FlyBase
QuickSearch Redesign

Use 'simple' search when:
- You aren't sure what type of data you're looking for (genes, alleles, insertions, constructs, etc.)
- A broad search is preferable (may be lots of hits!)
- You want to search all types of data in FlyBase at once.

Simple search hits report:

Use 'phenotype' search when:
- You want to search for a phenotype curated from the literature.
- You are interested in combinations of phenotypic classes and/or tissues affected.
- Example: Phenotypic class, 'lethal' and 'recessive', tissue/cell, 'motor neuron'.

Please note:
- The more boxes you fill in, the greater the chance of no hits. Consider starting your search broadly.
- Autocomplete within this tab works separately on the top search (phenotypic class) and the bottom search (tissue/cell affected).

High Throughput Expression Search

Use 'expression' search when:
- You want to search for genes with a certain expression pattern.
- You are interested in specific patterns as reported in the literature.

Please note:
- High throughput RNA-Seq expression data can be searched by clicking the link at the bottom (green arrow).
- Autocomplete within this tab restricts you to only choosing terms that will return results. Please see 'QuickSearch Help' for more information (purple arrow).

Use 'high throughput expression' search when:
- You want to search temporal expression patterns.
- You want to search genomic expression data for ALL FlyBase genes

Note: Please read 'Documentation' for explanation of how the search works (red circle).
D. melanogaster GBrowse data tracks have been subdivided into various “Views”. All views include gene models and other commonly viewed tracks (such as transgenic insertion sites). Additional genomic data are divided by category:

**Gene Models/Evidence** view includes:
cDNAs and ESTs, RNA-Seq exon junctions, gene predictions, orthologs, etc.

**Expression/Regulation** view includes:
RNA-Seq expression data, chromatin domains, transcription factor binding sites, insulators, enhancers, etc.

**MegaView** view includes:
Deletions and duplications, tiling BACs, and allows a whole chromosome arm to be viewed at once.

**Gene Disruptions, Stocks, and Reagents** view includes:
Indels, point mutations, fly stocks, RNAi amplicons, etc.

New and notable GBrowse tracks

- RNA-Seq exon junctions
- Transcription Factor Binding Sites (TFBS).
  Hot spot track: mousing over the hot spots pops up a box indicating which TFs bind in that region. Also available are tracks for various transcription factor types (homeodomain, HLH, etc.)
- Enhancers (none in this screenshot, see ‘abd-A’ gene for example)
- Silencers
- Putative brain enhancers, carried in transgenic fly stocks.
- RNA A→I editing sites (none in this screenshot, see ‘eag’ gene for example)
- Stranded RNA-Seq coverage data by tissue type (‘CNS and adult head’ and four other tissue groupings) and by tissue culture cell type.

Note: Help documentation and references for all tracks are available either by clicking the track name, or by clicking “Help and key for FlyBase Evidence Tiers” at the top of the tracks section.