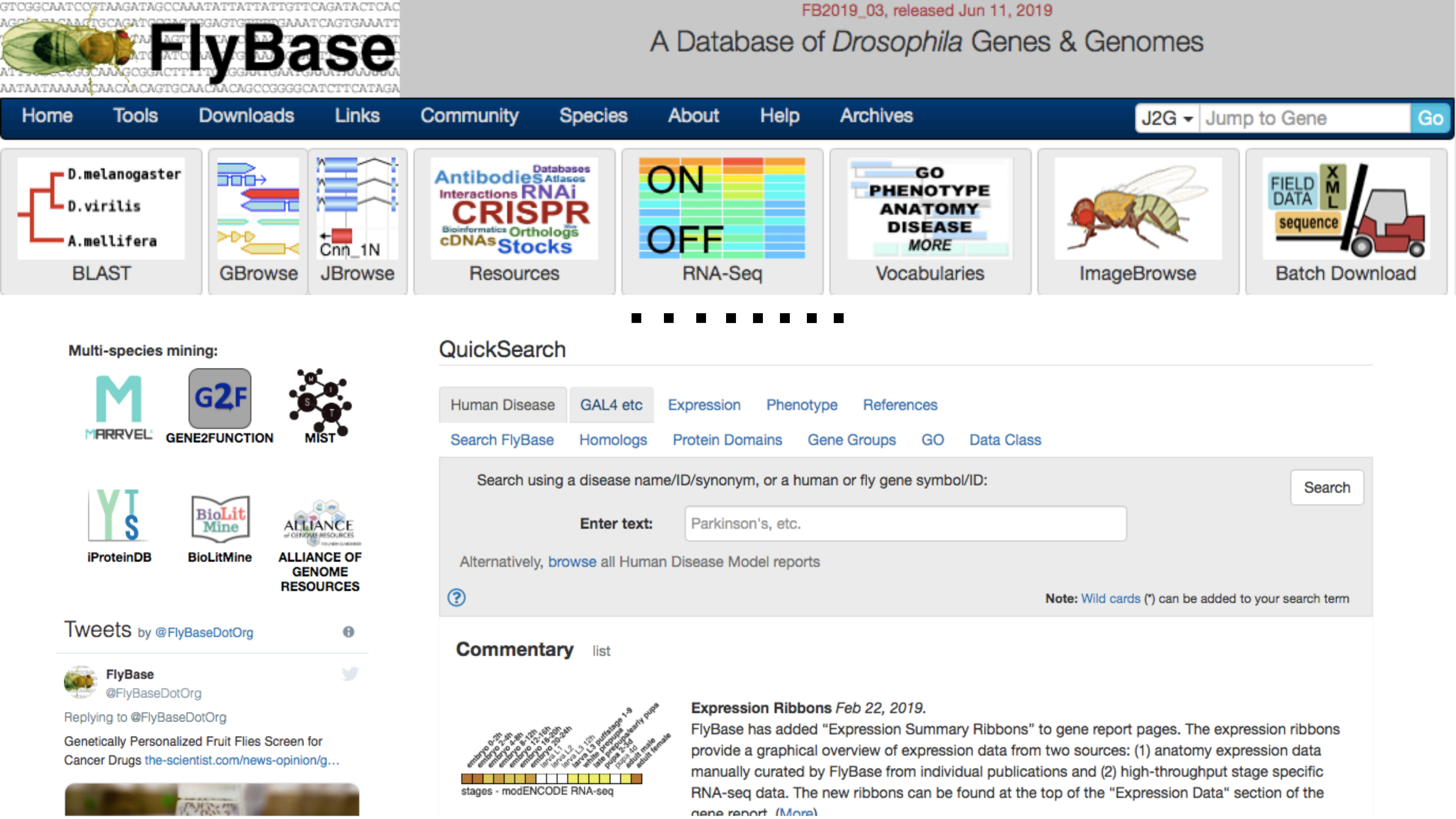
What’s new in FlyBase?

Lynn Crosby

CanFly XV 2019



Search using a disease name/ID/synonym, or a human or fly gene symbol/ID:

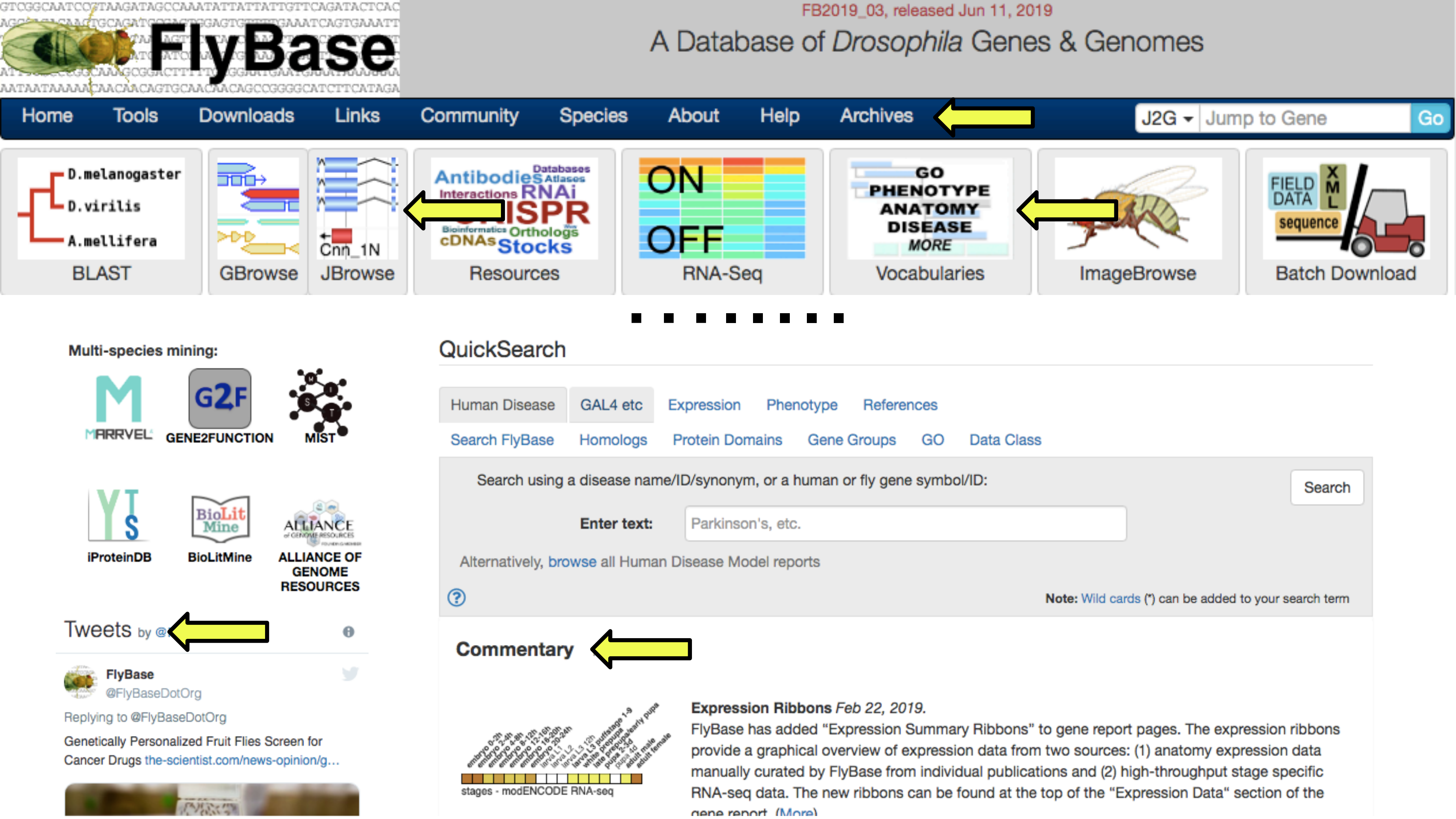
Enter text: Parkinson's, etc.

Alternatively, browse all Human Disease Model reports

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

FlyBase
@FlyBaseDotOrg
Replying to @FlyBaseDotOrg
Genetically Personalized Fruit Flies Screen for Cancer Drugs the-scientist.com/news-opinion/g…

Expression Ribbons *Feb 22, 2019.*
FlyBase has added "Expression Summary Ribbons" to gene report pages. The expression ribbons provide a graphical overview of expression data from two sources: (1) anatomy expression data manually curated by FlyBase from individual publications and (2) high-throughput stage specific RNA-seq data. The new ribbons can be found at the top of the "Expression Data" section of the gene report. (More)



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Genetically Personalized Fruit Flies Screen for Cancer Drugs the-scientist.com/news-opinion/g…

Commentary

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Overview

- → Answering the question yourself
  - Follow us on Twitter, subscribe to newsletter
  - ‘New in This Release’ page
  - Commentaries (current and past)
- Information for developers (github)
  - FlyBase APIs
- New resource for finding reagents
  - New experimental tool reports
- New data tracks in JBrowse
  - sgRNAs (predicted guide RNAs)
  - SRA aggregated RNA-Seq data

FlyBase twitter account

Home page, lower left -- quick view and link:

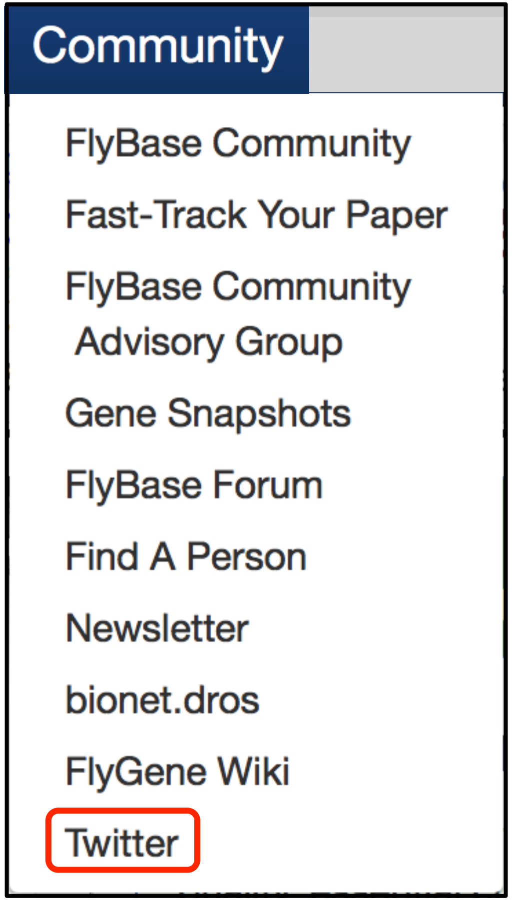
Tweets by @FlyBaseDotOrg

FlyBase
@FlyBaseDotOrg

Replying to @FlyBaseDotOrg

Genetically Personalized Fruit Flies Screen for Cancer Drugs the-scientist.com/news-opinion/g…

Navigation bar -- link:

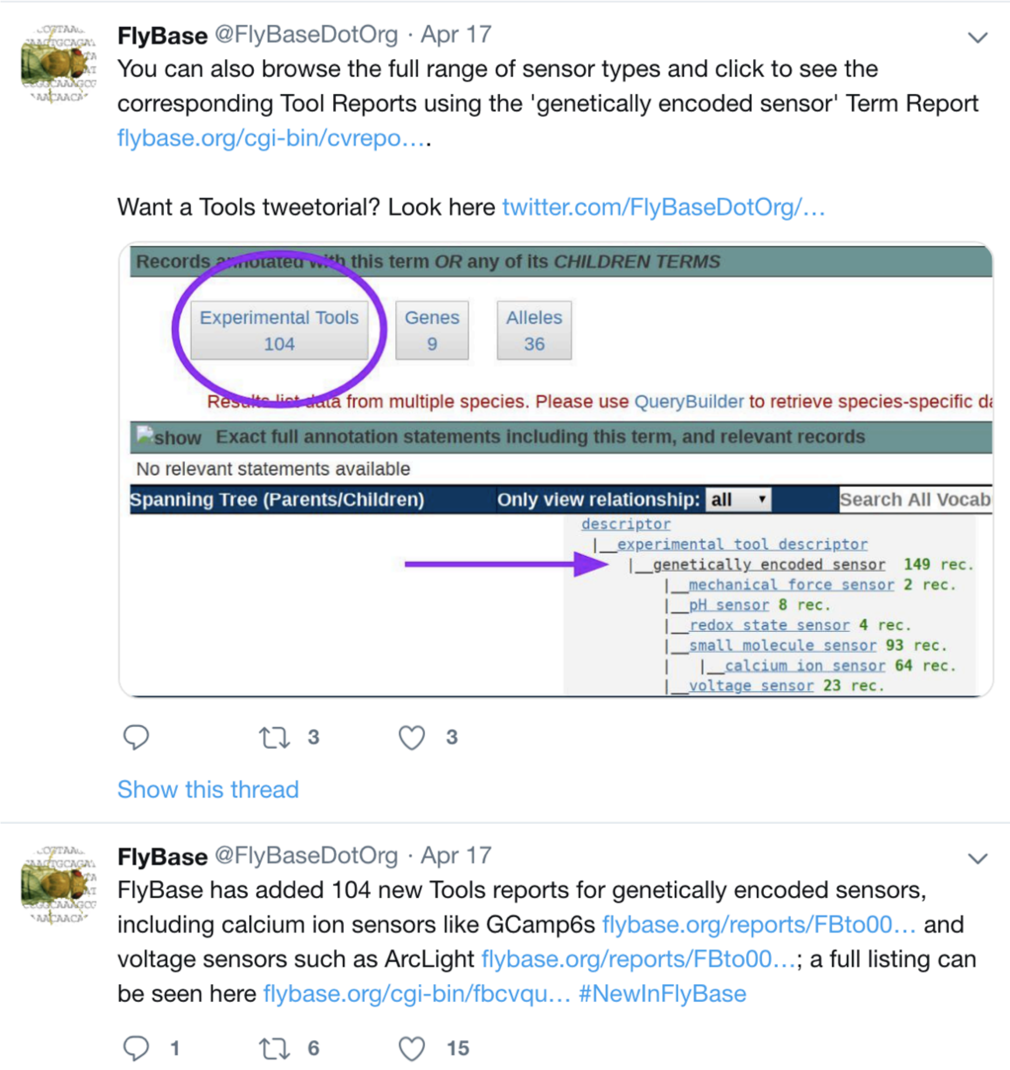


Community

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

FlyBase Twitter page

- News and retweets
- ‘Tweetorials’
- New-in-this-release descriptions #NewInFlyBase



FlyBase @FlyBaseDotOrg · Apr 17

You can also browse the full range of sensor types and click to see the corresponding Tool Reports using the 'genetically encoded sensor' Term Report flybase.org/cgi-bin/cvrepo….

