



What's New at FlyBase

Gil dos Santos, FlyBase Consortium

Presented at the 62nd Annual Drosophila Research Conference, 2021

A banner for the 62nd Annual Drosophila Research Conference. The background is black with a purple and yellow textured pattern on the right side, resembling a fly's wing or body. The text is white and bold.

62nd Annual *Drosophila*
Research Conference

March 23 – April 1 2021 | Anywhere and Everywhere

Questions please

Join us at
Slido.com

Using event code
#FlyBase



A screenshot of the Slido website's header and a participant entry field. The header is white with the 'slido' logo in green on the left. Navigation links for 'Product', 'Solutions', 'Pricing', 'Resources', and 'Enterprise' are in the center, and 'Log In' and a green 'Sign Up' button are on the right. Below the header is a black bar with the text 'Joining as a participant?' on the left, a white input field containing '# Enter code here' in the middle, and a green arrow button on the right. A green arrow from the text '#FlyBase' above points to the input field.

Overview

1. Reagents: responsive tables
2. Pathway reports
3. Disease models: potential models and summary "ribbons"
4. Sequence Ontology update
5. JBrowse
6. ID validator (for batch queries and downloads)
7. Fast-Track Your Paper (FTYP): tool updates

Overview

- 1. Reagents: responsive tables**
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Reagents: responsive allele tables

Alleles, Insertions, Transgenic Constructs, and Aberrations

Classical and Insertion Alleles (41)

For All Classical and Insertion Alleles Show

Export Other available columns: Mutagen(s), Encoded tool use(s), Tag use(s), Also carries Show/Hide Columns

All 10 100 « 1 2 3 ... 5 »

Allele	Allele class	Known lesion?	Insertion	Inserted element type	Regulatory region	Encoded tool	Tagged with	# Stocks ↓	# Refs
<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>
bt ^{l2E11}		<input checked="" type="checkbox" value="Yes"/>	P{lacW}bt ^{l2E11}	enhancer trap		lacZ	Tag:NLS(P)	2	7
bt ^{ldev1}	hypomorphic allele - genetic evidence	<input type="checkbox"/>						2	18
bt ^{EY01638}		<input checked="" type="checkbox" value="Yes"/>	P{EPgy2}bt ^{EY01638}	misexpression element	UASp			2	3
bt ^{l1187}	hypomorphic allele - genetic evidence	<input checked="" type="checkbox" value="Yes"/>						1	3
bt ^{MI03286}		<input checked="" type="checkbox" value="Yes"/>	Mi{MIC}bt ^{MI03286}	gene trap RMCE target element				1	1
bt ^{MI03286-TG4.0}		<input checked="" type="checkbox" value="Yes"/>	Mi{Trojan-GAL4.0}bt ^{MI03286-TG4.0}	gene trap		GAL4		1	2
bt ^{FW-3}		<input checked="" type="checkbox" value="Yes"/>	P{ST.lexA::HG}bt ^{FW-3}	enhancer trap		lexA::GAD		1	1

Reagents: responsive allele tables

Alleles, Insertions, Transgenic Constructs, and Aberrations

Classical and Insertion Alleles (41)

For All Classical and Insertion Alleles Show Pre-selected data Choose specific data

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

All 10 100 « 1 2 3 ... 5 »

Allele	Allele class	Known lesion?	Insertion	Inserted element type ↑	Regulatory region	Encoded tool	Tagged with	# Stocks	# Refs
<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>	<input type="text" value="Filter..."/>
bt ^l 2E11		<input type="checkbox"/> Yes	P{lacW}bt ^l 2E11	enhancer trap		lacZ	Tag:NLS(P)	2	7
bt ^l 00208		<input type="checkbox"/> Yes	P{PZ}bt ^l 00208	enhancer trap		lacZ	Tag:NLS(P)	0	10
bt ^l FW-3		<input type="checkbox"/> Yes	P{ST.lexA::HG}bt ^l FW-3	enhancer trap		lexA::GAD		1	1
bt ^l 6-81		<input type="checkbox"/> Yes	P{lacW}bt ^l 6-81	enhancer trap		lacZ	Tag:NLS(P)	0	3
bt ^l NP6593		<input type="checkbox"/> Yes	P{GawB}bt ^l NP6593	enhancer trap		GAL4		1	1
bt ^l S084401		<input type="checkbox"/> Yes	P{lacW}bt ^l S084401	enhancer trap		lacZ	Tag:NLS(P)	0	3
bt ^l 04727			P{PZ}bt ^l 04727	enhancer trap		lacZ	Tag:NLS(P)	0	3
bt ^l MI03286-TG4.0		<input type="checkbox"/> Yes	Mi{Trojan-GAL4.0}bt ^l MI03286-TG4.0	gene trap		GAL4		1	2

