

New: Experimental Tool Reports

The 'Classical and Insertion Alleles' and 'Transgenic Constructs' tables on Gene Reports now include data from our new **Experimental Tool** reports. These reports make it easier to identify reagents with particular characteristics, such as those that are tagged with a fluorescent protein or subcellular localization signal.

Transgenic constructs containing regulatory region of ey		
Characterization construct	Name	Expression Data
	P(ey1x-GAL4.Exel)	NA
	P(ey3.5-FLP.B)	NA
	P(ey3.5-GAL4.Exel)	NA
	P(ey-FLP.B)	NA
	P(ey-FLP.N)	NA
	P(ey-FLP.U)	NA
	P(ey-GAL80.3.5)	NA
	P(UAS-Pax-6.mus)	NA
GAL4 construct		
	Name	Expression Data
	P(ey-GAL4.S)	Yes
	P(ey-GAL4.U)	No
	P(ey-IT4)	No
	P(GAL4-ey.B)	Yes
	P(GAL4-ey.H)	Yes
vital-reporter construct		
	Name	Expression Data
	P(ey3.6-GFP.mcutx3)	No
	P(ey3.6-GFP.mcutx3+mthx2)	No
	P(ey3.6-GFP.mthx2)	No
	P(ey3.6-GFP)	No
reporter construct		
	Name	Expression Data
	P(ey3.5-lacZ)	No
	P(ey.12E-lacZ)	No
	P(ey.12ER-lacZ)	No
	P(ey.12-lacZ)	No

Construct components	
Component allele	Product class / Tool use(s)
Avic1GFP	green fluorescent protein
Encoded product / tool	GFP
Description	GFP expression is driven by a 3.6kb fragment from the ey enhancer. (Wang and Sun, 2012)

You can also identify reporter alleles by whether they contain regulatory/enhancer or coding regions of the gene of interest.

On the Experimental Tool report, we describe molecular and genetic characteristics of the experimental tool. For fluorescent markers, a Linkout connects to the Fluorescent Protein Database (FPbase), where you can find further details about specific fluorophores.

General Information			
Symbol	EGFP	FlyBase ID	FBto0000027
Name	Enhanced green fluorescent protein		
Description			
Description	EGFP is a green fluorescent protein with an excitation peak of 488nm and an emission peak of 507-509nm in vitro. It is an artificial derivative of the naturally occurring fluorescent protein encoded by the Aequorea victoria GFP gene (UniProtKB:P42212), containing the mutations F64L and S65T (PMID:9759496).		
Uses	green fluorescent protein		
External Crossreferences and Linkouts			
	FPbase - A database for users of fluorescent proteins. egfp		

A specialized section of Experimental Tool reports is the **Frequently Used GAL4 Drivers** table, a tabular summary of more than 200 commonly used GAL4 driver alleles that can be found in the GAL4 etc. tab of QuickSearch.

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 expression pattern: Search

Driver/Reporter: GAL4 binary driver

Output format: integrated table

refine search by adding qualifier terms

Developmental Stage: e.g., third instar larval stage

Anatomy/Cell Type: e.g., neuron

Cellular Component: e.g., neuromuscular junction

Fill only as many fields as you need

Frequently Used GAL4 Drivers table

Spotlight: improved ncRNA representation

Several improvements have been made to representation of **non-coding RNAs**. Now, all *D. melanogaster* genes producing non-coding RNAs have a standardized prefix based on their class, and are cross-referenced with RNAcentral's Unique RNA Sequence (URS) identifiers. For transfer RNAs, we now link to the Genomic tRNA Database (GtRNadb), which contains transfer RNA gene predictions and associated analyses.

General Information			
Symbol	Dme tRNA:Gly-GCC-1-1	Species	<i>D. melanogaster</i>
Name	transfer RNA:Glycine-GCC 1-1	Annotation Symbol	CR31667
Feature Type	tRNA_gene	FlyBase ID	FBgn0011859
Gene Model Status	Current	Stock Availability	None publicly available
Other Summaries			
Auto summary		Gene Group	
Also Known As			
tRNA:gly3:22BCa			
Key Links			
ALLIANCE GENOME RESOURCES		NCBI Gene	Ensembl
RNAcentral			
External Crossreferences and Linkouts (7)			
Sequence Crossreferences			
RNAcentral - A comprehensive ncRNA sequence collection representing all ncRNA types from a broad range of organisms			
URS0003429B0_7227			
Linkouts			
GtRNadb Genomic tRNA Database: tRNA gene predictions from tRNAscan-SE analysis of complete genomes			
tRNA-Gly-GCC-1-1			



a database of *Drosophila* genes and genomes

Other New FlyBase Features

Graphical Abstracts are now included in Reference Reports and as thumbnails in HitLists. This initial integration comprises more than 900 graphical abstracts from papers in journals published by Cell Press.

