)

☰ External Data

Linkouts

FlyCyc Pathways - Pathways from a BioCyc PGDB for Dmel

glycolysis III (from glucose) glycolysis I (from glucose 6-phosphate) glycolysis II (from fructose 6-phosphate)

KEGG Pathways - Wiring diagrams of molecular interactions, reactions and relations.

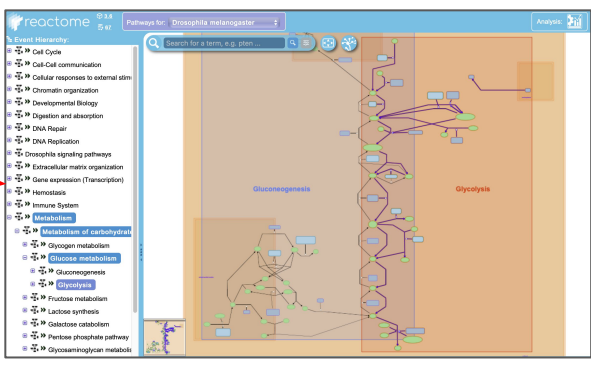
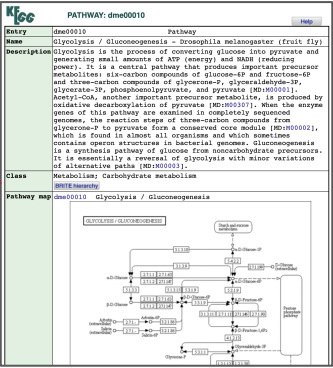
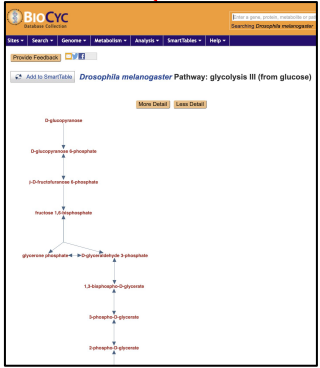
Glycolysis / Gluconeogenesis Pentose phosphate pathway Fructose and mannose metabolism

Galactose metabolism Metabolic pathways Carbon metabolism

Biosynthesis of amino acids RNA degradation

Reactome - An open-source, open access, manually curated and peer-reviewed pathway database.

Glycolysis Neutrophil degranulation



Improved enzyme data

| General Information | | | |
|--|--|--------------------|------------------------|
| Symbol | Dmelaay | Species | <i>D. melanogaster</i> |
| Name | astray | Annotation Symbol | CG3705 |
| Feature Type | protein_coding_gene | FlyBase ID | FBgn0023129 |
| Gene Model Status | Current | Stock Availability | 10 publicly available |
| Enzyme Name (EC) | Phosphoserine phosphatase (3.1.3.3) | | |
| Families, Domains and Molecular Function | | | |
| Catalytic Activity (EC) | <p>Experimental Evidence</p> <p>-</p> <p>Predictions / Assertions</p> <p>O-phospho-L(or D)-serine + H(2)O = L(or D)-serine + phosphate (3.1.3.3)</p> | | |

| Enzyme class | #Genes | #Genes added / removed |
|-----------------|--------|------------------------|
| Oxidoreductases | 649 | 72 / 39 |
| Transferases | ~1,400 | TBD |
| Hydrolases | ~1,900 | TBD |
| Lyases | 130 | 23 / 14 |
| Isomerases | 104 | 13 / 6 |
| Ligases | 121 | 27 / 18 |



Gene Groups

New links - from the homepage

Multi-species mining:

MARRVEL GENE2FUNCTION MIST

iProteinDB BioLitMine ALLIANCE OF GENOME RESOURCES

QuickSearch

Human Disease GAL4 etc Expression Phenotype **References**

Search FlyBase Orthologs Protein Domains Gene Groups GO Data Class

Search by Author Year Title/Abstract Journal Pub type ID Any field

Author e.g. 'Smith NOT Johnson'

Title/Abstract search Title and Abstract text

or search fly preprints at Europe PMC

Note: Wild cards (*) can be added to your search term

Europe PMC About Tools Developers Help **Explore the beta version**

Search worldwide, life-sciences literature

("drosophila" OR "melanogaster") AND (PUB_TYPE:"Preprint") Search Advanced Search

E.g. "breast cancer" HER2 Smith J

Results RSS Save Search Recent Activity Export


1 - 25 of 1554 results Sort by: Relevance | Date | Times Cited

- Select results 1 - 25
- Co-expression network analysis identifies specific hub genes in association with developmental neuronal remodeling in *Drosophila melanogaster*. Preprint. Liu Y, Sun X, Qu A. PeerJ Preprints [13 Mar 2019]. Cited: 0 times (PPR:PPR73424)
- Multiple genetic loci affect place learning and memory performance in *Drosophila melanogaster*. Preprint. Williams-Simon P, Posey C, Mitchell S, Ngoma E, Mrkwicka J, Zars T, King E. bioRxiv [16 Mar 2019]. Cited: 0 times (PPR:PPR73334)
- Characterisation of the genetic architecture underlying eye size variation within *Drosophila melanogaster* and *Drosophila simulans*. Preprint. Gaspar P, Arif S, Sumner-Rooney L, Kittelmann M, Stern DL, Nunes MDS, McGregor AP. bioRxiv [21 Feb 2019]. Cited: 0 times (PPR:PPR71163)

Content types: Free full text (4), Open access (4), Preprints (1554)

Date: 2019 (149), 2018 (665), 2017 (408), 2016 (174), 2015 (89), Custom date range

New links - from Gene Reports

| General Information | | | |
|---------------------|--|--------------------|------------------------|
| Symbol | Dmel\Prp8 | Species | <i>D. melanogaster</i> |
| Name | pre-mRNA processing factor 8 | Annotation Symbol | CG8877 |
| Feature Type | protein_coding_gene | FlyBase ID | FBgn0033688 |
| Gene Model Status | Current | Stock Availability | 10 publicly available |
| Key Links |  | | |

RNAcentral



GtRNAdb
tRNAscan-SE analysis








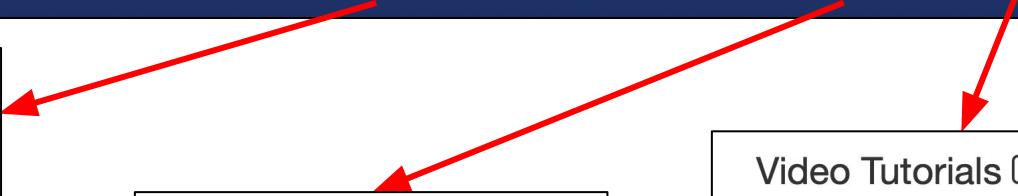


More information & keeping in touch

- FlyBase Community
- Fast-Track Your Paper
- FlyBase Community Advisory Group
- Gene Snapshots
- FlyBase Forum
- Find A Person
- Newsletter**
- bionet.dros
- FlyGene Wiki
- Twitter**

- Release Notes
- New In This Release
- Release Schedule
- FlyBase Positions
- Citing FlyBase
- FlyBase Consortium
- FlyBase Publications
- FlyBase Presentations**
- FlyBase Support

- Video Tutorials 
- Tool help
- Report help
- Info for Authors 
- Linking to/from FlyBase
- Nomenclature
- Curation documentation 
- New to Flies
- Help Index
- Contact FlyBase**



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