



# New and Classic Features in FlyBase

Beverley Matthews, FlyBase Consortium

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# Overview

1. Building a genetic toolkit
2. Expression data
3. Improvements to functional data
4. Cell line gene associations
5. Variants
6. Fly lab list
7. Connecting with FlyBase

# Building a Genetic “toolkit”

## New: Transgenic Products class column

New column describes the nature of the encoded product in transgenic constructs, (e.g. wild type, missense mutation, RNAi reagent)

In gene report in Alleles/Transgenic Constructs section

Transgenic Constructs ( 118 )

For All Alleles Carried on Transgenic Constructs Show  Pre-selected data  Choose specific data

Transgenic constructs containing/affecting coding region of hh

Export  Other available columns: Mutagen(s), Known lesion?, Encoded tool use(s), Tag use(s) [Show/Hide Columns](#)

All 10 100 << 1 2 3 ... 12 >>

Component Allele	Transgenic construct	Transgenic Product Class	Regulatory region	Encoded product/tool	Tagged with	Also carries	# Stocks ↓	# Refs
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
hh <sup>HMS00492</sup>	P{TRIP.HMS00492}	RNAi_reagent	UAS	hh		loxP	2	12
hh <sup>GD193</sup>	P{GD193}	RNAi_reagent	UAS <sup>t</sup>	hh			2	10
hh <sup>UAS.cHa.EGFP</sup>	P{UAS-hh.EGFP.H}	cDNA_wild_type	UAS <sup>t</sup>	hh	EGFP		2	2
hh <sup>TOE.GS00191</sup>	P{TOE.GS00191}	sgRNA		hh			2	3
hh <sup>TKO.GS00602</sup>	P{TKO.GS00602}	sgRNA		hh			1	1
hh <sup>WKO.P1-C1</sup>	M{WKO.P1-C1}	sgRNA		hh			1	1
hh <sup>JF01804</sup>	P{TRIP.JF01804}	RNAi_reagent	UAS	hh		loxP	1	10
hh <sup>N.UAS.cGa</sup>	P{UAS-hh.N.G}	stop_gained	UAS <sup>t</sup>	hh			1	3
hh <sup>N.UAS.cHa.EGFP</sup>	P{UAS-hh.N.EGFP.H}	inframe_deletion	UAS <sup>t</sup>	hh	EGFP		1	2
hh <sup>C85S.N.UAS</sup>	P{UAS-hh.C85S.N}	missense_variant, stop_gained	UAS <sup>t</sup>	hh			1	2

All 10 100 << 1 2 3 ... 12 >>

# Interactive allele tables

Export ▾

Other available columns: Mutagen(s), Encoded tool use(s), Tag use(s), Also carries

Show/Hide Columns

All 10 100

Component Allele	Known lesion?	Transgenic construct	Transgenic Product Class ↓	Encoded product/tool	Regulatory region	Tagged with
Filter...	Filter...	Filter...	wild	Filter...	Filter...	Filter...
hh <sup>hs.PI</sup>	<input type="checkbox"/> Yes	P{HShh.I}	wild_type	hh	Hsp70	
hh <sup>UAS.EGFP.cVa</sup>	<input type="checkbox"/> Yes	P{UAS-hh.EGFP.V}	wild_type	hh	UAS	EGFP
hh <sup>FRT.Rnor\Cd2.smo.αTub84B</sup>	<input type="checkbox"/> Yes	P{αTub84B(FRT.smo+CD2)hh.D}	wild_type	hh	αTub84B	
hh <sup>UAS.cKb</sup>	<input type="checkbox"/> Yes	P{UAS-hh.Kb}	wild_type	hh	UAS	
hh <sup>UAS.cUa.GFP</sup>	<input type="checkbox"/> Yes	P{UAS-hh.GFP.U}	wild_type	hh	UAS	GFP
hh <sup>UAS.RFP(Unk)</sup>	<input type="checkbox"/> Yes	P{UAS-hh.RFP}	wild_type	hh	UAS	RFP(Unk)
hh <sup>UAS.CFP</sup>	<input type="checkbox"/> Yes	P{UAS-hh.mCFP}	wild_type	hh	UAS	CFP
hh <sup>UAS.cJa</sup>	<input type="checkbox"/> Yes	P{UAS-hh.J}	wild_type	hh	UAS	