Reagents: responsive allele tables

Alleles, Insertions, Transgenic Constructs, and Aberrations

Classical and Insertion Alleles (41)

For All Classical and Insertion Alleles Show

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

All 10 100 « 1 »

Allele	Allele class	Known lesion?	Insertion	Inserted element type	Regulatory region	Encoded tool	Tagged with	# Stocks ↓	# Refs
Filter...	Filter...	Filter...	Filter...	Filter...	Filter...	Filter...	mChe	Filter...	Filter...
bt ^{mCherry.endo}		<input type="button" value="Yes"/>	T1{T1}bt ^{mCherry.endo}				mCherry	0	3

All 10 100 « 1 »

Reagents: responsive driver hitlist

QuickSearch

[Human Disease](#) [Protein Domains](#) [Gene Groups](#) [Pathways](#) [GO](#) [Data Class](#)

[Search FlyBase](#) [Homologs](#) [GAL4 etc](#) [Expression](#) [Phenotype](#) [References](#)

Search for GAL4 and other drivers and reporters in *curated data* [?](#)

[by curated expression pattern](#)

[don't use qualifier terms](#)

Developmental Stage:

qualifier:

Anatomy/Cell Type:

qualifier:

Cellular Component:

qualifier:

Fill only as many fields as you need

[reflecting expression of a particular gene](#)

[Frequently Used GAL4 Drivers table](#)

Search for drivers by expression pattern

Search for drivers by gene (new)

Browse frequently used GAL4s

Reagents: responsive driver hitlist

Query

Anatomy:

of results:

neuron

4523

Export

Other available columns: Allele class, Mutagen(s), Known lesion?, Also carries

Show/Hide Columns

All 20 100

« 1 2 3 ... 13 »

Allele	Expression terms	Insertion / Construct	Inserted element type	Regulatory region	Encoded tool	Encoded tool use(s)	Tagged with	Tag use(s)	# Stocks ↓	# Refs
Filter...	Filter...	Filter...	Filter...	Filter...	lexA	Filter...	Filter...	Filter...	Filter...	Filter...
Ecol\lexA ^{GMR57C10}	neuron	P{GMR57C10-lexA} PBac{GMR57C10-lexA}			lexA::p65	binary expression system - driver			8	12
Ecol\lexA ^{GMR48A07}	mechanosensory neuron of hair plate	P{GMR48A07-lexA}			lexA::p65	binary expression system - driver			2	2
Ecol\lexA ^{QF.nSyb}	neuron	P{nSyb-lexA.DBD::QF.AD}		nSyb	lexA::QF	binary expression system - driver			2	5
Ecol\lexA ^{P65.nompC}	sensory system neuron mechanosensory system neuron larval abdominal sensory neuron lch1 neuron	PBac{nompC-lexA::p65}		nompC	lexA::p65	binary expression system - driver			2	15
Ecol\lexA ^{P65.lav}	mechanosensory system neuron larval abdominal sensory neuron mechanosensory neuron of leg chordotonal organ lch1 neuron	PBac{lav-lexA::p65}		lav	lexA::p65	binary expression system - driver			2	4

Overview

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- 2. Pathway reports**
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Pathway reports

