

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

Steven Marygold

- JBrowse
- Gene Snapshots
- Gene Groups
- Orthologs
- Human Disease Models
- GAL4 search
- New website: FlyBase 2.0
- Gene2Function
- Alliance of Genome Resources

Outline

1. Recent additions to FlyBase
2. New features in FlyBase 2.0
3. Multi-species databases
4. Further information/feedback

Outline

1. Recent additions to FlyBase
2. New features in FlyBase 2.0
3. Multi-species databases
4. Further information/feedback



BLAST	GBrowse	Resources	RNA-Seq	Vocabularies	ImageBrowse	Batch Download
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FAST-TRACK YOUR PAPER	FLYBASE NEWS
FLY BOARD	COMMUNITY NEWS

MEETINGS COURSES	FLYBOOK
Resources for:	
PUBLIC, TEACHERS, STUDENTS	BIOMEDICAL RESEARCH
Multi-species mining:	
MARRVEL	G2F
MIST	Gene2Function

QuickSearch

Human Disease GAL4 etc Expression Phenotype References

Simple Orthologs Protein Domains Gene Groups GO Data Class

Species: include non-Dmel species

Enter text:

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

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)



FlyBase wishes to congratulate our colleagues Jeffrey C. Hall, Michael Rosbash, and Michael W. Young, joint recipients of the 2017 Nobel Prize in Physiology or Medicine.



Tweets by [@FlyBaseDotOrg](#)

FlyBase [@FlyBaseDotOrg](#)

Survey results up: Curation of phenotypes induced or modified by chemical treatments or nutritional challenges

General Information			
Symbol	Dmel\Egfr	Species	<i>D. melanogaster</i>
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, Efp, dEGFR, Egf-r, c-erbB		
Gene Snapshot	Epidermal growth factor receptor (Egfr) is the transmembrane tyrosine kinase receptor for signaling ligands in the TGF α 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		

<p>Genomic Maps</p> <p>GBrowse</p> <p>JBrowse</p>		<p>Decorated FASTA</p> <p>Get genome region</p> <p>Gene region <input type="text" value=""/></p> <p>Get FastA</p>
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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

JBrowse File View Help

0 5,000,000 10,000,000 15,000,000 20,000,000 25,000,000

3R 3R:15257302..15264371 (7.07 Kb) Go

5,257,500 15,258,750 15,260,000 15,261,250 15,262,500

Gene

- Su(var)3-9-RA
- Su(var)3-9
- eIF2gamma-RB
- eIF2gamma-RC
- eIF2gamma-RD
- eIF2gamma
- Set-RA
- Set

RNA-seq exon junctions

Protein domains (PFAM)

- TIF2_gsu_C
- EFTU-like_2
- SET_dom
- Pre-SET_dom
- Chromo_domain

TRIP RNAi amplicons

- dsRNA-JF01404

VDRC RNAi amplicons

- dsRNA-GD15421

NIG-Fly RNAi amplicons

- dsRNA-6476R
- dsRNA-6476R

Point mutation

- Su(var)3-9[22]
- Su(var)3-9[318]
- Su(var)3-9[319]
- Su(var)3-9[25]
- Su(var)3-9[8]
- Su(var)3-9[10]
- dsRNA-HMS00704
- dsRNA-HMS00279
- dsRNA-GL01471
- dsRNA-GD15258
- dsRNA-GD15421
- dsRNA-KK108870

Gene Snapshots


General Information			
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Epidermal growth factor receptor (Egfr) is the transmembrane tyrosine kinase receptor for signaling ligands in the TGF α 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


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

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

QuickSearch 

Human Disease  GAL4 etc Expression Phenotype References


Simple Orthologs Protein Domains **Gene Groups** GO Data Class

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

Enter text:

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	<i>D. melanogaster</i>
Symbol	RTK	FlyBase ID	FBgg0000220
Date last reviewed	2015-08-26	Number of members	20
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	In other metazoans, <i>otk</i> orthologous kinases are inactive. <i>otk</i> deviates in some consensus kinase motifs, indicating that it may be a pseudokinase. However, FBrf0055961 have shown a kinase activity associated with immunoprecipitated <i>otk</i> . 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). Wस्क is predicted to be a pseudokinase based on sequence analysis in FBrf0209106 .		
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 (20)			
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	DAIk	(Sopko and Perrimon, 2013, Manning et al., 2002, Sopko et al., 2014, Vogel et al., 2013)
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			
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)
drl	derailed	lio, derailed	(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


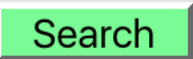
Links to external resources


Orthology search tool

QuickSearch 

Human Disease  GAL4 etc Expression Phenotype References

Simple **Orthologs** Protein Domains Gene Groups GO Data Class

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


Input:
Species: Gene(s): 


Output:
HUMAN AND MODEL ORGANISMS (via [DIOPT](#))

<input checked="" type="checkbox"/> <i>H. sapiens</i> (Human)	<input checked="" type="checkbox"/> <i>D. melanogaster</i> (Fruit fly)
<input checked="" type="checkbox"/> <i>R. norvegicus</i> (Norway rat)	<input checked="" type="checkbox"/> <i>C. elegans</i> (Nematode, roundworm)
<input checked="" type="checkbox"/> <i>M. musculus</i> (Laboratory mouse)	<input checked="" type="checkbox"/> <i>S. cerevisiae</i> (Brewer's yeast)
<input checked="" type="checkbox"/> <i>X. tropicalis</i> (Western clawed frog)	<input checked="" type="checkbox"/> <i>S. pombe</i> (Fission yeast)
<input checked="" type="checkbox"/> <i>D. rerio</i> (Zebrafish)	


un/check all: or [search Drosophila species, insects etc.](#)

Orthology search tool

QuickSearch 

Human Disease  GAL4 etc Expression Phenotype References

Simple **Orthologs** Protein Domains Gene Groups GO Data Class

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

Input:



