

# New Features in FlyBase:

## FlyBase 2.0 (beta)



# A Database of *Drosophila* Genes & Genomes

Home Tools Downloads Links Community Species About Help Archives

**BLAST**

**GBrowse**

Antibodies  
Databases  
Interactions  
**CRISPR**  
Bioinformatics  
Orthologs  
cDNAs  
Stocks  
**RNAi**

**Resources**

**RNA-Seq**

GO  
**PHENOTYPE**  
**ANATOMY**  
**DISEASE**  
MORE

**Vocabularies**

**ImageBrowse**

FIELD DATA  
XML  
sequence

**Batch Download**

**FAST-TRACK YOUR PAPER**

**FLYBASE NEWS**

**FLY BOARD**

**COMMUNITY NEWS**

**MEETINGS**

**COURSES**

Resources for:

**PUBLIC, TEACHERS, STUDENTS**

**BIOMEDICAL RESEARCH**

Multi-species mining:

**MARRVEL**

**G2F**  
Gene2Function

## QuickSearch

Human Disease Expression GO Phenotype References  
Simple Orthologs Protein Domains Gene Groups 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](http://beta.flybase.org)... (More)



# A Database of *Drosophila* Genes & Genomes

**D.melanogaster**  
**D.virilidis**  
**A.mellifera**

BLAST

GBrowse

Databases  
Interactions  
Antibodies  
RNAi  
CRISPR  
Bioinformatics  
Orthologs  
cDNAs  
Stocks

Resources

RNA-Seq

GO  
PHENOTYPE  
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DISEASE  
MORE

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NEWS

FLY BOARD

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### Resources for:

PUBLIC TEACHERS  
STUDENTS

BIOMEDICAL  
RESEARCH

### Multi-species mining:

MARRVEL

G2F  
Gene2Function

## QuickSearch

Human Disease Expression Phenotype GO References

Simple Orthologs Protein Domains Gene Groups Data Class

Enter text:

Search

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

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[beta.flybase.org](http://beta.flybase.org) ... (More)

# Disclaimer!

*If you see some missing data on the new site, don't worry. We are actively working on importing all existing data and do not anticipate dropping anything at this time.*

# New features include:

- **New/Improved tools**
  - New hit-list management
  - Sequence Downloader
  - Revised Jump-to-Gene/Search box
- **Enhanced Gene Reports**
  - Navigation panel
  - GO summary ribbons
  - Protein domain graphics
  - Reference filtering
- **Mobile device friendly**

# New hit-lists

## QuickSearch

[Human Disease](#)

[Expression](#)

[Phenotype](#)

[GO](#)

[References](#)

[Simple](#)

[Orthologs](#)

[Protein Domains](#)

[Gene Groups](#)

[Data Class](#)

**Enter text:**

Search

Cdk1

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

# New hit-lists

Cdk1  analysis tools here View As

1-50 of 485

← Previous **1** 2 3 ... 10 → Next

**Show results for**

- 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)

**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 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)

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

**Stumpff et al. (2004)** (FBF0183813)

**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 485

← Previous **1** 2 3 ... 10 → Next

**Show results for** clear

- Aberration (12)
- Allele (135)
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- Transgenic Construct (51)

[show empty](#)

**Cdk1** Cyclin-dependent kinase 1 (CG5363, FBgn0004106)   **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)** (FBF0183813) **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

