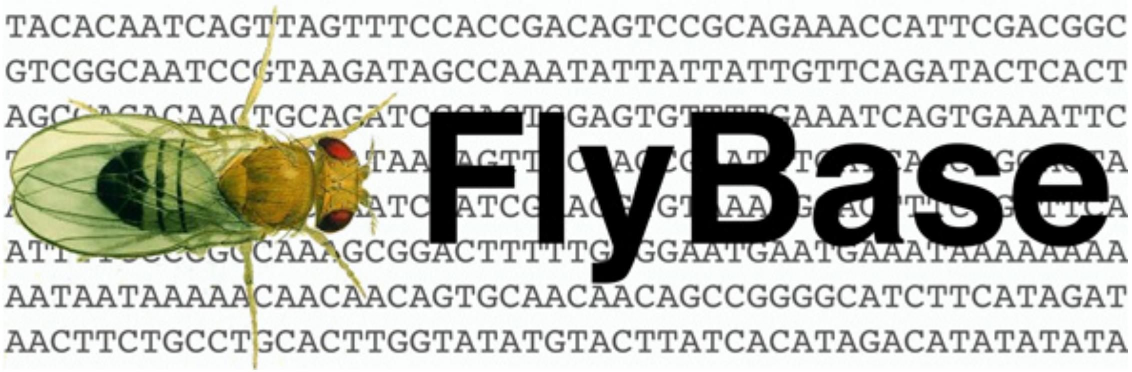
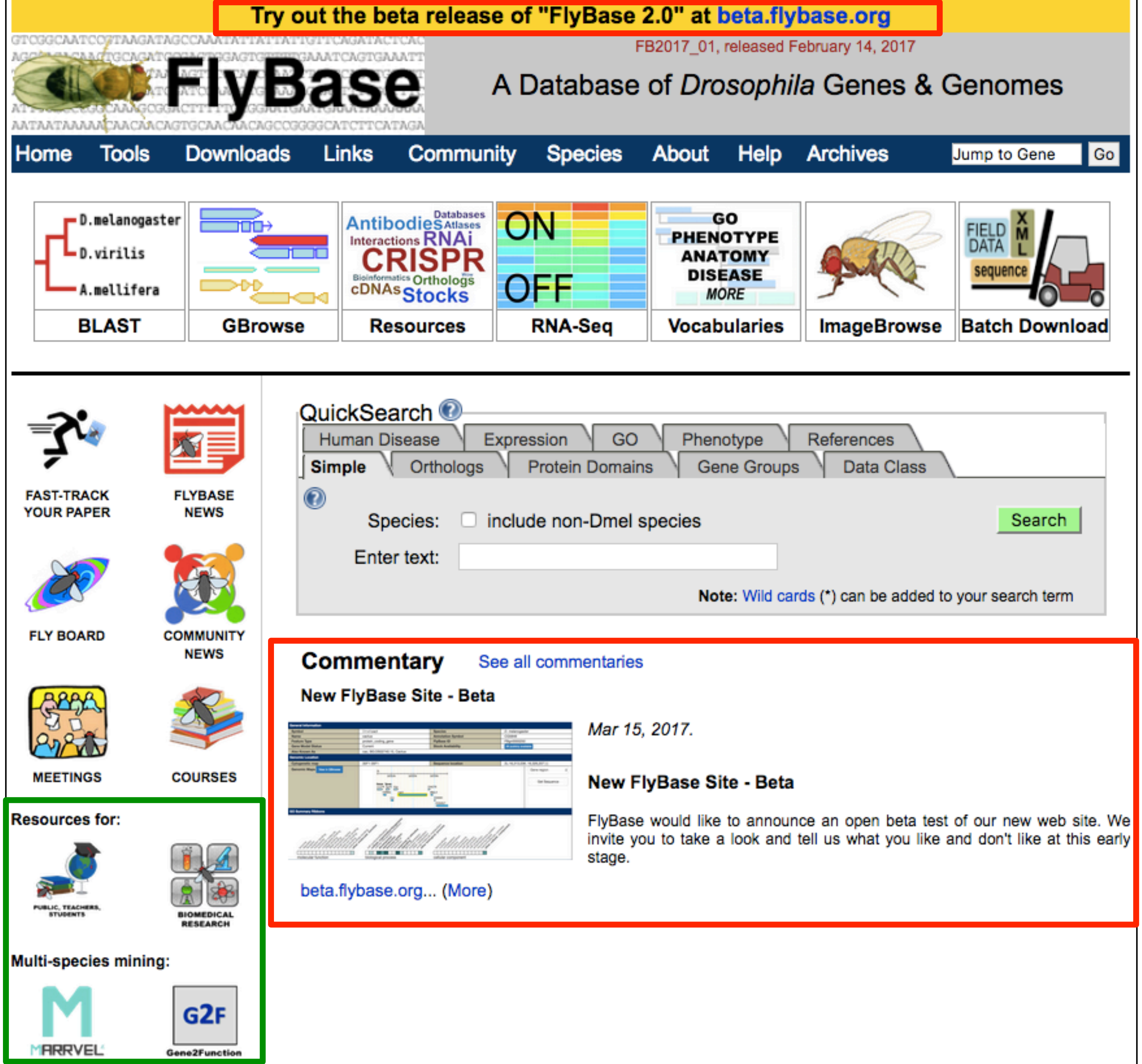


What’s new in FlyBase (in its 25th year)

Steven Marygold

- JBrowse
- Gene Snapshots
- Gene Groups
- Orthologs

- Human Disease Models
- Gene2Function
- Community interactions
- New website



Try out the beta release of "FlyBase 2.0" at beta.flybase.org

FB2017_01, released February 14, 2017

FlyBase

A Database of *Drosophila* Genes & Genomes

QuickSearch

Species: ☐ include non-Dmel species

Enter text:

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

Resources for:

Multi-species mining:

Commentary See all commentaries

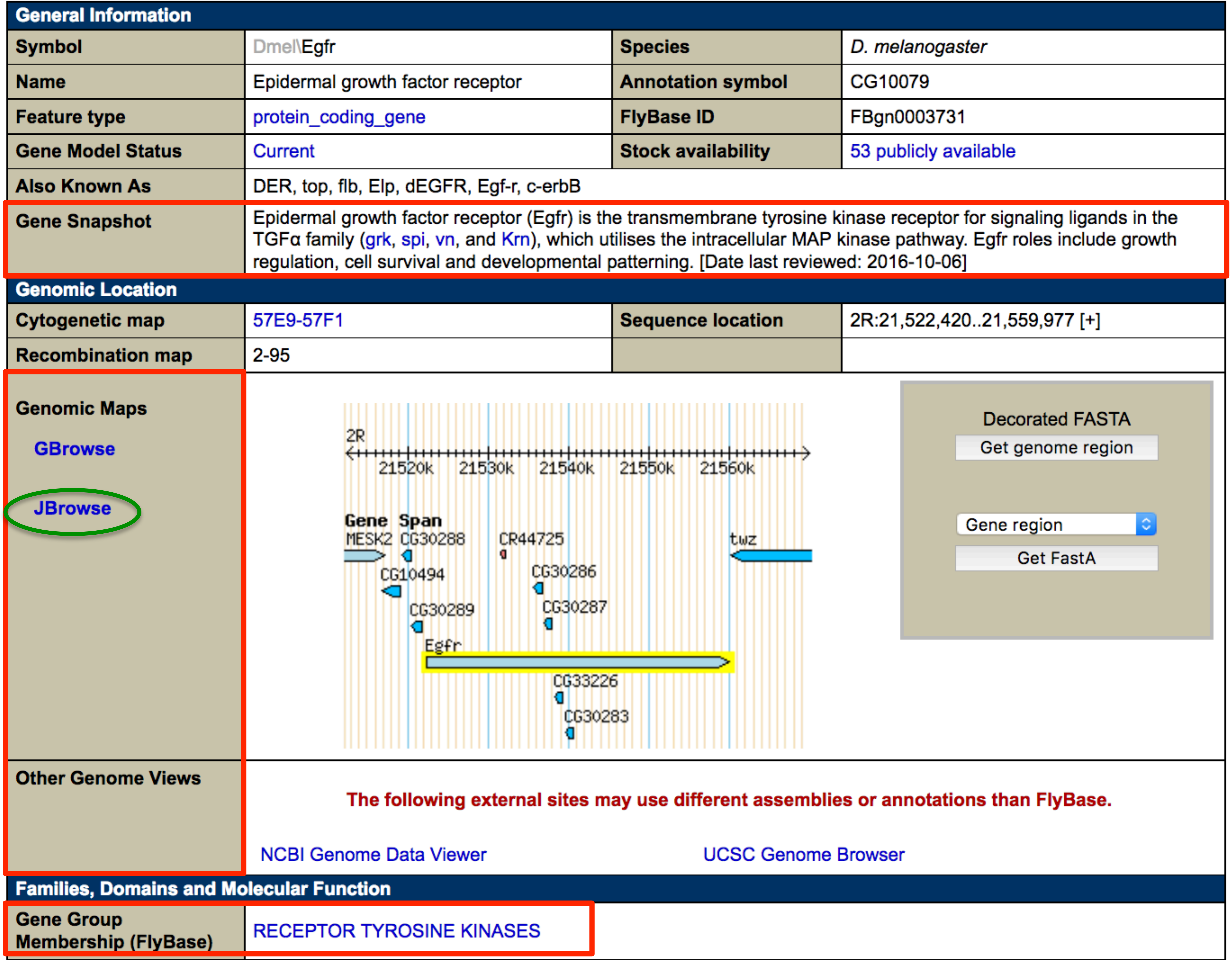
New FlyBase Site - Beta

Mar 15, 2017.

New FlyBase Site - Beta

FlyBase would like to announce an open beta test of our new web site. We invite you to take a look and tell us what you like and don't like at this early stage.

beta.flybase.org... (More)



General Information

Symbol	Dmel\Egfr	**Species**	*D. melanogaster*
Name	Epidermal growth factor receptor	**Annotation symbol**	CG10079
Feature type	protein_coding_gene	**FlyBase ID**	FBgn0003731
Gene Model Status	Current	**Stock availability**	53 publicly available
Also Known As	DER, top, flb, Elp, dEGFR, Egf-r, c-erbB		
Gene Snapshot	Epidermal growth factor receptor (Egfr) is the transmembrane tyrosine kinase receptor for signaling ligands in the TGFα family (grk, spi, vn, and Krn), which utilises the intracellular MAP kinase pathway. Egfr roles include growth regulation, cell survival and developmental patterning. [Date last reviewed: 2016-10-06]		

Genomic Location

Cytogenetic map	57E9-57F1	**Sequence location**	2R:21,522,420..21,559,977 [+]
Recombination map	2-95		

Genomic Maps

GBrowse

JBrowse

Other Genome Views

The following external sites may use different assemblies or annotations than FlyBase.

