

An open source integrated database of genomic, expression and protein data for *Drosophila*, *Anopheles* and other insects.



**Log in to save queries and bags.**

**Upload your own lists of identifiers to run queries against**

**Quick Search**

**Quickly navigate to an entry for a particular identifier**

**Browse FlyMine by type of data/data source**

**Search descriptions of predefined template queries**

**Navigate to a query builder starting point**

**Template search**

**FlyMine QueryBuilder**

## What can I do with FlyMine?

FlyMine is an integrated database of genomic, expression and protein data from *Drosophila*, *Anopheles* and other insects. As an integrated resource it is possible to run data mining queries that span domains of biological knowledge. Inclusion of InParanoid orthologues allows comparative analysis between organisms.

### Quick Search

Enter any identifier, symbol or gene name in the search box on the FlyMine home page to access details pages and integrated tools.

### Browse Aspects

FlyMine presents data as 'aspects', with each aspect providing a view of a particular type of data (for example Gene Expression or Protein Interactions). Use the aspect icons on the FlyMine home page to run a predefined template query or to build your own query (see below).

### Run Template Queries

Dozens of useful queries have been predefined. These range from simple queries to retrieve a particular type of data to more complex queries that span the different types of data. Find lists of template queries on each aspect page or use the Template Search box on the home page and in the top menu.

### Use the FlyMine QueryBuilder

Advanced users can use a flexible query interface to construct their own data mining queries across the multiple integrated data sources, to modify existing template queries or to create new template queries. Access the FlyMine QueryBuilder via the home page or choose a query starting point on an aspect page.

### Operate on Lists

All queries in FlyMine can be performed on lists (or 'bags') that you create yourself. Bags can be created by typing or pasting in a list of identifiers, or uploading a file containing the list. Data from previous queries can also be saved into a bag using the boxes displayed underneath the query results. Saved bags of data can be used to constrain new queries, perform logical operations and can be exported.

### Save Queries

You can save your bags, queries and templates between sessions by creating an account using the 'Log in' box in the top menu on every page.

### FlyMine data sources include:

- *D. melanogaster* and *D. pseudoobscura* genome annotation - FlyBase
- *A. gambiae* and *A. mellifera* genome annotation - Ensembl
- InParanoid orthologues between multiple organisms
- UniProt protein data for multiple organisms
- Protein-protein interactions (multiple experiments) for *D. melanogaster* and *C. elegans* - IntAct
- Protein Family and Domain data for *D. melanogaster*, *A. gambiae* and *C. elegans* - InterPro
- *D. melanogaster* protein domain 3-D structure predictions - Kenji Mizuguchi, University of Cambridge
- RNAi phenotypes for *C. elegans* genes - WormBase
- The Gene Ontology
- GO annotations for *D. melanogaster*, *A. gambiae*, *C. elegans*, *A. mellifera* and other organisms
- FlyReg DNase I footprints for *D. melanogaster*
- Microarray gene expression data, including Arbeitman et al (2002) *D. melanogaster* time course experiment
- *D. melanogaster* P-element insertion and deletion locations - DrosDel
- Homophila human disease to *Drosophila* gene data set
- INDAC microarray oligo set for *D. melanogaster* - INDAC Consortium
- *D. melanogaster* whole genome tiling amplicon set

# FlyMine details page

For every FlyMine database entry there is a details page. Below is an example for the zen gene. A summary of the entry is provided at the top of the page and further details are grouped into aspects. You can navigate to other, related entries and quickly view results of relevant template queries.

**Callouts for FlyMine details page:**

- Your navigation trail**: Points to the top navigation bar.
- Quick summary for the entry**: Points to the 'Summary for selected Gene' section.
- Link-outs to other sites**: Points to links for FlyBase and FBgn0004053.
- Navigate to a related entry**: Points to the 'Genome browser view (GBrowse)' section.
- Export FASTA sequence**: Points to the 'FASTA...' link under the 'synonyms' section.
- View a collection of entries related to this entry**: Points to the 'Other details by aspect' section.
- Inline template queries. Relevant template queries are automatically executed**: Points to the 'TFBindingSite' table.
- Some template queries return no results for the viewed object**: Points to the '2 UTR' section.
- Navigate to this template query**: Points to a link in the 'TFBindingSite' table.
- Show all results for the template query**: Points to the 'Show in table...' link.

**Table: TFBindingSite**

TFBindingSite > factor	identifier	organismDbId	symbol	TFBindingSite	identifier	TFBindingSite > chromosomeLocation > obje
Gene [details...]	CG1046	FBgn0004053	zen	TFBindingSite [details...]	FPID004210	2L
Gene [details...]	CG1046	FBgn0004053	zen	TFBindingSite [details...]	FPID004211	2L
Gene [details...]	CG1046	FBgn0004053	zen	TFBindingSite [details...]	FPID006353	2R
Gene [details...]	CG1046	FBgn0004053	zen	TFBindingSite [details...]	FPID006356	2R
Gene [details...]	CG1046	FBgn0004053	zen	TFBindingSite [details...]	FPID006148	3R

# FlyMine QueryBuilder

Advanced users can use the QueryBuilder to construct their own queries, customise existing template queries or create new template queries. Access the FlyMine QueryBuilder via the FlyMine home page or choose a query starting point on an aspect page.

**Callouts for FlyMine QueryBuilder:**

- Quickly move to a different aspect**: Points to the 'Go to: -- Choose aspect --' dropdown.
- Constrain an attribute**: Points to the 'Constrain?' section.
- Remove constraint**: Points to the 'Remove constraint' button.
- Edit existing constraint**: Points to the 'Edit...' button.
- After clicking CONSTRAIN to the left or an edit icon to the right, constraint settings are displayed here**: Points to the 'Constraint logic' section.
- Edit the logic between constraints**: Points to the 'AND/OR' logic buttons.
- Clicking SHOW will add an attribute to the output table**: Points to the 'SHOW' button.
- Click the disclosure boxes to navigate down into the model**: Points to the disclosure boxes in the 'Fields selected for output?' section.
- Click and drag (on the blue background) to reorder the output columns**: Points to the blue background of the output columns.
- Export your query to share with others**: Points to the 'Export this query as XML or IQL' button.
- Save a query to your profile**: Points to the 'Save query' button.
- Remove attribute from the output table**: Points to the 'Remove' button.

**Fields selected for output?**

Gene > organismDbId	Gene > identifier	Gene > symbol	Gene > goAnnotation > name	Gene > goAnnotation > identifier
String	String	String	String	String