Want a Tools tweetorial? Look here twitter.com/FlyBaseDotOrg/…

Records annotated with this term *OR* any of its *CHILDREN TERMS*

Results list data from multiple species. Please use QueryBuilder to retrieve species-specific da

show Exact full annotation statements including this term, and relevant records

No relevant statements available

Spanning Tree (Parents/Children) **Only view relationship:** all ▾ Search All Vocab

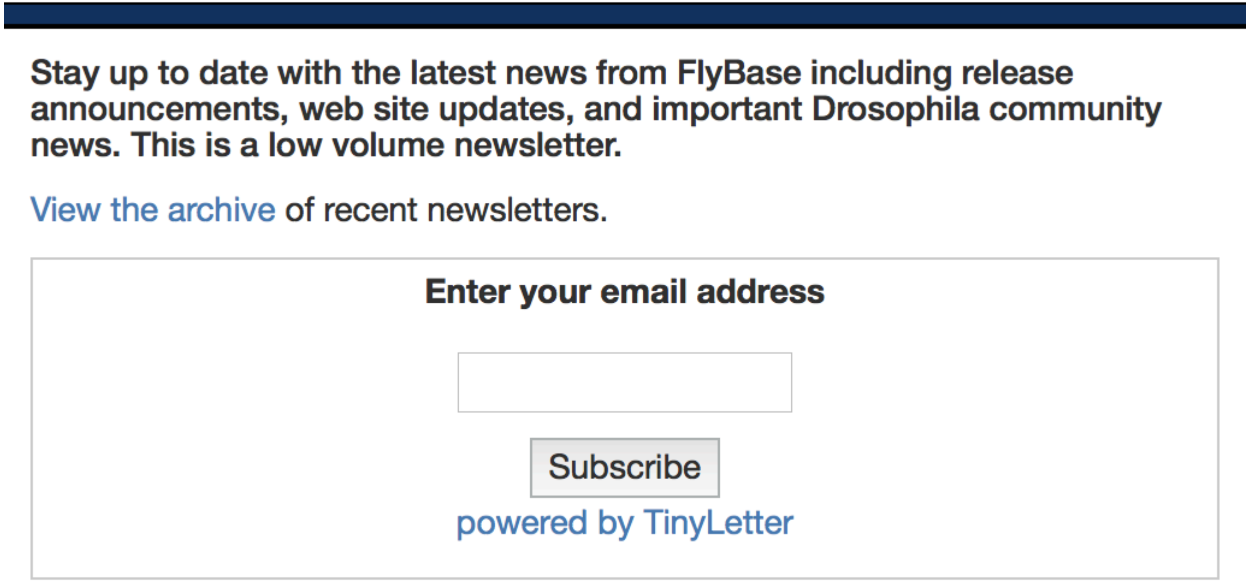
```
descriptor
 |__experimental tool descriptor
    |__genetically encoded sensor  149 rec.
       |__mechanical force sensor 2 rec.
       |__pH sensor 8 rec.
       |__redox state sensor 4 rec.
       |__small molecule sensor 93 rec.
       |   |__calcium ion sensor 64 rec.
       |__voltage sensor 23 rec.
```

Show this thread

FlyBase @FlyBaseDotOrg · Apr 17

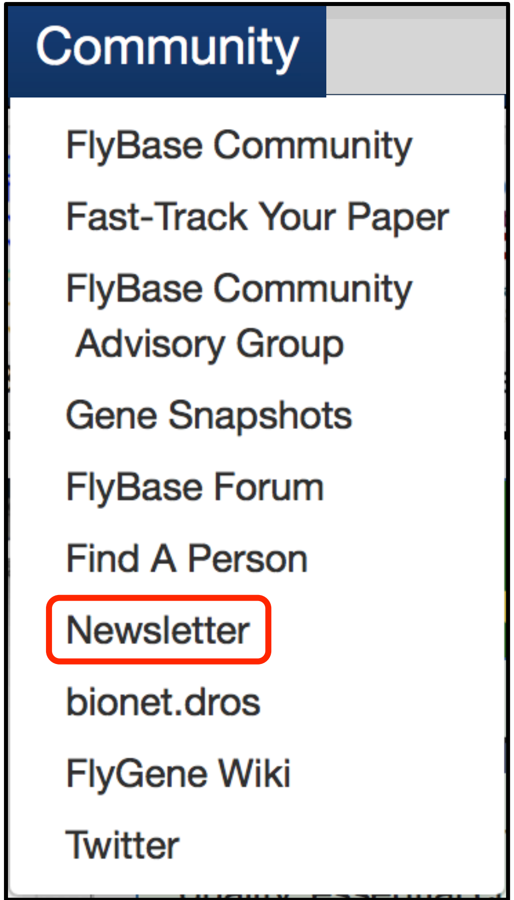
FlyBase has added 104 new Tools reports for genetically encoded sensors, including calcium ion sensors like GCamp6s flybase.org/reports/FBto00… and voltage sensors such as ArcLight flybase.org/reports/FBto00…; a full listing can be seen here flybase.org/cgi-bin/fbcvqu… #NewInFlyBase

FlyBase newsletter

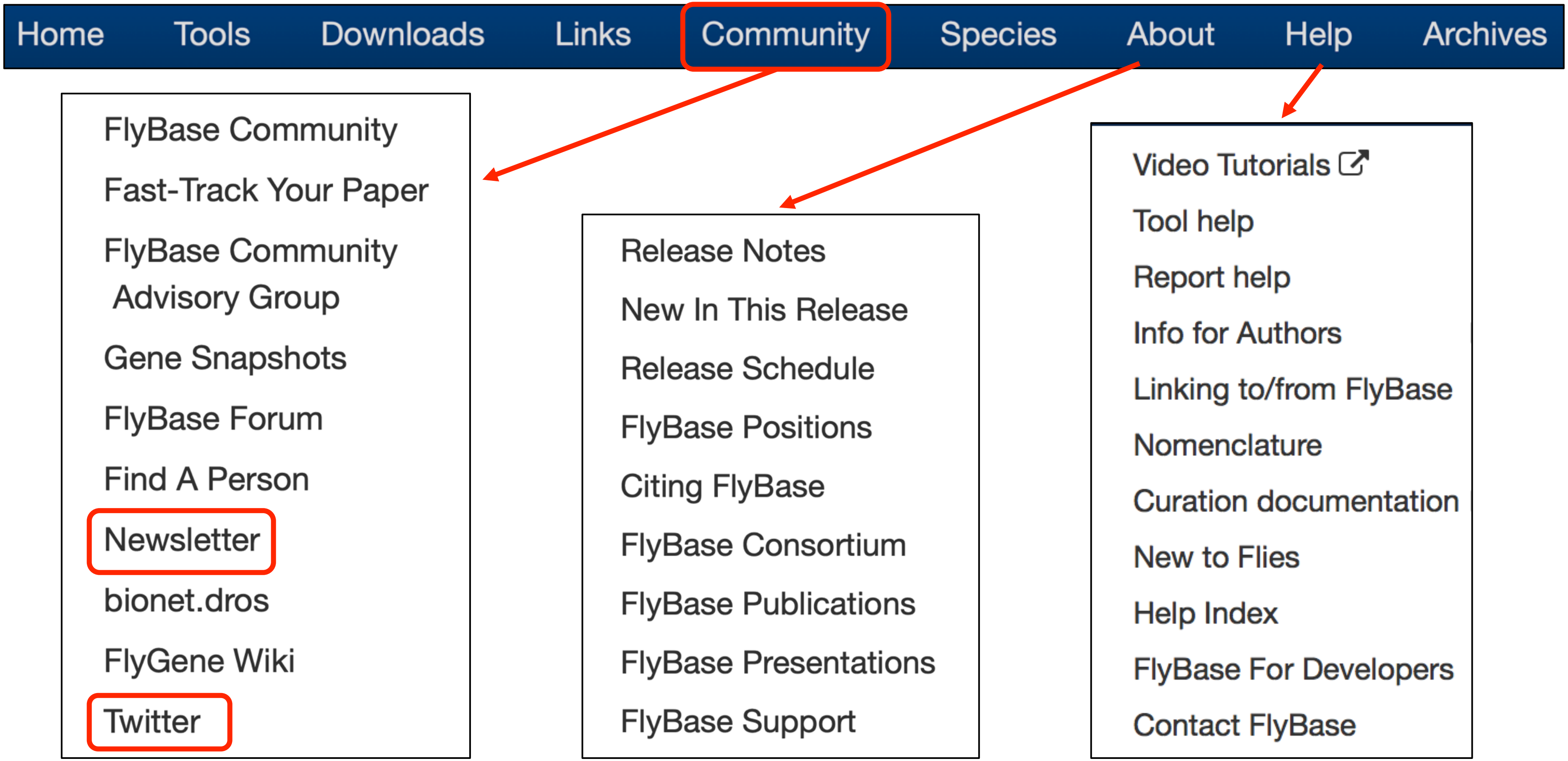

Stay up to date with the latest news from FlyBase including release announcements, web site updates, and important Drosophila community news. This is a low volume newsletter.

View the archive of recent newsletters.

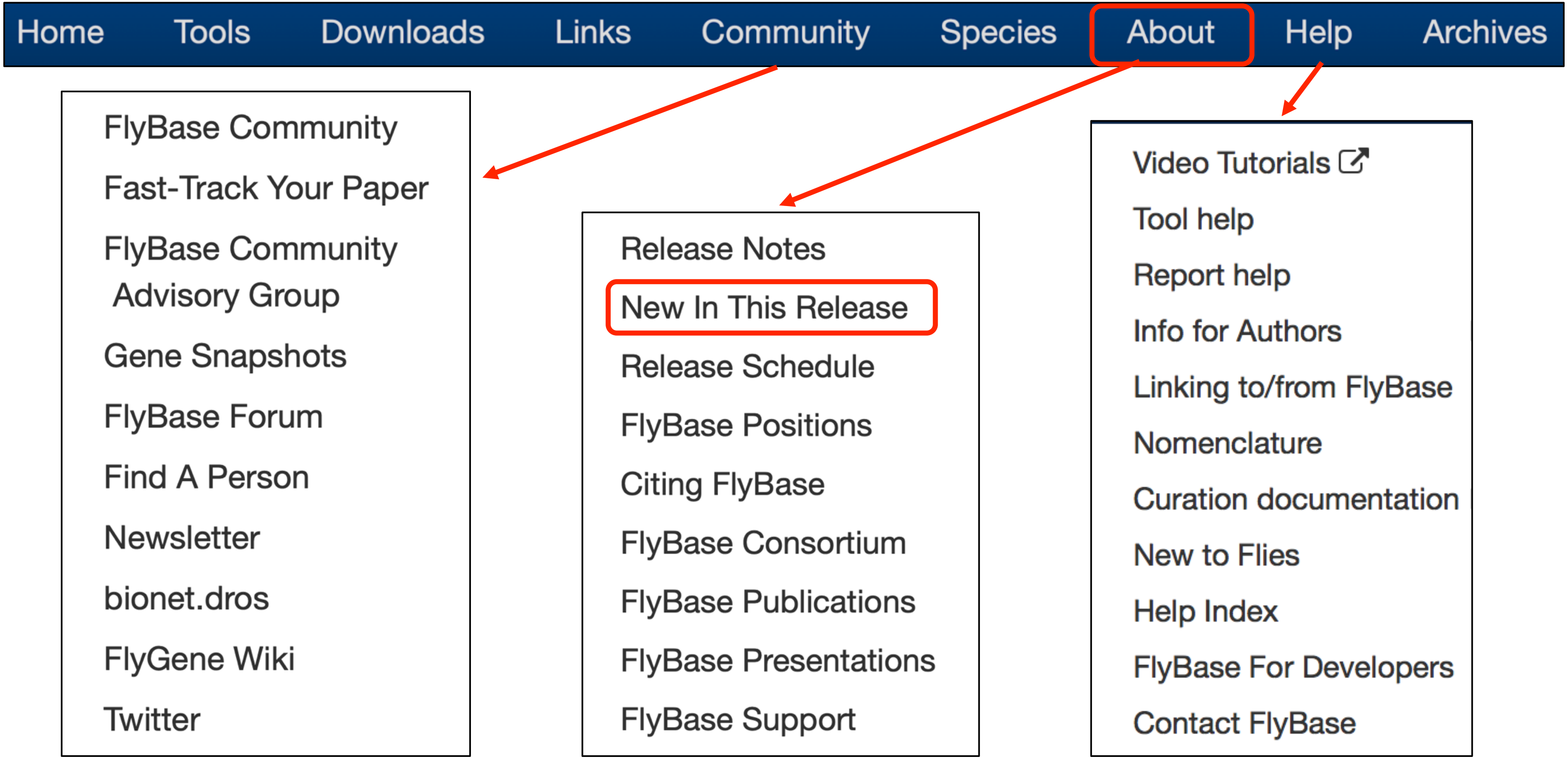
Navigation bar -- link:

