

FlyBase



@FlyBaseDotOrg



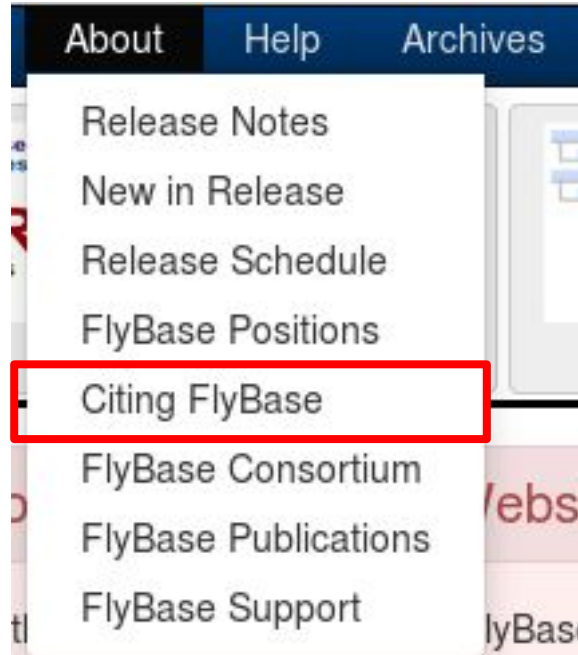
FlyBase TV

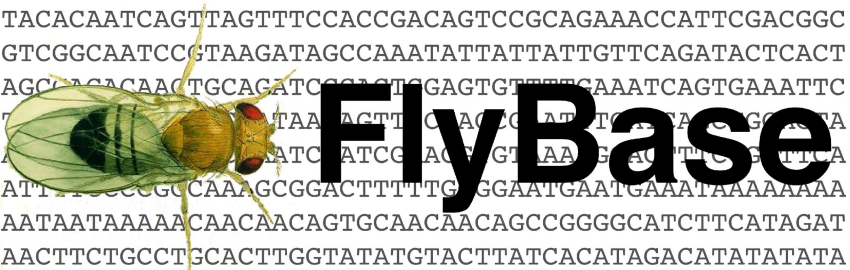


alliancegenome.org

Thank you for your support.

How to Help FlyBase





FlyBase 2018: New look, new features

Josh Goodman, FlyBase
ADRC 2018



Annual Drosophila
Research Conference

Overview

- Jump to Gene
- HitLists
- Reports
 - Summaries
 - Ribbons
 - Domains
 - References
- Human Disease
- GAL4
- Orthologs
- Sequence Downloader

FlyBase 2.0



FB2018_02, released Apr 3, 2018

A Database of *Drosophila* Genes & Genomes

Home Tools Downloads Links Community Species About Help Archives

J2G Jump to Gene Go

BLAST

GBrowse

Resources

RNA-Seq

Vocabularies

ImageBrowse

Batch Download

FlyBase 2.0: It's here!

FLYBASE 2.0
IT'S HERE!



FAST-TRACK
YOUR PAPER



FLYBASE
NEWS



FLY BOARD



COMMUNITY
NEWS



MEETINGS
COURSES



FLYBOOK

QuickSearch

Human Disease GAL4 etc Expression Phenotype References

Search FlyBase Orthologs Protein Domains Gene Groups GO Data Class

Enter text:

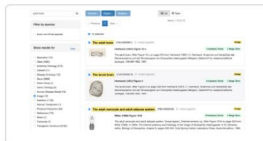
Search



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

Commentary

commentary archive



FlyBase 2.0 Dec 31, 2017.

With the final release of 2017, "FlyBase 2.0" becomes the main FlyBase website. This major rework of the FlyBase website comes with new features, new tools, and improved mobile device browsing and stability. The look and feel of the site has also been updated, but should still look familiar to long-time users. Here's a [video teaser](#), showing some of the new features. ([More](#))

Jump to Gene



Navigation



General Information			
Symbol	Dmel\Fne	Species	<i>D. melanogaster</i>
Name	found in neurons	Annotation Symbol	CG4396
Feature Type	protein_coding_gene	FlyBase ID	FBgn0086675
Gene Model Status	Current	Stock Availability	publicly available
Gene Snapshot	Found in neurons (Fne) is an RNA binding protein that works as a post-transcriptional regulator. It is present in the cytoplasm of all neurons. Lack of Fne produces fusion of the mushroom body β -lobes and altered male courtship behaviour. [Date last reviewed: 2016-09-01]		
Other Summaries	Auto summary		
Comparative Info	Integrated model organism details available at the ALLIANCE of GENOME RESOURCES		
Genomic Location			
Cytogenetic map	11D3-11D4	Sequence location	X:12,917,477..12,950,417 [-]
Recombination map			
Genomic Maps	GBrowse JBrowse		
		A genomic map showing gene spans (e.g., hspL49CR4525, Bra1, CR4525, Fne, CG4645) and features (e.g., hnc, CG3264) on a chromosome. The Fne gene is highlighted with a yellow arrow.	Gene region Get Sequence



