Several improvements have been made to representation of non-coding RNAs. Now, all *D. melanogaster* genes producing non-coding RNAs have a standardized prefix based on their class, and are cross-referenced with RNAcentral’s Unique RNA Sequence (URS) identifiers. For transfer RNAs, we now link to the Genomic tRNA Database (GtRNAdb), which contains transfer RNA gene predictions and associated analyses.

**Graphical Abstracts** are now included in Reference Reports and as thumbnails in HitLists. This initial integration comprises more than 900 graphical abstracts from papers in journals published by Cell Press.

**Connections** to more sources have been added to many Report pages, in the Key Link section near the top and the External Cross-References and Linkouts section. These include the DRSC’s Molecular Interaction Search Tool (MIST), and antibody information provided by Cell Signaling Technologies. On the front page, we have added links to the BioLitMine MeSH term literature mining tool and the iProteinDB post-translational modification database.

There is now a link to search for *Drosophila* preprint articles in Europe PMC, from the References tab of QuickSearch.

FlyBase is supported by a grant from the National Human Genome Research Institute at the U.S. National Institutes of Health U41HG000739. Support is also provided by the British Medical Research Council. To contact us, please email helpfb@morgan.harvard.edu.

A specialized section of Experimental Tool reports is the **Frequently Used GAL4 Drivers** table, a tabular summary of more than 200 commonly used GAL4 driver alleles that can be found in the GAL4 etc. tab of QuickSearch.
FlyBase is pleased to introduce our new Pathway Reports that list genes that have been experimentally shown to act within a pathway or to regulate it. These form a subset of our Gene Group resource and can be searched via the ‘Gene Groups’ QuickSearch tab or a browsable list. This resource is under development and we welcome any feedback to help improve the usefulness and accuracy of these gene lists.

Gene Reports now feature new Expression Summary Ribbons giving an at-a-glance view of expression data from two sources. In the manually curated anatomy expression data ribbon, a filled tile indicates that data has been curated from the research literature for that particular cell type, tissue or system.

A summary of high-throughput stage specific RNA-Seq expression data from modENCODE is presented as a heat map (increased expression is darker).

Enzyme Nomenclature and Metabolic Pathways:
FlyBase Gene Reports now show improved information on enzyme nomenclature and reactions, as well as links to metabolic pathway resources KEGG, Reactome, and BioCyc on the Gene Report pages. We have added many new Gene Groups for families of enzymes.

Quantitative protein expression data from the proteomic study of Casas-Vila et al., 2017, has been incorporated into Gene Reports for more than half of annotated protein coding genes. The proteome is available for the complete fly life cycle (17 time points) and/or embryogenesis (14 time points).

The data are presented as histograms, color-coded by expression level, in the “High-Throughput Expression Data” sub-section of Gene Reports’ “Expression Data” section. The display can be viewed at log or linear scale, with options to scale the data relative to the gene’s maximum expression or relative to global “low” or “moderate” expression levels.

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