

FlyGene Wiki and FTYP

At the top of every gene report there is a link to our community-generated gene wiki

Simply register on the wiki to be able to edit the gene summaries and add your take on a particular gene

Fast Track Your Paper

Six steps:

1. Find your paper
2. Identify yourself
3. Indicate the data-types in the publication
4. Identify the genes
5. Provide information on new antibodies
6. Confirm your submission

Indicate Data Types in Publication

Search for Gene Symbol or Name in FlyBase

Check the genes that appear in the publication and press "Continue"

1 result for "PINK1"

Refine your search (above) or enter a gene unknown to FlyBase (below) if

QuickSearch

"Simple" searches all text in all fields on every report

QuickSearch (Simple) Human Disease NEW Expression Phenotype GO References Data Class

Species: include non-Dmel species

Enter text:

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

Six other tabs, many allowing controlled vocabulary searches:

QuickSearch (Simple) Human Disease NEW Expression Phenotype GO References Data Class

Phenotypic class:

refinement: and:

Autocomplete: aging defective, apoptosis defective, auditory perception defective, auditory system affected, auxotroph, back specification defective, cell adhesion defective, delayed aging, dorsal/ventral axis specification defective, increased adult mortality, lethal - all die before end of embryonic stage, lethal - all die before end of first instar larval stage, lethal - all die before end of larval stage, lethal - all die before end of pupal stage, lethal - all die before end of adult stage, lethal - all die before end of life cycle, lethal - all die during embryonic stage, lethal - all die during larval stage, lethal - all die during pupal stage, lethal - all die during adult stage, lethal - all die during life cycle, lethal - all die during development, lethal - all die during embryonic development, lethal - all die during larval development, lethal - all die during pupal development, lethal - all die during adult development, lethal - all die during life cycle development, lethal - all die during embryonic life cycle, lethal - all die during larval life cycle, lethal - all die during pupal life cycle, lethal - all die during adult life cycle, lethal - all die during life cycle development.

Note: The more boxes you fill out, the greater the chance you'll not get any hits. Try starting more broadly

Autocomplete in every controlled vocabulary box

QuickSearch (Simple) Human Disease NEW Expression Phenotype GO References Data Class

Phenotypic class: apoptosis defective

refinement: larval and:

Autocomplete: larval stage, third instar, larval stage

Tissue/cell affected: and:

refinement:

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

87 matches to query (apoptosis defective)embryonic stage

#	Symbol	Class	Inserted Element	Stocks #	Mutagen	HitList	Conversion Tools
1	DNase1 ¹	hypomorphic allele - genetic evidence		3	ethyl methanesulfonate		Yes
2	dn1 ¹	loss of function allele					

EXPORT selected HITS TO:

- Batch Download
- QueryJvarkit (new session)
- FlyBase IDs file (to store on your computer)
- Cross-referencing FlyBase Records Table
- Get FlyBase-curated external data links (for associated genes):
 - Nucleotide Sequences
 - Protein Data
 - Protein Domains
 - Get LinkOut external data links (for associated genes):
 - FlyExpress - Expression Pattern Search
 - Fly GRID Interaction Data
 - FlyAtlas - Drosophila adult expression atlas
 - FLIGHT - Integrating Genomic and High-Throughput data
 - DRSC - Drosophila RNAi Screening Center
 - DEDS - Drosophila melanogaster Exon Database
 - FlyMine - integrated genomics and proteomics
 - NCBI Gene Expression Omnibus (GEO)
 - Heidelberg Database for RNAi Phenotypes

Continue your search using the Refinement and HitList Conversion Tools



A Database of *Drosophila* Genes and Genomes

What's New 2014

Genomic data and how to search for it

GBrowse 2 and FeatureMapper

Human Disease Models

FlyGene Wiki and FTYP

QuickSearch

www.flybase.org

FlyBase is supported by a grant from the National Human Genome Research Institute (NHGRI) at NIH #P41 HG000739. Support is also provided by the British Medical Research Council and the Indiana Genomics Initiative.

Searching large datasets


Large Dataset Metadata (LDM) Reports

These reports contain information such as:

- Description of dataset
- Experimental procedures
- List of related datasets (parent or child)
- Link to list or file of dataset members


Search Options


- QuickSearch allows you to search all fields on the LDM reports at once. To search for modENCODE data sets:

 The image cannot be displayed. Your computer may not have enough memory to open the image, or the image may have been corrupted. Restart your computer, and then open the file again. If the red x still appears, you may have to delete the image and then insert it again.

- QueryBuilder allows searches by specific field


GBrowse Track labels link to relevant LDM reports

 The image cannot be displayed. Your computer may not have enough memory to open the image, or the image may have been corrupted. Restart your computer, and then open the file again. If the red x still appears, you may have to delete the image and then insert it again.

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GBrowse1
GBrowse2

Sequence Feature reports contain links to datasets of which the feature is a member

 The image cannot be displayed. Your computer may not have enough memory to open the image, or the image may have been corrupted. Restart your computer, and then open the file again. If the red x still appears, you may have to delete the image and then insert it again.