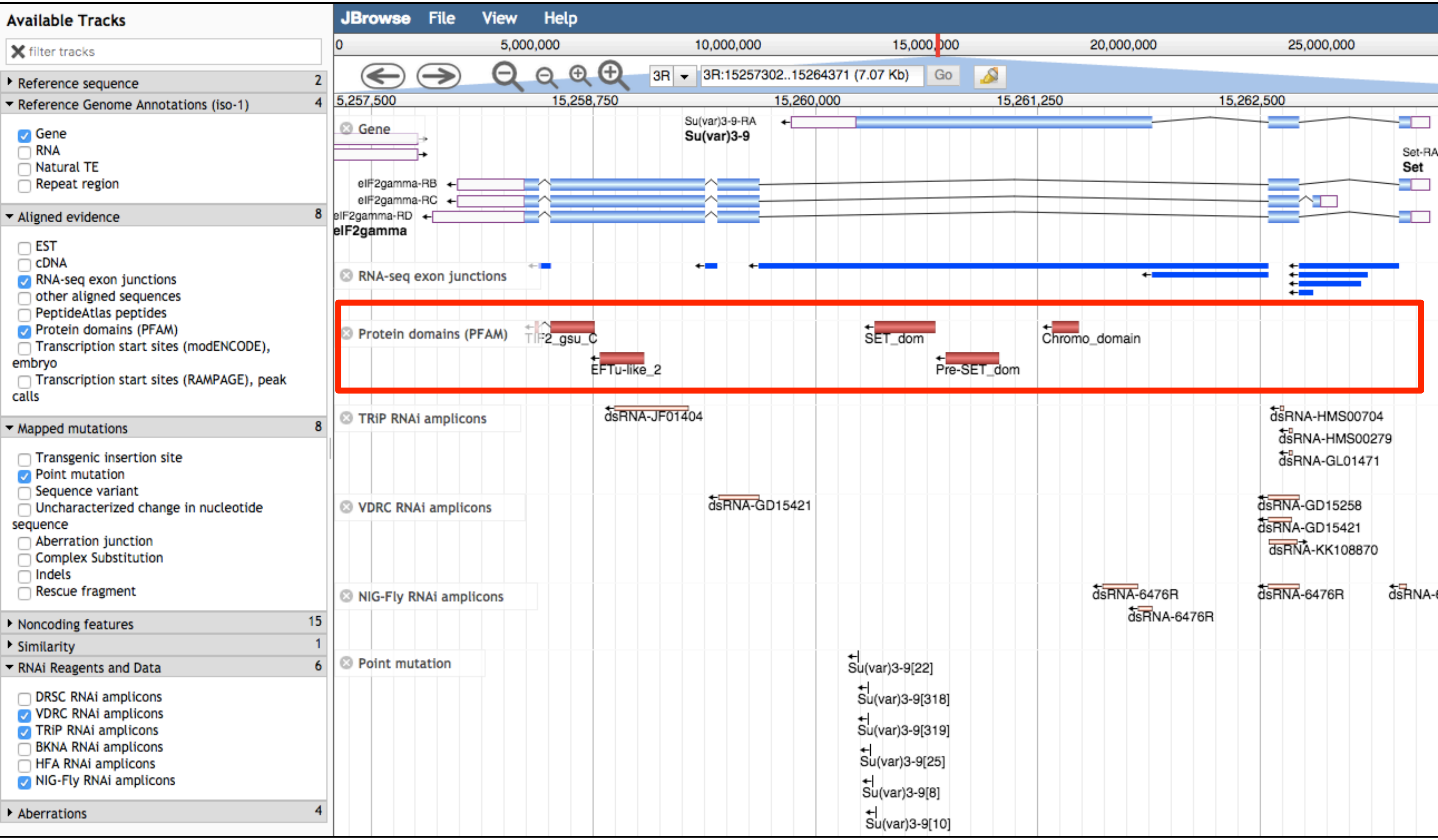
NCBI Genome Data Viewer

UCSC Genome Browser

Families, Domains and Molecular Function

Gene Group Membership (FlyBase)	RECEPTOR TYROSINE KINASES

JBrowse



Available Tracks

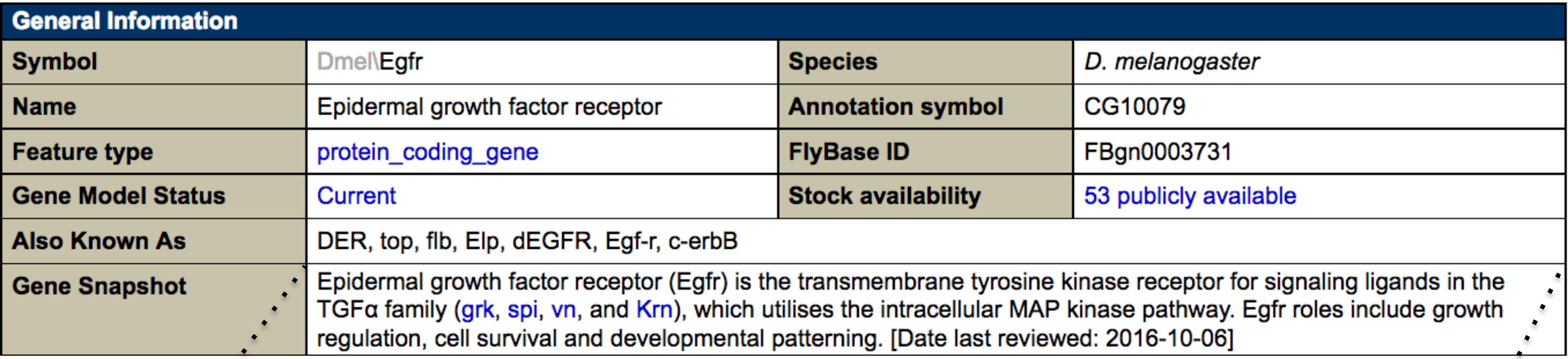
filter tracks

- Reference sequence 2
- Reference Genome Annotations (iso-1) 4
  - ☑ Gene
  - ☐ RNA
  - ☐ Natural TE
  - ☐ Repeat region
- Aligned evidence 8
  - ☐ EST
  - ☐ cDNA
  - ☑ RNA-seq exon junctions
  - ☐ other aligned sequences
  - ☐ PeptideAtlas peptides
  - ☑ Protein domains (PFAM)
  - ☐ Transcription start sites (modENCODE), embryo
  - ☐ Transcription start sites (RAMPAGE), peak calls
- Mapped mutations 8
  - ☐ Transgenic insertion site
  - ☑ Point mutation
  - ☐ Sequence variant
  - ☐ Uncharacterized change in nucleotide sequence
  - ☐ Aberration junction
  - ☐ Complex Substitution
  - ☐ Indels
  - ☐ Rescue fragment
- Noncoding features 15
- Similarity 1
- RNAi Reagents and Data 6
  - ☐ DRSC RNAi amplicons
  - ☑ VDRC RNAi amplicons
  - ☑ TRiP RNAi amplicons
  - ☐ BKNA RNAi amplicons
  - ☐ HFA RNAi amplicons
  - ☑ NIG-Fly RNAi amplicons
- Aberrations 4

3R

3R:15257302..15264371 (7.07 Kb)

Gene Snapshots



General Information

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Name	Epidermal growth factor receptor	**Annotation symbol**	CG10079
Feature type	protein_coding_gene	**FlyBase ID**	FBgn0003731
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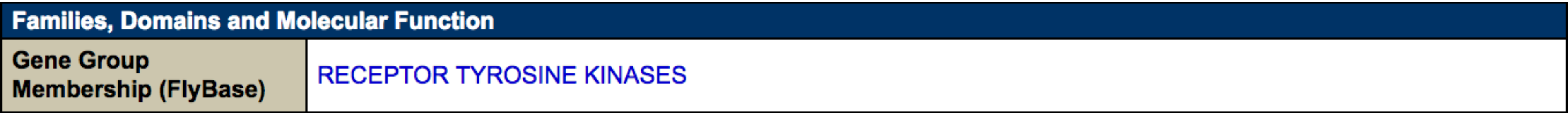
Epidermal growth factor receptor (Egfr) is the transmembrane tyrosine kinase receptor for signaling ligands in the TGFα family (grk, spi, vn, and Krn), which utilises the intracellular MAP kinase pathway. Egfr roles include growth regulation, cell survival and developmental patterning.

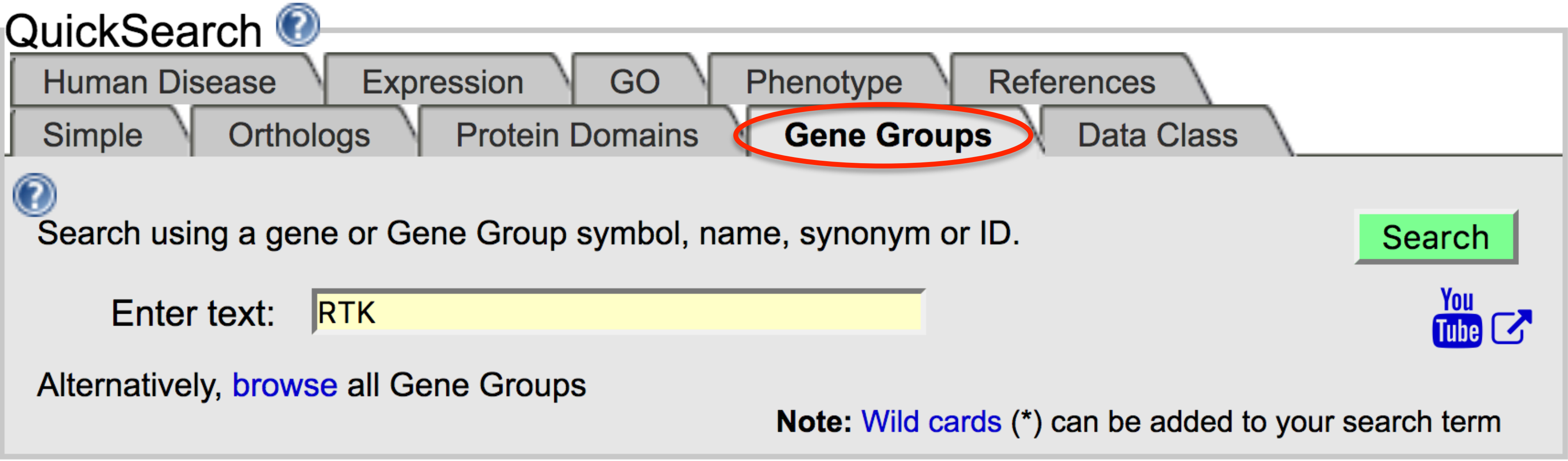
Gene Groups



Families, Domains and Molecular Function	
Gene Group Membership (FlyBase)	RECEPTOR TYROSINE KINASES