Cdk1  analysis tools here View As

1-50 of 485

← Previous **1** 2 3 ... 10 → Next

**Show results for**

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**44 Alleles**

**Gene model status:** Current  
**Cytogenetic Map:** 31D11-31D11

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# New hit-lists

View As

List

Table

1-44 of 44

Modify your query



analysis tools here

Show results for

clear

Allele (44)

show empty

← Previous **1** → Next

- Cdk1<sup>216A</sup>** (FBal0001571) Allele
- Allele class:** [hypomorphic allele - genetic evidence](#)  
**Mutagen:** ethyl methanesulfonate  
**Associated insertions:**  
# Phenotype (class) statements: 3  
# Disease model annotations: 0  
[0 Stocks](#) [3 References](#)
- Known lesion?** yes  
**Carried in construct:**  
# Phenotype (anatomy) statements: 1
- Cdk1<sup>D57</sup>** (FBal0001572) Allele
- Allele class:** [amorphic allele - genetic evidence](#)  
**Mutagen:** ethyl methanesulfonate  
**Associated insertions:**  
# Phenotype (class) statements: 3  
# Disease model annotations: 0  
[0 Stocks](#) [4 References](#)
- Known lesion?** yes  
**Carried in construct:**  
# Phenotype (anatomy) statements: 1
- Cdk1<sup>E1-23</sup>** (FBal0001573) Allele
- Allele class:** [amorphic allele - genetic evidence](#)  
**Mutagen:** ethyl methanesulfonate  
**Associated insertions:**  
# Phenotype (class) statements: 3  
# Disease model annotations: 0  
[1 Stock](#) [10 References](#)
- Known lesion?** yes  
**Carried in construct:**  
# Phenotype (anatomy) statements: 3

# New hit-lists

View As

List

Table

1-44 of 44

Modify your query



analysis tools here

Show results for

clear

Allele (44)

show empty

← Previous 1 → Next

<input type="checkbox"/>	Symbol	Class	Inserted Elements	# Stocks	Mutagens
<input type="checkbox"/>	Cdk1 <sup>216A</sup>	hypomorphic allele - genetic evidence		0	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>D57</sup>	amorphic allele - genetic evidence		0	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>E1-23</sup>	amorphic allele - genetic evidence		1	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>E1-24</sup>	heat sensitive loss of function allele		1	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>E1-9</sup>	amorphic allele - genetic evidence		0	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>216P</sup>	hypomorphic allele - genetic evidence	P{ $\lambda$ Cdk1 <sup>216P</sup>	0	PM hybrid dysgenesis; P-element activity
<input type="checkbox"/>	Cdk1 <sup>B47</sup>	amorphic allele - genetic evidence loss of function allele		1	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>E10</sup>	amorphic allele - genetic evidence		0	ethyl methanesulfonate
<input type="checkbox"/>	Cdk1 <sup>hs.PS</sup>			0	in vitro construct
<input type="checkbox"/>	Cdk1 <sup>+15.8</sup>			0	in vitro construct
<input type="checkbox"/>	Cdk1 <sup>A171T</sup>			0	in vitro construct
<input type="checkbox"/>	Cdk1 <sup>P131S</sup>			0	in vitro construct
<input type="checkbox"/>	Cdk1 <sup>G43E</sup>			0	in vitro construct

# 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	53 publicly available
Also Known As	DER, top, flb, Efp, dEGFR, EGF-R, Efp-B1, top/DER, torpedo/egfr, Efp-1		