- Component Allele
- Mutagen(s)
- Known lesion?
- Transgenic construct
- Transgenic Product Class
- Regulatory region
- Encoded product/tool
- Encoded tool use(s)
- Tagged with
- Tag use(s)
- Also carries
- # Stocks
- # Refs

# Expression: Split System Combination

FB2024\_02, released April 23, 2024 HitList J2G Jump to Gene Go

R72B05      View As

Filter by species

- D. melanogaster* (5)
- H. sapiens* (transgenes in files) (0)
- other *Drosophila* species (0)
- Other species (0)

Filter by data class

- Allele (3)
- Gene (1)
- Insertion (5)
- Split System Combination (5)
- Stock (14)
- Transgenic Construct (4)

5 selected   1

**ScerGAL4<sup>DBD.R72B05</sup> nHsapIRELA<sup>AD.R82C10</sup>** FBco0000021 **Split System Combination**

Component alleles: ScerGAL4[DBD.R72B05], HsapIRELA[AD.R82C10]  
Expression Data:  Image(s):

**ScerGAL4<sup>DBD.R72B05</sup> nHsapIRELA<sup>AD.ple</sup>** FBco0000023 **Split System Combination**

Component alleles: ScerGAL4[DBD.R72B05], HsapIRELA[AD.ple]  
Expression Data:  Image(s):

**ScerGAL4<sup>DBD.R72B05</sup> nHsapIRELA<sup>AD.VT026773</sup>** FBco0000453 **Split System Combination**

Component alleles: ScerGAL4[DBD.R72B05], HsapIRELA[AD.VT026773]  
Expression Data:  Image(s):

## New report type: Split System Combination

FB2024\_02, released April 23, 2024 Split System Combination: SsssScerGAL4<sup>DBD.R72B05</sup> nHsapIRELA<sup>AD.ple</sup> J2G Jump

General Information			
Symbol	ScerGAL4 <sup>DBD.R72B05</sup> nHsapIRELA <sup>AD.ple</sup>	FlyBase ID	FBco0000023
Feature Type	split system combination	Component Alleles	ScerGAL4[DBD.R72B05] HsapIRELA[AD.ple]

Expression Data		
Reporters Expression		
distribution deduced from reporter (Gal4 UAS)		
Stage	Tissue/Position (including subcellular localization)	Reference
third instar larval stage	larval mushroom body dopaminergic neuron c1	(Truman et al., 2023, Eschbach et al., 2020)
	larval mushroom body dopaminergic neuron f1	(Truman et al., 2023, Eschbach et al., 2020)
adult stage	MB-alpha neuron of the dopaminergic PPL1 cluster	(Zhang et al., 2022, Aso and Rubin, 2016, Aso et al., 2014)
	MB-alpha' neuron of the dopaminergic PPL1 cluster   faint	(Aso et al., 2014)
	mushroom body medial-vertical lobe arborizing neuron 1	(Zhang et al., 2022, Aso and Rubin, 2016, Aso et al., 2014)
	mushroom body vertical lobe arborizing neuron 1	(Zhang et al., 2022, Aso and Rubin, 2016, Aso et al., 2014)
	MB-alpha' neuron of the dopaminergic PPL1 cluster	(Zhang et al., 2022, Aso and Rubin, 2016)

Additional Information	
Statement	Reference
<input type="button" value="Stocks (1)"/>	
Bloomington	68281 w <sup>1118</sup> ; P[ple-p65.AD]attP40; P[R72B05-GAL4.DBD]attP2

Publication Types  2015, Smith, cell, etc.  Year (descending)

All publications

Research paper

Truman et al., 2023, eLife 12: e80594  
Metamorphosis of memory circuits in *Drosophila* reveals a strategy for evolving a larval brain. [FBri0255928]

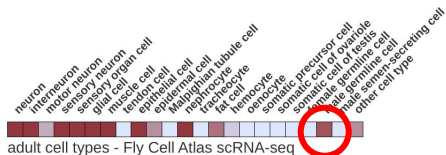
New data class in hitlists:  
Split System Combination

# Expression: scRNA-seq

## scRNA-seq expression data

Explore expression in specific cell types.