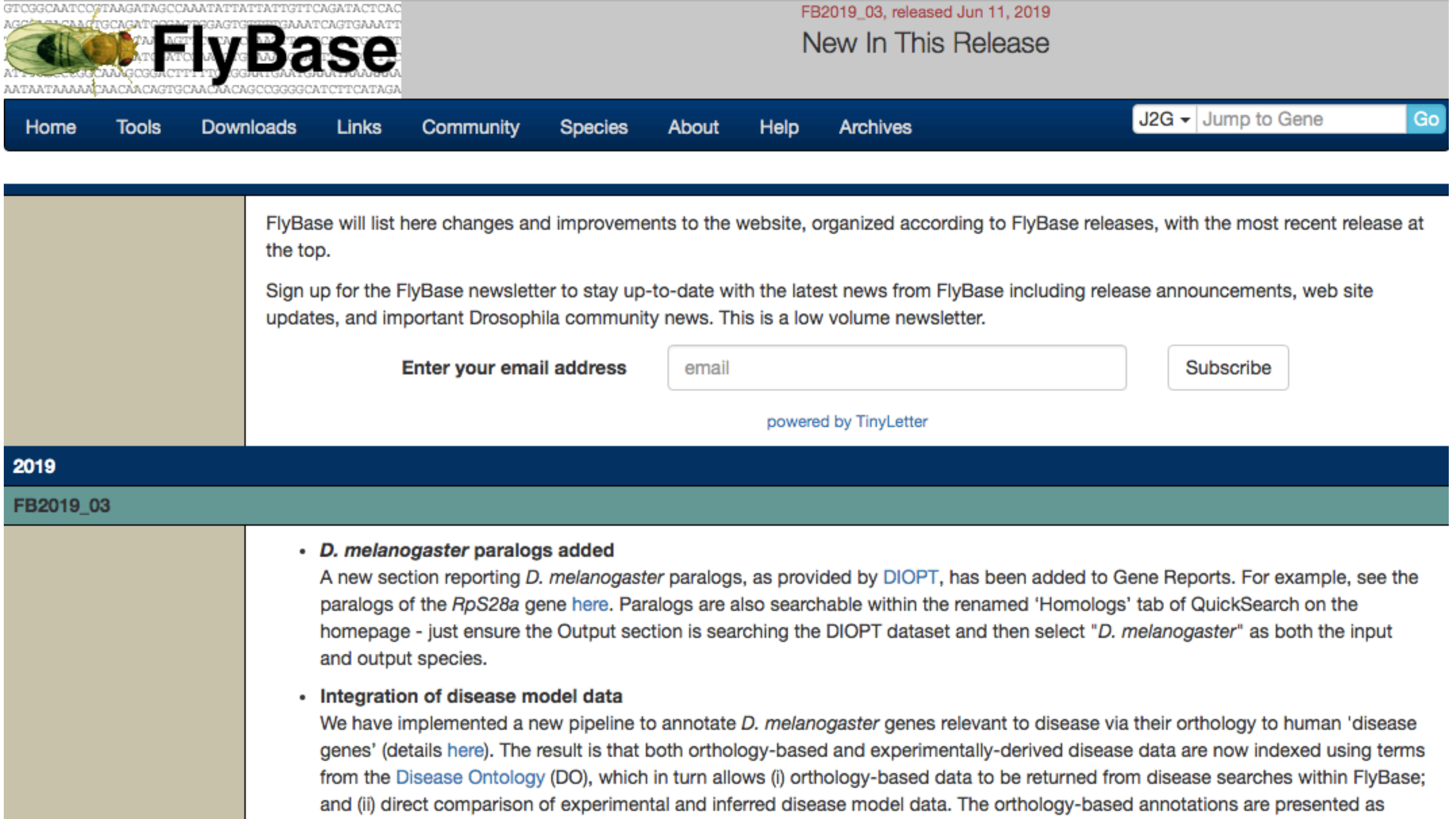


More information -- links from the navigation bar



More information -- links from the navigation bar





FB2019_03, released Jun 11, 2019

New In This Release

FlyBase will list here changes and improvements to the website, organized according to FlyBase releases, with the most recent release at the top.

Sign up for the FlyBase newsletter to stay up-to-date with the latest news from FlyBase including release announcements, web site updates, and important Drosophila community news. This is a low volume newsletter.

Enter your email address

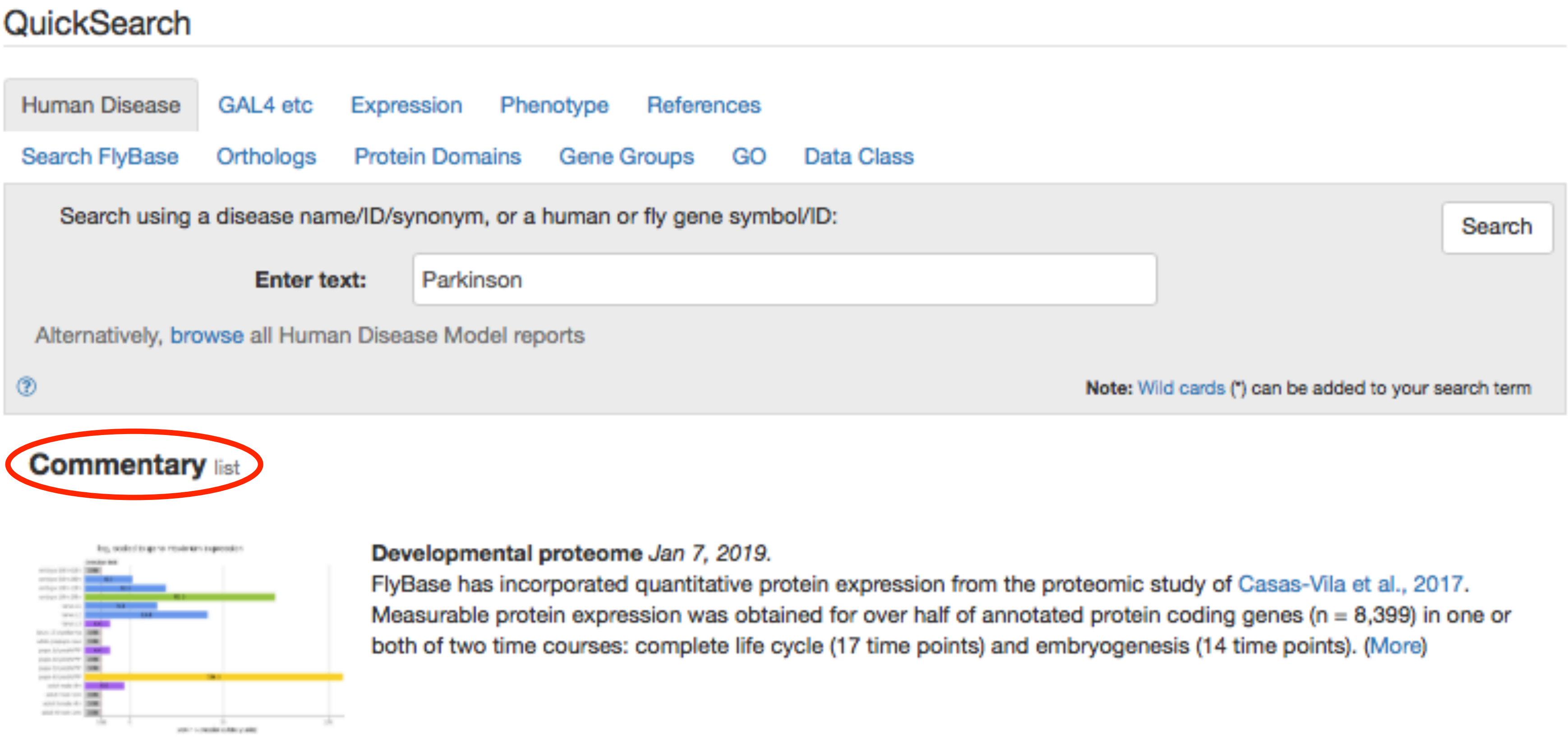
powered by TinyLetter

2019

FB2019_03

- ***D. melanogaster*** **paralogs added**
  A new section reporting *D. melanogaster* paralogs, as provided by DIOPT, has been added to Gene Reports. For example, see the paralogs of the *RpS28a* gene here. Paralogs are also searchable within the renamed 'Homologs' tab of QuickSearch on the homepage - just ensure the Output section is searching the DIOPT dataset and then select "*D. melanogaster*" as both the input and output species.
- **Integration of disease model data**
  We have implemented a new pipeline to annotate *D. melanogaster* genes relevant to disease via their orthology to human 'disease genes' (details here). The result is that both orthology-based and experimentally-derived disease data are now indexed using terms from the Disease Ontology (DO), which in turn allows (i) orthology-based data to be returned from disease searches within FlyBase; and (ii) direct comparison of experimental and inferred disease model data. The orthology-based annotations are presented as

Commentaries -- bottom of the home page



QuickSearch

Search using a disease name/ID/synonym, or a human or fly gene symbol/ID:

Enter text: Parkinson

Alternatively, browse all Human Disease Model reports

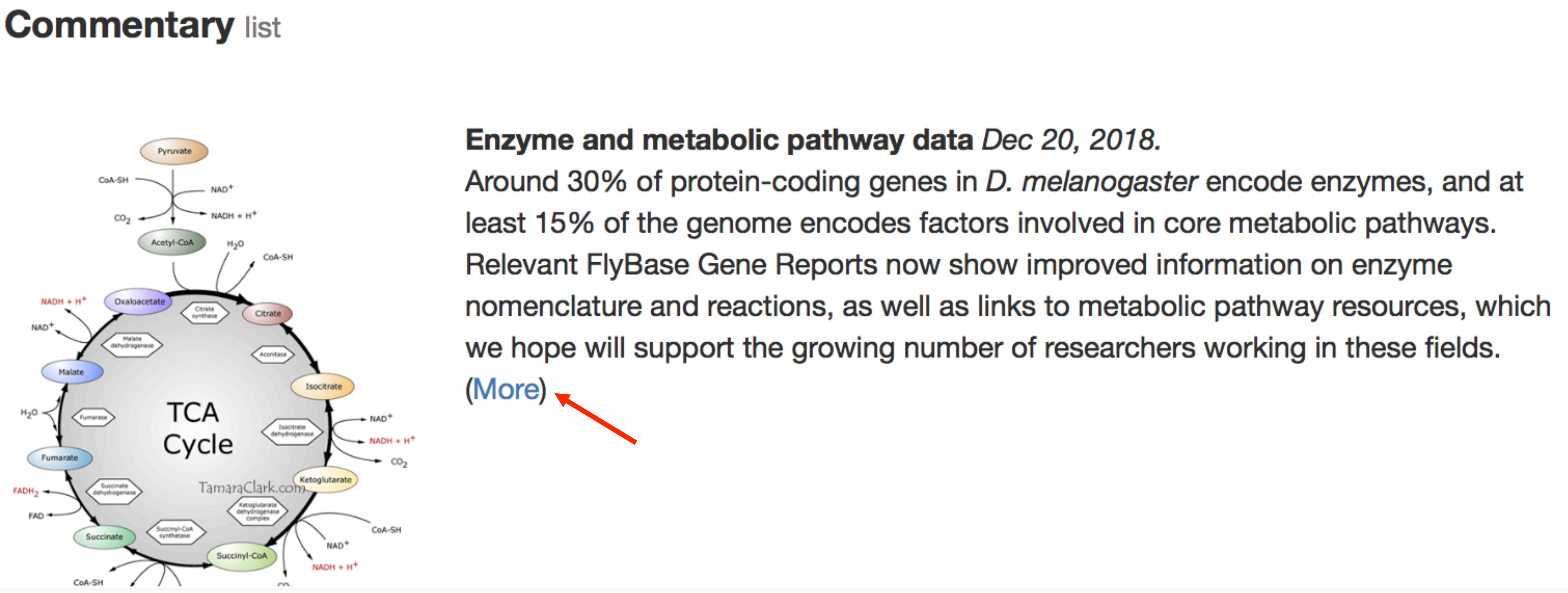
Note: Wild cards (*) can be added to your search term

Commentary list

Developmental proteome *Jan 7, 2019.*
FlyBase has incorporated quantitative protein expression from the proteomic study of Casas-Vila et al., 2017. Measurable protein expression was obtained for over half of annotated protein coding genes (n = 8,399) in one or both of two time courses: complete life cycle (17 time points) and embryogenesis (14 time points). (More)

Commentaries provide more details

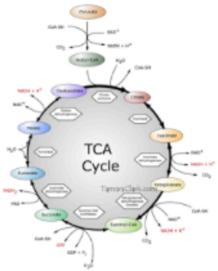
Home page, bottom (rotating entries):



Commentary list

Enzyme and metabolic pathway data *Dec 20, 2018.*
Around 30% of protein-coding genes in *D. melanogaster* encode enzymes, and at least 15% of the genome encodes factors involved in core metabolic pathways. Relevant FlyBase Gene Reports now show improved information on enzyme nomenclature and reactions, as well as links to metabolic pathway resources, which we hope will support the growing number of researchers working in these fields. (More)

