FlyBase
QuickSearch Redesign

QuickSearch
Simple | Expression | Phenotype | GO | References | Data Type

QuickSearch help

Enter text: en-GAL4   Search

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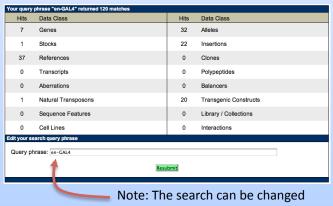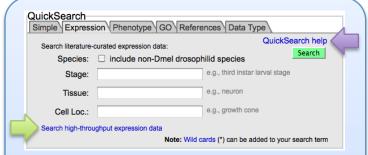
Use 'simple' search when:
- You aren't sure what type of data you're looking for (genes, alleles, insertions, constructs, etc.)
- A broad search is preferable (may be lots of hits!)
- You want to search all types of data in FlyBase at once.

Simple search hits report:

Your query phrase "en-GAL4" returned 120 matches

Hits	Data Class	Hits	Data Class
7	Genes	32	Alleles
1	Stocks	22	Insertions
37	References	0	Clones
0	Transcripts	0	Polypeptides
0	Aberrations	0	Balancers
1	Natural Transposons	20	Transgenic Constructs
0	Sequence Features	0	Library / Collections
0	Cell Lines	0	Interactions

Edit your search query phrase

Query phrase: en-GAL4

Resubmit

Note: The search can be changed directly from this page if you don't see what you want.

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Phenotypic class: lethal   Search

refinement: recessive   and:

Autocomplete coordinates only within each of the two groups of fields.

Tissue/cell affected: motor neuron

refinement: and:

Note: Wild cards (*) can be added to your search term

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).

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QuickSearch help

Search literature-curated expression data:

Species: ☐ include non-Dmel drosophilid species   Search

Stage: e.g., third instar larval stage

Tissue: e.g., neuron

Cell Loc.:   e.g., growth cone

Search high-throughput expression data

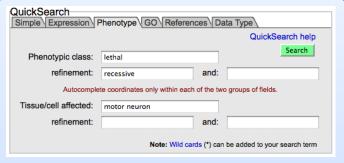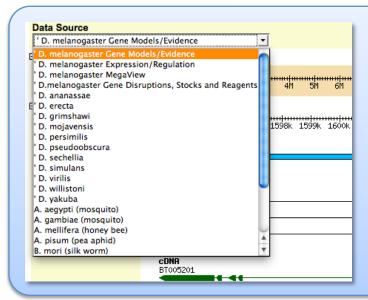**Note:** Wild cards (*) can be added to your search term

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).

High Throughput Expression Search

modENCODE expression by stage data

'Expression Off' means a peak expression level[1] no more than:

Low expression

Graveley et al., 2010.03.15

Expression Off	Stage	Expression On
	embryo, 0-2 hr	
	embryo, 2-4 hr	
	embryo, 4-6 hr	
	embryo, 6-8 hr	
	embryo, 8-10 hr	
	embryo, 10-12 hr	
	embryo, 12-14 hr	
	embryo, 14-16 hr	
	embryo, 16-18 hr	
	embryo, 18-20 hr	
	embryo, 20-22 hr	
	embryo, 22-24 hr	
	larva, L1	
	larva, L2	
	larva, L3 12 hrs old	
	larva, L3 puff stage 1-2	
	larva, L3 puff stage 3-6	
	larva, L3 puff stage 7-9	
	white prepupa, new	
	white prepupa, 12 hr	
	white prepupa, 24 hr	
	pupa, 2 days post-WPP	
	pupa, 3 days post-WPP	
	pupa, 4 days post-WPP	
	adult male, 1 day	
	adult male, 5 days	
	adult male, 30 days	
	adult female, 1 day	
	adult female, 5 days	
	adult female, 30 days	

'Expression On' means a peak expression level[1] no less than:

Moderate expression

submit search

⊞ Documentation

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).

FlyBase
GBrowse Redesign

Data Source

' D. melanogaster Gene Models/Evidence

' D. melanogaster Gene Models/Evidence
' D. melanogaster Expression/Regulation
' D. melanogaster MegaView
' D.melanogaster Gene Disruptions, Stocks and Reagents
' D. ananassae
' D. erecta
' D. grimshawi
' D. mojavensis
' D. persimilis
' D. pseudoobscura
' D. sechellia
' D. simulans
' D. virilis
' D. willistoni
' D. yakuba
' A. aegypti (mosquito)
' A. gambiae (mosquito)
' A. mellifera (honey bee)
' A. pisum (pea aphid)
' B. mori (silk worm)

4M   5M   6M

1598k 1599k 1600k

cDNA
BT005201

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.
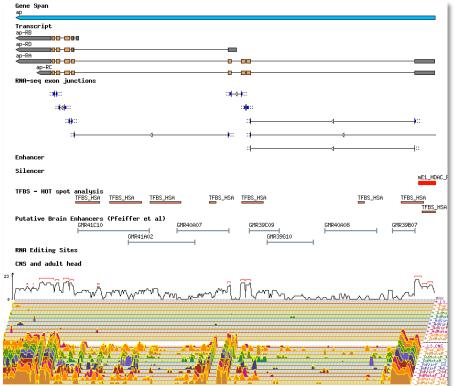**Expression/Regulation** view includes:
   RNA-Seq expression data, chromatin domains, transcription factor binding sites, insulators, enhancers, etc.
MegaView view includes:
   Deletions and duplications, tiling BACs, and allows a whole chromosome arm to be viewed at once.
Gene Disruptions, Stocks, and Reagents view includes:
   Indels, point mutations, fly stocks, RNAi amplicons, etc.

New and notable GBrowse tracks

Gene Span
ap

Transcript
ap-RB
ap-RD
ap-RA
ap-RC

RNA-seq exon junctions

Enhancer

Silencer

mE1_HDAC_

TFBS - HOT spot analysis
TFBS_HSA TFBS_HSA TFBS_HSA   TFBS_HSA TFBS_HSA   TFBS_HSA   TFBS_HSA
TFBS_HSA

Putative Brain Enhancers (Pfeiffer et al)
   GMR41C10   GMR40A07   GMR39C09   GMR40A08   GMR39B07
     GMR41A02   GMR39G10

RNA Editing Sites
CNS and adult head

23

- 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.

[**Help and key for FlyBase evidence tiers**]

⊟**Tracks**
  ⊟ **Reference Genome Annotations (Iso-1)** Select all | Clear all
    ☑ Gene Span   ☐ CDS   ☑ Repeat region
    ☑ Transcript   ☑ Natural TE (only visible below 300Kb)
  ⊟ **General** Select all | Clear all
    ☐ 3-frame translation (forward)   ☐ DNA/GC Content   ☐ 3-frame translation (reverse)
  ⊟ **Aligned Evidence** Select all | Clear all
    ☑ cDNA   ☐ mRNA   ☑ RNA-seq exon junctions