Species: Gene(s):

Output:

DROSOPHILA SPECIES, OTHER INSECTS, etc. (via [OrthoDB](#))

- Drosophila species (*D. pseudoobscura*, *D. virilis*, etc.)
- non-Drosophila Dipterans (mosquitoes and flies)
- non-Dipteran Insects (bees, beetles, etc.)
- non-Insect Arthropods (arachnids, water flea, etc.)
- non-Arthropod Metazoa (chicken, sea urchin, etc.)

un/check all: [or search human and model organisms](#)

Orthology search results

[Save results as tsv file](#) | [Exclude scores <3](#) | [Help](#)

Search Term: Psn Species: <i>Drosophila melanogaster</i> (Fruit fly) Gene: Psn Reports: NCBI FlyBase								
Ortholog Gene	Ortholog Gene Reports	Via DIOPT (v6.0)					Align	Transgene in Fly
		Score	Best Score	Best Rev Score	Source			
<i>Homo sapiens</i> (Human)								
PSEN2	NCBI HGNC OMIM	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam		(+)	Yes
PSEN1	NCBI Ensembl OMIM HGNC	9 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, Isobase, OMA, orthoMCL, Panther, Phylome, TreeFam		(+)	Yes
<i>Mus musculus</i> (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		(+)	
<i>Rattus norvegicus</i> (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		(+)	
<i>Xenopus tropicalis</i> (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		(+)	
<i>Danio rerio</i> (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		(+)	
<i>Caenorhabditis elegans</i> (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		(+)	
<i>Saccharomyces cerevisiae</i> (Brewer's yeast) - no orthologs found								
<i>Schizosaccharomyces pombe</i> (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		<input type="button" value="Models Data"/> <input type="button" value="Interaction data"/>		
Models				
Allele	Disease	Evidence	References	
tefu^{atm-8}	model of ataxia telangiectasia	inferred from mutant phenotype	<i>(Petersen et al., 2012)</i>	
tefu^{dsRNA.Scer\UAS}	model of ataxia telangiectasia	inferred from mutant phenotype	<i>(Petersen et al., 2012)</i>	
Interactions				
Allele	Disease	Interaction	References	
tefu^{atm-8}	model of neurodegenerative disease	is ameliorated by Rel^{E20}	<i>(Petersen et al., 2013)</i>	
	model of neurodegenerative disease	is ameliorated by Rel^{E38}	<i>(Petersen et al., 2013)</i>	
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; this kinase belongs to family of proteins that respond to DNA damage by phosphorylating key substrates involved in DNA repair and/or cell cycle control. There is a single fly ortholog, [tefu](#), for which loss-of-function alleles, RNAi targeting constructs, and alleles caused by insertional mutagenesis 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](#)).

The human ATM gene has not yet been introduced into flies.

Animals homozygous for the more severe loss-of-function alleles of *Dmel\tefu* are semi-lethal; surviving adults exhibit rough eyes, notched wings, and shorter or missing bristles; females are sterile. Homozygous mutant neuroblast cells display severe mitotic abnormalities that are characterised by a high frequency of end-to-end fusions of chromosomes during mitosis, leading to the hypothesis that normal function of [tefu](#) is required to protect the linear ends of chromosomes. A mutation that results in reduction of kinase activity causes neuron and glial cell death in the adult brain and a reduction in mobility and longevity. ATM knockdown in glial cells, but not neurons, is sufficient to cause neuron and glial cell death, a reduction in mobility and longevity, and elevated expression of innate immune response genes in glial cells, indicating that a non-cell-autonomous mechanism contributes to the neurodegeneration and related phenotypes. Physical and genetic interactions of *Dmel\tefu* have been described; see below and in the gene report for [tefu](#).

[updated Jun. 2017 by FlyBase; [FBr0222196](#)]

- + 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 (11)


Manually written summary of disease and model

Links to related diseases/fly models


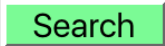
List of fly stocks used in model

'GAL4 etc.' search tool

GAL4 binary driver
QF binary driver
LexA binary driver
lacZ reporter
GFP reporter

QuickSearch 

Human Disease **★ GAL4 etc** Expression Phenotype References
Simple Orthologs Protein Domains Gene Groups GO Data Class

 Search for GAL4 and other drivers and reporters by expression pattern: 

Driver/Reporter:

refine search by adding qualifier terms (such as 'ventral')

Developmental Stage: e.g., third instar larval stage

Anatomy/Cell Type: e.g., neuron

Cellular Component: e.g., neuromuscular junction

Fill only as many fields as you need

(Coming soon: Search by gene or identifier)

Search for GAL4 and other drivers and reporters:

by gene:

by identifier:

'GAL4 etc.' search results

Query: GAL4 | adult stage | fat body

Group #	Relevant Expression Statements	Allele	Construct	Insertion	Stock
1	adult fat body adult stage embryonic/larval fat body fat body	Scer\GAL4[c564]	P{GawB}	P{GawB}c564	FBst0006982 FBst0067100
2	adult fat body adult stage embryonic/larval fat body fat body	Scer\GAL4[Lsp2.PH]	P{Lsp2-GAL4.H}		FBst0006357 FBst0307394
3	adult fat body adult stage	Scer\GAL4[yolk]	P{yolk-GAL4}		FBst0058814
4	adult fat body adult stage embryonic/larval fat body fat body	Scer\GAL4[ppl.PP]	P{ppl-GAL4.P}		FBst0058768
5	adult fat body adult stage embryonic/larval fat body fat body	Scer\GAL4[Cg.PA]	P{Cg-GAL4.A}		FBst0007011 FBst0063147
6	adult fat body adult stage fat body	Scer\GAL4[Switch1.106]	P{Switch1}	P{Switch1}106	FBst0008151
7	adult fat body adult stage embryonic/larval fat body	Scer\GAL4[r4]	P{r4-GAL4}		FBst0033832
8	adult fat body adult stage	Scer\GAL4[AkhR.PB]	P{AkhR-Gal4.B}		
9	adult stage fat body	Scer\GAL4[bun-Switch1.32]	P{Switch1}	P{Switch1}bun[Switch1.32]	
10	adult fat body adult stage	Scer\GAL4[Desat1-1573-1]	P{GawB}	P{GawB}Desat1[1573-1]	
11	adult fat body adult stage embryonic/larval fat body	Scer\GAL4[dsx.KI]	TI{GAL4}	TI{GAL4}dsx[KI.GAL4]	
12	adult fat body adult stage embryonic/larval fat body	Scer\GAL4[fat]	P{GAL4}	P{GAL4}fat	
13	adult stage	Scer\GAL4[Il k6-D.I6341]	P{GawB}	P{GawB}Il k6[D.I6341]	