Commentary for ‘Enzyme and metabolic pathway data”



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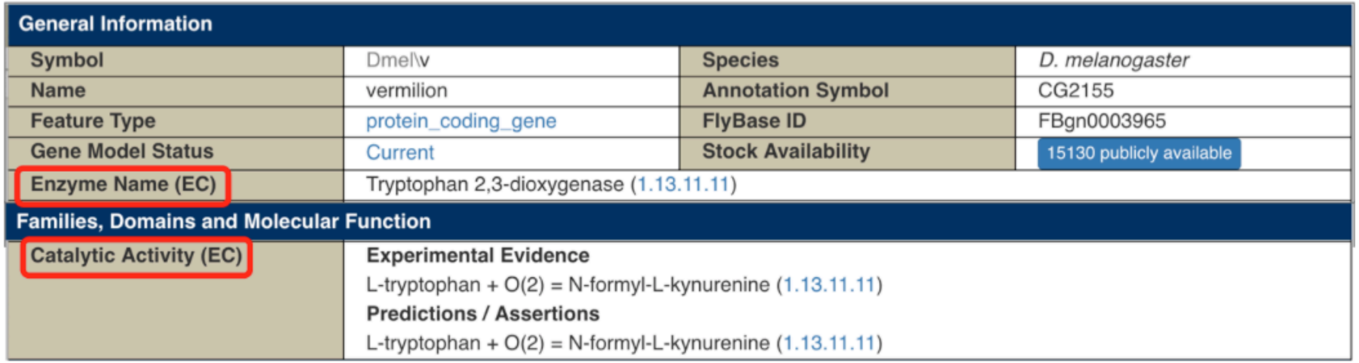
The uppermost ‘General Information’ panel on Gene Reports now contains an ‘Enzyme Name (EC)’ field that displays the systematic name for a given enzyme together with its Enzyme Commission (EC) number. (Showing the systematic name is especially useful where the fly gene is either unnamed or has been named based on its mutant phenotype rather than its wild type function.) Further down the page, in the ‘Families, Domains and Molecular Function’ section, the new ’Catalytic activity (EC)’ field displays the reaction(s) catalyzed by the enzyme. The EC data in both these new fields are derived from our Gene Ontology (GO) Molecular Function annotations, taking advantage of the EC cross-references within the GO itself. This allows the catalytic activities to be separated into those based on experimental evidence versus those based only on predictions or computational assertions, using the evidence code associated with the underlying GO annotations.



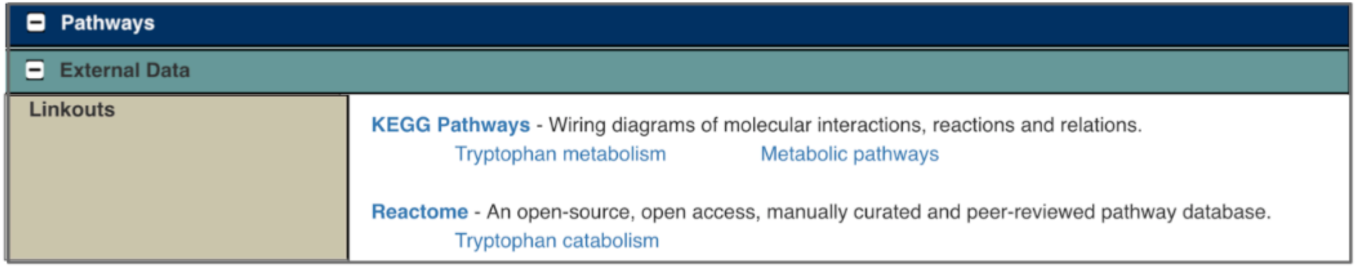
General Information

Symbol	Dmel\v	**Species**	*D. melanogaster*
Name	vermilion	**Annotation Symbol**	CG2155
Feature Type	protein_coding_gene	**FlyBase ID**	FBgn0003965
Gene Model Status	Current	**Stock Availability**	15130 publicly available
Enzyme Name (EC)	Tryptophan 2,3-dioxygenase (1.13.11.11)		

Families, Domains and Molecular Function

Catalytic Activity (EC)	**Experimental Evidence** L-tryptophan + O(2) = N-formyl-L-kynurenine (1.13.11.11) **Predictions / Assertions** L-tryptophan + O(2) = N-formyl-L-kynurenine (1.13.11.11)

We have also introduced a new ‘Pathways’ section within the Gene Report. Where relevant, this section now includes the names of metabolic (and other) pathways in which the gene product is involved, with links to the respective reports at KEGG and Reactome. Additional links to BioCyc are due in the near future. This section also includes a link to and description of our growing collection of FlyBase-curated reports for signalling pathways, where relevant.



Pathways

External Data

Linkouts	**KEGG Pathways** - Wiring diagrams of molecular interactions, reactions and relations. Tryptophan metabolism Metabolic pathways **Reactome** - An open-source, open access, manually curated and peer-reviewed pathway database. Tryptophan catabolism

Commentaries -- past commentaries are available

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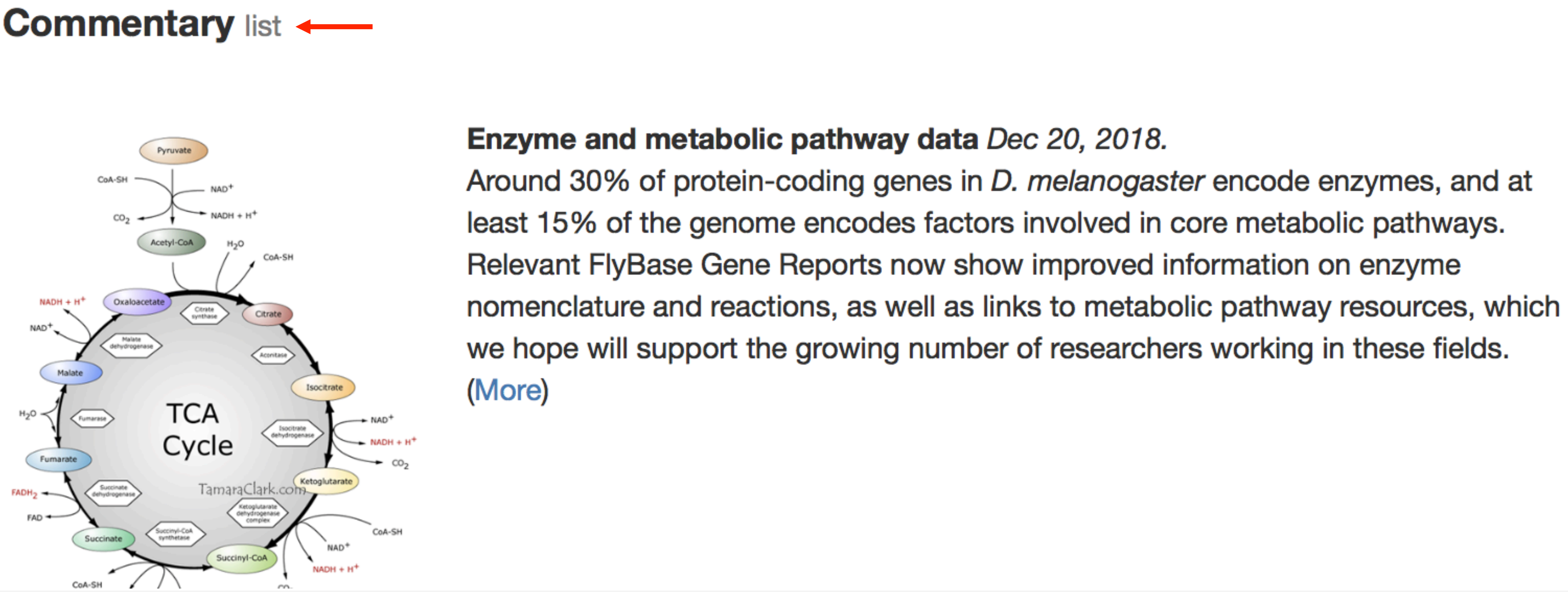

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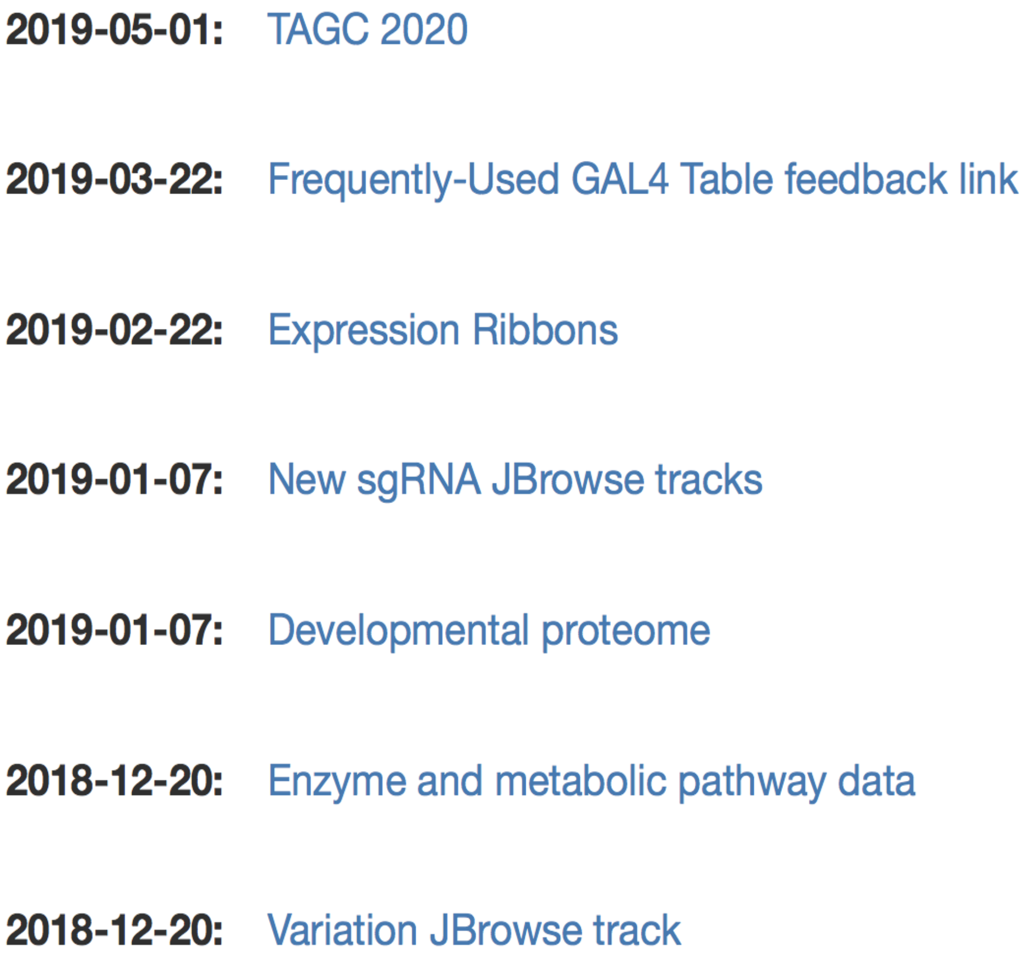
Commentary ‘list’

Access to archived commentaries



2019-05-01: TAGC 2020

2019-03-22: Frequently-Used GAL4 Table feedback link

2019-02-22: Expression Ribbons

2019-01-07: New sgRNA JBrowse tracks

2019-01-07: Developmental proteome

2018-12-20: Enzyme and metabolic pathway data

2018-12-20: Variation JBrowse track

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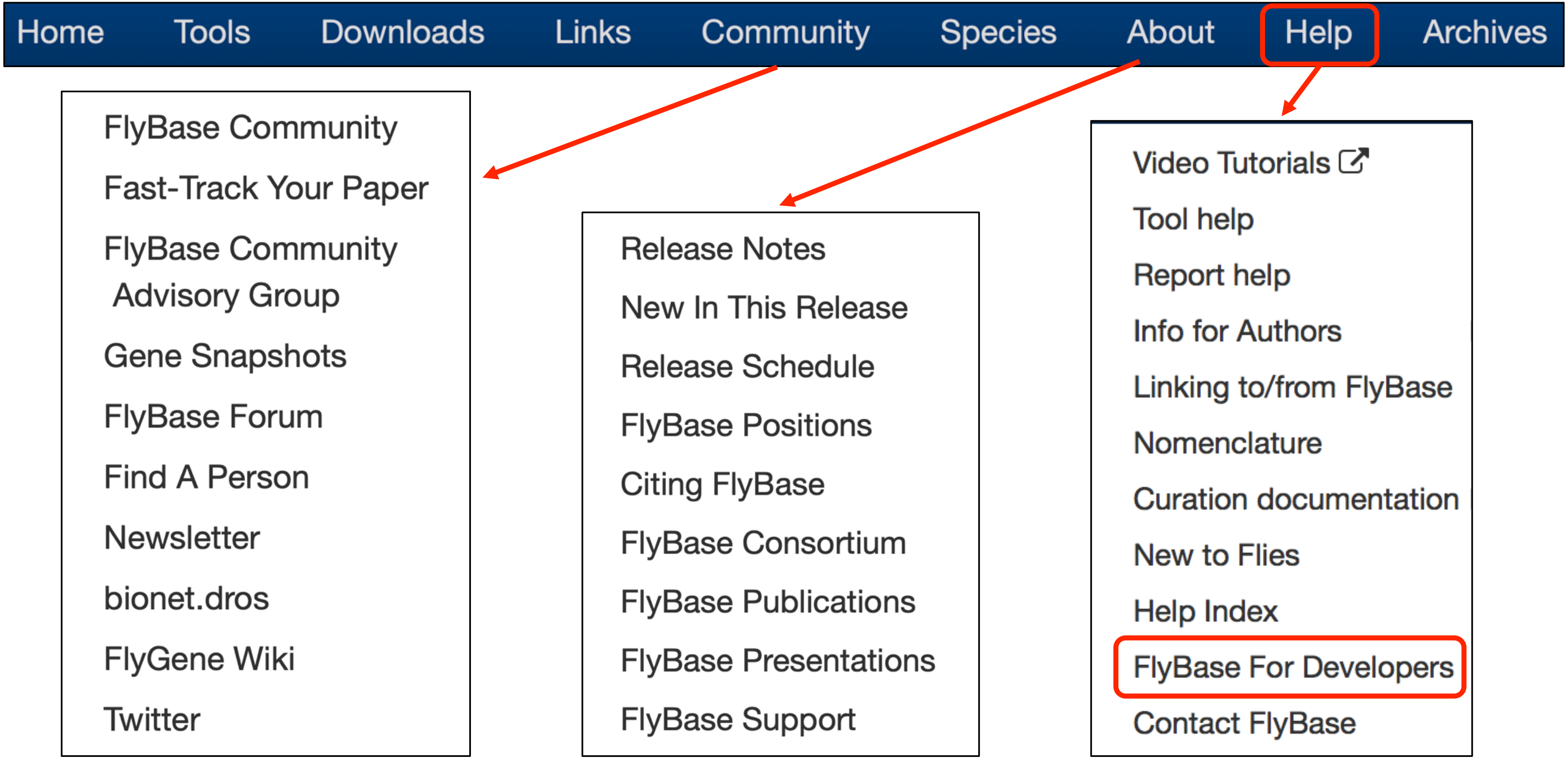
- → Information for developers (github)
  - FlyBase APIs