Kim et al. (2017) (FBri0236443)

Title: Spatial Activation of TORC1 Is Regulated by Hedgehog and E2F1 Signaling in the *Drosophila* Eye.

Citation: Dev. Cell. 2017;42:363-375.e4

Publication type: paper

PubMed PMCID EuropePMC Journal website

Abstract >

1 Cell Line 1 Natural Transposon 2 Insertions 1 Aberration 1 Reference

33 Genes 42 Alleles 27 Transgenic Constructs

Ma et al. (2016) (FBri0235873)

Title: Regulation of Smoothed Trafficking and Hedgehog Signaling by the SUMO Pathway.

Citation: Dev. Cell. 2016;39:438-451

Publication type: paper

PubMed PMCID EuropePMC Journal website

Abstract >

4 Experimental Tools 10 Genes 2 Natural Transposons 26 Alleles

21 Transgenic Constructs 2 Insertions

Connections to more sources have been added to many Report pages, in the Key Link section near the top and the External Cross-References and Linkouts section. These include the DRSC's Molecular Interaction Search Tool (MIST), and antibody information provided by Cell Signaling Technologies. On the front page, we have added links to the BioLitMine MeSH term literature mining tool and the iProteinDB post-translational modification database.

There is now a link to search for *Drosophila* **preprint** articles in Europe PMC, from the References tab of QuickSearch.

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 Search

Author: e.g., 'Smith NOT Johnson'

Journal: e.g., 'Dev. Biol.'

or search fly preprints at Europe PMC

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

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new tools, features, and resources for 2019

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New: Pathway Reports

FlyBase is pleased to introduce our new **Pathway Reports** that list genes that have been experimentally shown to act within a pathway or to regulate it. These form a subset of our Gene Group resource and can be searched via the 'Gene Groups' QuickSearch tab or a browsable list. This resource is under development and we welcome any feedback to help improve the usefulness and accuracy of these gene lists.

General Information				
Name	Notch Signaling Pathway Core Components	Species	<i>D. melanogaster</i>	
Symbol	NTCH-C	FlyBase ID	FBgg0001064	
Date last reviewed	2019-01-23	Number of members	12	
Description				
Description	The Notch receptor signaling pathway is activated by the binding of the transmembrane receptor Notch (N) to transmembrane ligands, <i>Delta</i> or <i>Serrate</i> , presented on adjacent cells. This results in the proteolytic cleavage of N, releasing the intracellular domain (NICD). NICD translocates into the nucleus, interacting with <i>Su(H)</i> and <i>Mam</i> to form a transcription complex, which up-regulates transcription of Notch-responsive genes. (Adapted from FBrt0225731 and FBrt0192604).			
Biological Process Gene Ontology (GO) term(s)	Notch signaling pathway			
Related Gene Groups				
Parent group(s)	Notch Signaling Pathway			
Protein Complex group(s)	CSL-NOTCH-MASTERMIND TRANSCRIPTION FACTOR COMPLEX GAMMA SECRETASE COMPLEX			
Other related group(s)	NOTCH LIGANDS			
Members (12)				
For all members:	View Orthologs	Export to HitList	Export to E	
Gene Symbol	Gene Name	Gene Group Membership	GO Molecular Function (Experimental)	# Refs
aph-1	anterior pharynx defective 1	GAMMA SECRETASE COMPLEX	endopeptidase activity	2
DI	Delta	NOTCH LIGANDS	Notch binding receptor ligand activity	9
kuz	kuzbanian	ADAM METALLOPROTEASES	metalloendopeptidase activity	5

Links to complexes and other functional groups

Export for further analysis

Gene Ontology (GO) annotation used to show experimentally characterized function and relevant pathway publications

