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-tTA}	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+mhthx2}	No
	P{ey3.6-GFP.mhthx2}	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

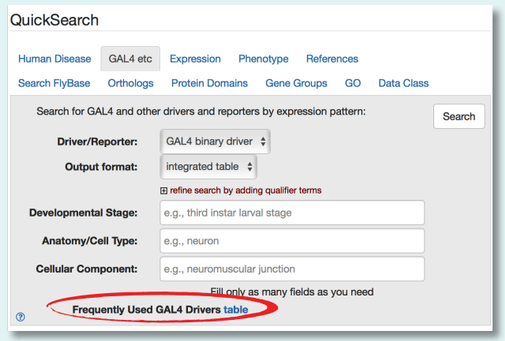
You can also identify reporter alleles by whether they contain regulatory/ enhancer or coding regions of the gene of interest.

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

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.

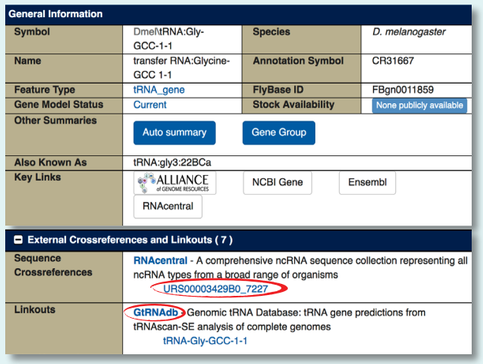
General Information			
Symbol	EGFP	**FlyBase ID**	FBto0000027
Name	Enhanced green fluorescent protein		
Description			
Description	EGFP is a green fluorescent protein with an excitation peak of 488nm and an emission peak of 507-509nm in vitro. It is an artificial derivative of the naturally occurring 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.



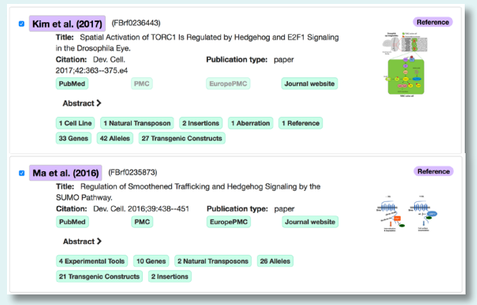
Spotlight: improved ncRNA representation

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.



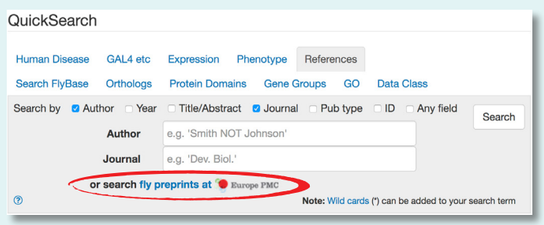
Other New FlyBase Features

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.

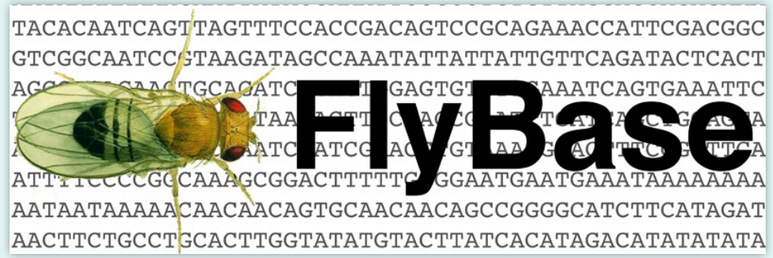


Connections to more sources have been added to many Report pages, in the Key Link section near the top and the External Cross-References and Linkouts section. These include the DRSC's Molecular Interaction Search Tool (MIST), and antibody information provided by Cell Signaling Technologies. On the front 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.



FlyBase is supported by a grant from the National Human Genome Research Institute at the U.S. National Institutes of Health #U41HG000739. Support is also provided by the British Medical Research Council. To contact us, please email helpfb@morgan.harvard.edu.