General Information			
Name	Wnt-TCF Signaling Pathway	Species	<i>D. melanogaster</i>
Symbol	WNT-TCF	FlyBase ID	FBgg0000889
Date last reviewed	2019-11-14	Number of members	94
Description			
Description	The Wnt-TCF (canonical Wnt) signaling pathway is initiated by the binding of a Wnt ligand to a frizzled family receptor on the cell surface. In the absence of a Wnt ligand, cytoplasmic levels of β -catenin (arm), the transcriptional effector of the pathway, are kept low through its constitutive degradation. Activation of the pathway leads to the inhibition of cytoplasmic β -catenin (arm) degradation and its subsequent accumulation in the nucleus, where it regulates the transcription of target genes. (Adapted from FBrf0218499 and FBrf0223299).		
Notes and selected reviews	Selected publications for background information: Modulating and measuring Wingless signalling (FBrf0225263), Powerful Drosophila screens that paved the wingless pathway (FBrf0228944), Function of the Wingless Signaling Pathway in Drosophila (FBrf0206499), The wingless signalling pathway and the patterning of the wing margin in Drosophila (FBrf0072872), Wnt/Wingless Signaling in Drosophila (FBrf0218499) and Wingless/Wnt signaling in Drosophila: the pattern and the pathway (FBrf0223299).		
	Note: Pathway Pages in FlyBase are under development. The pathway gene tables display genes that have been experimentally shown to act within the pathway or modify pathway activity. We welcome any feedback to help improve the usefulness and accuracy of these gene lists.		
Biological Process Gene Ontology (GO) term(s)			
Related Gene Groups			
Component group(s)	Negative Regulators of Wnt-TCF Signaling Pathway Positive Regulators of Wnt-TCF Signaling Pathway Wnt Production Wnt-TCF Signaling Pathway Core Components		

16 curated Pathways:

- 6 receptor tyrosine kinase pathways
- major developmental pathways such as Hedgehog, Notch and Wnt

Pathway reports: members table

Members (94)

For all members:

View Orthologs

Export to HitList

Export to Batch Download

Negative Regulators of Wnt-TCF Signaling Pathway

Export Other available columns: # All Research Refs, Also Known As, Antibody, Classical / Insertion Alleles, Transgenic constructs, Disease Models (Experimental), Potential Disease Models, Other Pathways, Human orthologs

Show/Hide Columns

All 10 100

« 1 2 3 4 »

Gene Symbol ↑	Gene Name	Gene Group Membership	GO Molecular Function (Experimental)	# Pathway Refs
Filter...	Filter...	Filter...	Filter...	Filter...
aop	anterior open	ETS DOMAIN TRANSCRIPTION FACTORS	DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription repressor activity, RNA polymerase II-specific protein domain specific binding RNA polymerase II cis-regulatory region sequence-specific DNA binding	1
Apc	APC-like	BETA CATENIN DESTRUCTION COMPLEX	beta-catenin binding	9
Apc2	Adenomatous polyposis coli 2	BETA CATENIN DESTRUCTION COMPLEX	beta-catenin binding molecular adaptor activity	12
Axn	Axin	BETA CATENIN DESTRUCTION COMPLEX	beta-catenin binding molecular adaptor activity protein kinase binding signaling receptor binding	13

Pathway members are presented in "responsive tables".

Pathway reports: how to find them

QuickSearch

Human Disease Protein Domains Gene Groups **Pathways** GO Data Class

Search FlyBase Homologs GAL4 etc Expression Phenotype References

Search using a gene or Pathway symbol, name, synonym or ID:

Enter text:

Alternatively, browse [Pathway reports](#)

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

Search/browse pathways from the homepage.

[-] Pathways

[-] Signaling Pathways (FlyBase)

Wnt-TCF Signaling Pathway Core Components -
The canonical Wnt signaling pathway is initiated by the binding of a Wnt ligand to a frizzled family receptor on the cell surface. Activation of the pathway leads to the inhibition of cytoplasmic β -catenin (*arm*) degradation and its subsequent accumulation in the nucleus, where it regulates the transcription of target genes. (Adapted from FBrf0218499 and FBrf0223299).

