



Data in FlyBase

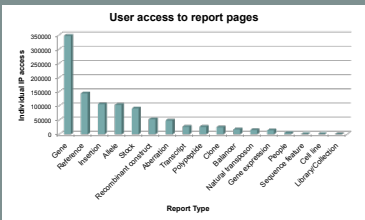
Have your say

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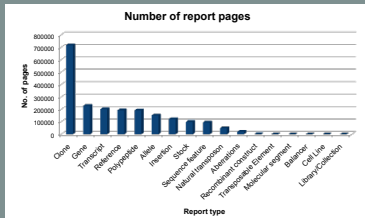


Report pages in FlyBase

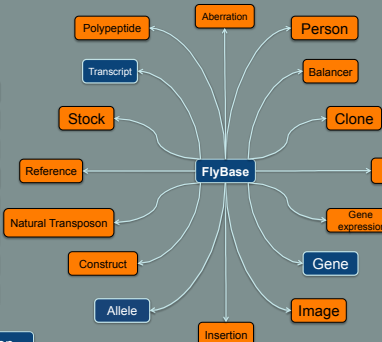
- General Information
- cDNA Clones Consistent with the Transcript
- Sequence
- Other Products of this Gene
- Comments
- External Crossreferences
- Synonyms
- References



User activity is focused heavily towards the gene report pages. Did you know about all the other reports available in FlyBase?



While gene reports might be the most viewed, we actually have more clone reports. We have just under 230,000 gene reports, across over 400 species of *Drosophila*. We also have reports for non-*Drosophila* genes like Human Huntingtin and *Manduca sexta* Synaptotagmin, to allow us to record phenotypic data when they are expressed in the fly.



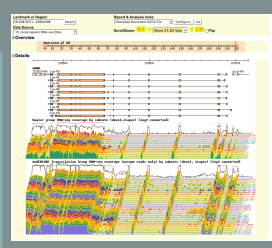
There are 16 different datatypes/reports available in FlyBase. They are all interlinked and browsable. Each report contains nested subsections containing further information on each datatype, and links to other reports and external databases.

- General Information
- Nature of the Allele
- Phenotypic Data
- Interactions
- Complementation & Rescue Data
- Stocks
- Notes on Origin
- Comments
- Synonyms & Secondary IDs
- References

- General Information
- Genomic Location
- Summary Information
- Detailed Mapping Data
- Gene Model & Products
- Expression Data
- Alleles & Phenotypes
- Gene Ontology
- Sequence Ontology
- Interactions & Pathways
- Orthologs
- Stocks & Reagents
- Other Information
- External Crossreferences & linkouts
- Synonyms & Secondary IDs
- References

New datatypes

As the data that scientists generate changes over time, so FlyBase must continually refine and change the datatypes that we curate. We have recently introduced Sequence feature (e.g., RNAi reagent), Cell line (e.g., Kc167), and Library/collection reports (e.g., CH clone library). These data are also searchable using our many search tools. As more data comes online we hope users will become familiar with these new reports and find all the reports in FlyBase useful.



With the advent of Next Generation sequencing technologies, along with genome tiling array technologies, an enormous and ever-increasing amount of high-throughput data anchored onto one or another of the *Drosophila* genomes is being produced. FlyBase is working with data producers to incorporate these data into FlyBase so that they can be examined in GBrowse and interrogated through our query engines in the context of other community genome-wide and literature-based information.

To see the RNA-Seq GBrowse data, go to GBrowse and select <D. melanogaster RNA-Seq Data> in the Data Source pull down menu.

Have your say

Use the red dots provided to answer the following questions:

If FlyBase had to lose one report (shown on the diagram above), which one would you miss the least?

If FlyBase had to lose one subsection from the reports above, which one would you miss the least?

Were you aware of all the datatypes shown on the diagram above?

Yes

No

Were you aware of the 'Fast-track your Paper' submission tool, to get your paper into FlyBase?

Yes

No

Are there any datatypes that we don't currently capture, that you'd be grateful if we did? List them below using the post-it notes provided.

FlyBase is supported by a grant from the National Human Genome Research Institute at the U.S. National Institutes of Health #R15 HG000739. Support is also provided by the British Medical Research Council and the Indiana Genomics Initiative.

Get your data into FlyBase!

Use our quick and easy publication submission tool to see your paper listed online sooner.

- Tell us which genes feature in your paper, and we'll link your paper to those genes for the next release cycle.
- Provide additional information during the submission process about your publication and help our Curators to speed up your curculation.
- Just click the link in the sidebar on the FlyBase home page or in the tools menu to get started!