External Data	
Other resource(s)	<p>Illustration - Notch signaling (The Interactive Fly)</p> <p>Wikipathways - Notch Signaling Pathway (Drosophila melanogaster)</p> <p>Animation - The Notch signaling pathway (Wolpert, Tickle & Martinez Arias:Principles of Development International 5e)</p> <p>Reactome Pathway - Signaling by Notch (computed)</p> <p>KEGG pathway - Notch signaling pathway - Drosophila melanogaster</p>

Useful links to other pathway resources

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: e.g. ACTINS, ACT, Act5C

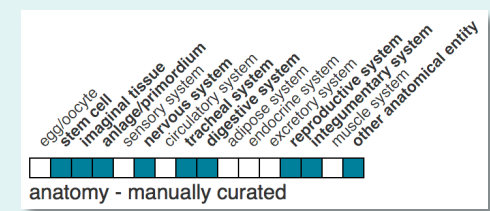
Alternatively, browse all Gene Group reports, or just **Pathway reports**

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

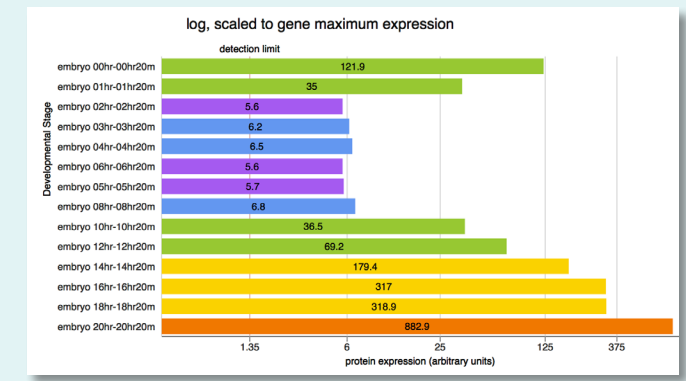
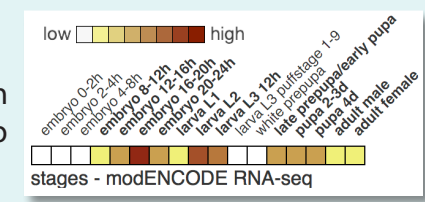
- ### FlyBase Pathway Report List
- Epidermal Growth Factor Receptor Signaling Pathway (EGFR-RTK)**
 - Effectors Negatively Regulated by Epidermal Growth Factor Receptor Signaling Pathway (EGFR-E)
 - Epidermal Growth Factor Receptor Ligand Biogenesis and Secretion (EGFR-S)
 - Epidermal Growth Factor Receptor Signaling Pathway Core Components (EGFR-C)
 - Negative Regulators of Epidermal Growth Factor Receptor Signaling Pathway (EGFR-N)
 - Positive Regulators of Epidermal Growth Factor Receptor Signaling Pathway (EGFR-P)
 - Fibroblast Growth Factor Receptor Signaling Pathway (FGFR)**
 - Effectors Negatively Regulated by Fibroblast Growth Factor Receptor Signaling Pathway (FGFR-E)
 - Fibroblast Growth Factor Receptor Signaling Pathway Core Components (FGFR-C)
 - Negative Regulators of Fibroblast Growth Factor Receptor Signaling Pathway (FGFR-N)
 - Positive Regulators of Fibroblast Growth Factor Receptor Signaling Pathway (FGFR-P)

New in Gene Reports: Expression Ribbons, Enzyme & Metabolic Pathways, Proteomics

Gene Reports now feature new **Expression Summary Ribbons** giving an at-a-glance view of expression data from two sources. In the manually curated **anatomy** expression data ribbon, a filled tile indicates that data has been curated from the research literature for that particular cell type, tissue or system.



A summary of high-throughput **stage specific RNA-Seq expression** data from modENCODE is presented as a heat map (increased expression is darker).



Quantitative protein expression data from the proteomic study of Casas-Vila *et al.*, 2017, has been incorporated into Gene Reports for more than half of annotated protein coding genes. The proteome is available for the complete fly life cycle (17 time points) and/or embryogenesis (14 time points).