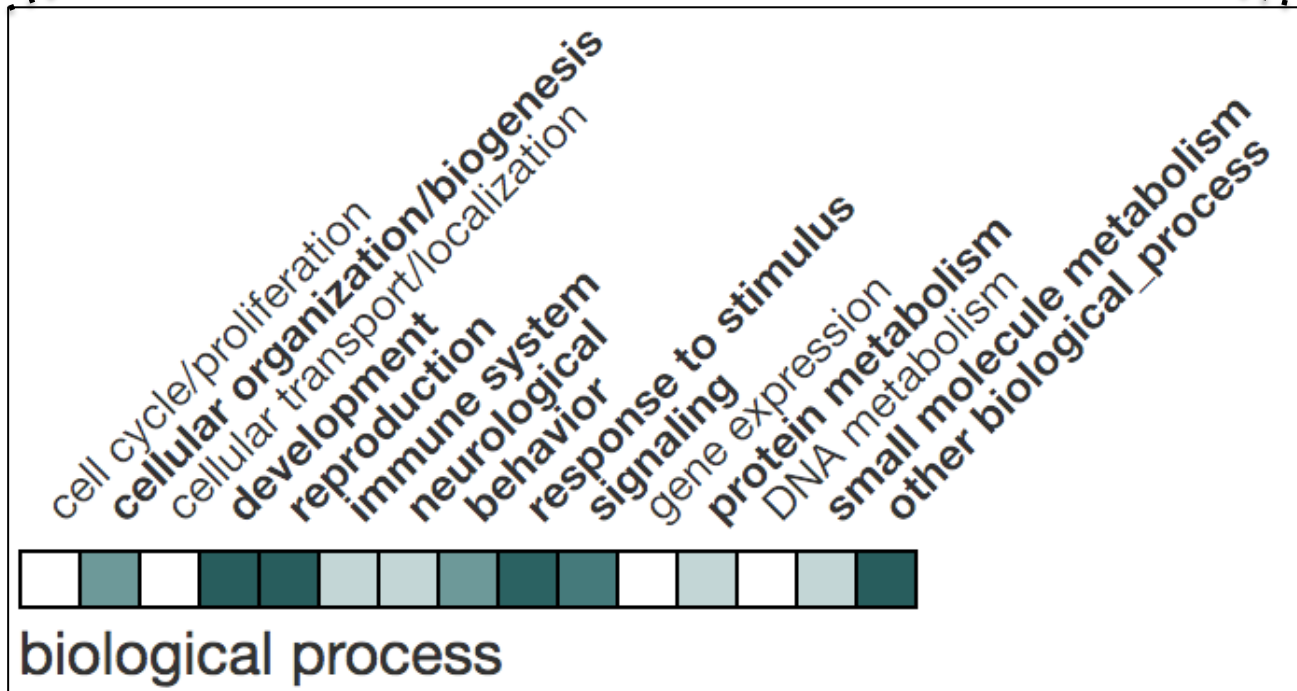
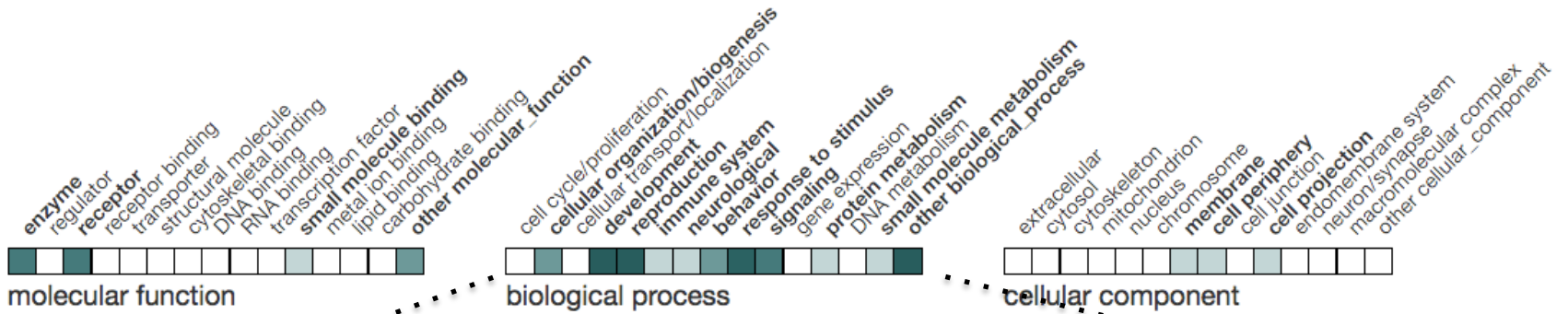
Genomic Location			
Cytogenetic map	57E9-57F1	Sequence location	2R:21,522,420..21,559,977 [+]
Genomic Maps	<a href="#">View in GBrowse</a>		