[+] Metabolic Pathways

[+] External Data

Find links to pathways on gene reports.



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Disease models: potential models

Automated pipeline:

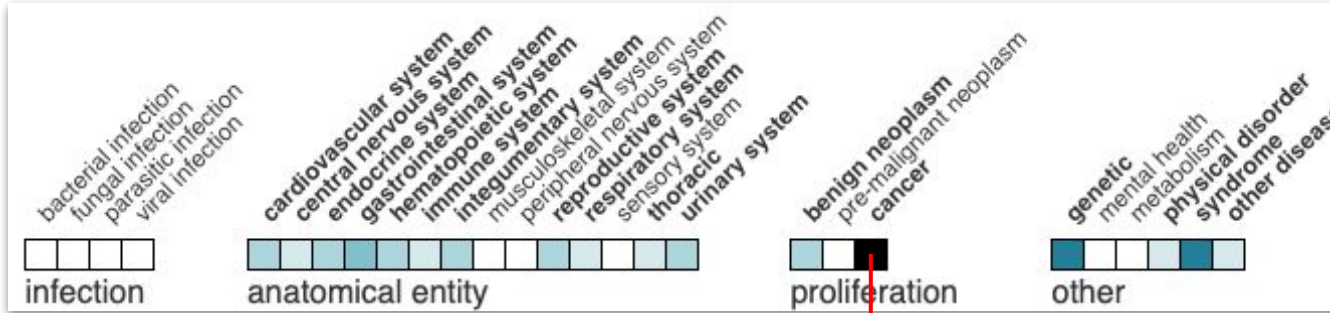
fly gene => human ortholog => OMIM disease annotation => Disease Ontology term

General Information 			
Symbol	DmelJHDM2	Species	<i>D. melanogaster</i>
Name	JmjC domain-containing histone demethylase 2	Annotation Symbol	CG8165
Disease Ontology (DO) Annotations			
[-] Models Based on Experimental Evidence (0) 			
Allele	Disease	Evidence	References
[-] Potential Models Based on Orthology (3)			
Human Ortholog	Disease	Evidence	References
HR; HR lysine demethylase and nuclear receptor corepressor	model of atrichia with papular lesions	IEA	(FlyBase, 2019-)
	model of alopecia universalis	IEA	(FlyBase, 2019-)
	model of hypotrichosis 4	IEA	(FlyBase, 2019-)

~4,800 annotations generated, available on gene reports and as a downloadable file.

Disease models: summary ribbons

General Information			
Symbol	Dmel\Ras85D	Species	<i>D. melanogaster</i>
Name	Ras oncogene at 85D	Annotation Symbol	CG9375
Feature Type	protein_coding_gene	FlyBase ID	FBgn0003205
Gene Model Status	Current	Stock Availability	290 publicly available



acute myeloid leukemia
adenocarcinoma
breast cancer
cancer
carcinoma
cervical cancer
colorectal cancer
hereditary diffuse gastric cancer
intestinal cancer
kidney cancer
leukemia
lung cancer
pancreatic carcinoma
prostate cancer
thyroid gland follicular carcinoma
urinary bladder cancer

Ribbons reflect experimental and computed annotations.

Mouse over a ribbon block to see specific annotations.

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Sequence Ontology update



General Information			
Symbol	DmelIncRNA:roX1	Species	<i>D. melanogaster</i>
Name	long non-coding RNA on the X 1	Annotation Symbol	CR32777
Feature Type	lncRNA_gene	FlyBase ID	FBgn0019601
Gene Model Status	Current	Stock Availability	7 publicly available

Comments on Gene Model	
	Gene model reviewed during 5.48
	Low-frequency RNA-Seq exon junction(s) not annotated.
	Gene model reviewed during 5.56

Sequence Ontology: Class of Gene	
	lncRNA_gene
	nuclear_gene

Gene
"Feature Type"

All Sequence Ontology annotations.

Sequence Ontology update

Before the Sequence Ontology update ...