Community Interactions

Community

Fast-Track Your Paper

FlyBase Community
Advisory Group

FlyBase Forum

Find A Person

Newsletter

bionet.dros

FlyGene Wiki

Twitter



Use this to accelerate incorporation of published data into FlyBase

You can:

- determin
- 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.



Welcome to the FlyBase forum.

Discussion categories

General

Questions or d

Job postings

Post your Dros

endorse any jo

FlyBase News

by FlyBase

February 17, 2017

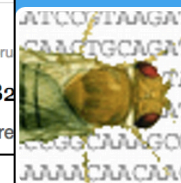
25th European Drosophila Research Conference

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

TWEETS

668

FOLLOWING

42

FOLLOWERS

1,447

LIKES

138

Follow

Tweets

Tweets & replies

Media

Pinned Tweet

FlyBase @FlyBaseDotOrg · Feb 15

The first FlyBase update of 2017, FB2017_01, has gone live.

Retweets

4

Likes

12

Outline

1. Recent additions to FlyBase
- 2. New features in FlyBase 2.0**
3. Multi-species databases
4. Further information/feedback



A Database of *Drosophila* Genes & Genomes

BLAST: D.melanogaster, D.virilis, A.mellifera

GBrowse: Genomic browser interface

Resources: Antibodies, Databases, Interactions, RNAi, CRISPR, Orthologs, cDNAs, Stocks

RNA-Seq: ON/OFF heatmap

Vocabularies: GO, PHENOTYPE, ANATOMY, DISEASE, MORE

ImageBrowse: Fly image

Batch Download: FIELD DATA, XML, sequence

FAST-TRACK YOUR PAPER

FLYBASE NEWS

FLY BOARD

COMMUNITY NEWS

MEETINGS COURSES

FLYBOOK

Resources for:

PUBLIC, TEACHERS, STUDENTS

BIOMEDICAL RESEARCH

Multi-species mining:

MARRVEL

GENE2FUNCTION

MIST

QuickSearch

Human Disease GAL4 etc Expression Phenotype References

Search FlyBase Orthologs Protein Domains Gene Groups GO Data Class

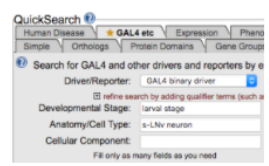
Enter text:

Search input field

Search

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

Commentary



GAL4 etc QuickSearch tab Aug 22, 2017.

FlyBase is pleased to announce the GAL4 etc QuickSearch tab. This tool allows FlyBase users to search by expression pattern for GAL4 drivers, as well as for the binary drivers QF and LexA, and the nonbinary reporters lacZ and GFP. ... (More)

Tweets by @FlyBaseDotOrg

Tweet from FlyBase (@FlyBaseDotOrg) about survey results on phenotypes induced by chemical treatments or nutritional challenges.

New features include:

- **New/Improved tools**

- New hit-list management
- Sequence Downloader
- Revised Jump-to-Gene/Search box

- **Enhanced Report pages**

- Navigation panel
- GO summary ribbons (Gene Report)
- Protein domain graphics (Gene/Polypeptide Report)
- Reference filtering

- **Mobile device friendly**

New hit-lists

[Human Disease](#)

[★ GAL4 etc](#)

[Expression](#)

[Phenotype](#)

[References](#)

[Search FlyBase](#)

[Orthologs](#)

[Protein Domains](#)

[Gene Groups](#)

[GO](#)

[Data Class](#)

Enter text:

Search

Cdk1



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

New hit-lists

analysis tools here

View As

1-50 of 499

Show results for

- Aberration (12)
- Allele (135)
- Clone (81)
- Dataset (2)
- Gene (54)
- Gene Group (3)
- Gene Ontology (4)
- Insertion (29)
- Natural Transposon (2)
- Physical Interaction (19)
- Polypeptide (1)
- Reference (444)
- Sequence Feature (18)
- Stock (17)
- Transcript (1)
- Transgenic Construct (51)

[show empty](#)

← Previous **1** 2 3 ... 10 → Next

Cdk1 Cyclin-dependent kinase 1 (CG5363, FBgn0004106) *D. melanogaster*

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 369 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 (CG5363-RA, FBtr0080051) *D. melanogaster*

Feature type: mRNA
Associated gene: Cdk1
Transcript length (nt): 1082
Associated polypeptide: Cdk1-PA (297 aa)

81 Supporting clones 0 References

Stumpff et al. (2004) (FBfr0183813)

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

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

New hit-lists

Cdk1 analysis tools here View As

1-50 of 499

← Previous **1** 2 3 ... 10 → Next

Show results for [clear](#)

- Aberration (12)
- Allele (135)
- Clone (81)
- Dataset (2)
- Gene (54)
- Gene Group (3)
- Gene Ontology (4)
- Insertion (29)
- Natural Transposon (2)
- Physical Interaction (19)
- Polypeptide (1)
- Reference (444)
- Sequence Feature (18)
- Stock (17)
- Transcript (1)
- Transgenic Construct (51)

[show empty](#)

