

Get your paper into FlyBase

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

FlyBase Community Advisory Group

The FlyBase Community Advisory Group (FCAG) was launched in September 2014 with the aim of gaining greater feedback from the community about changes in FlyBase. The group consists of representatives from any lab worldwide that uses FlyBase as part of its research, and in just 6 months we already have over 550 members from more than 40 countries. If you would like to be involved, please see <http://tinyurl.com/FlyBaseFCAG>.

Genomes: new assemblies, new gene models

2 New and Improved Genome Assemblies

- Release 6 is now the *Drosophila melanogaster* reference assembly

Get your release 5 data into release 6 coordinates using our coordinates converter tool

Drosophila Sequence Coordinates Converter

Species: D.melanogaster Input Assembly: 5 Output Assembly: 6 (current) Send results to: Browser

Enter Drosophila Coordinates: or Upload File of Coordinates: Choose File | No file chosen

- The new reference assembly for *D. simulans* is that of Hu *et al.* (FBrf0220370) on strain W[501] and is designated release 2.

- ❖ Due to the scale of changes between the two assemblies we are not providing a converter for this species but see NCBI's remap service for options <http://www.ncbi.nlm.nih.gov/genome/tools/remap>.

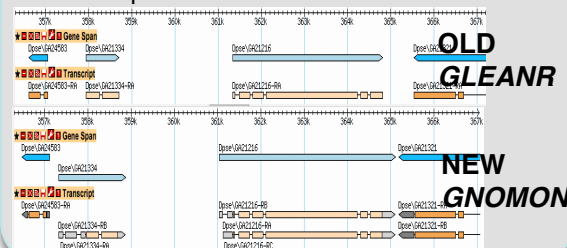
5 New and Improved Automated Annotation Sets based on NCBI Gnomon

<http://www.ncbi.nlm.nih.gov/genome/guide/gnomon.shtml>

- *D. simulans*
- *D. pseudoobscura*
- *D. erecta*
- *D. ananassae*
- *D. Yakuba*

- And Coming Soon**
- *D. virilis*
 - *D. mojavensis*
 - *D. willistoni*

- RNAseq input adds UTRs and alternate transcript models



A Database of *Drosophila* Genes and Genomes

What's New 2015

- Gene Groups
- New GBrowse2 options
- Human Disease Models
- Get your paper into FlyBase
- Community Advisory Group
- Genomes: new assemblies, new gene models

www.flybase.org

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Gene Group Reports

Gene Groups

These new Reports bring together genes that are acknowledged to form a biological group, such as members of a gene family (e.g. Actins, Wnts) or subunits of a protein complex (e.g. proteasome, ribosome).

Gene Group Reports include:

- Group description & membership criteria
- Table of members
- Key Gene Ontology terms
- Links to related groups in FlyBase
- External links to orthologous groups
- Export/Download options for further analysis
- Source references

General Information			
Name	WNTs	Species	<i>D. melanogaster</i>
Symbol	WNT	FlyBase ID	FBgg0000040
Group type	functional group	Number of members	7
Date last reviewed	2013-02-22		
Description			
Description	WNTs are evolutionarily conserved secreted Cys-rich glycoproteins, defined by sequence homology to the original members of the family - Wnt1 in mouse and wg in Drosophila. They are extracellular ligands for members of the Frizzled family of receptors as well as other receptors. (Adapted from PMID:23151663).		
Notes on membership			
Key GO terms			
Molecular Function	frizzled binding (FlyBase, 2014)		
Biological Process	Wnt signaling pathway (FlyBase, 2014)		
Cellular Component	extracellular region (FlyBase, 2014)		
Related Gene Groups			
Members (7)			
Gene Symbol	Gene Name	Annotation ID	Location
wg	wingless	CG4889	2L:7,307,159..7,316,265 [+]
Wnt10	Wnt oncogene analog 10	CG4971	2L:7,363,379..7,377,628 [+]
Wnt2	Wnt oncogene analog 2	CG1916	2R:9,494,166..9,503,188 [-]
Wnt4	Wnt oncogene analog 4	CG4698	2L:7,255,419..7,277,171 [-]
Wnt5	Wnt oncogene analog 5	CG8407	X:18,501,401..18,505,406 [-]
Wnt6	Wnt oncogene analog 6	CG4969	2L:7,333,714..7,352,542 [-]
wntD	Wnt inhibitor of Dorsal	CG8458	3R:13,292,052..13,293,198 [-]
External Data			
Orthologous group(s)	Human Wnt Genes		
Other resource(s)	The Wnt homepage (http://web.stanford.edu/group/russelsta/cgi-bin/wnt/drosophila)		
Synonyms and Secondary IDs			
References (2)			
FlyBase analysis	FlyBase, 2014. FlyBase Gene Group information. FlyBase Gene Group information. [FBrc022695]		
Research paper	Limargas and Lawrence, 2001, Proc. Natl. Acad. Sci. U.S.A. 98(25): 14487-14492 Seven Wnt homologues in Drosophila: a case study of the developing tracheae. [FBrc0141722]		