FeatureMapper

Purpose: to identify features within a sequence range of interest:

- Features include insulators, transcription factor binding sites, point mutations, RNA editing sites, etc.
- Can search within genes, upstream of genes, downstream of genes, or within any desired sequence (enter sequence coordinates directly into search box)


 The image cannot be displayed. Your computer may not have enough memory to open the image, or the image may have been corrupted. Restart your computer, and then open the file again. If the red x still appears, you may have to delete the image and then insert it again.

Output lists features found within each landmark (in this case, 10kb upstream of several genes, *abd-A* shown). Features can also be downloaded in GFF format.

abd-A				
TFBS - BTB/POZ domain	3R:12855496..12855581	->	TF_binding_site:mE1_TFBS_Tf1	TFBS_Tf1_004327
	3R:12855020..12855015	->	TF_binding_site:mE1_TFBS_bab1	TFBS_bab1_005832
TFBS - helix-loop-helix domain	3R:12854552..12855501	->	TF_binding_site:BDTNP1_TFBS_tw1	TFBS_tw1_008450
	3R:12855358..12855348	->	TF_binding_site:BDTNP1_TFBS_da	TFBS_da_008655
	3R:12856383..12855620	->	TF_binding_site:BDTNP1_TFBS_da	TFBS_da_008696
	3R:12856060..12855589	->	TF_binding_site:BDTNP1_TFBS_tw1	TFBS_tw1_008451
	3R:12858442..12859415	->	TF_binding_site:BDTNP1_TFBS_da	TFBS_da_008697
	3R:12864157..12868422	->	TF_binding_site:BDTNP1_TFBS_tw1	TFBS_tw1_008452
	3R:12864490..12865514	->	TF_binding_site:BDTNP1_TFBS_da	TFBS_da_008698
	3R:12865514..12866521	->	TF_binding_site:BDTNP1_TFBS_da	TFBS_da_008699
TFBS - homeodomain	3R:12851409..12855530	->	TF_binding_site:mE1_TFBS_cad	TFBS_cad_007589
	3R:12854508..12855501	->	TF_binding_site:BDTNP1_TFBS_z	TFBS_z_001772
	3R:12856546..12857558	->	TF_binding_site:BDTNP1_TFBS_z	TFBS_z_001773
	3R:12857150..12859079	->	TF_binding_site:mE1_TFBS_cad	TFBS_cad_007590
	3R:12857594..12858581	->	TF_binding_site:BDTNP1_TFBS_z	TFBS_z_001774
	3R:12858625..12859630	->	TF_binding_site:BDTNP1_TFBS_z	TFBS_z_001775
	3R:12859556..12859960	->	TF_binding_site:BDTNP1_TFBS_z	TFBS_z_001776
	3R:12863307..12863020	->	TF_binding_site:mE1_TFBS_tw1	TFBS_tw1_008453

Human disease models

We are now using Disease Ontology terms to annotate Drosophila alleles and transgenes and human transgenes inserted into Drosophila that reproduce a human disease phenotype.

QuickSearch  Simple | Expression | Phenotype | GO | References | Human Disease ^{NEW} | Data Class

Disease term:

Huntington's disease
acromesomelic dysplasia, Hunter-Thompson type
tolosa-hunt syndrome

TermLink Disease Report

Term	Huntington's disease	ID (Ontology)	DOID:12858 (Human Disease)
Definition	A neurodegenerative disease that has 'material_basis_in_expansion_of_CAG_repeats_resulting_in_neuron_degeneration_affecting_muscle_coordination_cognitive_abilities.'		
Comment			
Records annotated with this term or any of its children terms	Genes	Alleles	
	90	166	

Results list data from ALL species. Please use QueryBuilder to retrieve species specific data.

Spanning Tree (Parents/Children)

```

disease
├── disease_of_anatomical_entity
│   ├── nervous_system_disease
│   │   ├── central_nervous_system_disease
│   │   │   ├── neurodegenerative_disease
│   │   │   └── Huntington's_disease
    
```

Spanning Tree View Settings Show hierarchy levels: for parents, for children

#	Compound statement	Relevant reports
1	DOES NOT ameliorate Huntington's disease	1
2	DOES NOT exacerbate Huntington's disease	2
3	Does not model Huntington's disease	1
4	ameliorates Huntington's disease	91
5	exacerbates Huntington's disease	53
6	model of Huntington's disease	19

Interacting alleles that relieve the disease phenotype or make it more severe.

Allele Report

Symbol	HsppHTT128Q FL_SonLUAS	Species	<i>H. sapiens</i>
Name	FlyBase ID	Associated gene	FlyBase ID
Feature type	allele	Carried in construct	P(LAS-HTT.128Q.FL)
Caused by insertion			

Allele class	
Mutagen	in vitro construct - regulatory fusion

Model	Evidence	References
model of Huntington's disease	inferred from mutant phenotype	(Romero et al., 2008; Gonzales and Yin, 2010; Steinert et al., 2012)

Interactions	Interaction	References
model of Huntington's disease	is ameliorated by Cal^{1D}cup^{X10}¹cup¹	(Romero et al., 2008)

Comments Flies expressing HsppHTT1128Q FL_SonLUAS pan-neuronally show interruption and fragmentation of nighttime sleep resembling that seen in human Huntington's Disease patients. (Gonzales and Yin, 2010)