Expression Summary Ribbons



Colored tiles in ribbon indicate that the Fly Cell Atlas project found the gene expressed in that cell type. Darker colors mean that more cells of that cell type express the gene: low high. Colorless tiles indicate that there is no scRNAseq data for the gene in that cell type. Query the SCEA for this gene.

### MALE GERMLINE CELL:

cell types + gene expression spread (%) within related cluster :

- 59% : primary spermatocyte
- 34% : spermatocyte
- 7% : male germline cell
- 5% : mid-late elongation-stage spermatid
- 5% : spermatid
- 4% : early-mid elongation-stage spermatid
- 2% : early elongation stage spermatid
- 2% : primary gonial cell
- 1% : spermatogonium

View expression levels and proportion of cells with expression.

Fly Cell Atlas single-cell RNA-Seq

Fly Cell Atlas Cell Type Expression Data (scRNAseq\_2022\_FCA)

[download data (TSV)]

- Styles
- linear
  - logarithmic
  - heatmap
  - % -- level

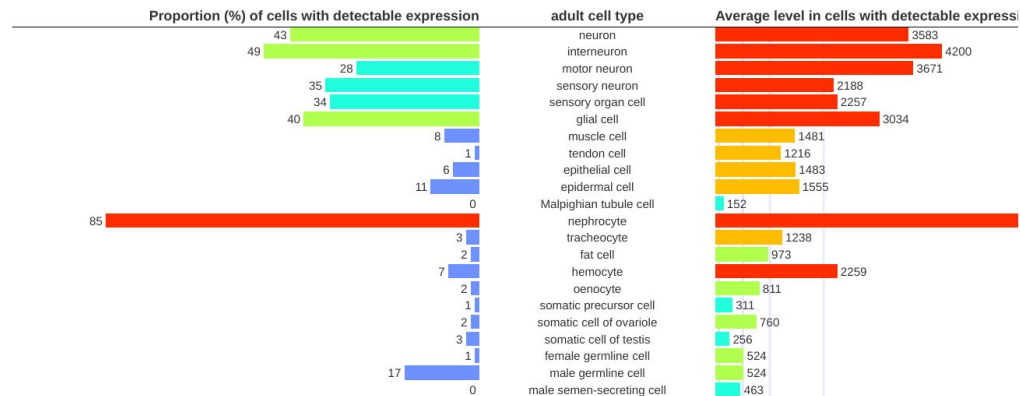
Guide to Fly Cell Atlas expression level colors

- very low expression (0 - 50)
- low expression (50 - 500)
- moderate expression (500 - 1000)
- high expression (1000 - 2000)
- very high expression (>2000)