Search



adult brain Items 1-12 of 12

Filter by species

show non-Dmel species

Show results for

- Aberration (15)
- Allele (4354)
- Anatomy Ontology (575)
- Dataset (17)
- Disease Ontology (12)
- Gene (2839)
- Gene Group (1)
- Gene Ontology (6)
- Human Disease Model (73)
- Image (12)
- Insertion (1190)
- Natural Transposon (1)
- Physical Interaction (25)
- Reference (170)
- Strain (1)
- Transcript (7)
- Transgenic Construct (2162)

The adult brain (FBim0000861) *D. melanogaster* [4 Anatomy Terms](#) [1 Stage Term](#)

Hertwick (1931) Figure 10 c

The adult brain. After Figure 10 c on page 572 from Hertwick (1931). H. Hertwick. Anatomie und Variabilität des Nervensystems und der Sinnesorgane von *Drosophila melanogaster* (Meigen). Zeitschrift für wissenschaftliche Zoologie, 139:560–663, 1931.

The larval brain (FBim0000870) *D. melanogaster* [6 Anatomy Terms](#) [1 Stage Term](#)

Hertwick (1931) Figure 4

The larval brain. After Figure 4 on page 568 from Hertwick (1931). H. Hertwick. Anatomie und Variabilität des Nervensystems und der Sinnesorgane von *Drosophila melanogaster* (Meigen). Zeitschrift für wissenschaftliche Zoologie, 139:560–663, 1931.

The adult oenocyte and adult adipose system (FBim0000049) *D. melanogaster* [18 Anatomy Terms](#) [1 Stage Term](#)

Miller (1950) Figure 16 B

The adult oenocyte and adult adipose system. Dorsal aspect. Oriented anterior up. After Figure 16 B on page 453 from Miller (1950). A. Miller. The internal anatomy and histology of the imago of *Drosophila melanogaster*. In M. Demerec, editor, *Biology of Drosophila*, chapter 6, pages 420-534. Cold Spring Harbor Laboratory Press, facsimile edition, 1994.

HitLists

18w

Filter by species

show non-Dmel species

Show results for

[clear](#)

- Aberration (3)
- Allele (69)
- Clone (18)
- Dataset (161)
- Gene (11)
- Insertion (13)
- Physical Interaction (3)
- Polypeptide (1)
- Reference (180)
- Sequence Feature (16)
- Stock (5)
- Transcript (1)
- Transgenic Construct (25)

[show empty](#)

[Convert](#) [Export](#) [Analyze](#)

View As

[List](#) [Table](#)

[← Previous](#) [1](#) [2](#) [3](#) [...](#) [11](#) [Next →](#)

Items 1-50 of 506

506 selected

18w  18 wheeler (CG8896, FBgn0004364) *D. melanogaster* [GBrowse](#) [JBrowse](#) **Gene**

Feature type: protein coding gene

Gene model status: Current

Sequence Location: 2R:20,111,511..20,116,932 [+]

Cytogenetic Map: 56F8-56F8

[27 Alleles](#)

[12 Stocks](#)

[1 Transcript](#)

[1 Polypeptide](#)

[159 References](#)

Gene Snapshot [▶](#)

BDSC:4372  (FBst0004372) *D. melanogaster* [Stock Center 4372](#) **Stock**

Genotype: $y^1 w^+$; 18w^{Δ7-35}/CyO

Collection: Bloomington Drosophila Stock Center

Kyoto:107712  (FBst0306360) *D. melanogaster* [Stock Center 107712](#) **Stock**

Genotype: $y^1 w^+$; 18w^{Δ7-35}/CyO

Collection: Kyoto Stock Center

18w⁰⁰⁰⁵³ (FBa0007942) *D. melanogaster* **Allele**

Allele class: hypomorphic allele - genetic evidence

Known lesion? yes

Mutagen: P-element activity

Associated insertion: P{PZ}18w⁰⁰⁰⁵³

1 Phenotype (Class) statement

[0 Stocks](#)

[6 References](#)

HitLists - Data Class

Show results for

Aberration (3)

Allele (69)

Clone (18)

Dataset (161)

Gene (11)

69 selected

18w⁰⁰⁰⁵³ (FBal0007942) *D. melanogaster* Allele

Allele class: [hypomorphic allele - genetic evidence](#)

Mutagen: P-element activity

Known lesion? yes

Associated insertion: [P{PZ}18w⁰⁰⁰⁵³](#)

1 Phenotype (Class) statement

0 Stocks 6 References

18w^{k02701} (FBal0065575) *D. melanogaster* Allele

Mutagen: P-element activity

Known lesion? no

Associated insertion: [P\[lacW\]18w^{k02701}](#)

4 Phenotype (Class) statements

2 Stocks 5 References

HitLists - Views

[Convert ▾](#) [Export ▾](#) [Analyze ▾](#)

View As

[List](#) [Table](#)

[← Previous](#) **1** [2](#) [Next →](#)

