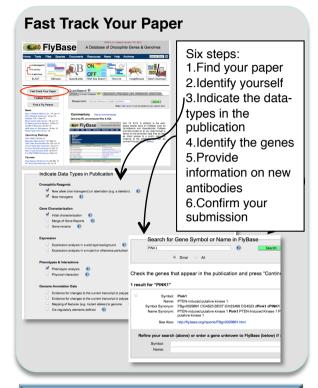
Get your paper into FlyBase



FlyBase Community Advisory Group

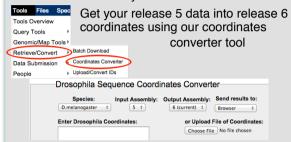
The FlyBase Community Advisory Group (FCAG) was launched in September 2014 with the aim of gaining greater feedback from the community about changes in FlyBase. The group consists of representatives from any lab worldwide that uses FlyBase as part of its research, and in just 6 months we already have 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



- ➤ 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 NCBIs remap service for options http://www.ncbi.nlm.nih.gov/genome/ tools/remap.

5 New and Improved Automated Annotation Sets based on NCBI Gnomon

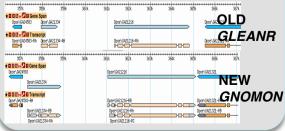
www.ncbi.nlm.nih.gov/genome/annotation euk/process

- 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



www.flybase.org

.FlyBase is supported by a grant from the National Human Genome Research Institute (NHGRI) at NIH #U41HG000739. Support is also provided by the British Medical Research Council and the Indiana Genomics Initiative.

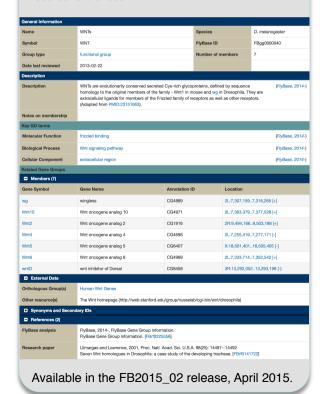
Gene Group Reports

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



New GBrowse2 options

Check out track toolbar options, including: > RNA-Seg track configuration options include linear scaling and increased spacing. 🖈 🖿 🖾 🖫 🛏 🍱 🖸 Gonads and male accessory glands, stranded Configure this track whitesmoke (default) \$ +_AdMateM_4d_testes _AdMateM_4d_acc_gland _AdVirF_4d_ovaries + AdMateF 4d ovaries Select samples to show -STRAND separator AdMateM 4d testes AdMateM_4d_acc_gland ·on _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. ★ ■ X M H Z M TFBS - zinc finger domain TFBS - zinc finger domain Track ID=tf_binding_site1 [Download ALL DATA for this 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.