‘Gene Groups’ encompass:

- gene products sharing molecular function (kinases, tRNAs…)
- gene families (actins, odorant receptors…)
- subunits of complexes (ribosome, spliceosome…)



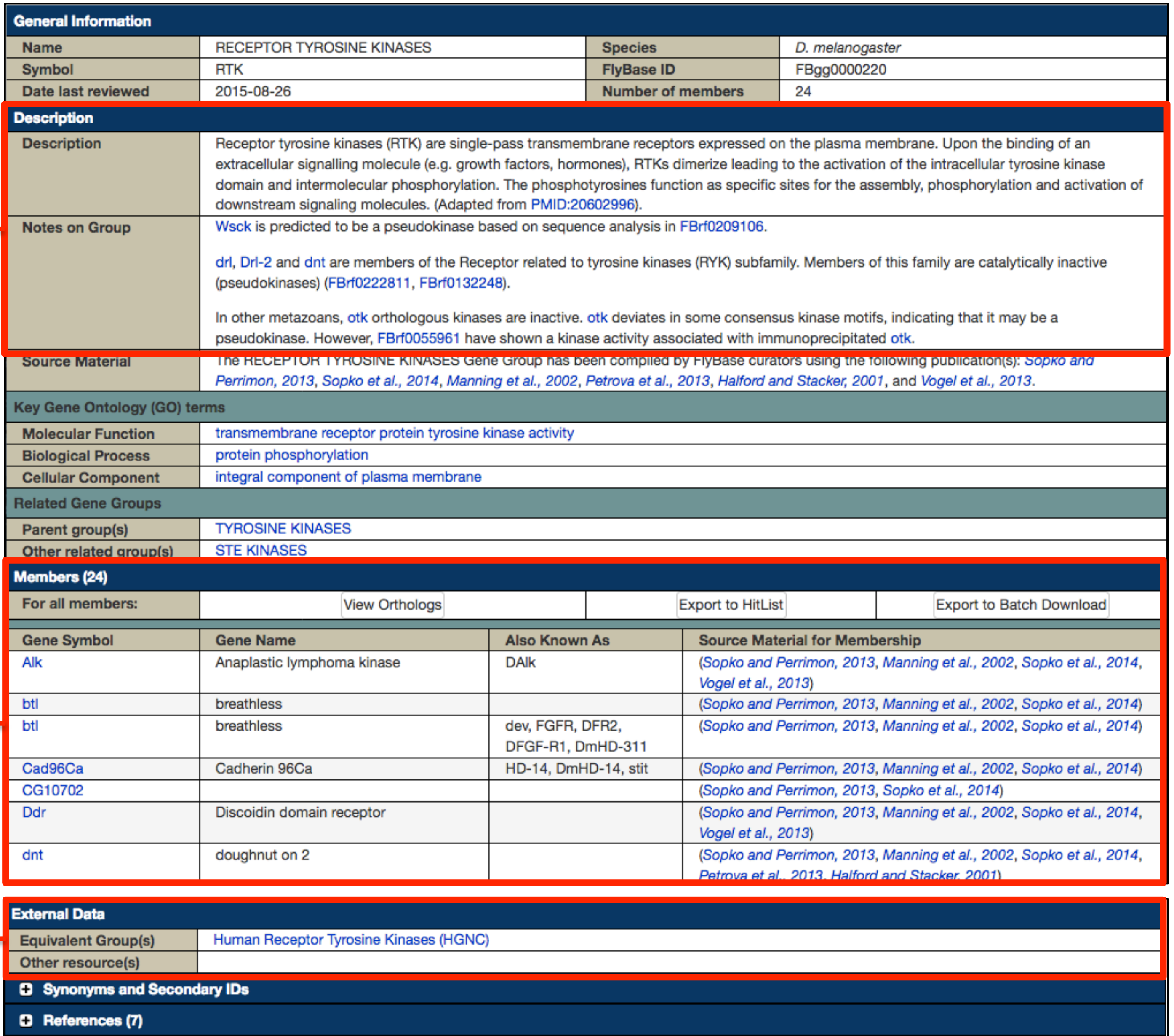
Search using a gene or Gene Group symbol, name, synonym or ID.

Enter text: RTK

Alternatively, browse all Gene Groups

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

Gene Group Reports



General Information

Name	RECEPTOR TYROSINE KINASES	**Species**	*D. melanogaster*
Symbol	RTK	**FlyBase ID**	FBgg0000220
Date last reviewed	2015-08-26	**Number of members**	24

Description

Description	Receptor tyrosine kinases (RTK) are single-pass transmembrane receptors expressed on the plasma membrane. Upon the binding of an extracellular signalling molecule (e.g. growth factors, hormones), RTKs dimerize leading to the activation of the intracellular tyrosine kinase domain and intermolecular phosphorylation. The phosphotyrosines function as specific sites for the assembly, phosphorylation and activation of downstream signaling molecules. (Adapted from PMID:20602996).
Notes on Group	Wsck is predicted to be a pseudokinase based on sequence analysis in FBrf0209106. drl, Drl-2 and dnt are members of the Receptor related to tyrosine kinases (RYK) subfamily. Members of this family are catalytically inactive (pseudokinases) (FBrf0222811, FBrf0132248). In other metazoans, otk orthologous kinases are inactive. otk deviates in some consensus kinase motifs, indicating that it may be a pseudokinase. However, FBrf0055961 have shown a kinase activity associated with immunoprecipitated otk.
Source Material	The RECEPTOR TYROSINE KINASES Gene Group has been compiled by FlyBase curators using the following publication(s): *Sopko and Perrimon, 2013*, *Sopko et al., 2014*, *Manning et al., 2002*, *Petrova et al., 2013*, *Halford and Stacker, 2001*, and *Vogel et al., 2013*.

Key Gene Ontology (GO) terms

Molecular Function	transmembrane receptor protein tyrosine kinase activity
Biological Process	protein phosphorylation
Cellular Component	integral component of plasma membrane

Related Gene Groups

Parent group(s)	TYROSINE KINASES
Other related group(s)	STE KINASES

Members (24)

For all members:	View Orthologs	Export to HitList	Export to Batch Download

Gene Symbol	Gene Name	Also Known As	Source Material for Membership
Alk	Anaplastic lymphoma kinase	DAlk	(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*, *Vogel et al., 2013*)
btl	breathless		(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*)
btl	breathless	dev, FGFR, DFR2, DFGF-R1, DmHD-311	(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*)
Cad96Ca	Cadherin 96Ca	HD-14, DmHD-14, stit	(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*)
CG10702			(*Sopko and Perrimon, 2013*, *Sopko et al., 2014*)
Ddr	Discoidin domain receptor		(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*, *Vogel et al., 2013*)
dnt	doughnut on 2		(*Sopko and Perrimon, 2013*, *Manning et al., 2002*, *Sopko et al., 2014*, *Petrova et al., 2013*, *Halford and Stacker, 2001*)

External Data

Equivalent Group(s)	Human Receptor Tyrosine Kinases (HGNC)
Other resource(s)	

⊞ Synonyms and Secondary IDs

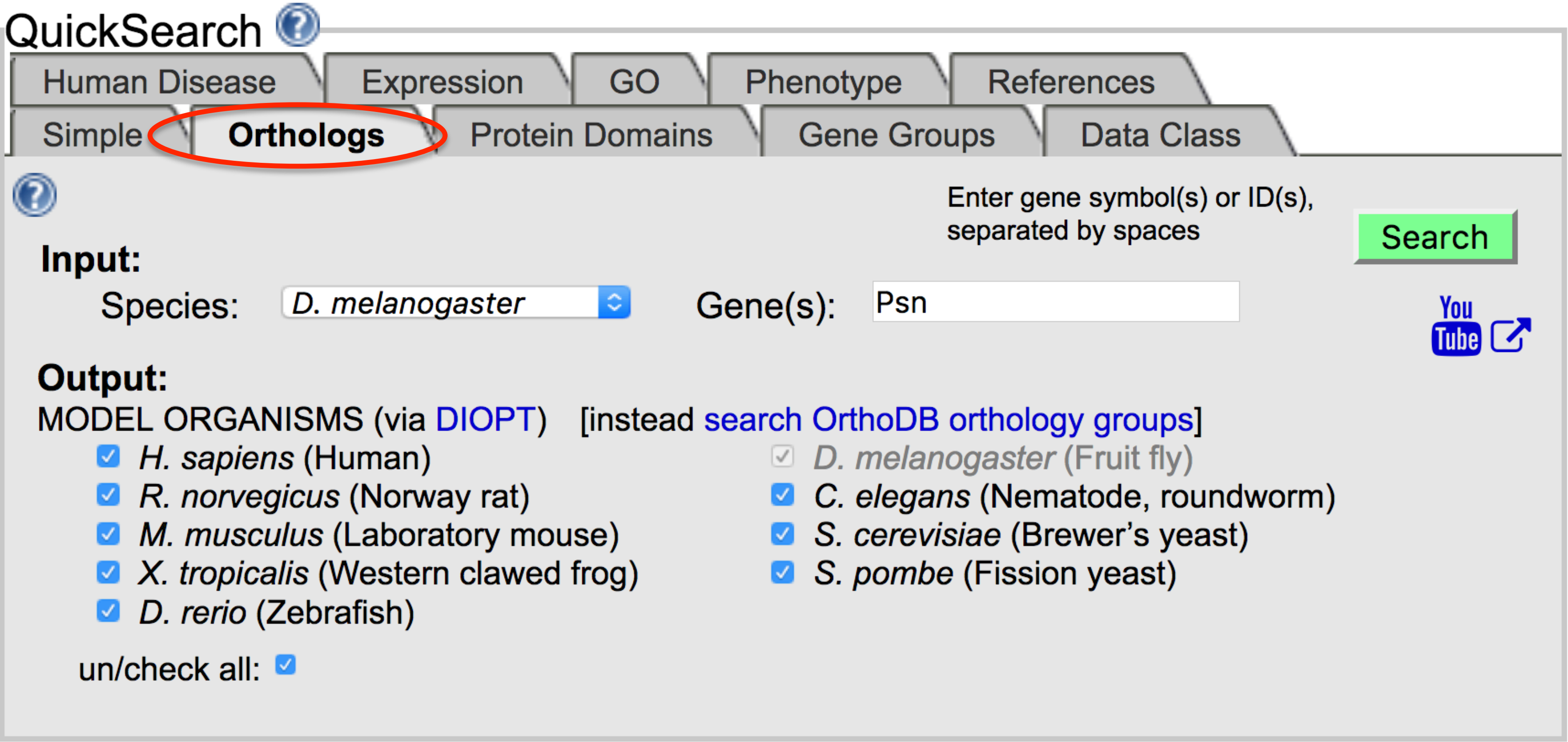
⊞ References (7)