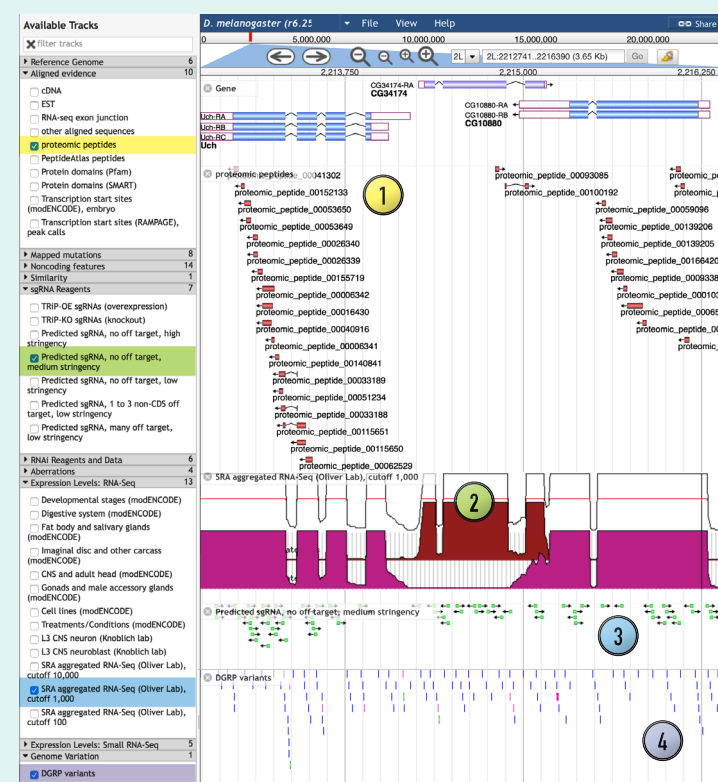
The data are presented as histograms, color-coded by expression level, in the "High-Throughput Expression Data" sub-section of Gene Reports' "Expression Data" section. The display can be viewed at log or linear scale, with options to scale the data relative to the gene's maximum expression or relative to global "low" or "moderate" expression levels.

General Information			
Symbol	Dmel ry	Species	<i>D. melanogaster</i>
Name	rosy	Annotation Symbol	CG7642
Feature Type	protein_coding_gene	FlyBase ID	FBgn0003308
Gene Model Status	Current	Stock Availability	3177 publicly available
Enzyme Name (EC)	Xanthine dehydrogenase (1.17.1.4) Xanthine oxidase (1.17.3.2)		
Families, Domains and Molecular Function			
Catalytic Activity (EC)	Experimental Evidence Xanthine + NAD(+) + H(2)O = urate + NADH (1.17.1.4) Predictions / Assertions Xanthine + NAD(+) + H(2)O = urate + NADH (1.17.1.4) Xanthine + H(2)O + O(2) = urate + H(2)O(2) (1.17.3.2)		
Pathways			
Linkouts	FlyCyc Pathways - Pathways from a BioCyc PGDB for Dmel urate biosynthesis/rosine adenosine nucleotides 5-phosphate degradation degradation II KEGG Pathways - Wiring diagrams of molecular interactions, reactions and relations. Purine metabolism Caffeine metabolism Metabolic pathways Peroxisome Reactome - An open-source, open access, manually curated and peer-reviewed pathway database. Purine catabolism Vitamins B6 activation to pyridoxal phosphate		

New Tracks in JBrowse: Proteomics, aggregated RNA-Seq, CRISPR reagents, DGRP variants

1 Proteomic peptides: Genomic alignments of over 150,000 peptides identified by mass spectroscopy from samples of Oregon-R can be seen at various developmental stages (Casas-Vila *et al.*, 2017). These peptides are shown in the proteomic peptides (uniquely mapping) track. Peptides from additional proteomic studies will be added to this track over time.

2 SRA Aggregated RNA-Seq tracks: New "aggregated" RNA-Seq tracks from Justin Fear and Brian Oliver combine thousands of high quality SRA RNA-Seq accessions to provide an "average" view of the transcriptome. The exceptional read depth provides insight into regions of low transcription. These tracks are offered with three signal cut-off points: high, medium, or low sensitivity.



3 sgRNAs for in vivo CRISPR: These pre-designed sgRNA sequences have been analyzed for predicted efficacy and off-target effects at various mismatch stringencies. Tracks include those showing TriP reagents that target genes for over-expression or mutation, and tracks covering over 10 million "Predicted sgRNAs" designs from the DRSC. Associated alleles and stocks are available in their respective section of Gene Reports.

4 Genome variation from the DGRP: Variation data from the Drosophila Genetics Reference Panel can now be visualized in JBrowse, providing information for 205 inbred lines from the DGRP.