Generic term annotation

General Information			
Symbol	DmelIncRNA.roX1	Species	<i>D. melanogaster</i>
Name	long non-coding RNA on the X 1	Annotation Symbol	CR32777
Feature Type	non_protein_coding_gene	FlyBase ID	FBgn0019661
Gene Model Status	Current	Stock Availability	7 publicly available


Comments on Gene Model	
	Gene model reviewed during 5.48
	Low-frequency RNA-Seq exon junction(s) not annotated.
	Gene model reviewed during 5.56
	lncRNA ; SO:0001877

Sequence Ontology: Class of Gene	
	non_protein_coding_gene
	nuclear_gene

More information in a free text comment.

Sequence Ontology update

After the Sequence Ontology update ...

General Information 			
Symbol	DmelIncRNA:roX1	Species	<i>D. melanogaster</i>
Name	long non-coding RNA on the X 1	Annotation Symbol	CR32777
Feature Type	lncRNA_gene	FlyBase ID	FBgn0019661
Gene Model Status	Current	Stock Availability	7 publicly available
Comments on Gene Model			
	Gene model reviewed during 5.48		
	Low-frequency RNA-Seq exon junction(s) not annotated.		
	Gene model reviewed during 5.56		
Sequence Ontology: Class of Gene			
	lncRNA_gene		
	nuclear_gene		

More specific annotations are now possible.
Click on the term to find similar annotations.

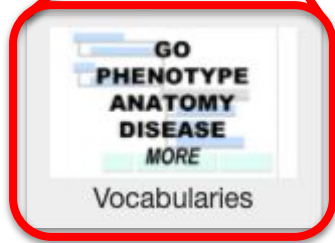
Sequence Ontology update

General Information			
Term	lncRNA_gene	ID (Ontology)	SO:0002127 (Sequence Ontology)
Definition	A gene that encodes a long non-coding RNA.		
Also Known As	"lnc RNA gene" ; "lnc_RNA_gene" ; "long_non_coding_RNA_gene"		
Comment			
Annotations			
Records annotated with this term <i>OR</i> any of its <i>CHILD TERMS</i>			
Genes 2500			
<small>Results list data from multiple species. Click on a button above and use the 'Filter by species' options on the resulting HitList to retrieve species-specific data.</small>			
Records annotated with this exact term (annotations to child terms are NOT included)			
Data Class	Field	Records	
Genes (FBgn)	SO_TERMS	1992	
<input checked="" type="checkbox"/> Full annotation statements including this term (annotations to child terms are NOT included), and relevant records			
Spanning Tree (Parents/Children)		Only view relationship: all	Search All Vocabularies for a New Term
<pre>gene _ncRNA_gene _lncRNA_gene 2500 rec. _antisense_lncRNA_gene 510 rec. _bidirectional_promoter_lncRNA _lincRNA_gene _sense_intronic_ncRNA_gene _sense_overlap_ncRNA_gene</pre>			
Spanning Tree View Settings	Show hierarchy levels: <input type="text" value="2"/> for parents, <input type="text" value="2"/> for children		<input type="button" value="Redraw"/>
hide Relationships			
Is a	ncRNA_gene		
Part of			

Easily find other FlyBase genes annotated to a specific term.

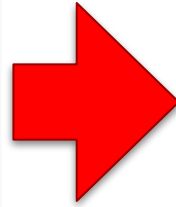
Browse the ontology

Sequence Ontology update



Gene Class

- |_engineered gene
- |_fusion gene
- |_non protein coding gene
 - |_cryptogene
 - |_miRNA gene
 - |_rRNA gene
 - |_scrRNA gene
 - |_snoRNA gene
 - |_snRNA gene
 - |_SRP RNA gene
 - |_strRNA gene
 - |_tmRNA gene
 - |_tRNA gene
- |_protein coding gene
- |_pseudogene attribute
- |_retron
- |_transgene
- |_transposable element gene