Cdk1 CG5363, FBgn0004106 *D. melanogaster* Gene

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

44 Alleles 24 Stocks 1 Transcript 1 Polypeptide 369 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 (CG5363-RA, FBtr0080051) *D. melanogaster* Transcript

Feature type: mRNA
Transcript length (nt): 1082
Associated gene: Cdk1
Associated polypeptide: Cdk1-PA (297 aa)

81 Supporting clones 0 References

Stumpff et al. (2004) (FBBr0183813) Reference

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1 Aberration 13 Genes 1 Transgenic Construct 6 Alleles 1 Insertion

New hit-lists

Cdk1



analysis tools here

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1-50 of 499

Show results for

clear

- Aberration (12)
- Allele (135)
- Clone (81)
- Dataset (2)
- Gene (54)
- Gene Group (3)
- Gene Ontology (4)
- Insertion (29)
- Natural Transposon (2)
- Physical Interaction (19)
- Polypeptide (1)
- Reference (444)
- Sequence Feature (18)
- Stock (17)
- Transcript (1)
- Transgenic Construct (51)

show empty

← Previous 1 2 3 ... 10 → Next

Cdk1 Cyclin-dependent kinase 1 (CG5363, FBgn0004106) *D. melanogaster* [GBrowse](#) [JBrowse](#) 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](#) [369 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 (CG5363-RA, FBtr0080051) *D. melanogaster* [GBrowse](#) [JBrowse](#) Transcript

Feature type: mRNA
Associated gene: Cdk1
Transcript length (nt): 1082
Associated polypeptide: Cdk1-PA (297 aa)

[81 Supporting clones](#) [0 References](#)

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](#)

New hit-lists

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Show results for

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Allele (44)

[show empty](#)

← Previous **1** → Next

- Cdk1^{216A}** (FBal0001571) *D. melanogaster* Allele

Allele class: [hypomorphic allele - genetic evidence](#)
Mutagen: ethyl methanesulfonate
Associated insertions:
3 **Phenotype (class) statements**
0 **Disease model annotations**
[0 Stocks](#) [3 References](#)

Known lesion? yes
Carried in construct:
1 **Phenotype (anatomy) statements**
- Cdk1^{D57}** (FBal0001572) *D. melanogaster* Allele

Allele class: [amorphic allele - genetic evidence](#)
Mutagen: ethyl methanesulfonate
Associated insertions:
3 **Phenotype (class) statements**
0 **Disease model annotations**
[0 Stocks](#) [4 References](#)

Known lesion? yes
Carried in construct:
1 **Phenotype (anatomy) statements**
- Cdk1^{E1-23}** (FBal0001573) *D. melanogaster* Allele

Allele class: [amorphic allele - genetic evidence](#)
Mutagen: ethyl methanesulfonate
Associated insertions:
3 **Phenotype (class) statements**
0 **Disease model annotations**
[1 Stock](#) [10 References](#)

Known lesion? yes
Carried in construct:
3 **Phenotype (anatomy) statements**

New hit-lists

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Table

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Show results for

[clear](#)

Allele (44)

[show empty](#)

← Previous **1** → Next

Allele Results

<input type="checkbox"/>	Symbol	Class	Inserted Elements	# Stocks	Mutagens	Known Lesion?
<input type="checkbox"/>	Cdk1^{216A}	hypomorphic allele - genetic evidence		0	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{D57}	amorphic allele - genetic evidence		0	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{E1-23}	amorphic allele - genetic evidence		1	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{E1-24}	heat sensitive loss of function allele		1	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{E1-9}	amorphic allele - genetic evidence		0	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{216P}	hypomorphic allele - genetic evidence	P{Cdk1^{216P}}	0	PM hybrid dysgenesis; P-element activity	yes
<input type="checkbox"/>	Cdk1^{B47}	amorphic allele - genetic evidence loss of function allele		1	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{E10}	amorphic allele - genetic evidence		0	ethyl methanesulfonate	yes
<input type="checkbox"/>	Cdk1^{hs-PS}			0	in vitro construct	yes
<input type="checkbox"/>	Cdk1^{+t5.8}			0	in vitro construct	yes
<input type="checkbox"/>	Cdk1^{A171T}			0	in vitro construct	yes
<input type="checkbox"/>	Cdk1^{P131S}			0	in vitro construct	yes

Revised Gene Reports

General Information			
Symbol	Dmel\Egfr	Species	<i>D. melanogaster</i>
Name	Epidermal growth factor receptor	Annotation Symbol	CG10079
Feature Type	protein_coding_gene	FlyBase ID	FBgn0003731
Gene Model Status	Current	Stock Availability	52 publicly available
Gene Snapshot	Epidermal growth factor receptor (Egfr) is the transmembrane tyrosine kinase receptor for signaling ligands in the TGF α family (<i>grk</i> , <i>spi</i> , <i>vn</i> , and <i>Krn</i>), which utilizes the intracellular MAP kinase pathway. Egfr roles include growth regulation, cell survival and developmental patterning. [Date last reviewed: 2016-10-06]		

Other Summaries

[Auto summary](#)
[Gene Group](#)
[UniProt](#)
[Red Book](#)

Also Known As: DER, top, flb, Efp, dEGFR, Egf-r, c-erbB

Genomic Location

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

Recombination map: 2-95

Genomic Maps

[GBrowse](#)
[JBrowse](#)

Gene region:

[Get Sequence](#)

Other Genome Views

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

[NCBI Genome Data Viewer](#)
[UCSC Genome Browser](#)

[Ensembl Genome Browser](#)
[PopFly Genome Browser](#)