Manually written description of group, with notes

List of members, with export to:
1. Hit-list
2. Batch Download
3. Orthologs tool

Links to external resources

Orthology search tool



Enter gene symbol(s) or ID(s), separated by spaces

Input:

Species: *D. melanogaster*

Gene(s): Psn

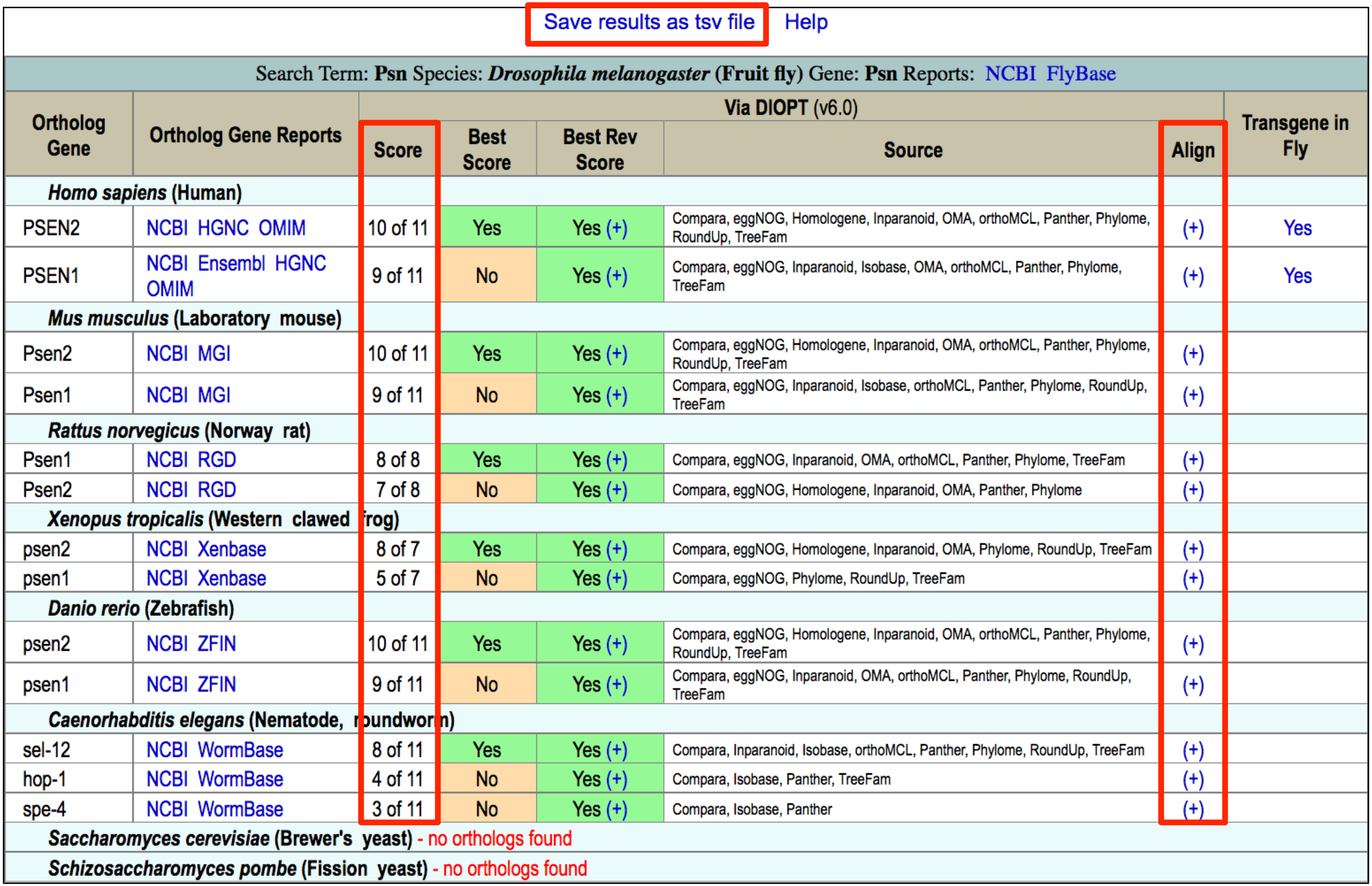
Output:

MODEL ORGANISMS (via DIOPT) [instead search OrthoDB orthology groups]

- ☑ *H. sapiens* (Human)
- ☑ *R. norvegicus* (Norway rat)
- ☑ *M. musculus* (Laboratory mouse)
- ☑ *X. tropicalis* (Western clawed frog)
- ☑ *D. rerio* (Zebrafish)
- ☑ *D. melanogaster* (Fruit fly)
- ☑ *C. elegans* (Nematode, roundworm)
- ☑ *S. cerevisiae* (Brewer's yeast)
- ☑ *S. pombe* (Fission yeast)

un/check all: ☑

Orthology search results

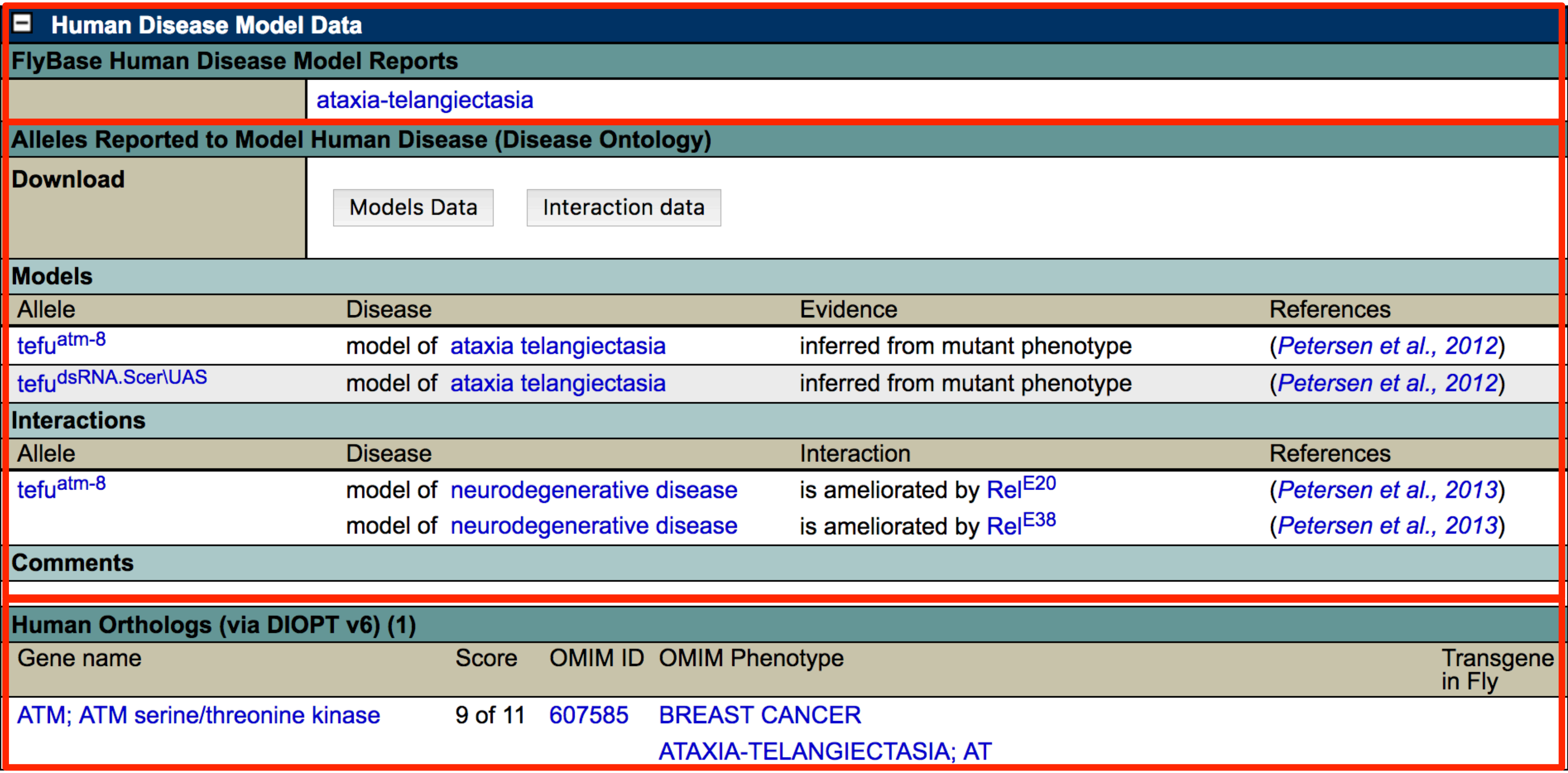


Save results as tsv file Help

Search Term: **Psn** Species: ***Drosophila melanogaster* (Fruit fly)** Gene: **Psn** Reports: NCBI FlyBase

Ortholog Gene	Ortholog Gene Reports	Via DIOPT (v6.0)					Transgene in Fly
		Score	Best Score	Best Rev Score	Source	Align	
***Homo sapiens* (Human)**							
PSEN2	NCBI HGNC OMIM	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	Yes
PSEN1	NCBI Ensembl HGNC OMIM	9 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, Isobase, OMA, orthoMCL, Panther, Phylome, TreeFam	(+)	Yes
***Mus musculus* (Laboratory mouse)**							
Psen2	NCBI MGI	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	
Psen1	NCBI MGI	9 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, Isobase, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	
***Rattus norvegicus* (Norway rat)**							
Psen1	NCBI RGD	8 of 8	Yes	Yes (+)	Compara, eggNOG, Inparanoid, OMA, orthoMCL, Panther, Phylome, TreeFam	(+)	
Psen2	NCBI RGD	7 of 8	No	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, Panther, Phylome	(+)	
***Xenopus tropicalis* (Western clawed frog)**							
psen2	NCBI Xenbase	8 of 7	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, Phylome, RoundUp, TreeFam	(+)	
psen1	NCBI Xenbase	5 of 7	No	Yes (+)	Compara, eggNOG, Phylome, RoundUp, TreeFam	(+)	
***Danio rerio* (Zebrafish)**							
psen2	NCBI ZFIN	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	
psen1	NCBI ZFIN	9 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	
***Caenorhabditis elegans* (Nematode, roundworm)**							
sel-12	NCBI WormBase	8 of 11	Yes	Yes (+)	Compara, Inparanoid, Isobase, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)	
hop-1	NCBI WormBase	4 of 11	No	Yes (+)	Compara, Isobase, Panther, TreeFam	(+)	
spe-4	NCBI WormBase	3 of 11	No	Yes (+)	Compara, Isobase, Panther	(+)	
***Saccharomyces cerevisiae* (Brewer's yeast)** - no orthologs found							
***Schizosaccharomyces pombe* (Fission yeast)** - no orthologs found							

Human Disease Model data



Human Disease Model Data

FlyBase Human Disease Model Reports

	ataxia-telangiectasia

Alleles Reported to Model Human Disease (Disease Ontology)