- New resource for finding reagents
  - New experimental tool reports

- New data tracks in JBrowse
  - sgRNAs (predicted guide RNAs)
  - SRA aggregated RNA-Seq data

More information -- links from the navigation bar



FlyBase for Developers

Developer docs for FlyBase API, Chado, bulk files, etc.

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→
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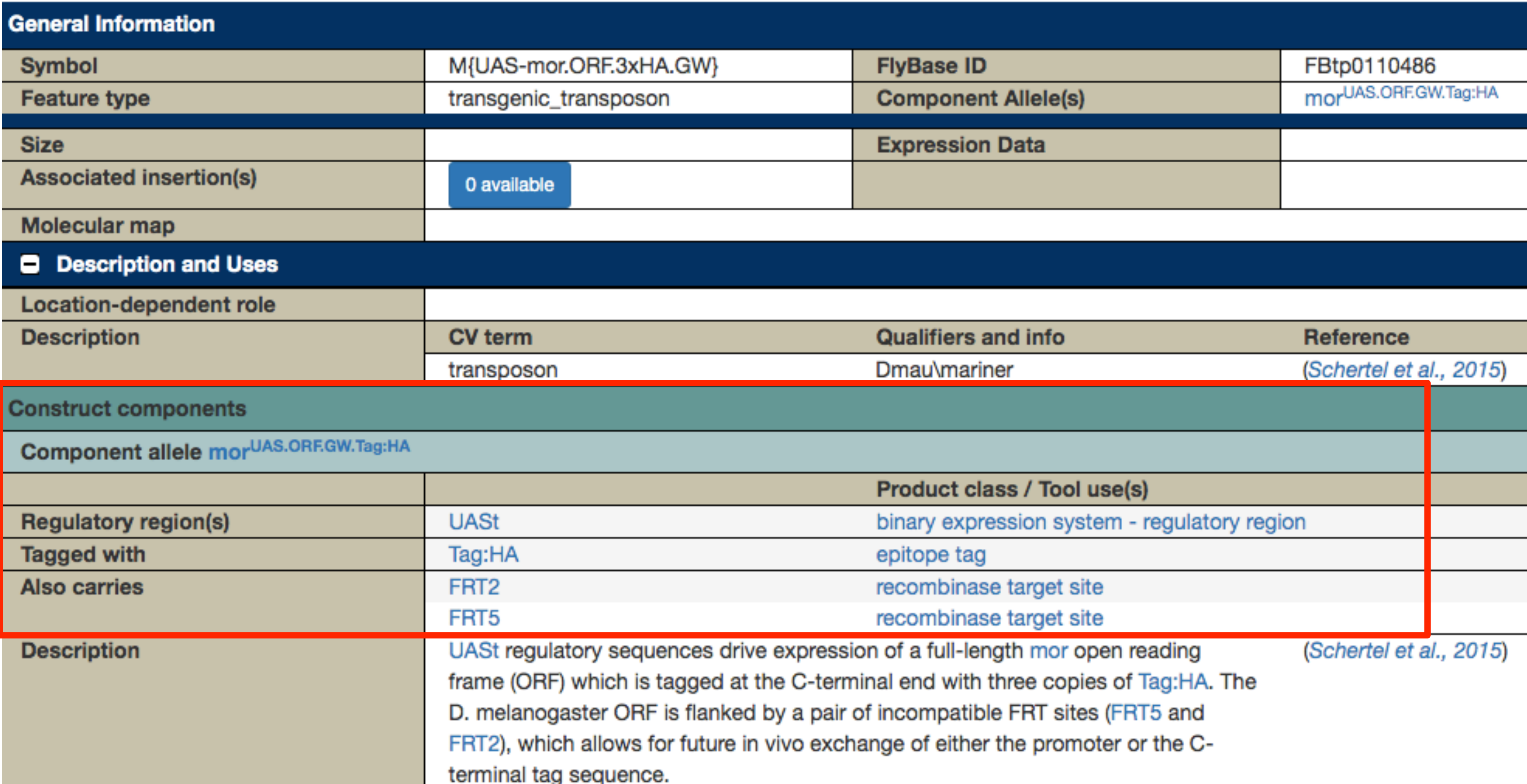
New: Experimental Tool reports

⇒ What are experimental tools?

Components of transgenic constructs:

- Localization tags
  - NLS
  - Signal peptide
  - Organelle localization
- Binary expression systems
  - GAL4/UAS
  - lexA/lexAop
  - tetR/tetO
  - QF/QUAS
- Insertional mutagenesis
  - Enhancer trap
  - Gene trap
- Detection tags
  - FLAG
  - EGFP
  - mCherry
- Genome engineering
  - FLP/FRT
  - phiC31/attB/attP
  - Cas9
- Sensors
  - pH sensor
  - Calcium sensor
  - Redox sensor

Experimental tools: “Construct components” in transgenic construct report



General Information

Symbol	M{UAS-mor.ORF.3xHA.GW}	**FlyBase ID**	FBtp0110486
Feature type	transgenic_transposon	**Component Allele(s)**	mor$^{\text{UAS.ORF.GW.Tag:HA}}$
Size		**Expression Data**	
Associated insertion(s)	0 available		
Molecular map			

Description and Uses

Location-dependent role

Description	**CV term**	**Qualifiers and info**	**Reference**
	transposon	Dmau\mariner	(*Schertel et al., 2015*)

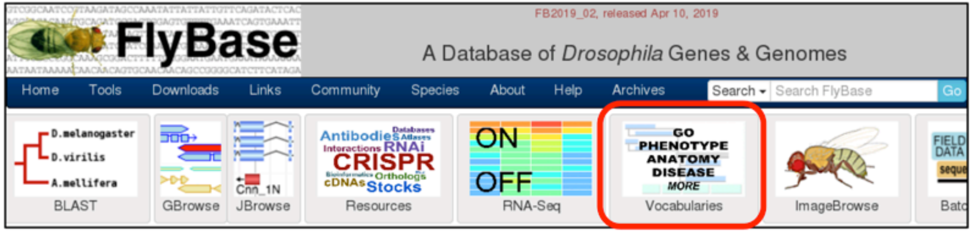
Construct components

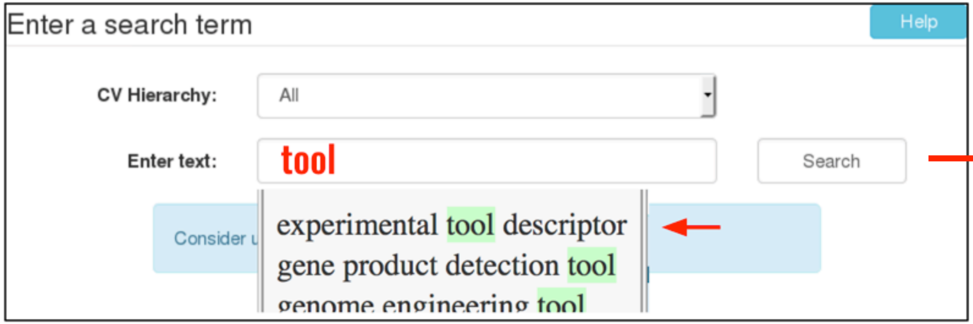
Component allele mor$^{\text{UAS.ORF.GW.Tag:HA}}$

		Product class / Tool use(s)
Regulatory region(s)	UASt	binary expression system - regulatory region
Tagged with	Tag:HA	epitope tag
Also carries	FRT2	recombinase target site
	FRT5	recombinase target site

Description	UASt regulatory sequences drive expression of a full-length mor open reading frame (ORF) which is tagged at the C-terminal end with three copies of Tag:HA. The D. melanogaster ORF is flanked by a pair of incompatible FRT sites (FRT5 and FRT2), which allows for future in vivo exchange of either the promoter or the C-terminal tag sequence.	(*Schertel et al., 2015*)

Browse experimental tools





CV Hierarchy: All

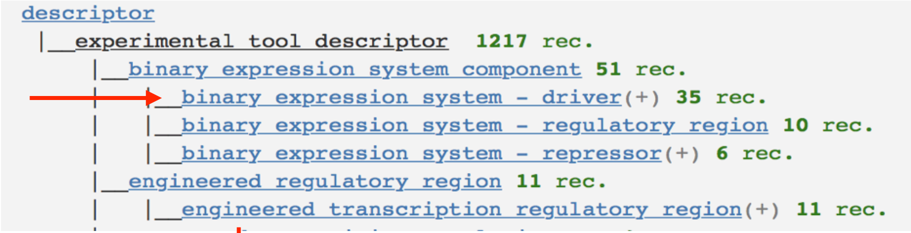
Enter text: tool

experimental tool descriptor
gene product detection tool
genome engineering tool

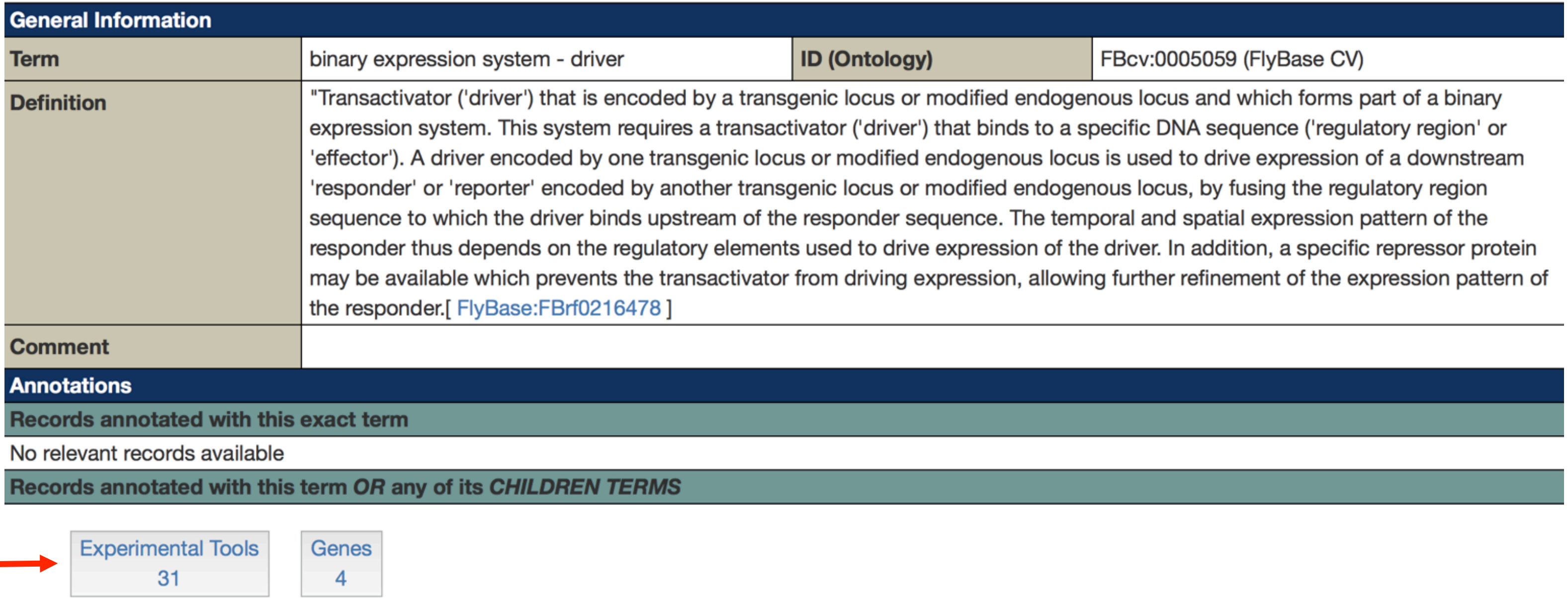
```
descriptor
 |__experimental tool descriptor  1217 rec.
     |__binary expression system component 51 rec.
     |    |__binary expression system - driver(+) 35 rec.
     |    |__binary expression system - regulatory region 10 rec.
     |    |__binary expression system - repressor(+) 6 rec.
     |__engineered regulatory region 11 rec.
     |    |__engineered transcription regulatory region(+) 11 rec.
     |__gene product activity regulation tag 4 rec.
     |    |__conditional activity regulation tag(+) 4 rec.
     |__gene product cleavage tag 4 rec.
     |    |__protein cleavage tag 4 rec.
     |__gene product degradation tag 10 rec.
     |    |__cell-cycle regulated gene product degradation tag 3 rec.
     |    |__small molecule-dependent gene product degradation tag 3 rec.
     |__gene product detection tool 293 rec.
     |    |__protein detection tool(+) 293 rec.
     |    |__RNA detection tool
     |__gene product localization tag 124 rec.
     |    |__protein localization tag(+) 124 rec.
     |__genetically encoded sensor 149 rec.
     |    |__mechanical force sensor 2 rec.
     |    |__pH sensor 8 rec.
     |    |__redox state sensor 4 rec.
     |    |__small molecule sensor(+) 93 rec.
     |    |__voltage sensor 23 rec.
     |__genome engineering tool 340 rec.
     |    |__integrase 49 rec.
     |    |__integrase target site 4 rec.
     |    |__nuclease(+) 4 rec.
     |    |__nuclease target site
     |    |__recombinase 261 rec.
     |    |__recombinase target site 23 rec.
     |__insertional mutagenesis tool 323 rec.
     |    |__enhancer trap 86 rec.
     |    |__gene trap 97 rec.
     |    |__misexpression element 22 rec.
     |    |__polyA trap 7 rec.
     |    |__promoter trap 25 rec.
     |    |__protein trap 107 rec.
     |__purification tag 11 rec.
     |__split system component 38 rec.
          |__split driver - DNA-binding fragment 5 rec.
          |__split driver - transcription activation fragment 9 rec.
          |__split fluorescent protein 20 rec.
```