GO Summary Ribbons

[Detailed GO annotations]

molecular function

biological process

cellular component

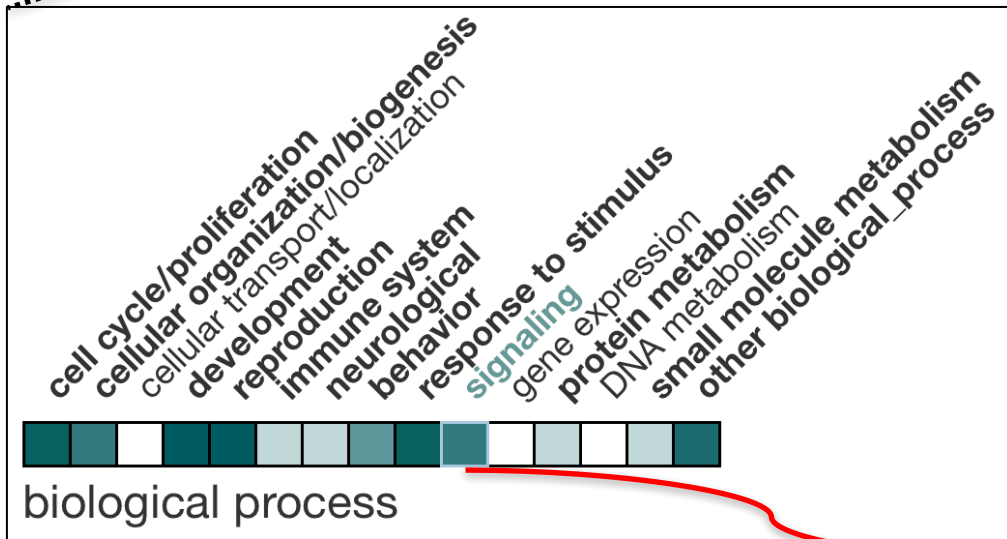
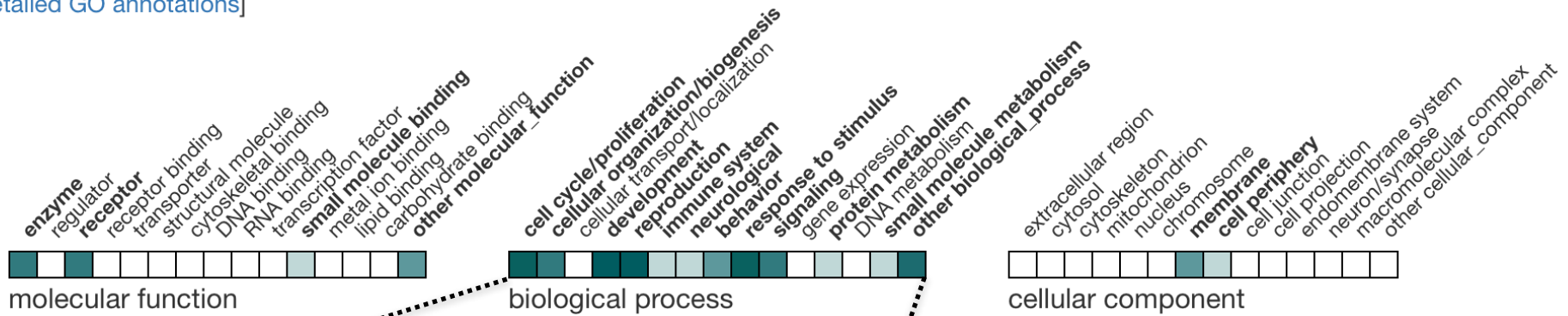
Report Sections

- General Information
- Genomic Location
- GO Summary Ribbons
- Families, Domains and Molecular Function
- Summaries
- Gene Model and Products
- Gene Ontology
- Expression Data
- Alleles, Insertions, Constructs, and Phenotypes
- Recent Updates
- Interactions and Pathways
- Genomic Location and Mapping
- Stocks and Reagents
- Other Information
- Crossreferences
- Synonyms and Secondary IDs
- References

Revised Gene Reports

GO Summary Ribbons

[\[Detailed GO annotations\]](#)



- SIGNALING:**
- epidermal growth factor receptor signaling pathway
 - negative regulation of apoptotic signaling pathway
 - transmembrane receptor protein tyrosine kinase signaling pathway

Revised Gene Reports

Gene Model and Products

Protein Domains (via Pfam)

Isoform displayed: [Egfr-PB](#)



Pfam protein

Ser-Thr/Tyr_kinase_cat_dom (PF07714)

Description:

Serine-threonine/tyrosine-protein kinase, catalytic domain [[pfam](#)]

Coordinates:

941 - 1192

InterPro name	start	end
Receptor L-domain (Rcpt_L-dom)	28	238
Furin-like cysteine-rich domain (Furin-like_Cys-rich_dom)	55	403
Receptor L-domain (Rcpt_L-dom)	119	547
Growth factor receptor domain 4 (GF_recep_IV)	572	682
Growth factor receptor domain 4 (GF_recep_IV)	740	852
Serine-threonine/tyrosine-protein kinase, catalytic domain	941	1192

Protein Domains (via SMART)

Isoform displayed: [Egfr-PB](#)



SMART protein domains

InterPro name	domain classification	start	end
Furin-like repeat (Furin_repeat)	undefined	255	295
Furin-like repeat (Furin_repeat)	undefined	299	343
Furin-like repeat (Furin_repeat)	undefined	563	612
Furin-like repeat (Furin_repeat)	undefined	617	660
Furin-like repeat (Furin_repeat)	undefined	662	717
Furin-like repeat (Furin_repeat)	undefined	734	779

Revised Gene Reports

References (1,568)

Publication Types

Representative publications **25**

All publications **1568**

Research paper **841**

Supplementary material **24**

Review **303**

Erratum **1**

Personal communication to FlyBase
27

Abstract **326**

FlyBase analysis **4**

Stock list **2**

DNA/RNA sequence record **16**

Conference report **5**



Filter

2015, Smith, cell, etc.