GO Summary Ribbons		
<p>enzyme regulator receptor receptor binding transporter structural molecule cytoskeletal binding DNA binding RNA binding transcription factor small molecule binding lipid binding metal ion binding carbohydrate binding other molecular_function</p> <p>molecular function</p>	<p>cell cycle/proliferation cellular organization/biogenesis cellular transport/localization development reproduction immune system neurological behavior response to stimulus signaling gene expression protein metabolism DNA metabolism small molecule metabolism other biological_process</p> <p>biological process</p>	<p>extracellular cytosol cytoskeleton mitochondrion nucleus chromosome membrane cell periphery cell junction cell protection endomembrane system neuron/synapse macromolecular complex other cellular_component</p> <p>cellular component</p>

Report Sections
<a href="#">General Information</a>
<a href="#">Genomic Location</a>
<a href="#">GO Summary Ribbons</a>
<a href="#">Families, Domains and Molecular Function</a>
<a href="#">Summaries</a>
<a href="#">Gene Model and Products</a>
<a href="#">Recent Updates</a>
<a href="#">Other Information</a>
<a href="#">Synonyms and Secondary IDs</a>
<a href="#">References</a>

# Revised Gene Reports

## GO Summary Ribbons



# Revised Gene Reports

## Gene Model and Products

### Protein Domains






#### Rcpt\_L-dom



**Description:**  
Receptor L-domain  
**Coordinates:**  
419 - 547

# Revised Gene Reports

**Publication Types**

- Representative publications 10**
- All publications 1537
- Research paper 820
- Supplementary material 22
- Review 299
- Erratum 1
- Personal communication to FlyBase 24

Filter 2015, Smith, cell, etc.  Sort by Year (descending) 

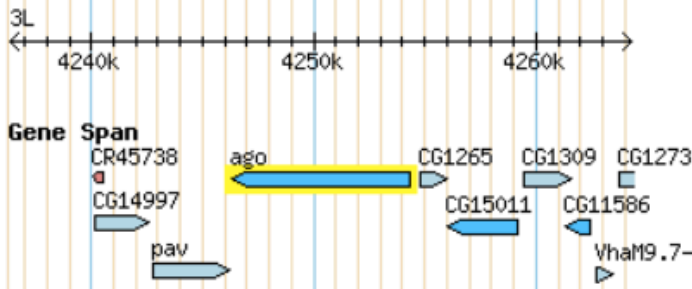
15, Nat. Commun. 6: 7102  
Drosophila glucone screening identifies Ck1alpha as a regulator of mammalian glucose metabolism. [\[FBrf0228532\]](#)

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

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. [\[FBrf0200831\]](#)

# New 'Sequence Downloader' tool

General Information			
Symbol	Dme\ago	Species	<i>D. melanogaster</i>
Name	archipelago	Annotation Symbol	CG15010
Feature Type	protein_coding_gene	FlyBase ID	FBgn0041171
Gene Model Status	Current	Stock Availability	10 publicly available
Also Known As			
Genomic Location			
Cytogenetic map	64A11-64A12	Sequence location	3L:4,246,343..4,254,306 [-]
Genomic Maps			<div data-bbox="1638 714 1893 778">Gene region ▾</div> <div data-bbox="1638 806 1893 878">Get Sequence</div>



# New 'Sequence Downloader' tool

Options ▾

## FlyBase Sequence Downloader

**ID mode**

**FlyBase ID**

**Type**

[View Sequence](#)