Experimental Tool Term Report

Find binary drivers other than GAL4



```
descriptor
 |__experimental tool descriptor  1217 rec.
     |__binary expression system component 51 rec.
     |   |__binary expression system - driver(+) 35 rec.
     |   |__binary expression system - regulatory region 10 rec.
     |   |__binary expression system - repressor(+) 6 rec.
     |__engineered regulatory region 11 rec.
     |   |__engineered transcription regulatory region(+) 11 rec.
```



General Information

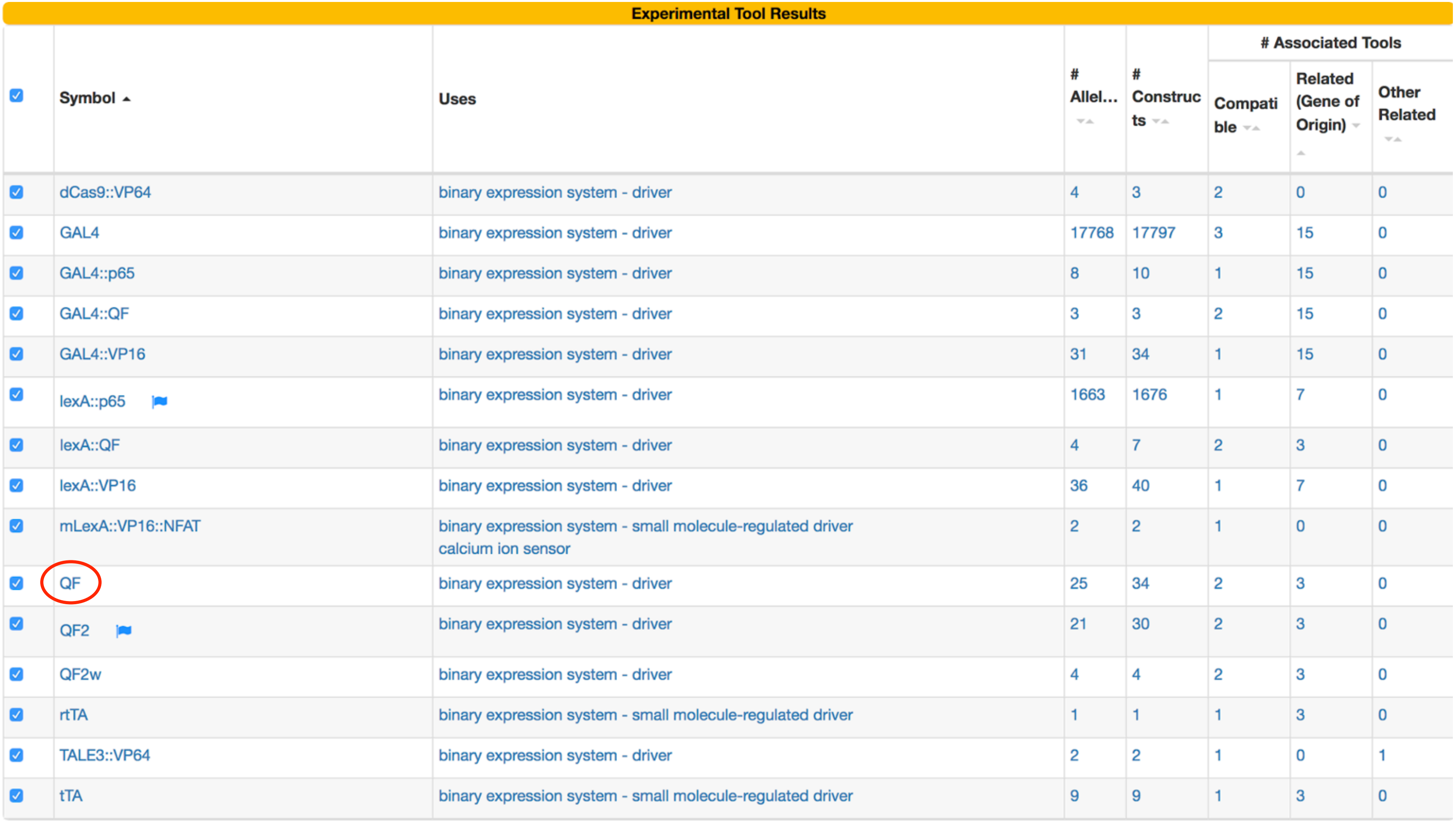
Term	binary expression system - driver	**ID (Ontology)**	FBcv:0005059 (FlyBase CV)
Definition	"Transactivator ('driver') that is encoded by a transgenic locus or modified endogenous locus and which forms part of a binary expression system. This system requires a transactivator ('driver') that binds to a specific DNA sequence ('regulatory region' or 'effector'). A driver encoded by one transgenic locus or modified endogenous locus is used to drive expression of a downstream 'responder' or 'reporter' encoded by another transgenic locus or modified endogenous locus, by fusing the regulatory region sequence to which the driver binds upstream of the responder sequence. The temporal and spatial expression pattern of the responder thus depends on the regulatory elements used to drive expression of the driver. In addition, a specific repressor protein may be available which prevents the transactivator from driving expression, allowing further refinement of the expression pattern of the responder.[FlyBase:FBrf0216478]		
Comment			

Annotations

Records annotated with this exact term

No relevant records available

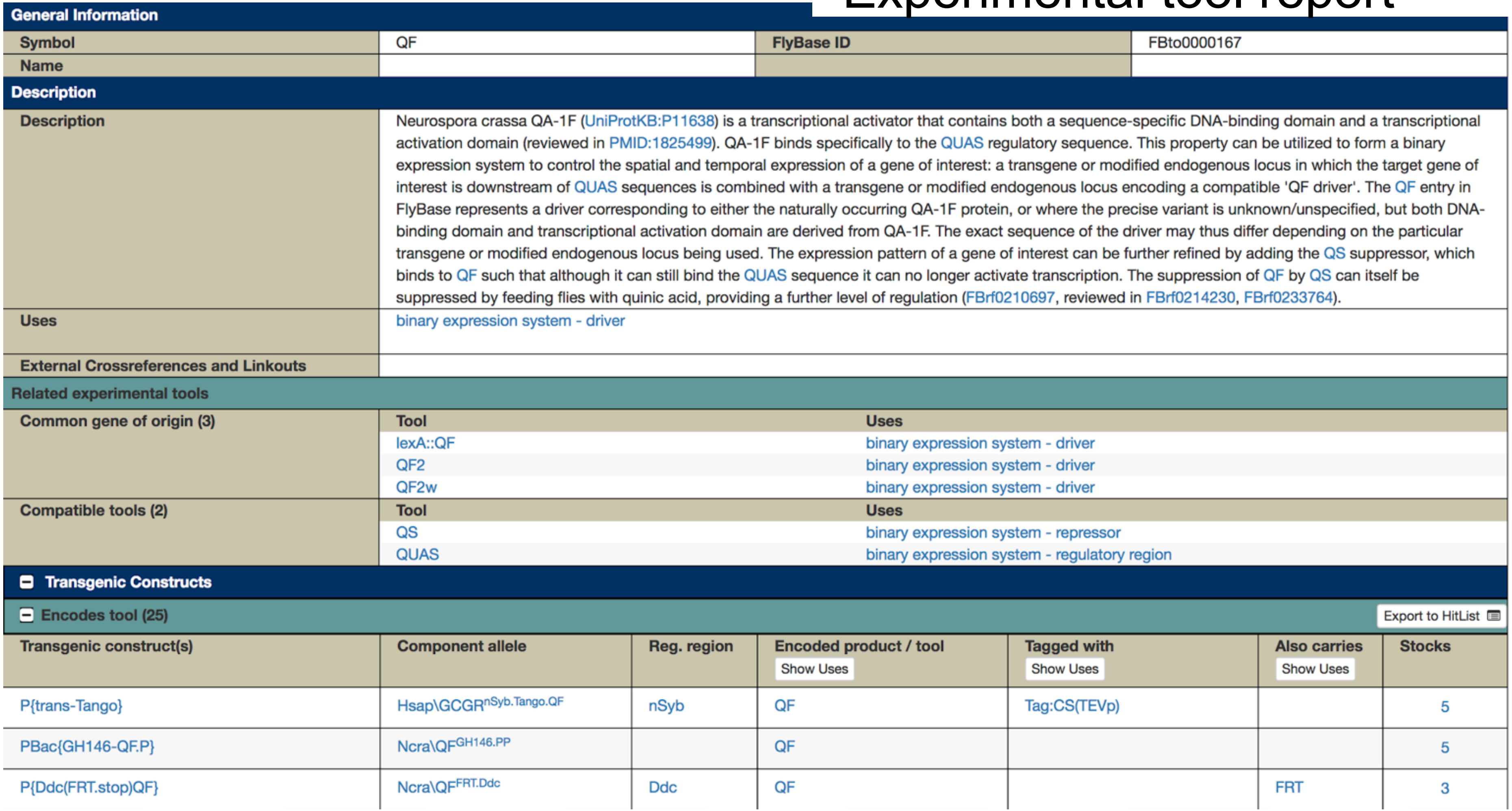
Records annotated with this term *OR* any of its *CHILDREN TERMS*



Experimental Tool Results

☑	Symbol ▲	Uses	# Allel…	# Constructs	# Associated Tools		
					Compatible	Related (Gene of Origin)	Other Related
☑	dCas9::VP64	binary expression system - driver	4	3	2	0	0
☑	GAL4	binary expression system - driver	17768	17797	3	15	0
☑	GAL4::p65	binary expression system - driver	8	10	1	15	0
☑	GAL4::QF	binary expression system - driver	3	3	2	15	0
☑	GAL4::VP16	binary expression system - driver	31	34	1	15	0
☑	lexA::p65 ⚑	binary expression system - driver	1663	1676	1	7	0
☑	lexA::QF	binary expression system - driver	4	7	2	3	0
☑	lexA::VP16	binary expression system - driver	36	40	1	7	0
☑	mLexA::VP16::NFAT	binary expression system - small molecule-regulated driver calcium ion sensor	2	2	1	0	0
☑	QF	binary expression system - driver	25	34	2	3	0
☑	QF2 ⚑	binary expression system - driver	21	30	2	3	0
☑	QF2w	binary expression system - driver	4	4	2	3	0
☑	rtTA	binary expression system - small molecule-regulated driver	1	1	1	3	0
☑	TALE3::VP64	binary expression system - driver	2	2	1	0	1
☑	tTA	binary expression system - small molecule-regulated driver	9	9	1	3	0

Experimental tool report



General Information

Symbol	QF	**FlyBase ID**	FBto0000167
Name			

Description

Description	Neurospora crassa QA-1F (UniProtKB:P11638) is a transcriptional activator that contains both a sequence-specific DNA-binding domain and a transcriptional activation domain (reviewed in PMID:1825499). QA-1F binds specifically to the QUAS regulatory sequence. This property can be utilized to form a binary expression system to control the spatial and temporal expression of a gene of interest: a transgene or modified endogenous locus in which the target gene of interest is downstream of QUAS sequences is combined with a transgene or modified endogenous locus encoding a compatible 'QF driver'. The QF entry in FlyBase represents a driver corresponding to either the naturally occurring QA-1F protein, or where the precise variant is unknown/unspecified, but both DNA-binding domain and transcriptional activation domain are derived from QA-1F. The exact sequence of the driver may thus differ depending on the particular transgene or modified endogenous locus being used. The expression pattern of a gene of interest can be further refined by adding the QS suppressor, which binds to QF such that although it can still bind the QUAS sequence it can no longer activate transcription. The suppression of QF by QS can itself be suppressed by feeding flies with quinic acid, providing a further level of regulation (FBrf0210697, reviewed in FBrf0214230, FBrf0233764).
Uses	binary expression system - driver
External Crossreferences and Linkouts	