Sort by

Default order

Jekely et al., 2005, Dev. Cell 9(2): 197--207

Regulators of endocytosis maintain localized receptor tyrosine kinase signaling in guided migration. [[FBrf0187407](#)]

Wang et al., 2000, Genes Dev. 14(18): 2271--2276

Dual role for Drosophila epidermal growth factor receptor signaling in early wing disc development. [[FBrf0130152](#)]

Liu et al., 1999, Genetics 151(2): 685--695

Identification of genes controlling Malpighian tubule and other epithelial morphogenesis in Drosophila melanogaster. [[FBrf0106865](#)]

Shen et al., 2013, PLoS ONE 8(4): e60180

Modulation of Morphogenesis by Egfr during Dorsal Closure in Drosophila. [[FBrf0221256](#)]

Buchon et al., 2010, BMC Biol. 8: 152

Drosophila EGFR pathway coordinates stem cell proliferation and gut remodeling following infection. [[FBrf0212840](#)]

Orian et al., 2007, Proc. Natl. Acad. Sci. U.S.A. 104(40): 15771--15776

A Myc-Groucho complex integrates EGF and Notch signaling to regulate neural development. [[FBrf0200831](#)]

Poulton and Deng, 2006, Proc. Natl. Acad. Sci. U.S.A. 103(34): 12775--12780

Dystroglycan down-regulation links EGF receptor signaling and anterior-posterior polarity formation in the Drosophila oocyte. [[FBrf0193906](#)]

Revised Jump to Gene/Search



FB2017_04, released Aug 22, 2017

A Database of *Drosophila* Genes & Genomes

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

J2G Jump to Gene Go



J2G Cdk1 Go



General Information			
Symbol	Dmel\Cdk1	Species	<i>D. melanogaster</i>
Name	Cyclin-dependent kinase 1	Annotation Symbol	CG5363
Feature Type	protein_coding_gene	FlyBase ID	FBgn0004106
Gene Model Status	Current	Stock Availability	24 publicly available
Also Known As	Cdc2, DmCdc2		

Genomic Location	
Cytogenetic map	31D11-31D11
Sequence location	2L:10,384,739..10,386,262 [-]

GO Summary Ribbons

Search Search FlyBase Go



Search Cdk1 Go



Cdk1 analysis tools here

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)

Cdk1 Cyclin-dependent kinase 1 (CG5363, FBgn0004106) **Gene**

Feature type: protein_coding_gene
Sequence Location: 44 Alleles, 24 Stocks, 1 Transcript, 1 Polypeptide, 380 References
Gene Snapshot >

Exelixis:FBst1006790 (FBst1006790) **Stock**

Collection: Exelixis at Harvard Medical School
Species: *melanogaster*
Genotype: PBac[PB]Cdk1¹⁰³⁴⁹⁵

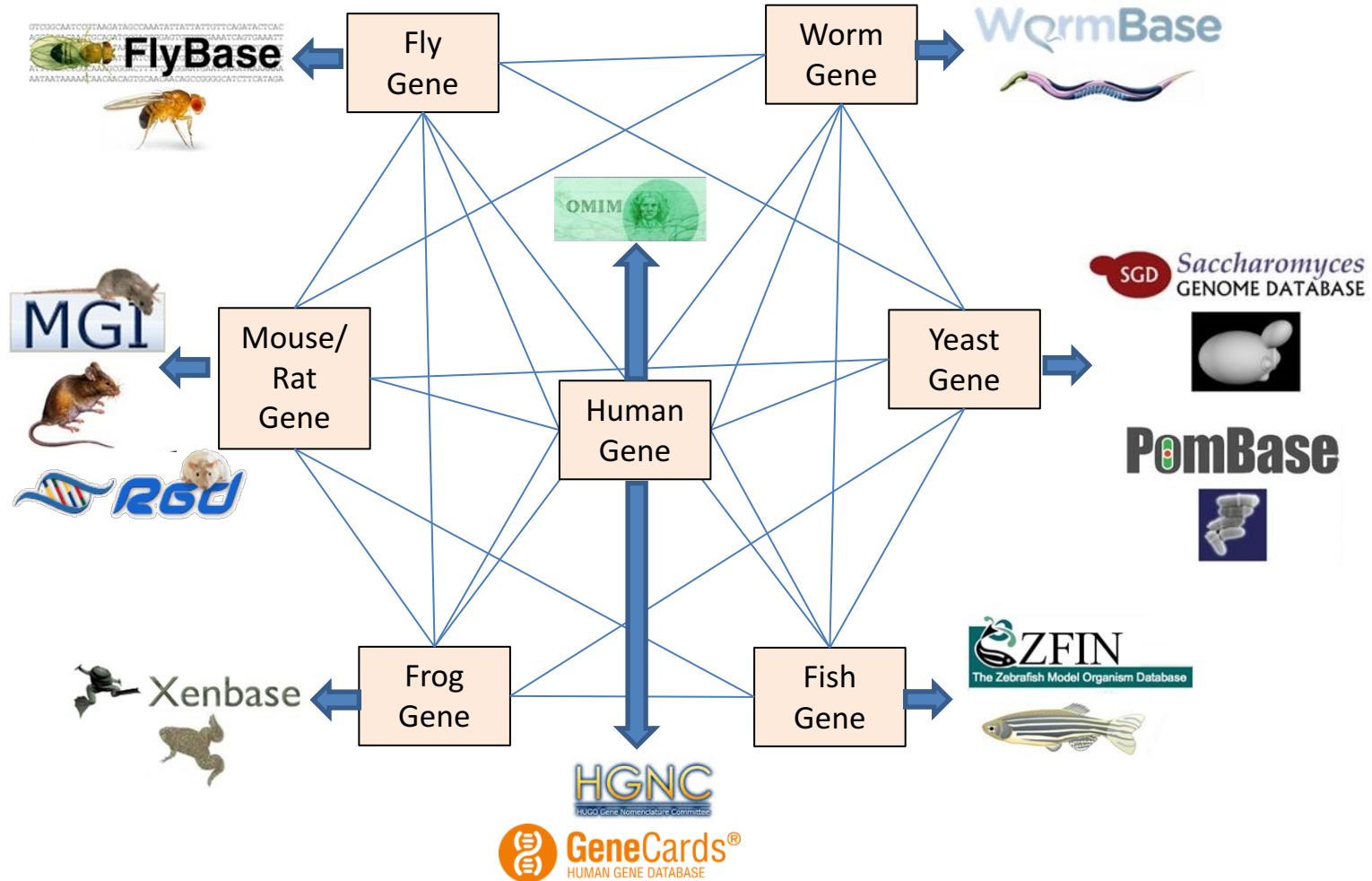
Cdk1^{216A} (FBal0001571) **Allele**

Allele class: hypomorphic allele - genetic evidence
Mutagen: ethyl methanesulfonate
Associated insertions:
Known lesion? yes
Carried in construct:

