

FlyMine

An integrated database for *Drosophila*
and *Anopheles* genomics



Outline

- What is FlyMine.
- Why do we need another database?
- Technical stuff.
- Data sources.
- Key features of querying FlyMine.
- Further Information and Feedback.



What is FlyMine

- A database that integrates several genomic and proteomic data sets in one place.
- Main focus is *Drosophila melanogaster* and *Anopheles gambiae* data but will be extended to include data from other insects.
- Includes data from other model organisms such as *C. elegans* for cross-species comparisons through orthologue data.



Why yet another database?



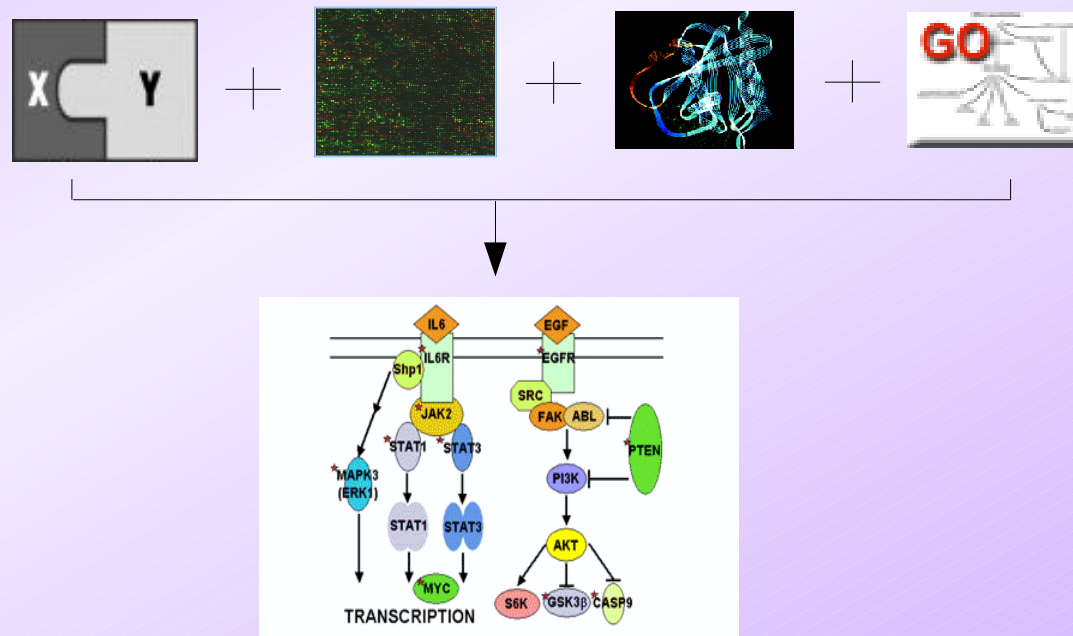
Many different databases...

- Currently lots of databases.
- Data stored in different format in each database.
- Hard to query across all these different sources.



Lots of data...

- Massive amounts of experimental data (microarray, proteomics) being produced.
- Data quality can vary significantly : high-throughput datasets tend to be noisy.
- Stronger inferences can be made when data are combined from different sources.

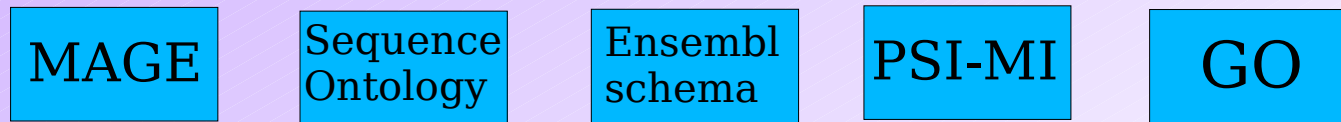


Key Points

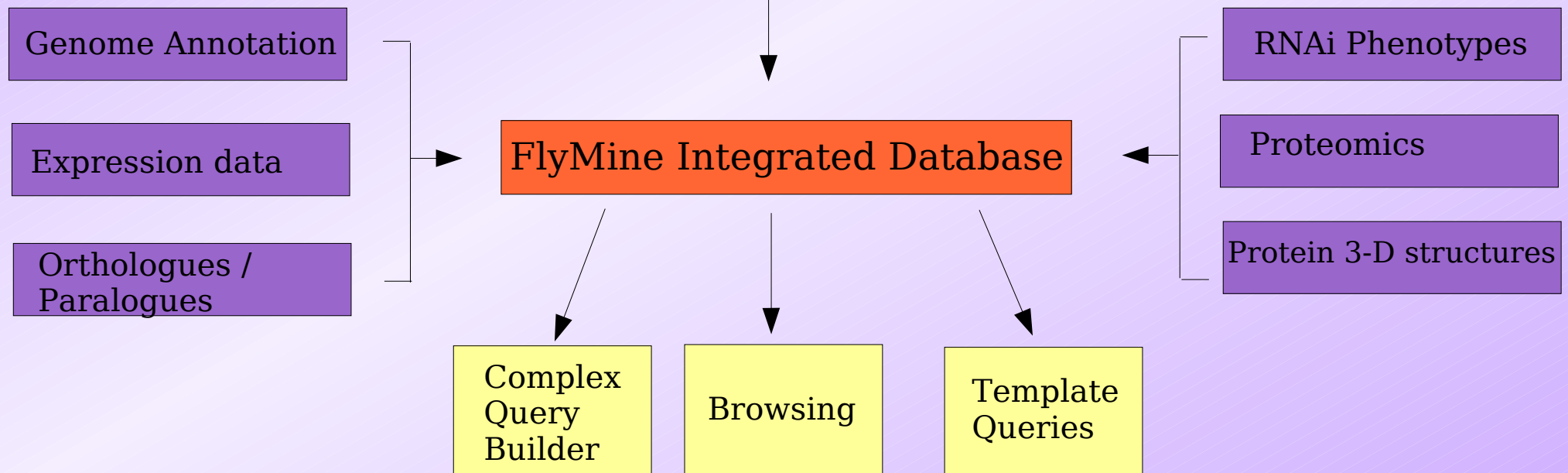
- Provide a powerful web-based query interface that allows construction of arbitrary and complex queries.
- Provide template queries for simpler access to the data.
- Provide link-ins from FlyBase and link-outs to FlyBase and other databases.
- Provide tools for the further viewing and analysis of data generated through a query.



