A Database of *Drosophila* Genes and Genomes

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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

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

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

www.ncbi.nlm.nih.gov/genome/annotation_euk/process

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

RNAseq input adds UTRs and alternate transcript models

And Coming Soon

- *D. virilis*
- *D. mojavensis*
- *D. willistoni*

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

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

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.
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.

Gene Group Reports

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

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.

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

Human disease models

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