Outline

1. Recent additions to FlyBase
2. New features in FlyBase 2.0
- 3. Multi-species databases**
4. Further information/feedback

Gene2Function



www.gene2function.org

Search by Gene

Species

Human

Gene

PARK2

Search By Gene

- Fission yeast
- Yeast
- Worm
- Fly
- Zebrafish
- Western clawed frog
- Human
- Mouse
- Rat

Result count: 6
Export (tab separated) Export to Excel

NCBI Gene ID	Symbol	Human Disease Count	Species Name	Species specific gene ID	Species specific database	DIOPT Score	Best Score	Best Score reverse	Confidence	Publication Counts	GO Component Count	GO Function Count	GO Process Count	Protein Interaction Counts	Genetic Interaction Counts	Mine Phenotype Data	Mine Expression Data	Mine Disruption Phenotype	RNAi Cell Data	Crispr Cell Data	3D Structure	ORF Clones	Protein Alignment
5071	PARK2	13	Human (Homo sapiens)	8607	HGNC	NA	-	-	-	622	17	25	69	420	3	0	376	0	283	865	9	3	[+] multiple seq alignment of best orthologs
50873	Park2		Mouse (Mus musculus)	1355296	MGI	13/13	NA	NA	high	199	5	2	31	26	1	0	0	1	NA	NA	3	0	[+] pairwise alignment
56816	Park2		Rat (Rattus norvegicus)	61797	RGD	5/11	NA	NA	high	0	0	0	0	13	0	NA	NA	0	NA	NA	0	0	[+] pairwise alignment
550328	park2		Zebrafish (Danio rerio)	ZDB-GENE-050417-109	ZFIN	10/12	NA	NA	high	7	1	0	5	0	0	0	9	0	NA	NA	0	0	[+] pairwise alignment
40336	park		Fly (Drosophila melanogaster)	FBgn0041400	FLYBASE	11/12	NA	NA	high	131	3	2	21	16	2	398	104	0	39	0	2	1	[+] pairwise alignment
176816	pdr-1		Worm (Caenorhabditis elegans)	WBGene00003967	WormBase	9/11	NA	NA	high	8	4	3	8	11	0	Wormbase	Wormbase	0	NA	NA	0	0	[+] pairwise alignment

Publication Counts?	GO Component Count?	GO Function Count?	GO Process Count?	Protein Interaction Counts?	Genetic Interaction Counts?	Mine Phenotype Data?	Mine Expression Data?
622	17	25	69	420	3	0	376

Search by Disease

Disease

breast cancer

Search By Disease

Select Disease Terms

select applicable and click to continue

Search

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]

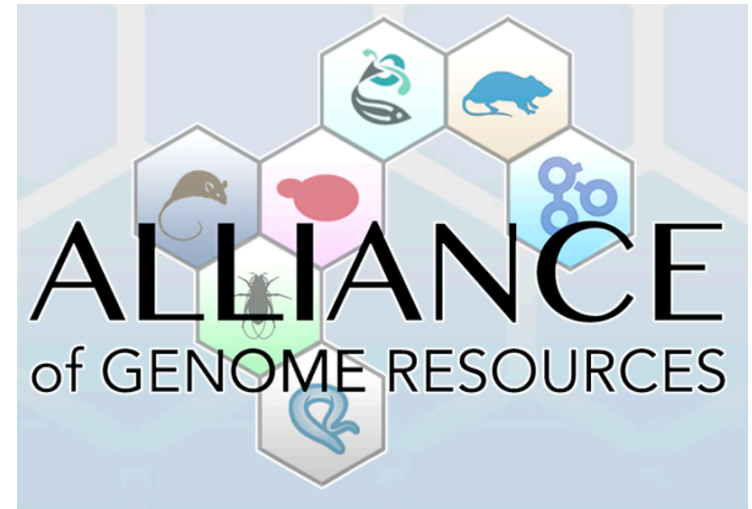
Disease Associated Genes

Gene Symbol	Gene ID	Count	Disease Terms	Orthologs Overview
TP53	7157	2	<ul style="list-style-type: none"> {Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1) 	TP53 Orthologs
SLC22A18	5002	2	<ul style="list-style-type: none"> {Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1) 	SLC22A18 Orthologs
ATM	472	2	<ul style="list-style-type: none"> {?Breast cancer susceptibility}, 114480 (1) {Breast cancer}, 114480 (1) 	ATM Orthologs
PPM1D	8493	2	<ul style="list-style-type: none"> {Breast cancer}, 114480 (1) {?Breast cancer susceptibility}, 114480 (1) 	PPM1D Orthologs
BARD1	590	2	<ul style="list-style-type: none"> {Breast cancer}, 114480 (1) 	BARD1

Alliance of Genome Resources (AGR)

- Current members:

- Saccharomyces Genome Database (SGD)
- WormBase
- FlyBase
- Zebrafish Information Network (ZFIN)
- Rat Genome Database (RGD)
- Mouse Genome Informatics (MGI)
- Gene Ontology Consortium