Items 1-50 of 69

Per page: 50 ▾



Allele Results						
<input checked="" type="checkbox"/>	Symbol ▾	Class ▾	Inserted Elements	# Stocks ▾	Mutagens	Known Lesion? ▾
<input checked="" type="checkbox"/>	18w ⁰⁰⁰⁵³	hypomorphic allele - genetic evidence	P{PZ}18w ⁰⁰⁰⁵³	0	P-element activity	yes
<input checked="" type="checkbox"/>	18w ^{k02701}		P{lacW}18w ^{k02701}	2	P-element activity	no
<input checked="" type="checkbox"/>	18w ^{unspecified}			0		no
<input checked="" type="checkbox"/>	18w ^{GD17}			3	in vitro construct	yes
<input checked="" type="checkbox"/>	18w ^{GD2513}			2	in vitro construct	yes
<input checked="" type="checkbox"/>	18w ^{GD14418}			1	in vitro construct	yes

HitLists - Convert, Export, and Analyze

View As
List Table

Items 1-50 of 69

← Previous 1 2 Next →

Convert Export

selected items to:

- Genes
- Transgenic Constructs
- Insertions
- Aberrations
- Balancers
- References
- Stocks
- Sequence Features

Export Analyze

selected items to a FlyBase tool:

- Batch Download
- QueryBuilder
- FeatureMapper

selected items as a file:

- ID list (download)
- FlyBase records crossreferencing table

Analyze

For the selected records, analyze frequencies of values of








- Phenotypic Class
- Anatomy Terms
- Mutagen

For the selected records, browse interactions


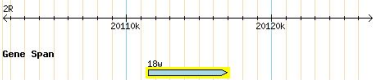
- Enhancement
- Enhancement + Suppression
- Suppression

HitLists - Convert, Export, and Analyze

Dataset: FBal Field: CV: phenotypic class

#	Most frequent CV Terms (out of 46461)		Related records
1	lethal		33
2	[empty field - no data available]		15
3	neuroanatomy defective		14
4	partially lethal - majority die		11
5	visible		10
6	viable		8
7	increased cell death		8

Reports


General Information			
Symbol	Dmel18w	Species	<i>D. melanogaster</i>
Name	18 wheeler	Annotation Symbol	CG8896
Feature Type	protein_coding_gene	FlyBase ID	FBgn0004364
Gene Model Status	Current	Stock Availability	12 publicly available
Gene Snapshot	18 wheeler (18w) encodes a member of the Toll-like receptor family. The 18w-encoded protein contributes to multiple processes including ovarian follicle cell migration, antibacterial humoral response and ventral cord development. A role in convergent extension during early embryogenesis is suggested by the genetic interaction of 18w with Toll-6 and Tollo. [Date last reviewed: 2018-01-25]		
Other Summaries	Auto summary Interactive Fly		
Also Known As	Toll-2		
Comparative Info	Integrated model organism details available at the  ALLIANCE of GENOME RESOURCES		
Genomic Location			
Cytogenetic map	56F8-56F8	Sequence location	2R:20,111,511..20,116,932 [+]
Recombination map	2-90		
Sequence	<div style="display: flex; justify-content: space-between;"> <div> <input type="text" value="Gene region"/> </div> <div> Decorated FASTA Get genome region </div> </div> <div style="margin-top: 10px;"> <input type="button" value="Get Sequence"/> </div>		
Genomic Maps			
Other Genome Views	<p>The following external sites may use different assemblies or annotations than FlyBase.</p> <div style="display: flex; justify-content: space-around;"> <div> NCBI Genome Data Viewer </div> <div> UCSC Genome Browser </div> </div> <div style="display: flex; justify-content: space-around; margin-top: 10px;"> <div> Ensembl Genome Browser </div> <div> PopFly Genome Browser </div> </div>		
GO Summary Ribbons			

General Information	
Symbol	Dmel18w
Species	<i>D. melanogaster</i>
Name	18 wheeler
Annotation Symbol	CG8896
Feature Type	protein_coding_gene
FlyBase ID	FBgn0004364
Gene Model Status	Current
Stock Availability	12 publicly available
Gene Snapshot	18 wheeler (18w) encodes a member of the Toll-like receptor family. The 18w-encoded protein contributes to multiple processes including ovarian follicle cell migration, antibacterial humoral response and ventral cord development. A role in convergent extension during early embryogenesis is suggested by the genetic interaction of 18w with Toll-6 and Tollo. [Date last reviewed: 2018-01-25]
Other Summaries	Auto summary Interactive Fly
Also Known As	Toll-2

Report Sections

- [General Information](#)
- [Overview](#)
- [Disease Summary](#)
- [Related Diseases](#)
- [Ortholog Information](#)
- [Dmel Gene Information](#)
- [Synthetic Gene\(s\) Used](#)
- [Experimental Findings](#)
- [Summary of Physical Interactions](#)
- [Alleles Reported to Model Human Disease](#)
- [Genetic Tools, Stocks and Reagents](#)
- [References](#)