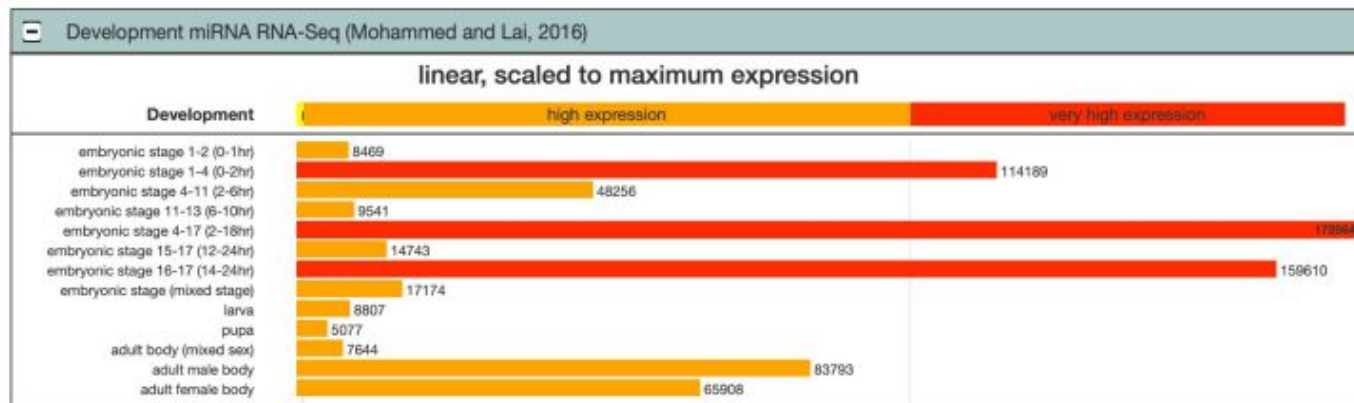
- Scales
- high expression bin max
  - moderate expression bin max
  - low expression bin max
  - gene maximum expression

Color palette: FlyBase

% ↔ level, scaled to maximum expression

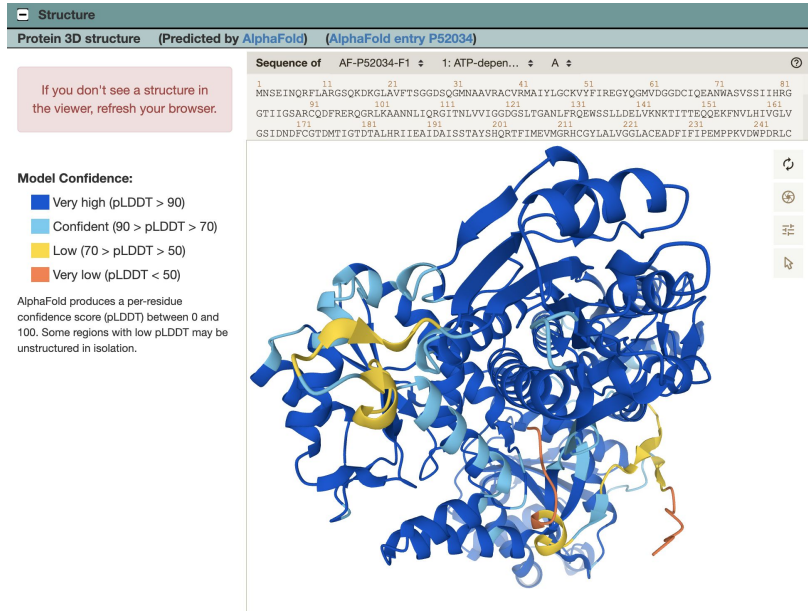


# Expression: miRNA RNA-seq

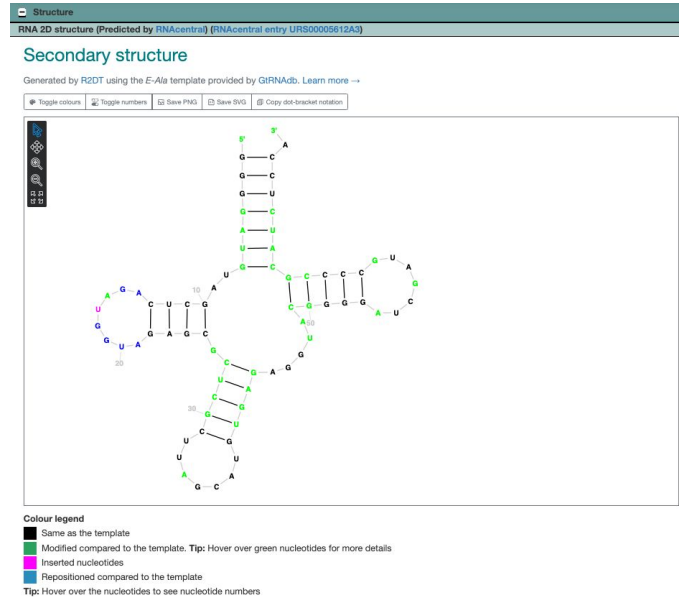


# Function: protein and ncRNA structures

## Genes/Gene Model and Products/Structure



3D Protein structure predicted by AlphaFold (Pfk)