Download	Models Data Interaction data

Models

Allele	Disease	Evidence	References
tefu^{atm-8}	model of ataxia telangiectasia	inferred from mutant phenotype	(*Petersen et al., 2012*)
tefu$^{dsRNA.Scer\backslash UAS}$	model of ataxia telangiectasia	inferred from mutant phenotype	(*Petersen et al., 2012*)

Interactions

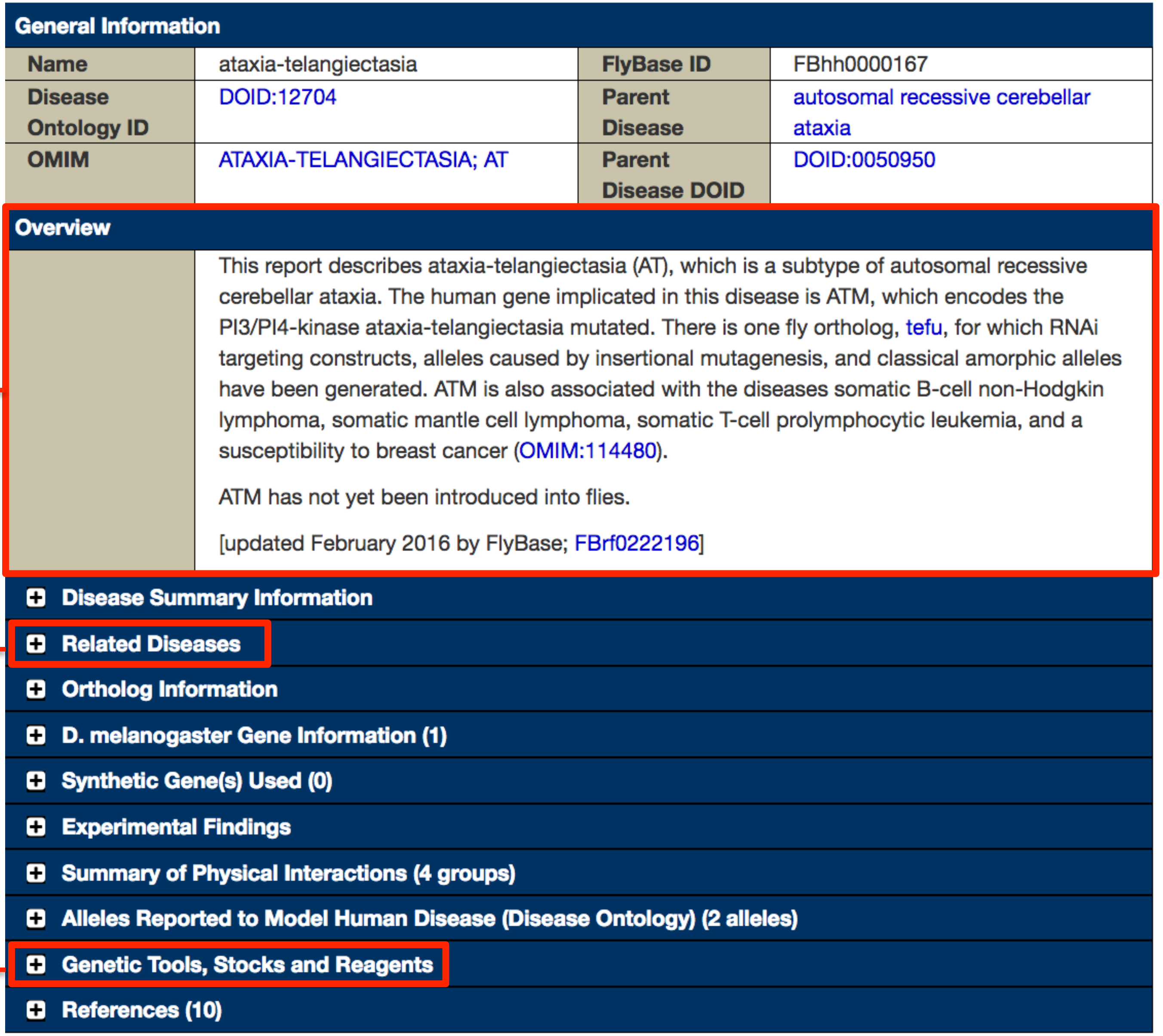
Allele	Disease	Interaction	References
tefu^{atm-8}	model of neurodegenerative disease	is ameliorated by Rel^{E20}	(*Petersen et al., 2013*)
	model of neurodegenerative disease	is ameliorated by Rel^{E38}	(*Petersen et al., 2013*)

Comments

Human Orthologs (via DIOPT v6) (1)

Gene name	Score	OMIM ID	OMIM Phenotype	Transgene in Fly
ATM; ATM serine/threonine kinase	9 of 11	607585	BREAST CANCER ATAXIA-TELANGIECTASIA; AT	

Human Disease Model Reports



General Information

Name	ataxia-telangiectasia	**FlyBase ID**	FBhh0000167
Disease Ontology ID	DOID:12704	**Parent Disease**	autosomal recessive cerebellar ataxia
OMIM	ATAXIA-TELANGIECTASIA; AT	**Parent Disease DOID**	DOID:0050950

Overview

This report describes ataxia-telangiectasia (AT), which is a subtype of autosomal recessive cerebellar ataxia. The human gene implicated in this disease is ATM, which encodes the PI3/PI4-kinase ataxia-telangiectasia mutated. There is one fly ortholog, tefu, for which RNAi targeting constructs, alleles caused by insertional mutagenesis, and classical amorphic alleles have been generated. ATM is also associated with the diseases somatic B-cell non-Hodgkin lymphoma, somatic mantle cell lymphoma, somatic T-cell prolymphocytic leukemia, and a susceptibility to breast cancer (OMIM:114480).

ATM has not yet been introduced into flies.

[updated February 2016 by FlyBase; FBrf0222196]

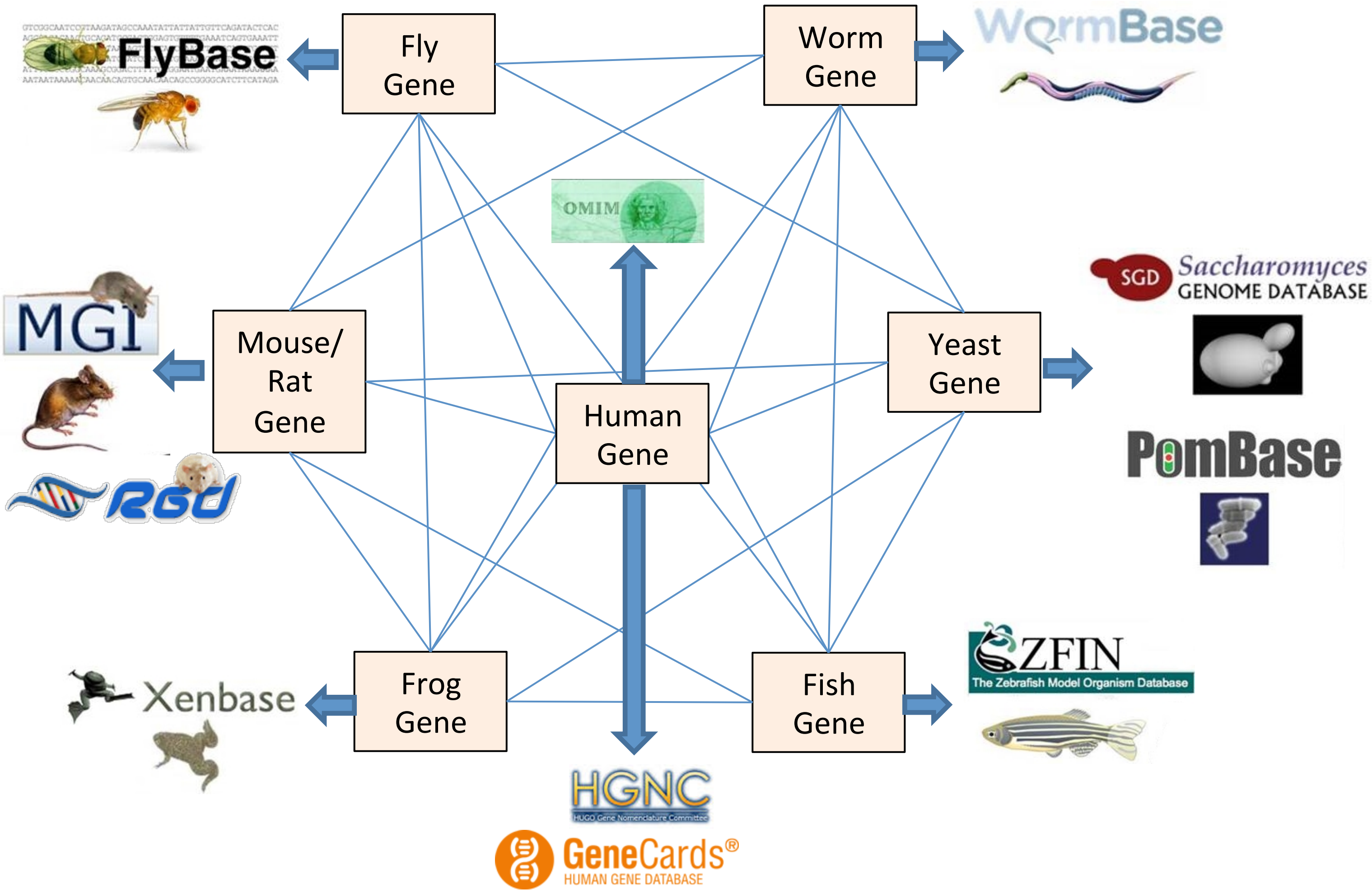
- ⊞ **Disease Summary Information**
- ⊞ **Related Diseases**
- ⊞ **Ortholog Information**
- ⊞ **D. melanogaster Gene Information (1)**
- ⊞ **Synthetic Gene(s) Used (0)**
- ⊞ **Experimental Findings**
- ⊞ **Summary of Physical Interactions (4 groups)**
- ⊞ **Alleles Reported to Model Human Disease (Disease Ontology) (2 alleles)**
- ⊞ **Genetic Tools, Stocks and Reagents**
- ⊞ **References (10)**