Related experimental tools

	Tool	**Uses**
Common gene of origin (3)	lexA::QF	binary expression system - driver
	QF2	binary expression system - driver
	QF2w	binary expression system - driver

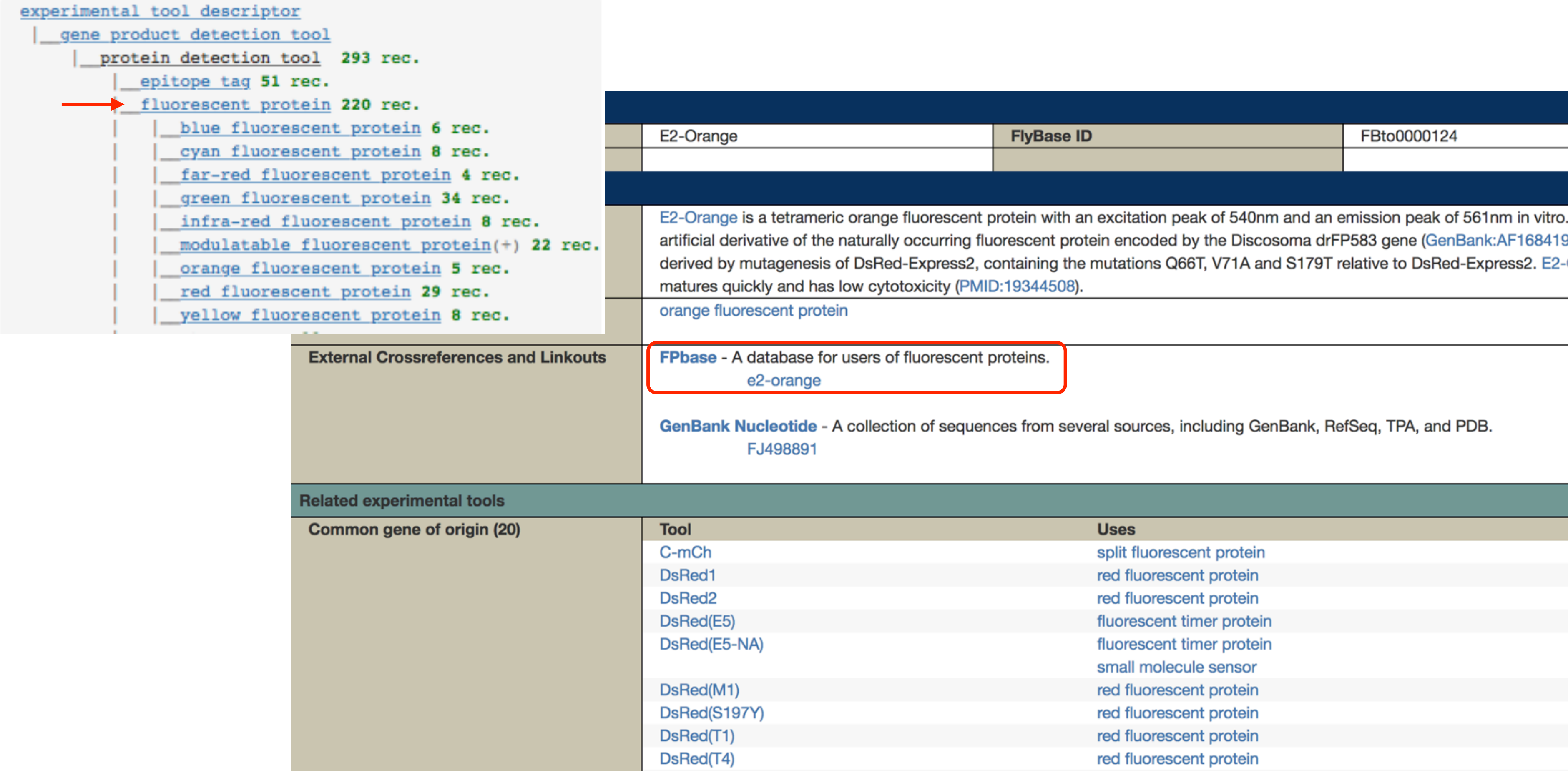
	Tool	**Uses**
Compatible tools (2)	QS	binary expression system - repressor
	QUAS	binary expression system - regulatory region

Transgenic Constructs

Encodes tool (25)

Transgenic construct(s)	Component allele	Reg. region	Encoded product / tool Show Uses	Tagged with Show Uses	Also carries Show Uses	Stocks
P{trans-Tango}	Hsap\GCGR$^{nSyb.Tango.QF}$	nSyb	QF	Tag:CS(TEVp)		5
PBac{GH146-QF.P}	Ncra\QF$^{GH146.PP}$		QF			5
P{Ddc(FRT.stop)QF}	Ncra\QF$^{FRT.Ddc}$	Ddc	QF		FRT	3

Experimental tools: fluorescent proteins



```
experimental tool descriptor
 |__gene product detection tool
     |__protein detection tool  293 rec.
         |__epitope tag 51 rec.
         |__fluorescent protein 220 rec.
         |   |__blue fluorescent protein 6 rec.
         |   |__cyan fluorescent protein 8 rec.
         |   |__far-red fluorescent protein 4 rec.
         |   |__green fluorescent protein 34 rec.
         |   |__infra-red fluorescent protein 8 rec.
         |   |__modulatable fluorescent protein(+) 22 rec.
         |   |__orange fluorescent protein 5 rec.
         |   |__red fluorescent protein 29 rec.
         |   |__yellow fluorescent protein 8 rec.
```

E2-Orange	**FlyBase ID**	FBto0000124

E2-Orange is a tetrameric orange fluorescent protein with an excitation peak of 540nm and an emission peak of 561nm in vitro.
artificial derivative of the naturally occurring fluorescent protein encoded by the Discosoma drFP583 gene (GenBank:AF168419
derived by mutagenesis of DsRed-Express2, containing the mutations Q66T, V71A and S179T relative to DsRed-Express2. E2-
matures quickly and has low cytotoxicity (PMID:19344508).

orange fluorescent protein

External Crossreferences and Linkouts

FPbase - A database for users of fluorescent proteins.
e2-orange

GenBank Nucleotide - A collection of sequences from several sources, including GenBank, RefSeq, TPA, and PDB.
FJ498891

Related experimental tools

Common gene of origin (20)

Tool	**Uses**
C-mCh	split fluorescent protein
DsRed1	red fluorescent protein
DsRed2	red fluorescent protein
DsRed(E5)	fluorescent timer protein
DsRed(E5-NA)	fluorescent timer protein small molecule sensor
DsRed(M1)	red fluorescent protein
DsRed(S197Y)	red fluorescent protein
DsRed(T1)	red fluorescent protein
DsRed(T4)	red fluorescent protein

Overview

- Answering the question yourself
  - Follow us on Twitter, subscribe to newsletter
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  - Commentaries (current and past)

- Information for developers (github)
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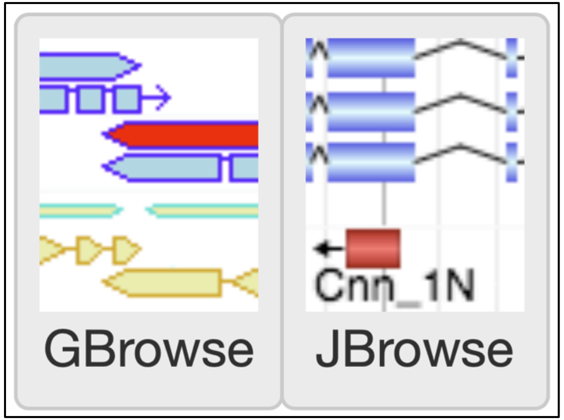
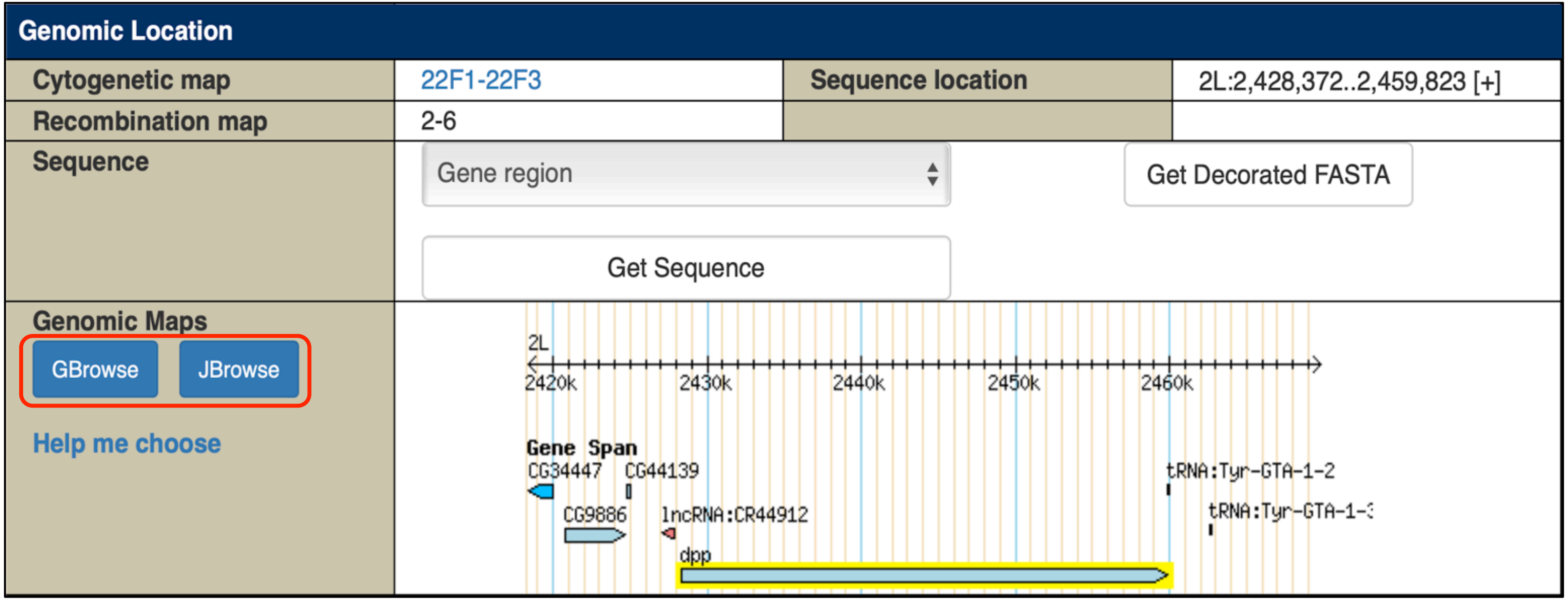
- New resource for finding reagents
  - New experimental tool reports

→
- New data tracks in JBrowse
  - sgRNAs (predicted guide RNAs)
  - SRA aggregated RNA-Seq data

JBrowse vs GBrowse

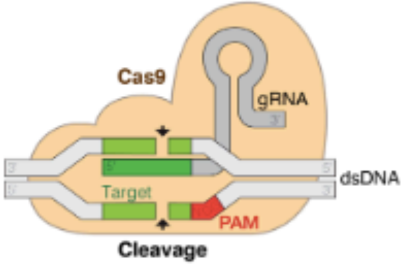




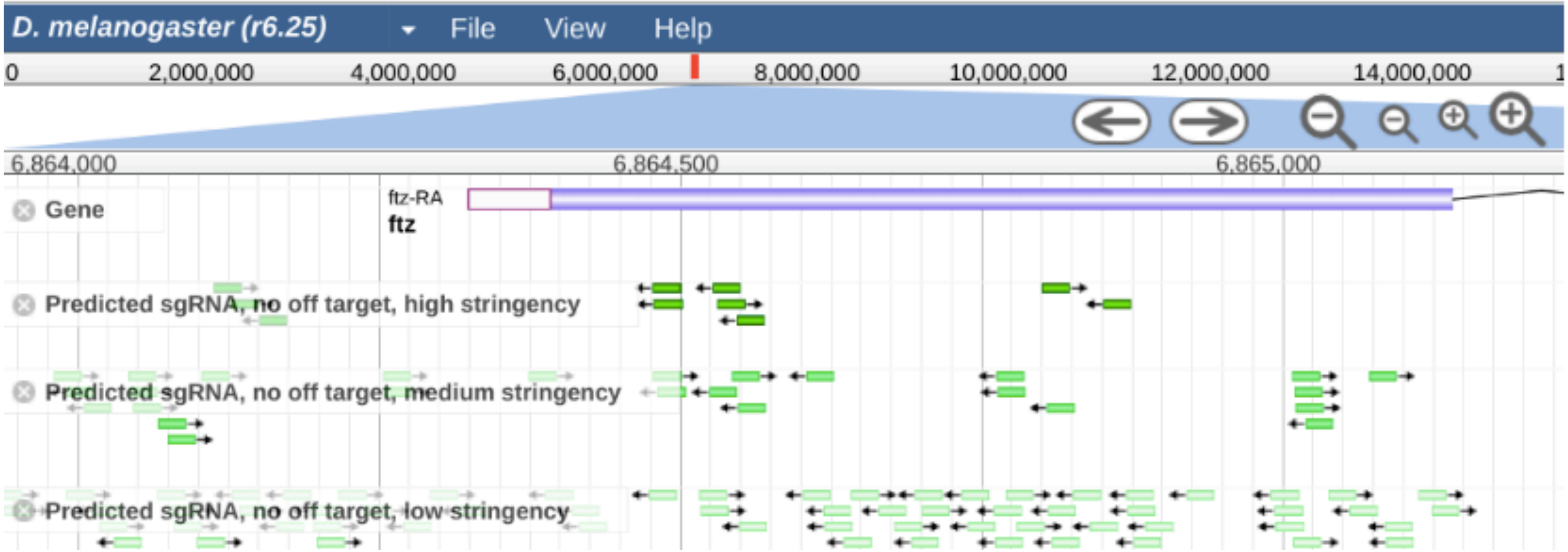
Genomic Location

Cytogenetic map	22F1-22F3	**Sequence location**	2L:2,428,372..2,459,823 [+]
Recombination map	2-6		
Sequence	Gene region Get Sequence		Get Decorated FASTA
Genomic Maps GBrowse JBrowse Help me choose			