Gene Class

- |_engineered gene
- |_foreign gene
- |_fusion gene
- |_gene with polycistronic transcript
- |_gene with trans spliced transcript
- |_mt gene
- |_ncRNA gene
 - |_lncRNA gene
 - |_miRNA gene
 - |_piRNA gene
 - |_RNase MRP RNA gene
 - |_RNase P RNA gene
 - |_rRNA gene
 - |_snoRNA gene
 - |_snRNA gene
 - |_SRP RNA gene
 - |_tRNA gene
- |_nuclear gene
- |_protein coding gene
- |_retrogene
- |_transposable element gene

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JBrowse

Available Tracks

- filter tracks
- Reference Genome [?] 9
- Aberrations [?] 7
- Transgenic Insertions [?] 2
- Mutations & Sequence Variants 7
- Misc. Reagents 25
- Genome Level Features 21
- Transcript Level Features 12
 - Transcript Sequences 3
 - Transcription Start Sites (TSS) [?] 6
 - RNA-Seq exon junctions [?]
 - Polyadenylation Sites [?] 6
 - RNA Editing Sites [?]
- Protein Level Features 4
 - Protein Domains [?] 2
 - Peptide Sequences [?] 2
 - Developmental Proteomes
 - Peptide Atlas
- Expression 26
 - RNA-Seq [?] 17
 - modENCODE transcriptomes 8
 - Knoblich lab L3 CNS transcriptomes 2
 - Oliver lab SRA Aggregated RNA-Seq 3
 - FlyAtlas2 transcriptomes 4
 - Nervous system
 - Digestive system
 - Reproductive system
 - Other systems and whole organism
 - Small RNA-Seq [?] 9
 - Gene Predictions [?] 2

D. melanogaster (r6.37) File View Help

0 2,000,000 4,000,000 6,000,000 8,000,000 10,000,000 12,000,000 14,000,000 16,000,000 18,000,000 20,000,000 22,000,000 24,000,000

24,785,500 24,786,000 24,786,500 24,787,000 24,787,500

CDS: PA
key-PA
key-PB

Polyadenylation Sites [?]
pA_site_074085
pA_site_034261
pA_site_074086
pA_site_034262
pA_site_023597
pA_site_074087

Developmental Proteomes
proteomic_peptide_00110843
proteomic_peptide_00179446
proteomic_peptide_00124519
proteomic_peptide_00063107
proteomic_peptide_00109641
proteomic_peptide_00103891
proteomic_peptide_00179443
proteomic_peptide_00047706
proteomic_peptide_00018340
proteomic_peptide_00102542
proteomic_peptide_00117757
proteomic_peptide_00179444
proteomic_peptide_00086327
proteomic_peptide_00019229
proteomic_peptide_00059650
proteomic_peptide_00153289
proteomic_peptide_00179447
proteomic_peptide_00024545
proteomic_peptide_00159203
proteomic_peptide_00092965