Manually written summary of disease and model

Links to related diseases/fly models

List of fly stocks used in model

Gene2Function



Fly Gene

Worm Gene

Mouse/ Rat Gene

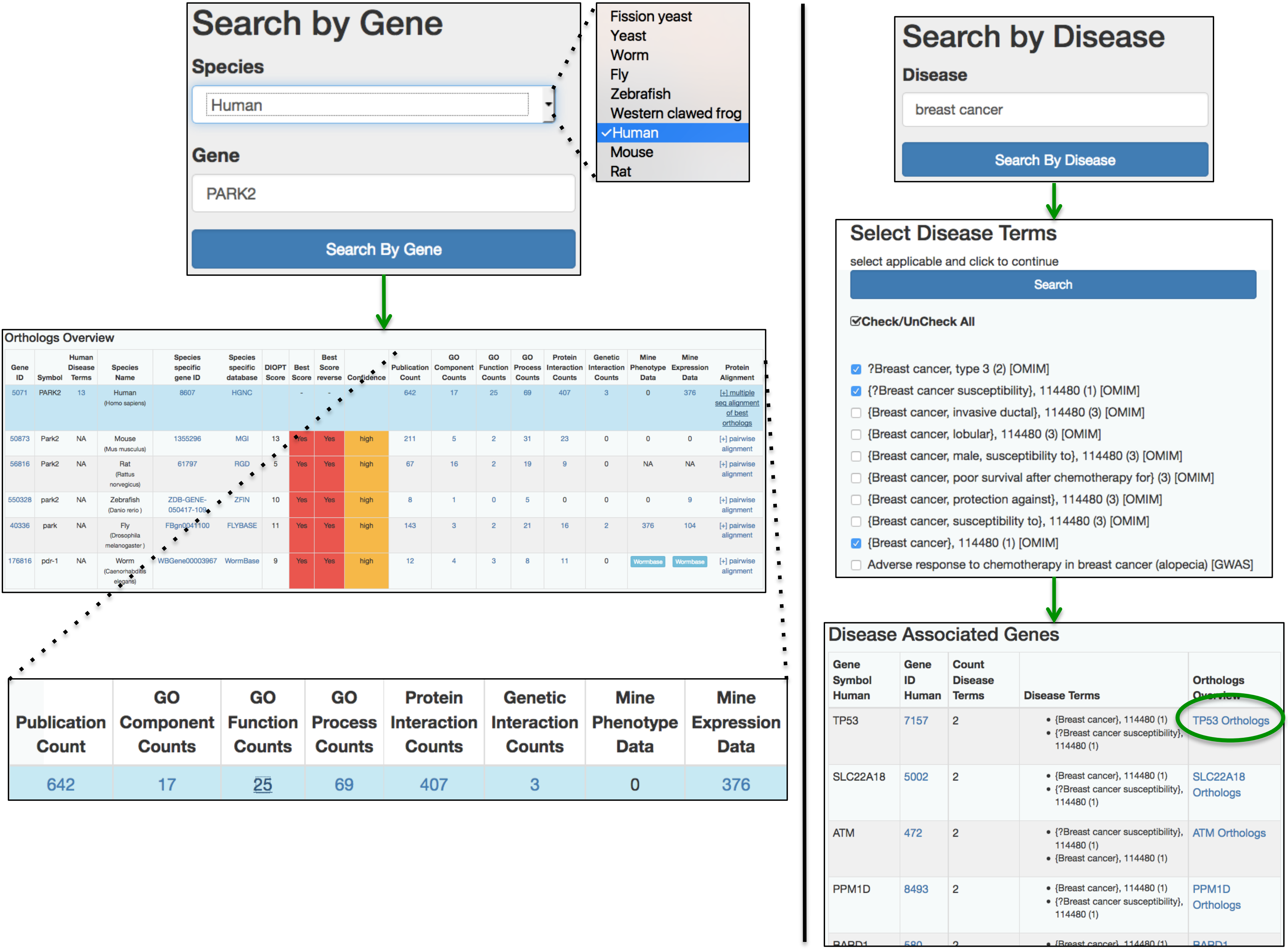
Human Gene

Yeast Gene

Frog Gene

Fish Gene

www.gene2function.org



Search by Gene

Species

Human

Gene

PARK2

Orthologs Overview

Gene ID	Symbol	Human Disease Terms	Species Name	Species specific gene ID	Species specific database	DIOPT Score	Best Score	Best Score reverse	Confidence	Publication Count	GO Component Counts	GO Function Counts	GO Process Counts	Protein Interaction Counts	Genetic Interaction Counts	Mine Phenotype Data	Mine Expression Data	Protein Alignment
5071	PARK2	13	Human (Homo sapiens)	8607	HGNC		-	-		642	17	25	69	407	3	0	376	[+] multiple seq alignment of best orthologs
50873	Park2	NA	Mouse (Mus musculus)	1355296	MGI	13	Yes	Yes	high	211	5	2	31	23	0	0	0	[+] pairwise alignment
56816	Park2	NA	Rat (Rattus norvegicus)	61797	RGD	5	Yes	Yes	high	67	16	2	19	9	0	NA	NA	[+] pairwise alignment
550328	park2	NA	Zebrafish (Danio rerio)	ZDB-GENE-050417-109	ZFIN	10	Yes	Yes	high	8	1	0	5	0	0	0	9	[+] pairwise alignment
40336	park	NA	Fly (Drosophila melanogaster)	FBgn0041100	FLYBASE	11	Yes	Yes	high	143	3	2	21	16	2	376	104	[+] pairwise alignment
176816	pdr-1	NA	Worm (Caenorhabditis elegans)	WBGene00003967	WormBase	9	Yes	Yes	high	12	4	3	8	11	0	Wormbase	Wormbase	[+] pairwise alignment

Publication Count	GO Component Counts	GO Function Counts	GO Process Counts	Protein Interaction Counts	Genetic Interaction Counts	Mine Phenotype Data	Mine Expression Data
642	17	25	69	407	3	0	376

Search by Disease

Disease

breast cancer

Select Disease Terms

select applicable and click to continue

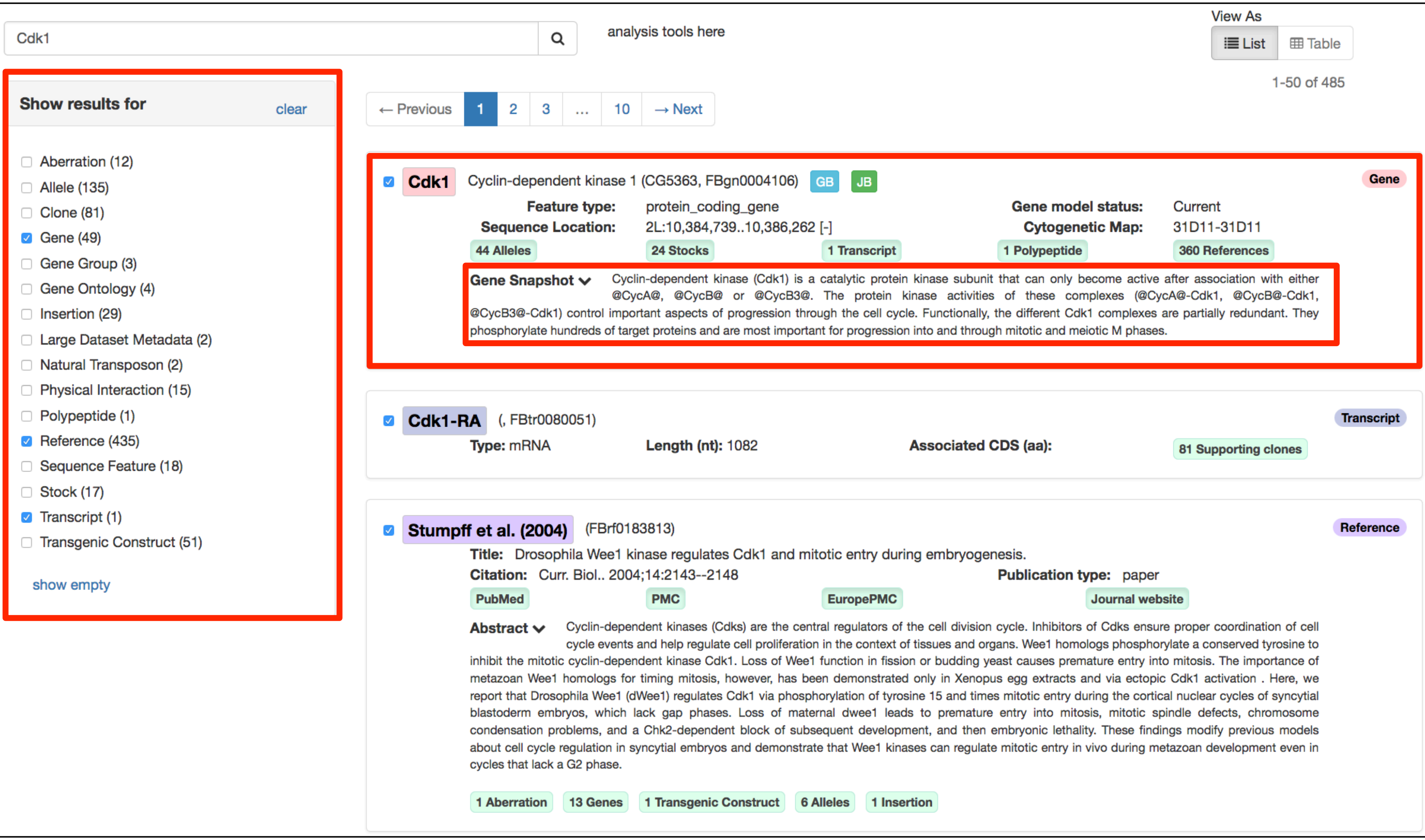
☑Check/UnCheck All

- ☑ ?Breast cancer, type 3 (2) [OMIM]
- ☑ {?Breast cancer susceptibility}, 114480 (1) [OMIM]
- ☐ {Breast cancer, invasive ductal}, 114480 (3) [OMIM]
- ☐ {Breast cancer, lobular}, 114480 (3) [OMIM]
- ☐ {Breast cancer, male, susceptibility to}, 114480 (3) [OMIM]
- ☐ {Breast cancer, poor survival after chemotherapy for} (3) [OMIM]
- ☐ {Breast cancer, protection against}, 114480 (3) [OMIM]
- ☐ {Breast cancer, susceptibility to}, 114480 (3) [OMIM]
- ☑ {Breast cancer}, 114480 (1) [OMIM]
- ☐ Adverse response to chemotherapy in breast cancer (alopecia) [GWAS]

Disease Associated Genes

Gene Symbol Human	Gene ID Human	Count Disease Terms	Disease Terms	Orthologs Overview
TP53	7157	2	{Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1)	TP53 Orthologs
SLC22A18	5002	2	{Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1)	SLC22A18 Orthologs
ATM	472	2	{?Breast cancer susceptibility}, 114480 (1) {Breast cancer}, 114480 (1)	ATM Orthologs
PPM1D	8493	2	{Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1)	PPM1D Orthologs
BARD1	580	2	{Breast cancer}, 114480 (1)	BARD1

New hit-lists



Cdk1

analysis tools here

View As

1-50 of 485

Show results for clear

- ☐ Aberration (12)
- ☐ Allele (135)
- ☐ Clone (81)
- ☑ Gene (49)
- ☐ Gene Group (3)
- ☐ Gene Ontology (4)
- ☐ Insertion (29)
- ☐ Large Dataset Metadata (2)
- ☐ Natural Transposon (2)
- ☐ Physical Interaction (15)
- ☐ Polypeptide (1)
- ☑ Reference (435)
- ☐ Sequence Feature (18)
- ☐ Stock (17)
- ☑ Transcript (1)
- ☐ Transgenic Construct (51)

show empty

☑ **Cdk1** Cyclin-dependent kinase 1 (CG5363, FBgn0004106) GB JB — Gene

Feature type: protein_coding_gene
Gene model status: Current
Sequence Location: 2L:10,384,739..10,386,262 [-]
Cytogenetic Map: 31D11-31D11

44 Alleles | 24 Stocks | 1 Transcript | 1 Polypeptide | 360 References

Gene Snapshot Cyclin-dependent kinase (Cdk1) is a catalytic protein kinase subunit that can only become active after association with either @CycA@, @CycB@ or @CycB3@. The protein kinase activities of these complexes (@CycA@-Cdk1, @CycB@-Cdk1, @CycB3@-Cdk1) control important aspects of progression through the cell cycle. Functionally, the different Cdk1 complexes are partially redundant. They phosphorylate hundreds of target proteins and are most important for progression into and through mitotic and meiotic M phases.