2D RNA structure predicted by R2DT/RNAcentral (tRNA:Ala-AGC-2-3)



# Function: Enzyme updates

Catalytic Activity section in gene reports gives EC (Enzyme Commission #) and Rhea information

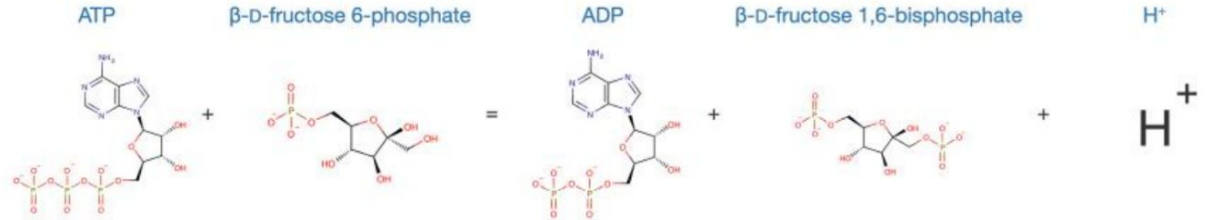
Rhea - knowledgebase of chemical and transport reactions of biological interest

## Catalytic Activity (EC/Rhea)

### 6-phosphofructokinase activity

ATP + beta-D-fructose 6-phosphate = ADP + beta-D-fructose 1,6- bisphosphate + H(+)

RHEA 16109:



# New cell line information in reports

New section added to [cell line reports](#) for genes that have been knocked out, overexpressed, tagged or are otherwise important features of the cell line.

Symbol	S2R+-Sec23-GFP-6	Species	<i>D. melanogaster</i>
Feature type	<a href="#">cultured cell-line</a>	FlyBase ID	FBtc0000294
Source			
Tissue Source	embryo	<i>(Drosophila Genomics Resource Center, 2015-)</i>	
Developmental Stage	late embryonic stage	<i>(Drosophila Genomics Resource Center, 2015-)</i>	
Lab of Origin	DRSC	<i>(Drosophila Genomics Resource Center, 2015-)</i>	
+ Characterization			
- Associated Genes (1)			
	Sec23		

New Cell line information section added to [gene reports](#).

- Stocks and Reagents	
+ Stocks (9)	
+ Genomic Clones (19)	
+ cDNA Clones (202)	
+ RNAi and Array Information	
+ Antibody Information	
- Cell Line Information	
Publicly Available Cell Lines	
	S2R+-Sec23-GFP-6
Other Stable Cell Lines	
	New stable cell line derived from S2- <a href="#">unspecified</a> : The following stable S2 cell lines were used: <a href="#">Delta-WTndeMYC</a> , <a href="#">fng-GFP</a> , <a href="#">Sar1[H74G]-GFP</a> or <a href="#">GFP-Sec23</a> . <i>(Ivan et al., 2008)</i>

# Variants - VEP analysis from ENSEMBL

## Variant Molecular Consequences

Variant Effect Predictor (VEP) Analysis of FlyBase variant data. See [this glossary](#) for definitions of terms used in the table below. Highlighted text in the table applies to the subject FBid of this report.