Digestive system

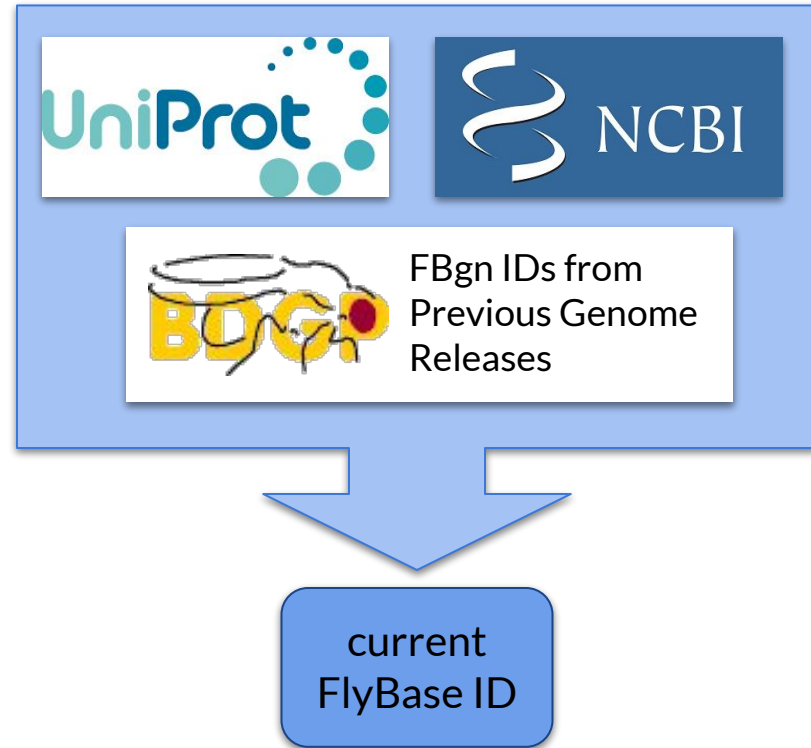
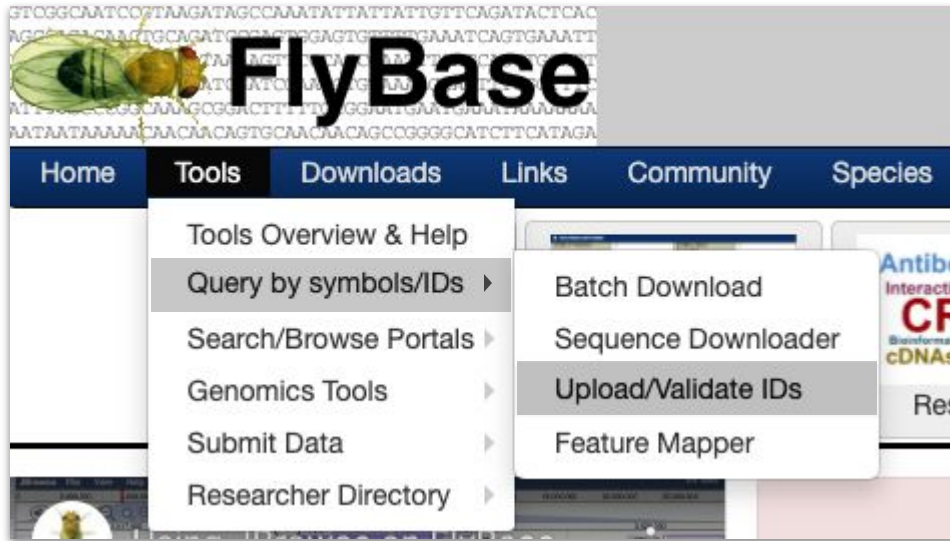
Female Cr
Male Cr
Female Mid
Male Mid
Female Gut
Male Gut
Female Saliv
Male Saliv

reorganized
track listings

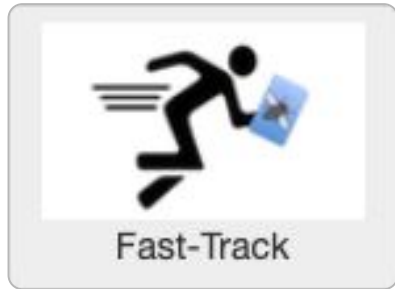
track
info

ID validator

A helpful first step for batch queries and downloads.



Fast-Track Your Paper



1 Publication — 2 Contact — 3 Data — 4 Genes — 5 Confirmation — 6 Finished

Choose a Publication to Annotate

enter key terms, author name, PubMed ID, etc.

Q Search ?

Preview the new
Fast-Track Your Paper steps at:

[https://wiki.flybase.org/wiki/FlyBase:Fast-Track Your Paper](https://wiki.flybase.org/wiki/FlyBase:Fast-Track_Your_Paper)

Links to papers where authors marked the
“contains technical advance” box can be found at:

[https://wiki.flybase.org/wiki/FlyBase:Papers with technical advances](https://wiki.flybase.org/wiki/FlyBase:Papers_with_technical_advances)

Staying in touch with FlyBase



FB2021_01, released Feb 18, 2021

A Database of *Drosophila* Genes & Genomes

Home Tools Downloads Links **Community** Species **About** **Help** Archives J2G ▾ Jump to Gene Go