Available in the FB2015_02 release, April 2015.

New GBrowse2 options

Check out track toolbar options, including:

- RNA-Seq track configuration options include linear scaling and increased spacing.

Configure this track

Fill color: whitesmoke (default)

Select samples to show:

- + _AdMateM_4d_testes
- + _AdMateM_4d_acc_gland
- + _AdVirF_4d_ovaries
- + _AdMateF_4d_ovaries
- STRAND_separator
- _AdMateM_4d_testes
- _AdMateM_4d_acc_gland
- _AdVirF_4d_ovaries
- _AdMateF_4d_ovaries

Signal scaling method: log2 (default)

Samples presentation style: Tilted (default)

Vertical spacing between samples (pixels): 7 (default)

Revert to defaults | Cancel | Apply changes

linear (default) | Vertical (default) | 30 (default)

- Data for any group of tracks may be downloaded via the 'About tracks' menu.

TFBS - zinc finger domain

Track ID=tf_binding_site1 [Download ALL DATA for this track]

[FlyBase track description](#)

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 | Data Class

Disease term: Hun Search

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

TermLink Disease Report

Term	ID (Ontology)	DOID:12806 (Human Disease)
Huntington's disease		

Definition: A neurodegenerative disease that has 'material_basis_in expansion of CAG repeats resulting in neuron degeneration affecting muscle coordination, cognitive abilities.

Records annotated with this term or any of its children terms:

GeneID	AlleleID
90	166

Spanning Tree (Parents/Children): Only view relationship(s):

Compound Statements:

#	Compound statement	Allele	Relevant reports
1	DOES NOT ameliorate Huntington's disease	1	
2	DOES NOT exacerbate Huntington's disease	2	
3	Doesn't worsen model Huntington's disease	1	
4	ameliorates Huntington's disease	91	
5	exacerbates Huntington's disease	53	
	model of Huntington's disease	19	

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

Allele Report

Symbol	Hsap HTT 128Q.FL_Scr UAS	Species	<i>H. sapiens</i>
Name		FlyBase ID	FBal0248417
Feature type	allele	Associated gene	Hsap HTT
Caused by Insertion		Carried in Construct	PQ UAS-HTT 128Q.FL
Allele class			
Mutagen	in vitro construct - regulatory fusion		
Recent Updates			
Human Disease Model Data			
Disease Ontology			
Models	Evidence	References	
model of Huntington's disease	inferred from mutant phenotype	(Romero et al., 2008, Gonzalez and Yin, 2010, Stewart et al., 2012)	
Interactions			
Disease	Interaction	References	
model of Huntington's disease	is ameliorated by Cal- α 1(Dr-cup1)>X10<v-up1a	(Romero et al., 2008)	
Comments			
Flies expressing Hsap HTT 128Q.FL_Scr UAS pan-neuronally show interruption and fragmentation of nighttime sleep resembling that seen in human Huntington's Disease patients. (Gonzalez and Yin, 2010)			