Variant	Affected Genes	Related Alleles	Affected Transcripts
deletion C > C <a href="#">3R:11,963,124..11,964,369</a> NT_033777.3:g.11963124_11964369del	<a href="#">aurA</a> <b>consequence:</b> splice_acceptor_variant, splice_donor_variant, start_lost, 5_prime_UTR_variant, intron_variant <b>impact:</b> HIGH	<a href="#">aurA<sup>ST</sup></a>	<a href="#">aurA-RA</a> <b>consequence:</b> splice_acceptor_variant, splice_donor_variant, start_lost, 5_prime_UTR_variant, intron_variant <b>impact:</b> HIGH
insertion C > C. <a href="#">3R:11,963,170..11,963,171</a> NT_033777.3:g.11963170_11963171ins	<a href="#">aurA</a> <b>consequence:</b> 5_prime_UTR_variant <b>impact:</b> MODIFIER	<a href="#">aurA<sup>EY03490</sup></a> assoc. with <a href="#">P{EPgy2}aurA[EY03490]</a>	<a href="#">aurA-RA</a> <b>consequence:</b> 5_prime_UTR_variant <b>impact:</b> MODIFIER
point_mutation C > T <a href="#">3R:11,963,298</a> NT_033777.3:g.11963298C>T	<a href="#">aurA</a> <b>consequence:</b> missense_variant <b>impact:</b> MODERATE	<a href="#">aurA<sup>3</sup></a>	<a href="#">aurA-RA</a> <b>consequence:</b> missense_variant <b>impact:</b> MODERATE
point_mutation A > C <a href="#">3R:11,963,623</a> NT_033777.3:g.11963623A>C	<a href="#">aurA</a> <b>consequence:</b> missense_variant <b>impact:</b> MODERATE	<a href="#">aurA<sup>3</sup></a>	<a href="#">aurA-RA</a> <b>consequence:</b> missense_variant <b>impact:</b> MODERATE



# Fly Lab List

## FlyBase:Fly Lab List

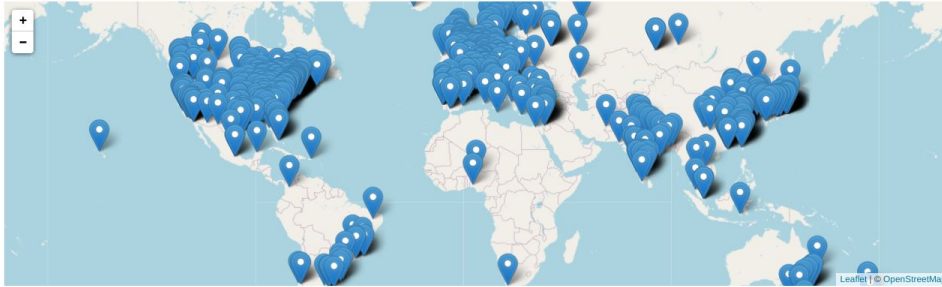
The "Fly Lab List" is an ongoing project aiming to generate an accurate list of all active labs undertaking a substantial fraction of their research using *Drosophila* (any species of *Drosophila*).

The table below can be **sorted** by any one column, and you can use your browser's 'Find' command to **search** the table. The current list can also be **downloaded** as an **Excel** file.

Lab locations are also shown on an interactive map. Click on a marker pin to view information about the lab(s) in that location. Note that map locations are only approximate, given the limited affiliation data collected in the Lab List.

The following feedback forms are available:

- If your lab is not on the list and you wish to **add** it, please use this [form](#). Note the PI/Lab must have a website to be included.
- If you wish to **revise** your lab's entry, please use this [form](#).
- If you wish to **remove** your entry from the list, or do not consider your lab to be an active Fly Lab, please opt out using this [form](#).
- If you wish to report a problem with the **map location** of your lab, please use this [form](#).



