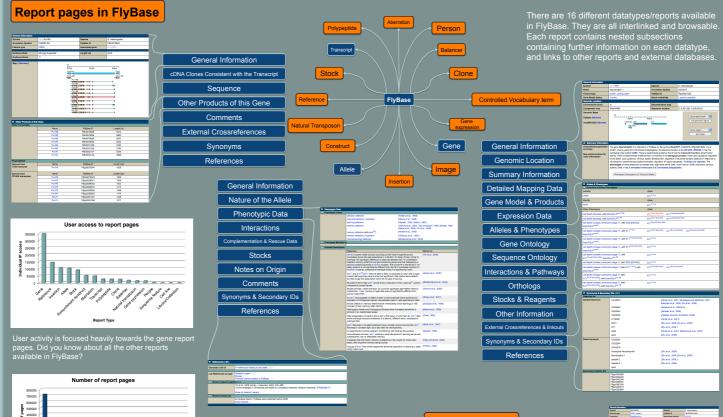


Data in FlyBase Have your say



Peter McQuilton, Gillian Millburn, Steven Marygold. The FlyBase Consortium. FlyBase.org



While gene reports might be the most viewed, we actually have more clone reports. We have just under

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.

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. GH clone library). These data are also fully 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.

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With the advent of Next Generation sequencing echnologies, along with genome tiling array echnologies, 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 clyBase so that they can be examined in SBrowse and interrogated through our query engines in the context of other community genome-wide and literature-based information.

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

	diagram above), which one would you miss the least?
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Vere you aware of the 'Fast-track your Paper' su	ubmission tool, to get your paper into FlyBase?
Are there any datatypes that we don't currently co	
f we did? List them below using the post-it notes	provided.

Get your data into FlyBase!

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se our quick and easy publication submission tool to see your paper listed

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