☑ **Cdk1-RA** (, FBtr0080051) — Transcript

Type: mRNA
Length (nt): 1082
Associated CDS (aa):

81 Supporting clones

☑ **Stumpff et al. (2004)** (FBrf0183813) — Reference

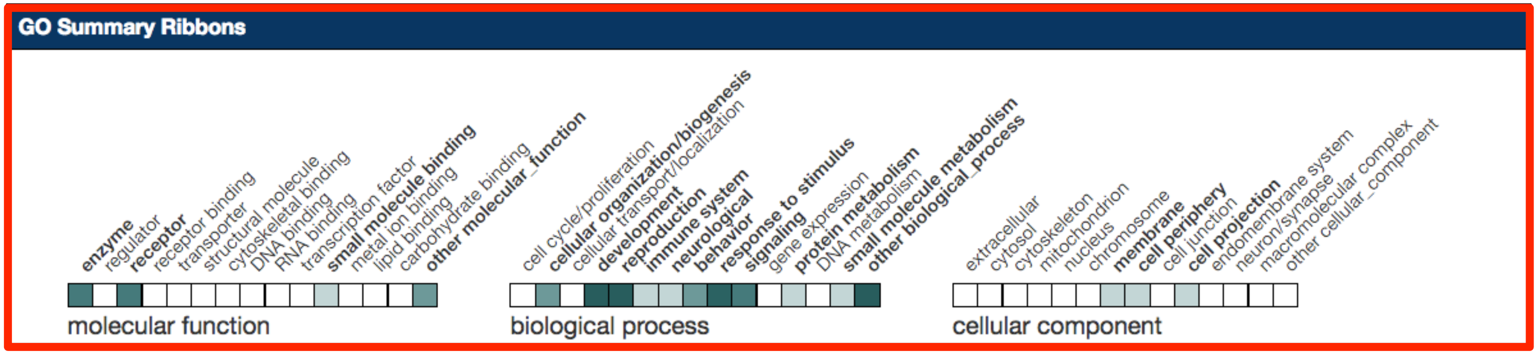
Title: Drosophila Wee1 kinase regulates Cdk1 and mitotic entry during embryogenesis.
Citation: Curr. Biol.. 2004;14:2143--2148
Publication type: paper

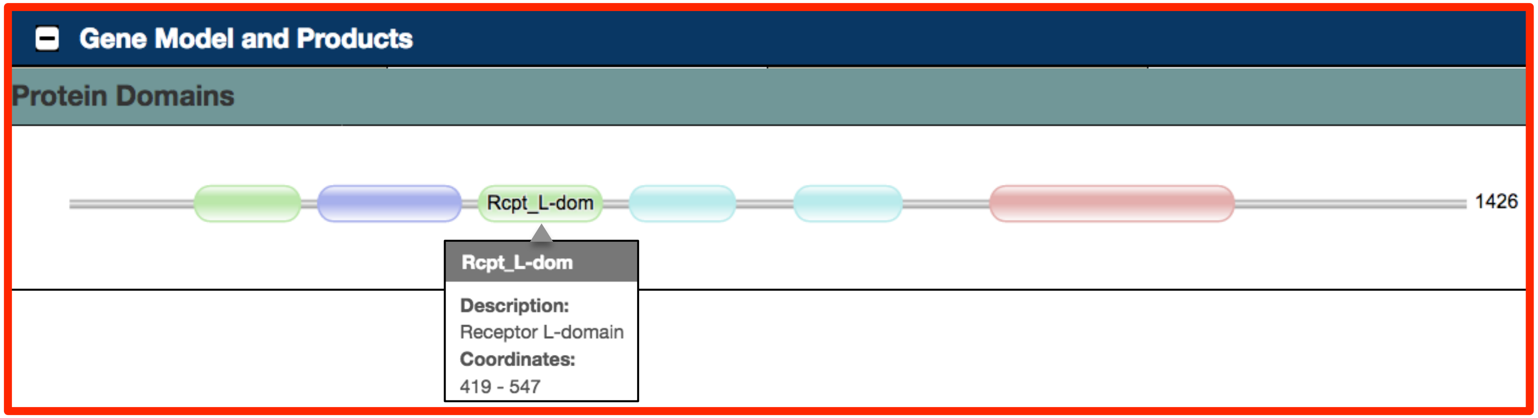
PubMed | PMC | EuropePMC | Journal website

Abstract Cyclin-dependent kinases (Cdks) are the central regulators of the cell division cycle. Inhibitors of Cdks ensure proper coordination of cell cycle events and help regulate cell proliferation in the context of tissues and organs. Wee1 homologs phosphorylate a conserved tyrosine to inhibit the mitotic cyclin-dependent kinase Cdk1. Loss of Wee1 function in fission or budding yeast causes premature entry into mitosis. The importance of metazoan Wee1 homologs for timing mitosis, however, has been demonstrated only in Xenopus egg extracts and via ectopic Cdk1 activation . Here, we report that Drosophila Wee1 (dWee1) regulates Cdk1 via phosphorylation of tyrosine 15 and times mitotic entry during the cortical nuclear cycles of syncytial blastoderm embryos, which lack gap phases. Loss of maternal dwee1 leads to premature entry into mitosis, mitotic spindle defects, chromosome condensation problems, and a Chk2-dependent block of subsequent development, and then embryonic lethality. These findings modify previous models about cell cycle regulation in syncytial embryos and demonstrate that Wee1 kinases can regulate mitotic entry in vivo during metazoan development even in cycles that lack a G2 phase.

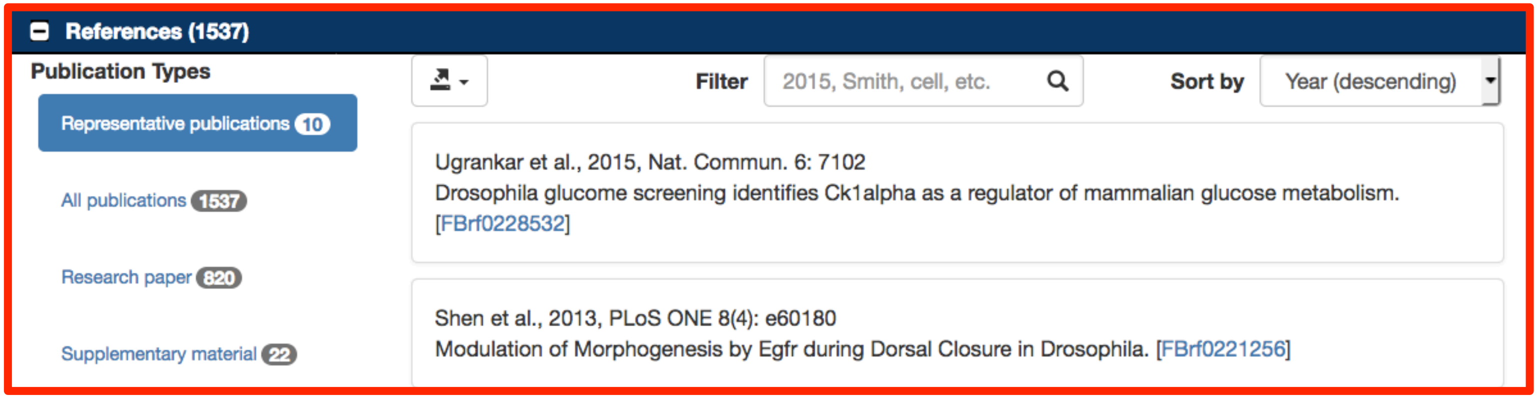
1 Aberration | 13 Genes | 1 Transgenic Construct | 6 Alleles | 1 Insertion