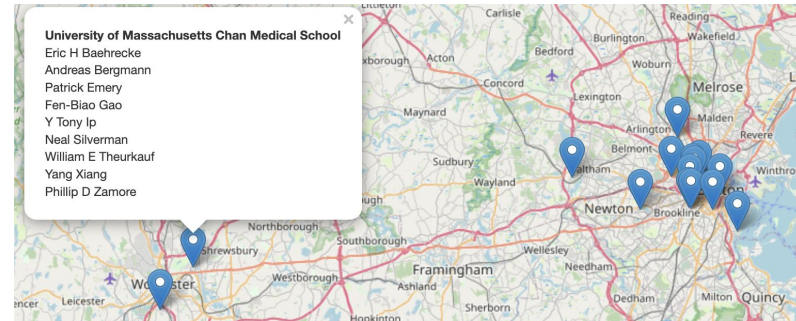
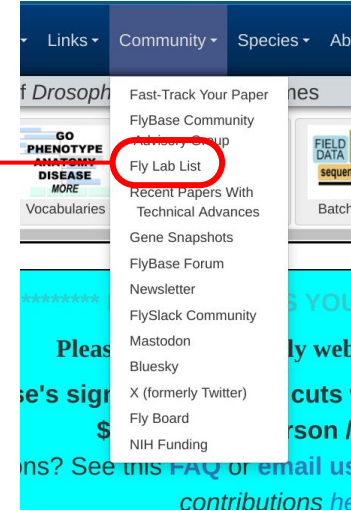
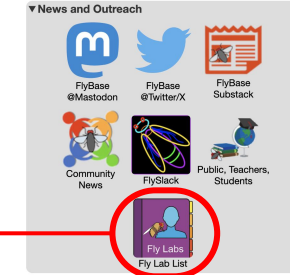
Last updated: 18th April 2024 (2,049 entries)

Lab head name				Website	Primary affiliation			
First	Middle	Last	Institution		City	State/Province/Prefecture	Country	
Jessica	K	Abbott	<a href="#">Link</a>	Lund University	Lund		Sweden	
Uri		Abdu	<a href="#">Link</a>	Ben-Gurion University of the Negev	Beer'Sheva		Israel	
Hermann		Aberle	<a href="#">Link</a>	Heinrich Heine University	Düsseldorf		Germany	



Citing FlyBase

### External Resources





# New: Fly Predictome link and Gene Set Enrichment Tools page

## FlyBase: External Resources

### Popular Resource Categories

All Resources	CRISPR	ScRNA-Seq	RNAi	Stocks	Antibodies	Neuroscience
Model Organism Databases	Images	Maps	Protocols <sup>Ⓢ</sup>	Papers with Technical Advances	Gene Set Enrichment Tools	

### All Resources

An extensive list of useful databases and reagent resources can be found on the pages linked below:

#### Drosophila Online Resources

Includes:

- Atlases, Images, and Videos
- Cell Lines and Cell Culture
- CRISPRs and TALENs
- Data Repositories
- Data and Metadata for Drosophila Genomes
- DNA Reagents
- Gene Expression Databases and Tools
- Gene Groups

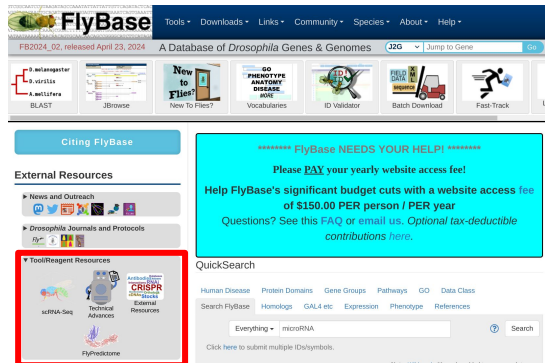
#### FlyBase:GSEA

##### Gene Set Enrichment Tools


Some examples of GSEA tools with links and information. A list of more GSEA tools can be found [here](#). It is recommended that users conduct their GSEA with more than one tool as all have different features, use statistically significant sets to further interpretation. With any GSEA, there will be genes within the analysis set that are not represented in the gene set library characterisation. These may be of interest for further study, even though they are not in an enriched set.