- Mission: *“To develop and maintain sustainable genome information resources that facilitate the use of diverse model organisms in understanding the genetic and genomic basis of human biology, health and disease”*
- 1st public release due October 2017
 - Press release etc
 - Basic gene data, genome browser, GO annotations, disease associations
 - Prominent links from FlyBase pages to AGR

Outline

1. Recent additions to FlyBase
2. New features in FlyBase 2.0
3. Multi-species databases
4. **Further information/feedback**

Further information

FB2017_04, released Aug 22, 2017



A Database of *Drosophila* Genes & Genomes

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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](#) (FBf0234167)

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](#) (FBf0233766) (PMC5107610)

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- Citing FlyBase
- FlyBase Consortium
- FlyBase Publications
- FlyBase Support

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*

Using the Orthology search tool
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Acknowledgements & funding

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Richard Cripps
Maggie Werner-
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MARRVEL

- **Model organism Aggregated Resources for Rare Variant ExpLoration**
- *MARRVEL allows users to search multiple public variant databases simultaneously and provides a unified interface to facilitate the search process.*

MARRVEL 1.0

Human Search Model Organisms Search About FAQ Feedback

MARRVEL

Human Gene Symbol:

Human Variant (hg19):

Example: [6:99365567 T>C / FBXL4](#) or [6:99365567 T>C or FBXL4](#) or [NM_012160.3:c.541A>G](#)

Search

INPUT
Variant
Gene
FBXL4

DATABASES
OMIM

ExAC / Geno2MP

ClinVar

DGV

MODEL ORGANISMS
Predicted Orthologs

Protein Domain

Protein Alignment

Human Gene Description (OMIM)

F-BOX AND LEUCINE-RICH REPEAT PROTEIN 4; FBXL4

MIM number: 605654

Description: The F box, named after cyclin F (CCNF; 600227), in which it was originally observed, is an approximately 40-amino acid motif that binds SKP1 (601434). F-box proteins, such as FBXL4, are components of modular E3 ubiquitin protein ligases called SCFs (SKP1, cullin (see 603134), F-box proteins), which function in phosphorylation-dependent ubiquitination.

Gene-Phenotype Relationships

OMIM

Phenotype	Phenotype MIM number	Inheritance
Mitochondrial DNA depletion syndrome 13 (encephalomyopathic type)	615471	Autosomal recessive

Reported Alleles From OMIM

FBXL4

Phenotype	Mutation	dbSNP
MITOCHONDRIAL DNA DEPLETION SYNDROME 13 (ENCEPHALOMYOPATHIC TYPE)	FBXL4, GLN519TER	rs398123059
MITOCHONDRIAL DNA DEPLETION SYNDROME 13 (ENCEPHALOMYOPATHIC TYPE)	FBXL4, ARG435TER	rs201889294
MITOCHONDRIAL DNA DEPLETION SYNDROME 13 (ENCEPHALOMYOPATHIC TYPE)	FBXL4, GLY568ALA	rs398123060
MITOCHONDRIAL DNA DEPLETION SYNDROME 13 (ENCEPHALOMYOPATHIC TYPE)	FBXL4, ARG482TRP	rs398123061
MITOCHONDRIAL DNA DEPLETION SYNDROME 13 (ENCEPHALOMYOPATHIC TYPE)	FBXL4, ASP565GLY	rs398123062

Control Population Gene Summary (ExAC Gene Table)

FBXL4

Constraint from ExAC	Expected no. variants	Observed no. variants	ConstraintMetric
Synonymous	71.0	77	z=-0.44
Missense	177.4	204	z=-0.98
LoF	19.2	7	pLI=0.01
CNV	5.3	2	z=0.59

Geno2MP Total Heterozygote Count
FBXL4

236

Geno2MP Total Homozygote Count
FBXL4

4

Disease Population (Geno2MP Database)

FBXL4

Variant	rsID	HPO Profiles	# het	# hom
6:99322069 A>C	NA	1	1	0
6:99322094 C>A	rs148574319	1	2	0
6:99322149 T>C	rs142988015	2	2	0
6:99322261 G>T	NA	1	1	0
6:99323254 C>T	rs371545985	2	2	0
6:99323294 A>G	rs183776114	1	0	1
6:99323308 T>C	NA	1	1	0
6:99323350 TCA>T	NA	2	3	0

Benign
ClinVar

6

Likely Benign
ClinVar

0

Pathogenic
ClinVar

24

Likely Pathogenic
ClinVar

8

Risk Factor
ClinVar

0

Uncertain Significance
ClinVar

4

Conflicting Interpretations
ClinVar

0

Reported Alleles From ClinVar

FBXL4

MIST

- Molecular Interaction Search Tool
- *MIST is a comprehensive resource of molecular interactions for several species, including fly, mouse and human. You can mine known physical interactions and infer interactions using other supportive evidence.*



Human

[Drosophila \(*D. melanogaster*\)](#)

[Mouse](#)

[Rat](#)

[C. elegans](#)

[S. cerevisiae](#)

[S. pombe](#)

[Zebrafish \(*D. rerio*\)](#)

[X. laevis](#)

[X. tropicalis](#)

1. Select Search Type:

Protein List

Protein Pairs

Find Interactors

2. Enter Genes:

Copy/Paste : [Fill in example genes](#)

[See examples](#)

A1BG,BGN,BGLAP,MRE11

Upload from the file:

Browse...

No file selected.

3. Choose Networks to Search

[Help](#)

Protein-protein interactions.

Filter By Rank

• Filter By Rank **Filter out Low Rank Results**

Other Filtering Options

Interologs: protein-protein interactions from other species

Filter By Rank

• Filter By Rank **Filter out Low Rank Results**

Other Filtering Options

Genetic interactions

Filter By Rank

• Filter By Rank **Filter out Low Rank Results**

Other Filtering Options

Interologs: genetic interactions from other species

Filter By Rank

• Filter By Rank **Filter out Low Rank Results**

Other Filtering Options

4. Submit Search

Submit