- FlyBase Community
- Fast-Track Your Paper
- FlyBase Community Advisory Group
- Gene Snapshots
- FlyBase Forum
- Find A Person
-
- FlySlack Community
-

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

- Video Tutorials [↗](#)
- Tool help
- Report help
- Info for Authors ▶
- Linking to/from FlyBase
- Nomenclature
- Curation documentation ▶
- New to Flies
- Help Index
- FlyBase For Developers
-

version FB2021_01, released Feb 18, 2021

[Cite FlyBase](#)



Tweetorials from @FlyBaseDotOrg

FlyBase @FlyBaseDotOrg · Aug 24, 2018

FlyBase has updated the 'Search FlyBase' QuickSearch tab. You can get the functionality you're used to, searching all of FlyBase by text string by choosing the (default) 'Everything' option, or narrow your search to only IDs, symbols & names.

QuickSearch

Human Disease GAL4 etc Expression Phenotype References

Search FlyBase Orthologs Protein Domains Gene Groups GO Data Class

Everything ▾ FBto*

- ID, Symbol, Name
- Everything

Commentary list

1 6 7

FlyBase @FlyBaseDotOrg · Aug 24, 2018

For example, we use the string 'FBto*', the identifier prefix for the new Experimental Tool reports. When 'Everything' is selected, the hitlist includes every FlyBase report with the string 'FBto' anywhere in it, while 'ID, Symbol, Name' includes only Experimental Tool reports.

The screenshot shows the FlyBase search results page for the query 'FBto*'. On the left, there are two filter panels. The 'Filter by species' panel has 'Everything' selected. The 'Filter by data class' panel has 'Experimental Tool (306)' selected. The main results area shows a list of items, with 'C-Cerulean' and 'C-EYFP' highlighted. Each item has a description and a '1 A/B/C' indicator.

1 1 1

FlyBase @FlyBaseDotOrg · Jan 7

Want to find a tweetorial? You can search Twitter using the hashtag **#FlyBaseTweetorial** + a hashtag for your feature of interest; this narrows your search to only tweets using both hashtags. The next few linked tweets alphabetically list all the FlyBaseDotOrg hashtags to date.

The screenshot shows a Twitter search bar with the query '#FlyBaseTweetorial #paralogs'. Below the search bar, the text 'Search for "#FlyBaseTweetorial #paralogs"' is displayed.



Acknowledgements

FlyBase @
University of
Cambridge:

Nick Brown (Co-PI)
Giulia Antonazzo
Helen Attrill
Phani Garapati
Aoife Larkin
Steven Marygold
Alex McLachlan
Gillian Millburn
Arzu Ozturk-Colak
Clare Pilgrim
Vitor Trovisco

FlyBase @
Harvard University:

Norbert Perrimon (PI)
Susan Russo Gelbart (PD)
Julie Agapite
Kris Broll
Lynn Crosby
Gil dos Santos
Kathleen Falls
L. Sian Gramates
Victoria Jenkins
Ian Longden
Beverley Matthews
Carol Sutherland
Christopher Tabone
Pinglei Zhou
Mark Zytkovicz

FlyBase @
Indiana University:

Thomas Kaufman (Co-PI)
Brian Calvi (Co-PI)
Josh Goodman
Victor Strelets
Jim Thurmond
Pravija Krishna

FlyBase @
University of New Mexico:

Richard Cripps (Co-PI)
TyAnna Lovato

**We thank FlyBase users
worldwide for their support.**



**NHGRI U41HG000739
MRC: MR/N030117/1
NSF: DBI-2035515, 2039324**

DROS21: even more FlyBase

DROS21 FlyBase posters

211A: Progress towards functional understanding of the gene repertoire of *Drosophila*. (Helen Attrill)

Tues 30th March: 10:00AM-12:00PM (Eastern)

Weds 31st March: 12:30PM-2:30PM (Eastern)

531C: An enzyme catalog for *Drosophila melanogaster* (Steven Marygold)

Weds 31st March: 10:00AM-12:00PM (Eastern)

Thurs 1st April: 12:30PM-2:30PM (Eastern)