##### Selected Gene Set Enrichment Tool Information


Tool	Backronym	Publication	Enrichment sets	Organism(s)	ID conversion	Multiple set enrichment available	Parallel gene list analysis
DAVID <sup>Ⓢ</sup>	Database for Annotation, Visualization and Integrated Discovery	PMID:35325185 <sup>Ⓢ</sup>	Many (e.g. GO, interaction, domains, UniProt Keyword, drug, human expression).	Large coverage	Yes	Yes	No



### ▼ Tool/Reagent Resources



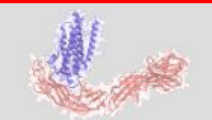
scRNA-Seq



Technical Advances

Databases  
Antibodies  
Interactions  
RNAi  
**CRISPR**  
Bioinformatics  
Orthologs  
cDNAs  
Stocks

External Resources



FlyPredictome

# Connecting with FlyBase

Ask a question, provide a suggestion, get news and helpful hints.

The screenshot shows the FlyBase website interface. At the top, a dark blue navigation bar contains the following menu items: Home, Tools, Downloads, Links, Community, Species, About, and Help. A red box highlights the 'Help' menu, which is expanded to show a list of options: Fast-Track Your Paper, FlyBase Community Advisory Group, Fly Lab List, Recent Papers With Technical Advances, Gene Snapshots, FlyBase Forum, Newsletter, FlySlack Community, Mastodon, Bluesky, X (formerly Twitter), Fly Board, and NIH Funding. Another red box highlights 'Citing FlyBase' in the 'Community' section. A third red box highlights 'Contact FlyBase' in the 'Help' section. A fourth red box highlights 'FlyBase Wiki' in the 'Help' section, which is expanded to show: Help Index, Tool help, Report help, FlyBase FAQ, Info for Authors, Linking to/from FlyBase, Nomenclature, Curation documentation, New to Flies?, Video Tutorials, and FlyBase For Developers. A red box highlights 'FlyBase' in the top left corner of the page. A red box highlights a central message: 'Please PAY your yearly website access fee! Help FlyBase's significant budget cuts with a website access fee of \$150.00 PER person / PER year. Questions? See this FAQ or email us. Optional tax-deductible contributions here.' A red box highlights the email address 'helpfb@morgan.harvard.edu' in the center of the page. A red box highlights the footer text: 'Grants Supporting FlyBase Copyright Statement. version FB2024\_02, released April 23, 2024'. A red box highlights the footer navigation links: 'Contact FlyBase', 'FAQ', and 'Citing FlyBase'. A red box highlights the footer social media icons: FlyBase logo, Mastodon, Twitter, and YouTube.

Home

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Advisory Group

Fly Lab List

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FlyBase Forum

Newsletter

FlySlack Community

Mastodon

Bluesky

X (formerly Twitter)

Fly Board

NIH Funding

Release Notes

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Report help

FlyBase FAQ

Info for Authors

Linking to/from FlyBase

Nomenclature

Curation documentation

New to Flies?

Video Tutorials

FlyBase For Developers

helpfb@morgan.harvard.edu

Grants Supporting FlyBase Copyright Statement.

version FB2024\_02, released April 23, 2024

Contact FlyBase

FAQ

Citing FlyBase



# Acknowledgements

FlyBase @  
University of  
Cambridge:

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FlyBase @  
University of  
New Mexico:

Richard Cripps (Co-PI)  
TyAnna Lovato

FlyBase @  
Harvard University:

Norbert Perrimon (PI)  
Susan Russo Gelbart (PD)  
Kris Broll  
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Victoria Jenkins  
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Mark Zytkovicz

FlyBase @  
Indiana University:

Thomas Kaufman (Co-PI)  
Brian Calvi (Co-PI)  
Seth Campbell  
Josh Goodman  
Victor Strelets  
Jim Thurmond

Collaborators:

DRSC (PANGAEA, DIOPT)  
Fly Cell Atlas / SCEA  
FlyAtlas2  
Eric Lai  
Rhea  
AlphaFold  
RNACentral  
Ensembl VEP  
OrthoDB



We thank FlyBase users  
worldwide for their support.



NHGRI U24HG013300,  
U24HG010859  
MRC: W024233/1  
NSF: DBI-2035515, 2039324  
NIDDK: 1R01DK136945-01  
BBSRC: BB/T014008/1  
Wellcome Trust: PLM13398  
FlyBase Users