✓ Gene Region

Extended Gene Region

CDS

Introns

Exons

Translations

Transcripts

5' UTR

3' UTR


Clones

Sequence Features

Recombinant Constructs

---

**Sequence (FBgn)**

<b>ID:</b>	FBgn0041171	
<b>Symbol:</b>	ago	
<b>Type:</b>	gene	
<b>Location:</b>	3L:complement(4246343..4254306)	
<b>Length:</b>	7964	
<b>Selected region:</b>	Displays residue numbers of region selected by mouse.	

```
1  GTCGAGCGGT  GGTCACTG  GATCCGATT  AGTTTTTTT  CGGGTCCAA  ATCTGTCAA
61  ATCCGCAAT  TGCACGATA  TTCTAGTATC  TGAAAACCAG  AAATTTAGAT  AGACTGGGTA
121 CAGAGTCATC  TGAAAAACGC  AAAAATTAGG  CAATCTCCGA  GGAGCAACGT  CCTTAAAACG
181 TATGTGAAAA  ATTCGATTGA  ACGTGTGTGT  GCTGTGTTGC  GCCTGTATGT  GTGAGAGTGG
241 GCCCCAAACG  CAAAAAGTTT  TACACGCGTT  AAATGTGCAG  TTGAAAACCT  GAAAACAAAT
301 TCTCCCGCGT  AAACTCGGCT  CTCTTTTFTT  ACTCCCGCGT  CCAGCTGCGT  TCCGCTTAAA
```

# New 'Sequence Downloader' tool

```
1  GTCGAGCGGT  GGTCACTG  GATCCGCATT  AGTTTTTTTT  CGGGTCCAAA  ATCTGTCCAA
61  ATCCGCAAAT  TGCACGCATA  TTCTAGTATC  TGAAAACCAG  AAATTTAGAT  AGACTGGGTA
121  CAGAGTCATC  TGAAAAACGC  AAAAATTAGG  CAATCTCCGA  GGAGCAACGT  CCTTAAAACG
181  TATGTGAAAA  ATTCGATTGA  ACGTGTGTGT  GCTGTGTTGC  GCCTGTATGT  GTGAGAGTGG
241  GCCCCAAACG  CAAAAAGTTT  TACACGCGTT  AAATGTGCAG  TTGAAAACCT  GAAAACAAAT
301  TGTGCCCGCT  AAAGTGGGGT  GTGTTTTTTT  AGTGCCCCCT  CCACGTTGGC  TGCCCTTAAA
361  GTTTATAAAC  AATGTGCAAG  GCACCACGCG  AACTCAAAC  TTAGCTGCGA  GCGAGCGAGC
421  GAGTGGGTTC  GTCTGTGTGC  GTGACTCTGC  CTGTGTGTAC  AACAAATGTC  ACATTTTTCT
481  TTTGTTGTTT  GCTCCACGAA  TTATGGGGCT  ATCCCCTCCG  TGTTCCAACC  GCTGCATTTG
541  CAGGTGCAGA  AAAGTGGGGT  TAGGATGGTC  AAAGAGTCCG  TAAGGAACGC  TCAGCGTGCT
601  GCAATCGCTG  CTCTGAATTT  GCAACGAAAG  TAATCTATTT  TTGGGGGATT  TGGGACCACA
661  GGTCTCTGCC  CATTATCCGC  GTTGGTGTGC  GTCTGTGTGT  ATGCAGCGAT  TATGACGACT
721  CCACACCCGT  GGCTAAATCC  ACAGAGAGAA  AATGTTCTCG  AGCGCATCCC  CGATGTTCTGA
781  CCAAAGTGTC  CTGTGTGGCA  CAGGTAAAAA  CGCGTATCGA  AATGCGGTGT  GAAAGCGGAG
841  ACCCTAAAAA  CATATTTTAC  GTTTTTTCGG  GAGGTCAACA  GCCAAAGGCC  ACGAGCCAGG
901  GGTGGGGAAG  GAGGAGGAGG  AGGAGAAGCA  GTAGAAGGAG  GGTGGGAAGA  GAATGAATAC
961  GAATATGGGA  AAATGTTTCGG  GAGAAATGCC  TGCACATCTG  ATCTGTTTCG  GCAGTGATGC
1021  AACAGCAGGA  GCGCTGAAAA  TTCCTTTGTG  ATCTCGCCCC  TTTTGTTCG  CGGATGCTGC
1081  GCTGCAATGG  CTGATCTTTG  CTTCTTCTCC  TTCTCCTTGG  TTTTCTTGTC  CCCTCCCTG
1141  GATCTTCCAA  TCTCTGCCTA  CGGCATCCC  TTTTCTACT  CTCTCGGGTG  CGTGTGTGTG
1201  TCTGTGCGCT  GGTAGGATGT  GATGGCCAGT  CAAGCTGCTG  TCAAACATCA  GAGATGCGCA
```