FlyBase

a database of *Drosophila* genes and genomes

new tools, features, and resources for 2019

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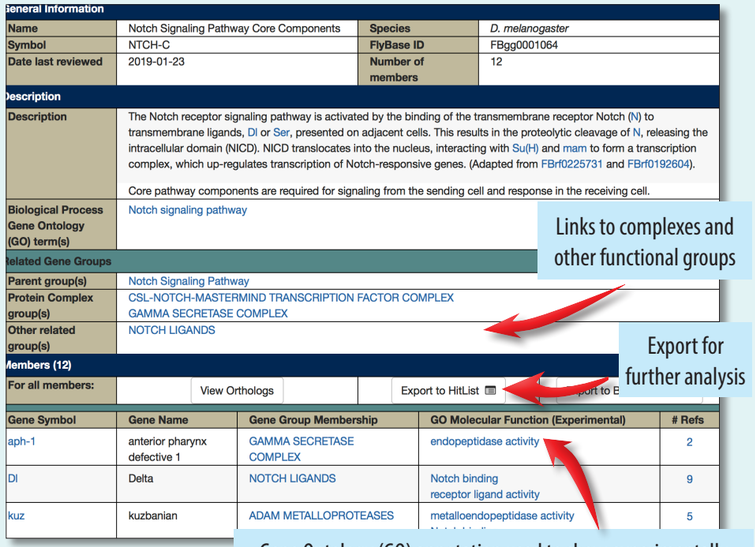
New: Pathway Reports

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.



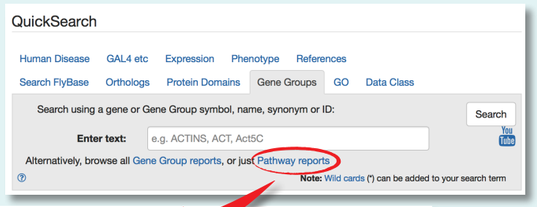
Links to complexes and other functional groups

Export for further analysis

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

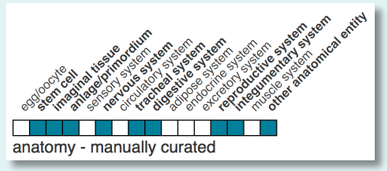
Useful links to other pathway resources

Pathway reports can be searched or browsed from the QuickSearch Gene Groups tab.

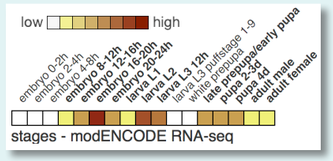


New in Gene Reports: Expression Ribbons, Enzyme & Metabolic Pathways, Proteomics

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.



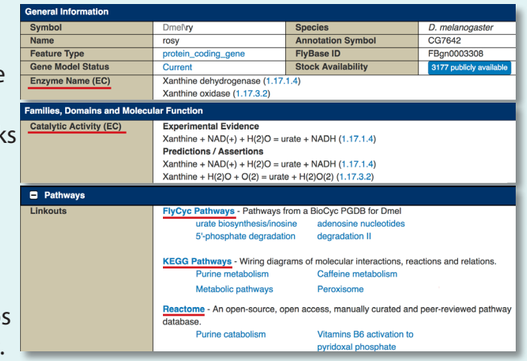
A summary of high-throughput **stage specific RNA-Seq expression** data from modENCODE is presented as a heat map (increased expression is darker).



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.

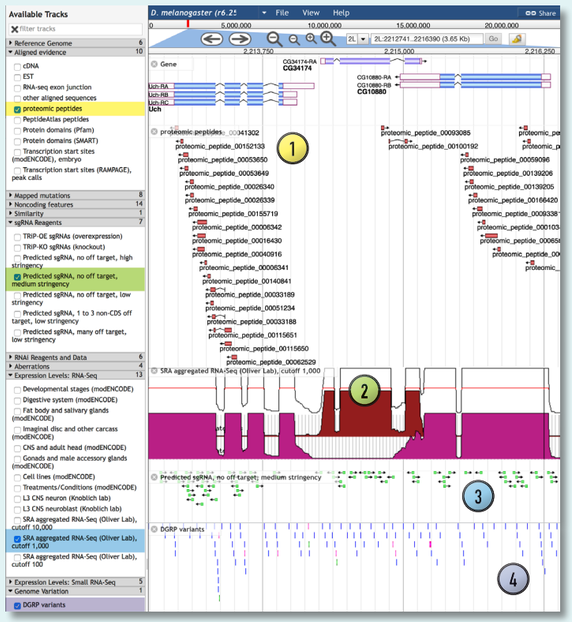
Enzyme Nomenclature and Metabolic Pathways:
FlyBase Gene Reports now show improved information on enzyme nomenclature and reactions, as well as links to metabolic pathway resources KEGG, Reactome, and BioCyc on the Gene Report pages. We have added many new Gene Groups for families of enzymes.



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.