Reports - General Information

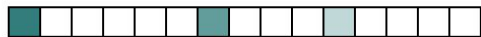
General Information					
Symbol	Dmel\Khc	Species	<i>D. melanogaster</i>		
Name	Kinesin heavy chain	Annotation Symbol	CG7765		
Feature Type	protein_coding_gene	FlyBase ID	FBgn0001308		
Gene Model Status	Current	Stock Availability	19 publicly available		
Gene Snapshot	Kinesin heavy chain (Khc) is the force generating subunit of kinesin-1, a microtubule motor protein. Khc functions in the long-distance transport of cytoplasmic "cargoes" such as mRNAs, protein complexes, and organelles. [Date last reviewed: 2016-06-09]				
Other Summaries	Auto summary	Gene Group	UniProt	Red Book	Interactive Fly
Also Known As	KIN, kinesin, DmKHC, DKH, kinesin-1				
Comparative Info	Integrated model organism details available at the				

Reports - GO Ribbons

GO Summary Ribbons

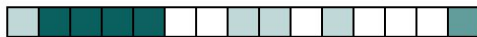
[\[Detailed GO annotations\]](#)

enzyme
regulator
receptor
receptor binding
transporter
structural molecule
cytoskeletal binding
DNA binding
RNA binding
transcription factor
small molecule binding
metal ion binding
lipid binding
carbohydrate binding
other molecular_function



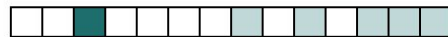
molecular function

cell cycle/proliferation
cellular organization/biogenesis
cellular transport/localization
development
reproduction
immune system
nervous system
behavior
response to stimulus
signaling
gene expression
protein metabolism
DNA metabolism
small molecule metabolism
other biological_process



biological process

extracellular region
cytosol
cytoskeleton
mitochondrion
nucleus
chromosome
membrane
cell periphery
cell junction
cell projection
endomembrane system
neuron/synapse
macromolecular complex
other cellular_component

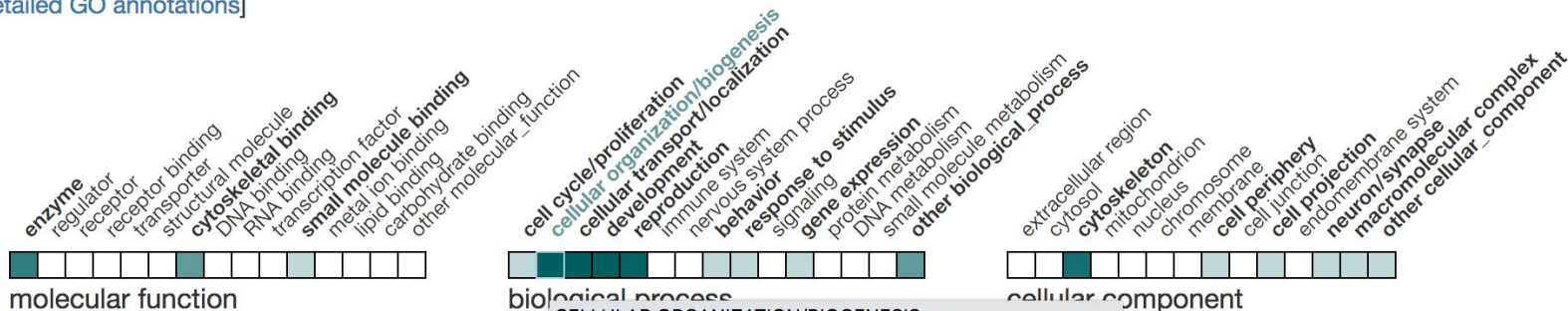


cellular component

Reports - GO Ribbons

GO Summary Ribbons

[Detailed GO annotations]



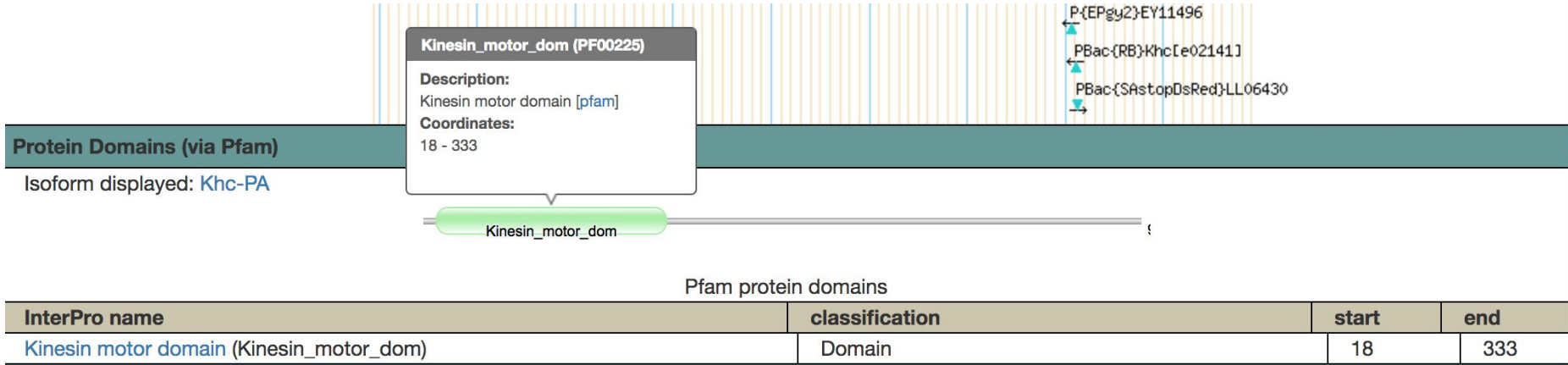
Families, Domains and Molecular Function