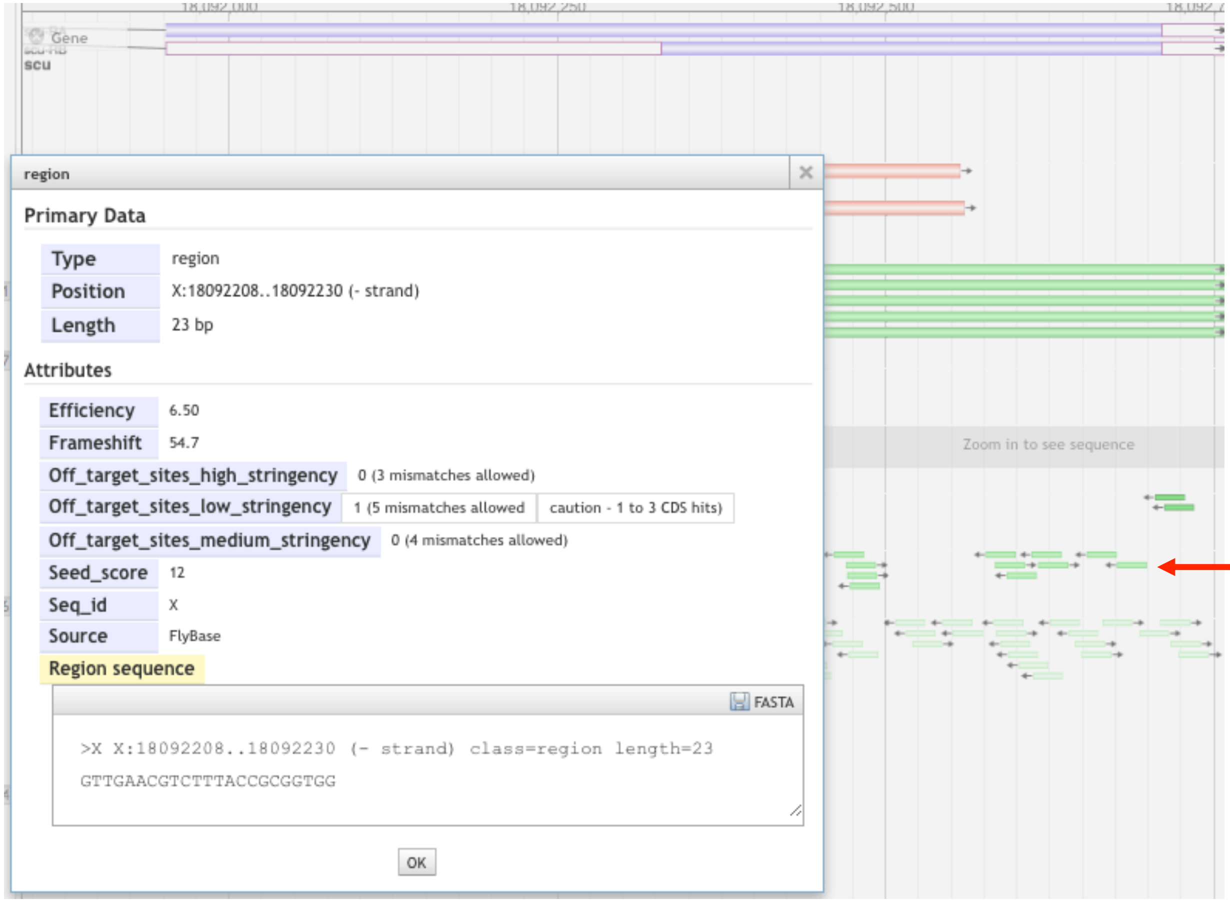
New: predicted sgRNAs (DRSC)



FlyBase has incorporated over 10 million short guide RNA (sgRNA) designs from the DRSC. These designs represent all possible 23-mers in the *D. melanogaster* genome containing a 3′ proto-adjacent motif (PAM) sequence (NGG) and a 15-base 3′ sequence that is unique to the genome. These designs have been further evaluated for predicted efficiency and off-target sites at various mismatch stringencies.



New: predicted sgRNAs (DRSC)



region

Primary Data

Type	region
Position	X:18092208..18092230 (- strand)
Length	23 bp

Attributes

Efficiency	6.50	
Frameshift	54.7	
Off_target_sites_high_stringency	0 (3 mismatches allowed)	
Off_target_sites_low_stringency	1 (5 mismatches allowed	caution - 1 to 3 CDS hits)
Off_target_sites_medium_stringency	0 (4 mismatches allowed)	
Seed_score	12	
Seq_id	X	
Source	FlyBase	

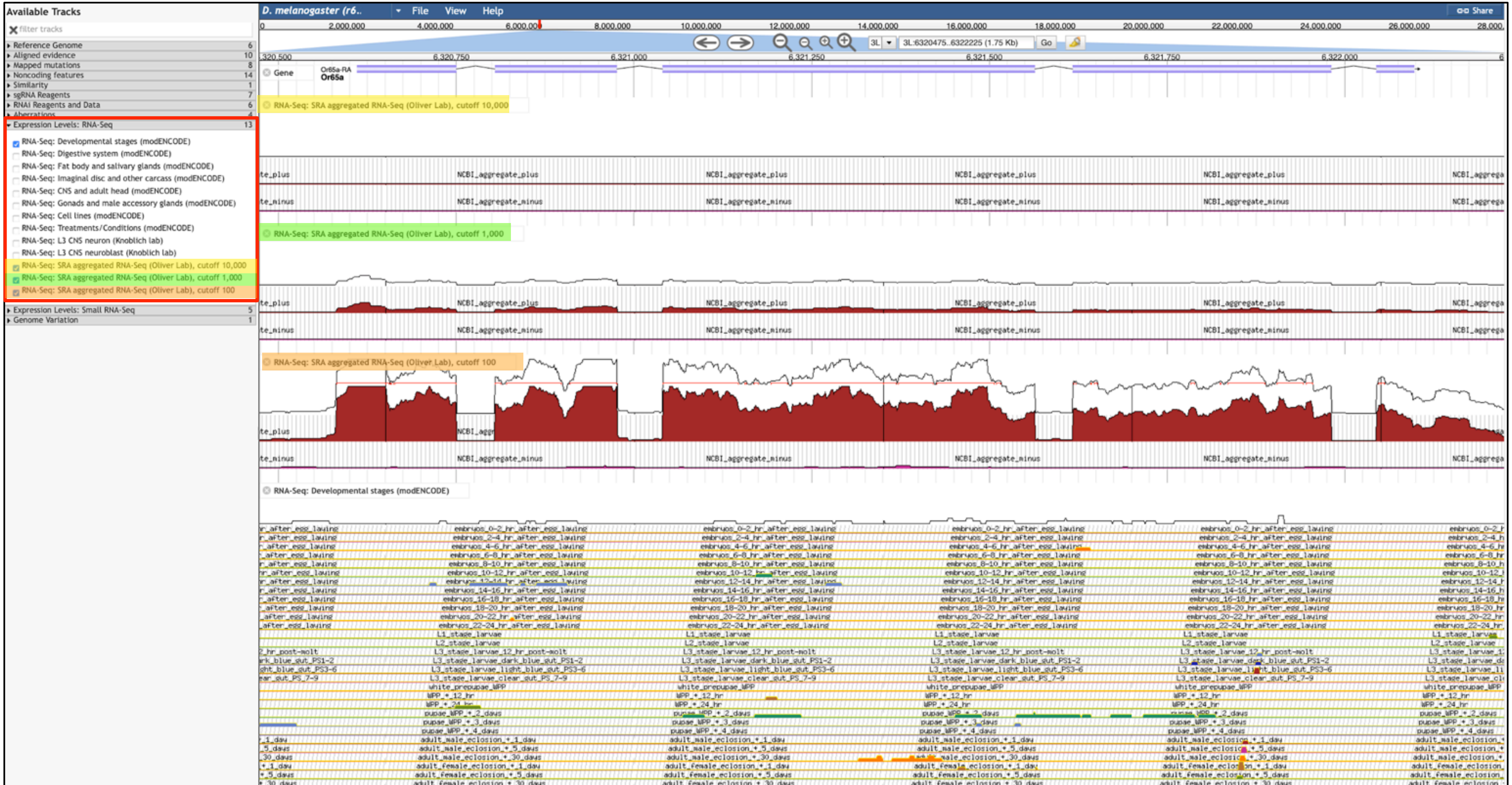
Region sequence

FASTA

```
>X X:18092208..18092230 (- strand) class=region length=23
GTTGAACGTCTTTACCGCGGTGG
```

Click on a specific sgRNA icon to bring up an informational pop-up

New: SRA aggregated RNA-Seq (Oliver lab)



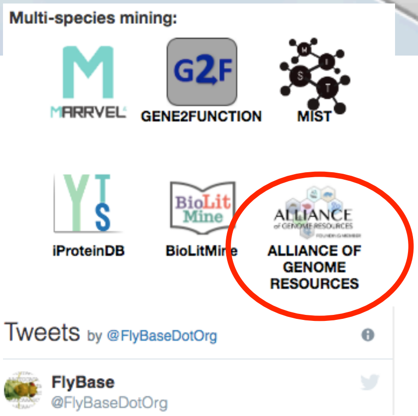
Available Tracks

filter tracks

- Reference Genome 6
- Aligned evidence 10
- Mapped mutations 8
- Noncoding features 14
- Similarity 1
- sgRNA Reagents 7
- RNAi Reagents and Data 6
- Aberrations
- Expression Levels: RNA-Seq 13
  - ☑ RNA-Seq: Developmental stages (modENCODE)
  - ☐ RNA-Seq: Digestive system (modENCODE)
  - ☐ RNA-Seq: Fat body and salivary glands (modENCODE)
  - ☐ RNA-Seq: Imaginal disc and other carcass (modENCODE)
  - ☐ RNA-Seq: CNS and adult head (modENCODE)
  - ☐ RNA-Seq: Gonads and male accessory glands (modENCODE)
  - ☐ RNA-Seq: Cell lines (modENCODE)
  - ☐ RNA-Seq: Treatments/Conditions (modENCODE)
  - ☐ RNA-Seq: L3 CNS neuron (Knoblich lab)
  - ☐ RNA-Seq: L3 CNS neuroblast (Knoblich lab)
  - ☑ RNA-Seq: SRA aggregated RNA-Seq (Oliver Lab), cutoff 10,000
  - ☑ RNA-Seq: SRA aggregated RNA-Seq (Oliver Lab), cutoff 1,000
  - ☑ RNA-Seq: SRA aggregated RNA-Seq (Oliver Lab), cutoff 100
- Expression Levels: Small RNA-Seq 5
- Genome Variation 1

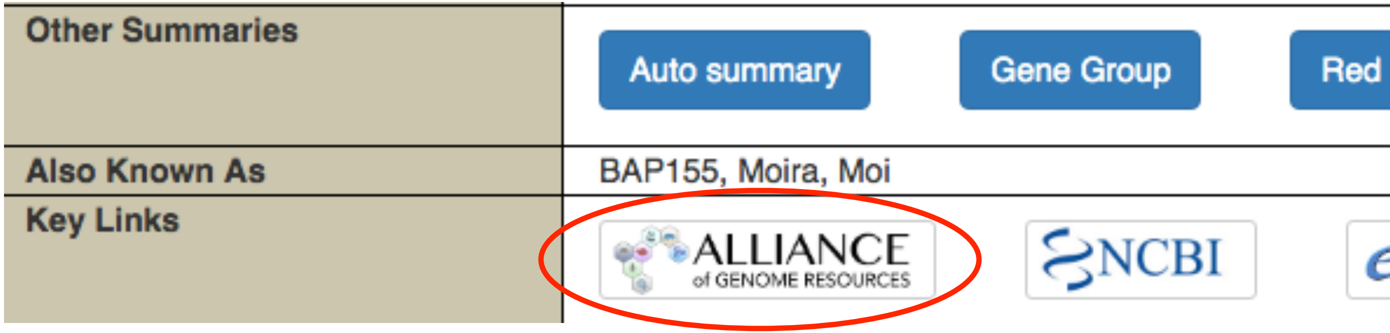
FlyBase is a member of the Alliance

The Gene Ontology Consortium and Six Model Organism Databases have joined together to form the Alliance of Genome Resources


Multi-species mining:

Tweets by @FlyBaseDotOrg

FlyBase
@FlyBaseDotOrg



Other Summaries	Auto summary Gene Group Red
Also Known As	BAP155, Moira, Moi
Key Links	ALLIANCE of GENOME RESOURCES NCBI

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FlyBase Users Worldwide

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