Revised Gene Reports



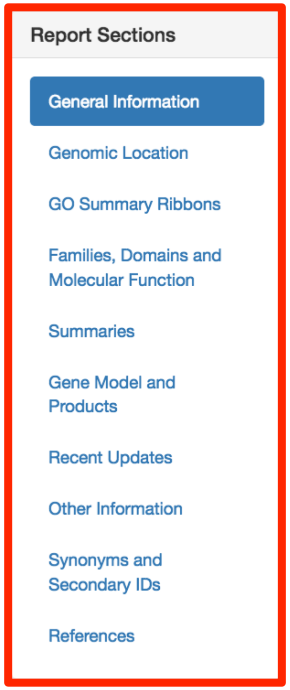


Description: Receptor L-domain
Coordinates: 419 - 547

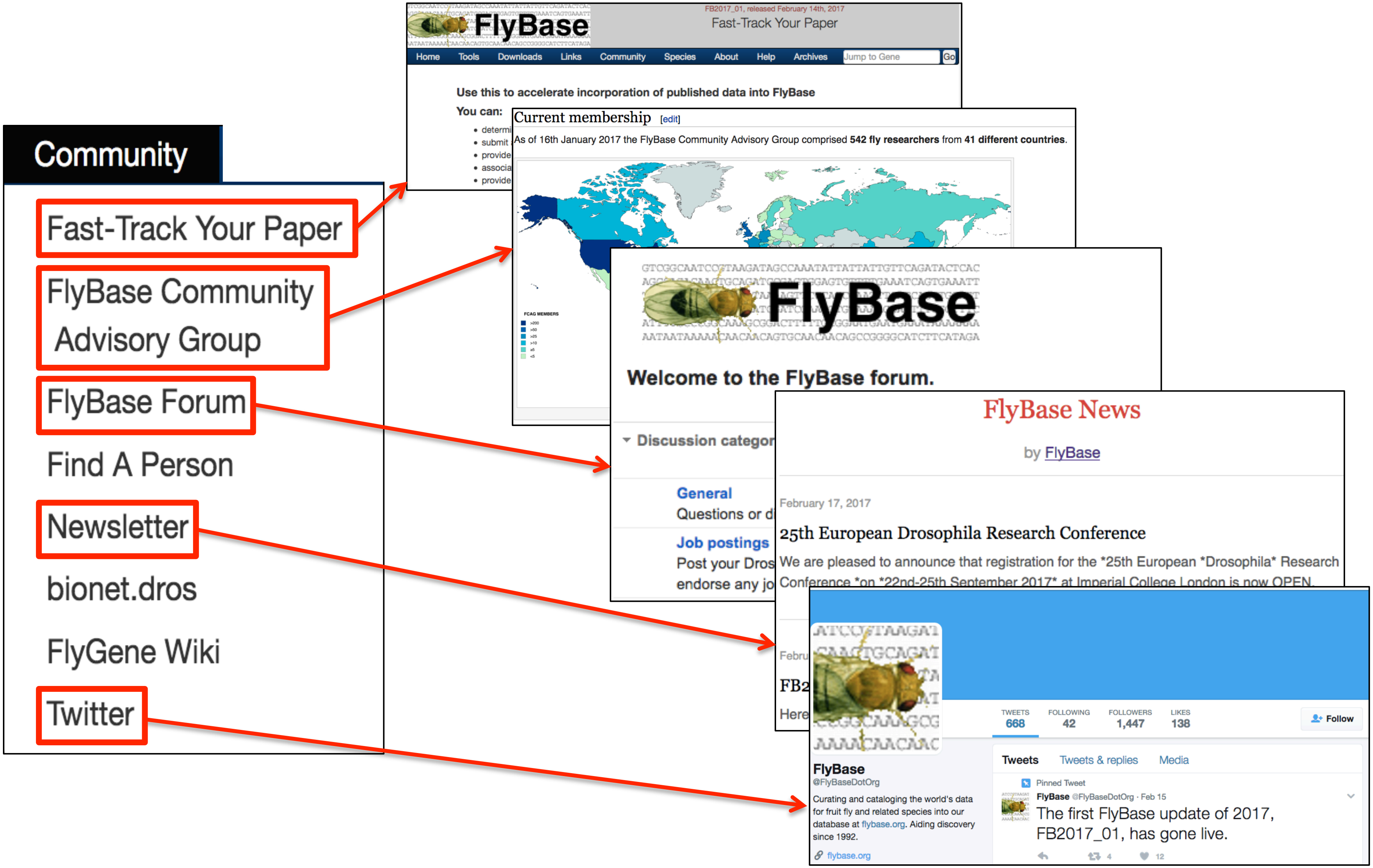


Ugrankar et al., 2015, Nat. Commun. 6: 7102
Drosophila glucome screening identifies Ck1alpha as a regulator of mammalian glucose metabolism. [FBrf0228532]

Shen et al., 2013, PLoS ONE 8(4): e60180
Modulation of Morphogenesis by Egfr during Dorsal Closure in Drosophila. [FBrf0221256]



Community Interactions



Community

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

FlyBase

FB2017_01, released February 14th, 2017

Fast-Track Your Paper

Use this to accelerate incorporation of published data into FlyBase

You can:

- determi
- submit
- provide
- associa
- provide

Current membership [edit]

As of 16th January 2017 the FlyBase Community Advisory Group comprised **542 fly researchers** from **41 different countries**.

FlyBase

Welcome to the FlyBase forum.

Discussion categor

General
Questions or d

Job postings
Post your Dros
endorse any jo

FlyBase News

by FlyBase

February 17, 2017

25th European Drosophila Research Conference

We are pleased to announce that registration for the *25th European *Drosophila* Research Conference *on *22nd-25th September 2017* at Imperial College London is now OPEN.

Febru

FB2

Here

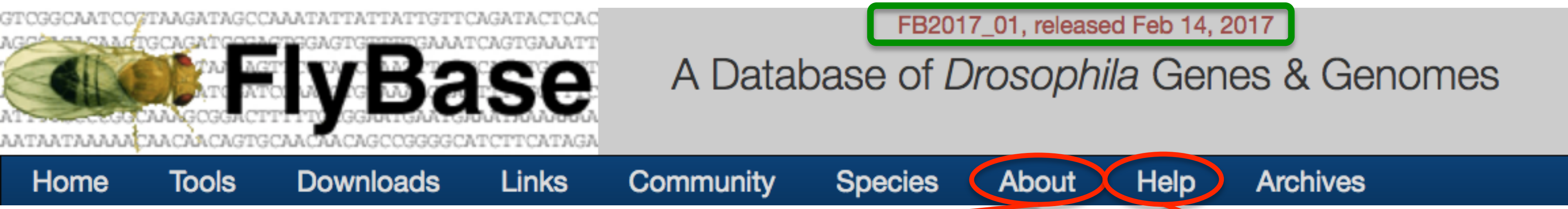
FlyBase
@FlyBaseDotOrg

Curating and cataloging the world's data for fruit fly and related species into our database at flybase.org. Aiding discovery since 1992.

flybase.org

FlyBase @FlyBaseDotOrg · Feb 15
The first FlyBase update of 2017, FB2017_01, has gone live.

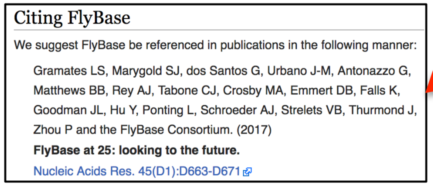
Further information


FB2017_01, released Feb 14, 2017


FlyBase 2017 Release Schedule

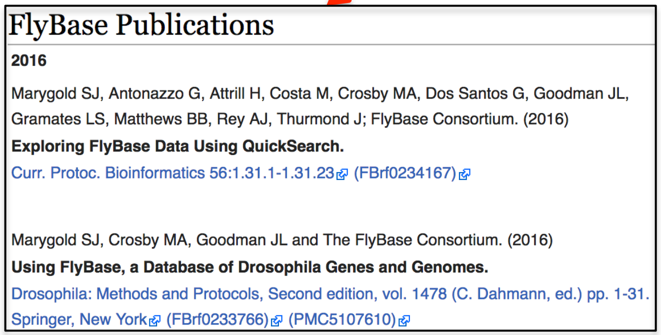
The following are the tentative dates of FlyBase releases in 2017. There will be 6 releases this year.

- FB2017_01 - February 14th
- FB2017_02 - April 18th
- FB2017_03 - June 20th
- FB2017_04 - August 22nd
- FB2017_05 - October 24th
- FB2017_06 - December 19th


Citing FlyBase

We suggest FlyBase be referenced in publications in the following manner:

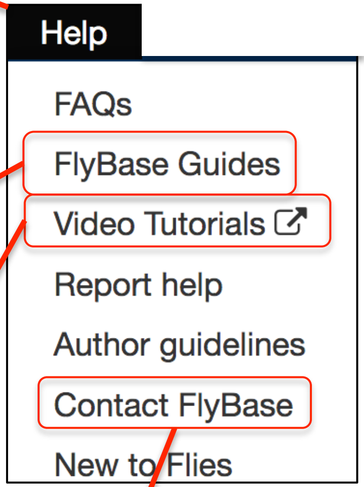
Gramates LS, Marygold SJ, dos Santos G, Urbano J-M, Antonazzo G, Matthews BB, Rey AJ, Tabone CJ, Crosby MA, Emmert DB, Falls K, Goodman JL, Hu Y, Ponting L, Schroeder AJ, Strelets VB, Thurmond J, Zhou P and the FlyBase Consortium. (2017)
FlyBase at 25: looking to the future.
Nucleic Acids Res. 45(D1):D663-D671

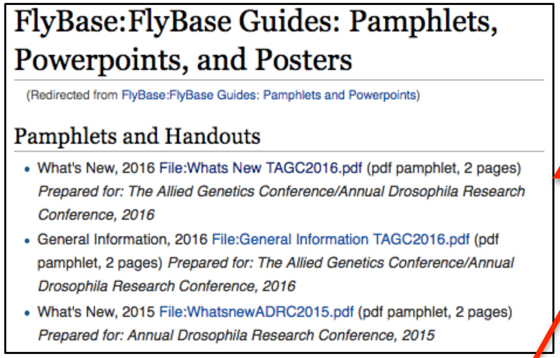

FlyBase Publications

2016

Marygold SJ, Antonazzo G, Attrill H, Costa M, Crosby MA, Dos Santos G, Goodman JL, Gramates LS, Matthews BB, Rey AJ, Thurmond J; FlyBase Consortium. (2016)
Exploring FlyBase Data Using QuickSearch.
Curr. Protoc. Bioinformatics 56:1.31.1-1.31.23 (FBrf0234167)

Marygold SJ, Crosby MA, Goodman JL and The FlyBase Consortium. (2016)
Using FlyBase, a Database of Drosophila Genes and Genomes.
Drosophila: Methods and Protocols, Second edition, vol. 1478 (C. Dahmann, ed.) pp. 1-31. Springer, New York (FBrf0233766) (PMC5107610)

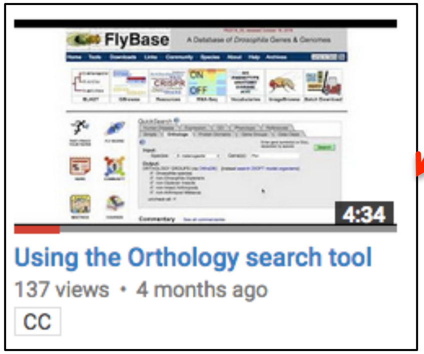



FlyBase:FlyBase Guides: Pamphlets, Powerpoints, and Posters

(Redirected from FlyBase:FlyBase Guides: Pamphlets and Powerpoints)

Pamphlets and Handouts

- What's New, 2016 File:Whats New TAGC2016.pdf (pdf pamphlet, 2 pages) *Prepared for: The Allied Genetics Conference/Annual Drosophila Research Conference, 2016*
- General Information, 2016 File:General Information TAGC2016.pdf (pdf pamphlet, 2 pages) *Prepared for: The Allied Genetics Conference/Annual Drosophila Research Conference, 2016*
- What's New, 2015 File:WhatsnewADRC2015.pdf (pdf pamphlet, 2 pages) *Prepared for: Annual Drosophila Research Conference, 2015*



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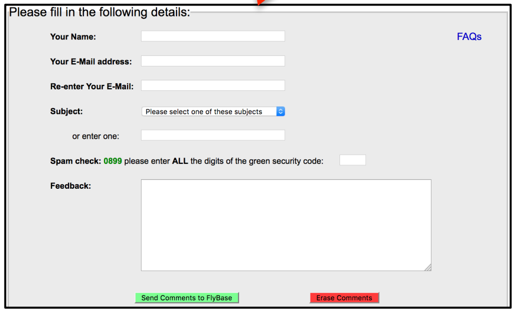
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