Gene Group Membership (FlyBase)	KINESINS
Protein Family (UniProt, Sequence Similarities)	Belongs to
Protein Domains/Motifs	InterPro Kinesin mo Kinesin-like
Molecular Function (see GO section for details)	Experimen

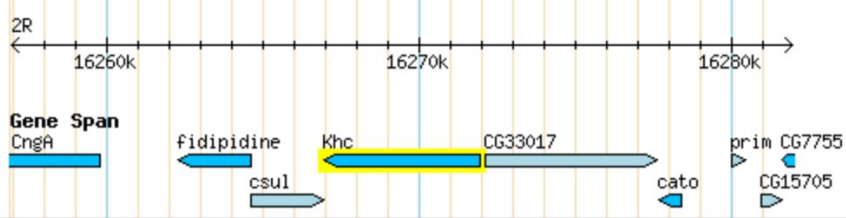
- CELLULAR ORGANIZATION/BIOGENESIS:**
- actin filament bundle organization
 - axon guidance
 - axonogenesis
 - centrosome separation
 - dendrite morphogenesis
 - dorsal appendage formation
 - heterochromatin organization involved in chromatin silencing
 - intracellular distribution of mitochondria
 - microtubule polymerization
 - mitochondrion distribution
 - oocyte microtubule cytoskeleton polarization
 - pole plasm assembly
 - pole plasm oskar mRNA localization
 - regulation of pole plasm oskar mRNA localization
 - stress granule disassembly

	y. Kinesin family. Kinesin subfamily. (P17210)
	loop containing nucleoside triphosphate hydrolase;