# New 'Sequence Downloader' tool

**FlyBase Sequence Downloader**

**ID mode**


**FlyBase ID**

**Type**

[View Sequence](#)

---

**Sequence (FBgn)**

**ID:** [FBgn0041171](#) 

**Symbol:** ago

**Type:** gene

**Location:** 3L:complement(4246343..4254306)

**Length:** 7964

**Selected region:** Displays residue numbers of region selected by mouse.

```
1  GTCGAGCGGT  GGTCACTG  GATCCGATT  AGTTTTTTT  CGGGTCCAA  ATCTGTCAA
61  ATCCGCAAT  TGCACGATA  TTCTAGTATC  TGAAAACCAG  AAATTTAGAT  AGACTGGGTA
121 CAGAGTCATC  TGAAAAACGC  AAAAATTAGG  CAATCTCCGA  GGAGCAACGT  CCTTAAAACG
181 TATGTGAAAA  ATTCGATTGA  ACGTGTGTGT  GCTGTGTTGC  GCCTGTATGT  GTGAGAGTGG
241 GCCCCAAACG  CAAAAAGTTT  TACACGCGTT  AAATGTGCAG  TTGAAAACCT  GAAAACAAAT
301 TCTCCCGCGT  AAACTCGGCT  CTCTTTTTF  ACTCCCGCGT  CCAGCTTCCG  TCCGCTTAAA
```

# Revised Jump to Gene/Search



FB2017\_01, released Feb 14, 2017

A Database of *Drosophila* Genes & Genomes

Home Tools Downloads Links Community Species About Help Archives

Go Jump to Gene J2G

Go Jump to Gene J2G

Go Cdk1 J2G

**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 [-]
-----------------	-------------	-------------------	-------------------------------

**Genomic Maps**

View in GBrowse

**GO Summary Ribbons**

Go Search FlyBase Search

Go Cdk1 Search

Cdk1 analysis tools here

View As List Table

1-50 of 855

Show results for clear

← Previous 1 2 3 ... 18 → Next

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- Polypeptide (1)
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- Sequence Feature (18)
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- Transcript (1)
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**Cdk1** Cyclin-dependent kinase 1 (CG5363, FBgn0004106) **Gene**

Feature type: protein\_coding\_gene

Sequence Location: 44 Alleles 24 Stocks 1 Transcript

Gene Snapshot >

Gene model status: Current

Cytogenetic Map: 31D11-31D11

References: 380

**Exelixis:FBst1006790** (FBst1006790) **Stock**

Collection: Exelixis at Harvard Medical School

Species: *melanogaster*

Genotype: PBac[PB]Cdk1<sup>103495</sup>

**Cdk1<sup>216A</sup>** (FBal0001571) **Allele**

Allele class: hypomorphic allele - genetic evidence

Mutagen: ethyl methanesulfonate

Associated insertions:

Known lesion? yes

Carried in construct:

# Feedback please!

Please fill in the following details:

Your Name:

[FAQs](#)

Your E-Mail address:

Re-enter Your E-Mail:

Subject:

or enter one:

Spam check: **0916** please enter **ALL** the digits of the green security code:

Feedback:

[Send Comments to FlyBase](#)

[Erase Comments](#)

# Acknowledgements & funding

## **FB-Harvard (USA):**

Norbert Perrimon  
Julie Agapite  
Kris Broll  
Lynn Crosby  
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