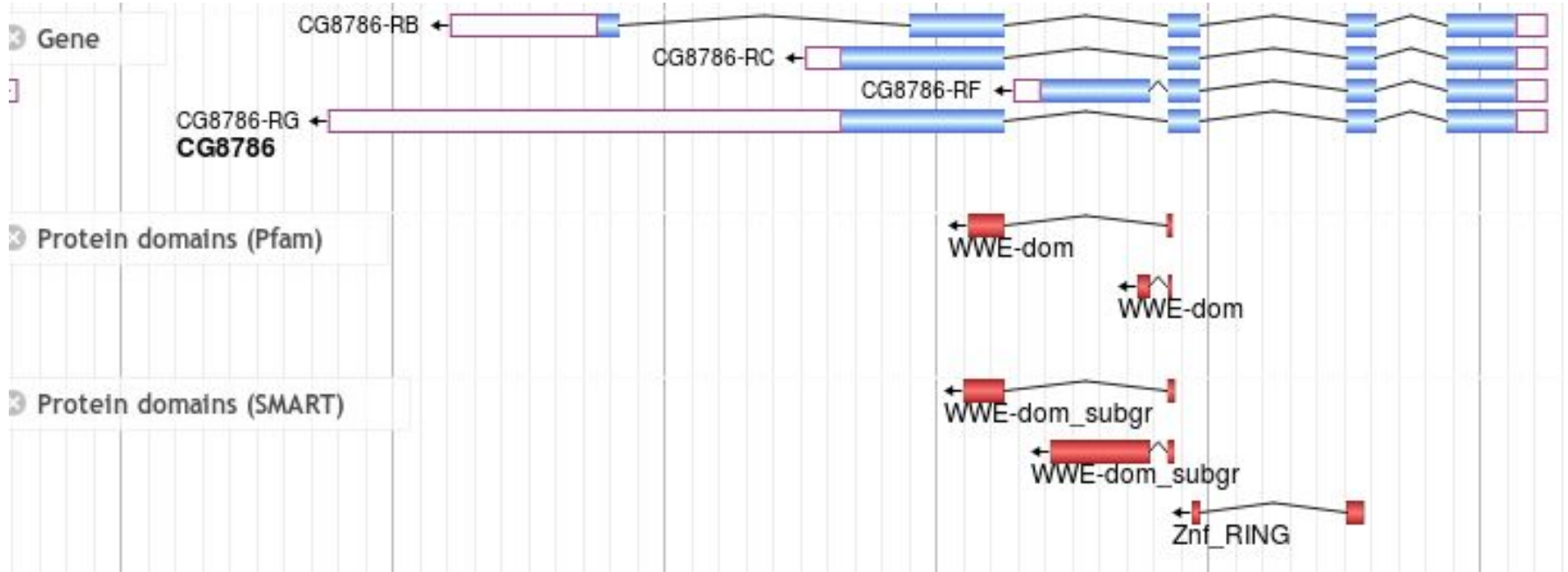
Reports - Protein Domains



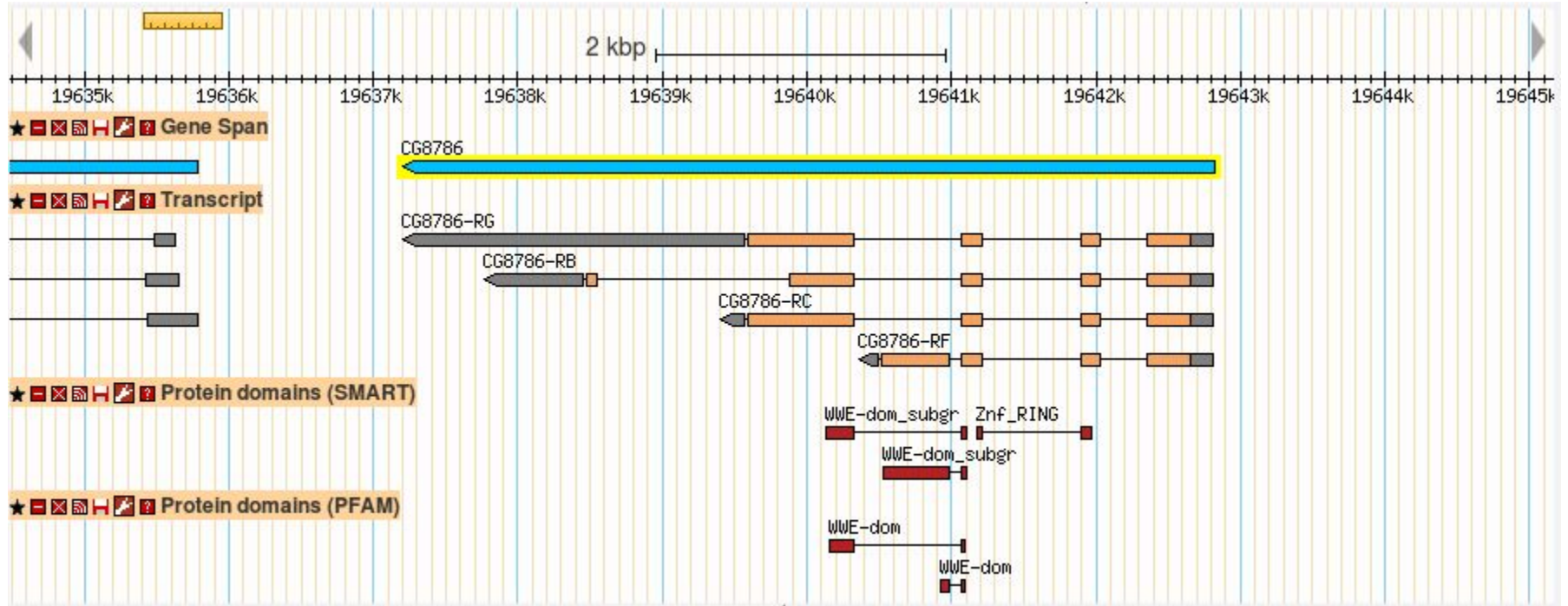
Reports - Protein Domains

Genomic Location			
Cytogenetic map	53A3-53A4	Sequence location	2R:16,266,960..16,271,971 [-]
Recombination map	2-79		
Sequence	<p>Gene region <input type="text" value="Gene region"/></p> <p>Decorated FASTA</p> <p>Get Sequence <input type="text" value="Get Sequence"/></p> <p>Get genome region <input type="text" value="Get genome region"/></p>		
Genomic Maps	<p>GBrowse JBrowse</p>  <p>2R ← 16260k 16270k 16280k →</p> <p>Gene Span CngA</p> <p>fidipidine</p> <p>csul</p> <p>Khc</p> <p>CG33017</p> <p>cato</p> <p>prim CG7755</p> <p>CG15705</p>		
Other Genome Views	<p>The following external sites may use different assemblies or annotations than FlyBase.</p> <p>NCBI Genome Data Viewer</p> <p>UCSC Genome Browser</p> <p>Ensembl Genome Browser</p> <p>PopFly Genome Browser</p>		

JBrowse - Protein Domains



GBrowse - Protein Domains



References

References (2,623)

Publication Types

Representative publications **25**

All publications **2623**

Research paper **1258**

Supplementary material **14**

Review **649**

Erratum **1**

Personal communication to FlyBase

28



- HitList
- Batch Download
- Citation Manager (RIS)

Filter

2015, Smith, cell, etc.



Sort by

Default order



(2): 296--306

Collagen Enhances BMP Signaling to Guide Renal Tubule Morphogenesis in

Teleman and Cohen, 2000, Cell 103(6): 971--980

Dpp gradient formation in the Drosophila wing imaginal disc. [[FBrf0132263](#)]

Deshpande et al., 2014, PLoS ONE 9(2): e88847

BMP Signaling and the Maintenance of Primordial Germ Cell Identity in Drosophila Embryos. [[FBrf0224203](#)]

Frandsen et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105(39): 14952--14957

Salmonella pathogenesis reveals that BMP signaling regulates blood cell homeostasis and immune responses in Drosophila. [[FBrf0205983](#)]

QuickSearch

QuickSearch

[Human Disease](#)

[GAL4 etc](#)

[Expression](#)

[Phenotype](#)

[References](#)

[Search FlyBase](#)

[Orthologs](#)

[Protein Domains](#)

[Gene Groups](#)

[GO](#)

[Data Class](#)

Enter text:



Human Disease

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

Enter text:

Alternatively, [browse](#) all Human Disease Model reports



Note: [Wild ca](#)

Human Disease

Arl6IP1 ADP-ribosylation factor-like 6 interacting protein 1 (CG10326, FBgn0038453) *D. melanogaster* Gene

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

Feature type: protein coding gene **Gene model status:** Current
Sequence Location: 3R:16,643,605..16,645,171 [+]

Cytogenetic Map: 89D6-89D6

[7 Alleles](#) [8 Stocks](#) [2 Transcripts](#) [2 Polypeptides](#) [30 References](#)

spastic paraplegia (FBhh0000032) Human Disease Model

Associated DO term: hereditary spastic paraplegia **Associated OMIM term:**
Human Genes implicated (HGNC): *D. melanogaster* Orthologs:

[11 Subtypes](#) [0 Related Disease Reports](#) [8 References](#)

spas^{5.75} (FBal0177736) *D. melanogaster* Allele

Allele class: [amorphic allele - molecular evidence](#)

Mutagen: Delta2-3 transposase **Known lesion?** yes

No associated insertions or constructs

24 Phenotype (Class) statements, **20** Phenotype (Anatomy) statements, and **1** Disease Model annotation

[0 Stocks](#) [15 References](#)

tropical spastic paraparesis (DOID:321) Disease Ontology

A viral infectious disease that results_in inflammation located_in spinal cord, has_material_basis_in Human T-lymphotropic virus 1, which is transmitted_by sexual contact, and transmitted_by breast feeding. The infection has_symptom spastic weakness of both legs, has_symptom muscle stiffness, has_symptom sensory disturbance, and has_symptom spasms.

GAL4 Search

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

Search

Driver/Reporter:

GAL4 binary driver

Output format:

integrated table

refine search by adding qualifier terms

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

Frequently Used GAL4 Drivers [table](#)

Frequently Used GAL4 Drivers

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

Driver/Reporter:

GAL4 binary driver

Output form

refine search by adding qualifier terms

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

Frequently Used GAL4 Drivers [table](#)

Frequently Used GAL4 Drivers

Export TSV

Allele ▼▲	Insertions / Constructs	Assoc. gene ▼▲	Common terms ▼▲	Major tissue ▼▲	Major stage ▼▲	Description	# Stocks ▼▲	# Refs ▼▲
Scer\GAL4 ^{Bx-MS1096}	P{GawB}Bx ^{MS1096} P{GawB}	Bx		wing disc dorsal compartment	larval stage	Drives expression in the dorsal wing pouch.	6	416
Scer\GAL4 ^{C-765}	P{GawB}C-765 P{GawB}		leg disc	ventral thoracic disc wing disc	larval stage	Drives expression in leg and wing discs.	1	140
Scer\GAL4 ^{C164}	P{GawB}C164 P{GawB}			motor neuron	larval stage adult stage	Drives expression in motor neurons.	1	29
Scer\GAL4 ^{C57}	P{GawB}C57 P{GawB}		body wall muscle	embryonic/larval hypodermal muscle somatic muscle	larval stage	Drives expression in larval body wall muscles.	2	91

Orthologs

Input:

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

Species:

D. melanogaster ▾

Gene(s):

e.g. Cdk1, CG5363, FBgn0004106, 34411

Output:

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

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:

instead [search Drosophila species, insects etc.](#)

Orthologs

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

Search Term: **Cdk1** Species: *Drosophila melanogaster* (Fruit fly) Gene: **Cdk1** 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)									
CDK1	NCBI Ensembl OMIM HGNC	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, OrthoDB, Panther, Phylome, RoundUp, TreeFam			(+)	
CDK2	NCBI Ensembl OMIM HGNC	4 of 11	No	No (+)	eggNOG, OrthoDB, orthoMCL, RoundUp			(+)	
CDK5	NCBI Ensembl OMIM HGNC	4 of 11	No	No (+)	eggNOG, OrthoDB, orthoMCL, RoundUp			(+)	Yes
CDK14	NCBI Ensembl OMIM HGNC	2 of 11	No	No (+)	eggNOG, OrthoDB			(+)	
CDK15	NCBI OMIM HGNC	2 of 11	No	No (+)	eggNOG, OrthoDB			(+)	
CDK16	NCBI Ensembl OMIM HGNC	2 of 11	No	No (+)	eggNOG, OrthoDB			(+)	
CDK18	NCBI Ensembl OMIM HGNC	2 of 11	No	Yes (+)	eggNOG, OrthoDB			(+)	

Orthologs

Input:

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

Species:

D. melanogaster ▾

Gene(s):

e.g. Cdk1, CG5363, FBgn0004106, 34411

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:

instead [search human and model organisms](#)

Sequence Downloader

Genomic Location			
Cytogenetic map	53A3-53A4	Sequence location	2R:16,266,960..16,271,971 [-]
Recombination map	2-79		
Sequence	<input type="text" value="Gene region"/>		Decorated FASTA
	<input type="button" value="Get Sequence"/>		<input type="button" value="Get genome region"/>

- Tools
- Downloads
- Links
- Community
- Spe

- Tools Overview
- Query Tools and Portals
- Genomic/Map Tools
 - BLAST
 - GBrowse
 - JBrowse
 - CytoSearch
 - Feature Mapper
 - RNA-Seq By Region
 - Chromosome Maps
 - Coordinates Converter
 - Sequence Downloader
- RNA-Seq
- Retrieve/Convert Tools
- Data Submission
- People

ummaries

own As

Sequence Downloader

[Help](#)

FlyBase Sequence Downloader

Mode

ID

FlyBase ID

FBgn0001308

Type

Gene Region

[View Sequence](#)

Sequence Downloader

ID: FBgn0000490
Symbol: dpp
Type: gene
Location: 2L:2428372..2459823
Length: 31452
Selected relative region: 71-463
Selected genomic region: 2L:2428442..2428834
of matches: 0

Search in sequence.. (Regex support)



```
1 ATTCAGTTTT TTGCGCTCAA CGCTCGTTGT ACGGAACCGA AAAACGCGTT CGTTCGTCCA
61 CAGAGTGTGC CCAAATCGAG GCGAAAGATC GCTGGTTACA ACCGAATATA CAGCCTCTAA
121 TCACTTTTTT TCTGCTCTGT AATCGTTCGC GTTTCTGCG GCCATAAAAT AAAGTAAATC
181 CGAGTTAAAC GCTGATAGTC GCGCCTGAAG AACCACAGAA AAAACAGAAA ATATCTCCCG
241 TCGTTTCTCG TTCTCGTTTC CGCGATCGCT CGTCAGCCAG CCAAAGCCTC TCCGATTTTT
301 GATACCGATT CCGTATCAGA TAATATATTC GTAACCATCG CCATTCTTGC GAGTGTGCCA
361 GTGTGAGTGA GTGATGTGTC TGTGTGCCAA ATCCAAATCG AAAATAGCCA AAGTCTGAGC
421 TTGGCCACCA TCGTCAGCAG CAAACATGTG AAGTGCCAGT GATTTCCATA AGCCAAAATC
481 GAAGTCGAAG TCGAATCGAA TCGAATCGAA GCCACAGCGA GATAGATAGG TCGAAAGTAT
541 TTGAGTGGAT ATCCGAGTCG AACCAGTGTA TAATGTATGC GACGTTTCGCG AACTGCCAGA
```


Sequence Downloader

ID: [FBpp0303224](#)

Symbol: Zif-PC

Parent features: [FBgn0037446](#), [FBtr0330191](#)

Type: protein

Location: 3R:join(6457287..6457430,6457493..6458109,6458167..6458301,6458403..6458673)

Length: 388

Selected relative region: 251-252

of matches: 2



```
1 MRVELTPQTC RVCLAQSERL QRLDEIREEG EESPNEMLIQ LLEVSYSNLN DREHIPDGIC
61 KSKVELNMA YQFREKALRK QMEIEEYCRE LGLLDES DVM MIKEEDGSQQ QCDEEMYILE
121 ETTTGEHHQ EEKGHEEYLE VDTSDQECI GDTIEYLEFN YTIEMNSDQT EIVLESEKQY
181 EETPSQQLAL QEAAKASLKA RRGRVRRGLN SLTSDGTEK GGYICDVCGN FYEKRRMME
241 HRRRHGICQ YACELCDAKF YRFQLRRHM YSHTGSKPYK CSFCSRQFFY ESVLKSHENV
301 HRGIKPYVCK VCDKAFYAH SLTKHELIHS DIKLYRCDYC NKDFRLLHHM RQHEETKLHQ
361 NAVMLAESMK VEMVAEQGGG NEIRIQAH
```

Acknowledgements

- Dr. Thom Kaufman
- Dr. Brian Calvi
- Victor Strelets
- Jim Thurmond
- FlyBase Consortium



Dr. Kathleen Matthews