Creating an Integrated database



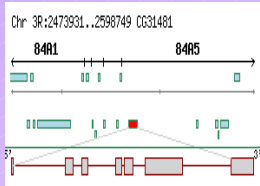
FlyMine Data Model



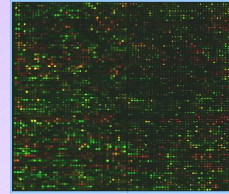
www.intermine.org

FlyMine

Data Sources



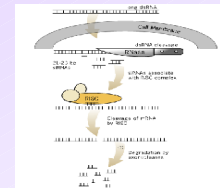
Genome Annotation



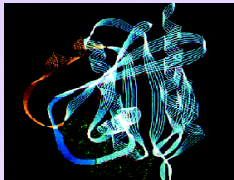
Microarray expression data



2-hybrid
Protein-Protein
Interactions



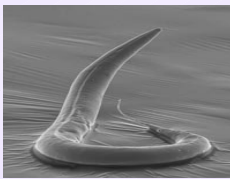
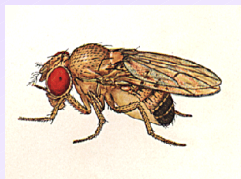
RNAi Phenotypes



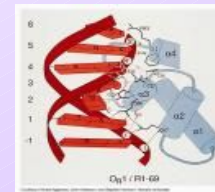
3-D structural
domain predictions



GO Annotation



Orthologues/
Paralogues



DNAase 1 footprints



Further Information, Help and Feedback

- FlyMine website: www.flymine.org: **release-2.0 Now Available.**
- On-line documentation: manual, tutorials, quick-start guide.
- Please give us feedback: Comments, suggestions, queries and data.
- Contact: email info@flymine.org / use the feedback form on the web site / contact Rachel Lyne: +44 1223 333377.
- Mailing list for announcements from the FlyMine web site.
- Drop-in for a tutorial/demonstration during the conference.



Acknowledgements

Richard Smith
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Tom Riley
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Markus Brosch
Debashis Rana
Andy Varley
Gos Micklem

More information at www.flymine.org



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FlyMine



Query Front Page:

FlyMine

An integrated database for *Drosophila* and *Anopheles* genomics

[Home](#) [Current query](#) [New query](#) [History](#) [Examples](#) [Templates](#) [Login](#) [Feedback form](#) [Help](#)

Build a query - choose a starting point

[\[help...\]](#)

Genomics

[Chromosome](#), [ChromosomeBand](#), [Gene](#), [Transcript](#), [Exon](#), [TRNA](#), [NcRNA](#), [Orthologue](#), [Paralogue](#), [GOTerm](#), [Phenotype](#), [RNAiExperiment](#)
or [view related template queries...](#)

[Create a bag of identifiers](#) ➤
[List all classes](#) ➤
[Browse model](#) ➤

Transcriptomics

[Transcript](#)

Proteomics

[Protein](#), [ProteinInteraction](#), [ProteinInteractionExperiment](#), [ProteinStructure](#)
or [view related template queries...](#)

Evidence

[AnalysisResult](#), [Experiment](#), [InfoSource](#), [Database](#), [Publication](#)

Others

[Organism](#)

Query Builder

Browse

[\[help...\]](#)

Browse
Enter an identifier or synonym (e.g. 'timeout')

Browse Mode

Predefined template queries

[\[help...\]](#)

Genomics

[Find an entry in the database using any identifier or synonym.](#) ➤

[Show the GO annotations for a particular gene](#) ➤

[For a particular genome database identifier, show all other identifiers and synonyms in FlyMine.](#) ➤

[Show the genes, transcripts and exons located between two points on a chromosome. Give the location of the exons.](#) ➤

[Show the chromosome location of the exons for a particular gene](#) ➤

[Show the predicted orthologues between two organisms.](#) ➤

[Show genes from Drosophila annotated with GO term.](#) ➤

[Show the predicted transcripts and the number of exons for a particular gene](#) ➤

[Show genes located on a particular chromosome.](#) ➤

Proteomics

[For the protein product of a particular gene, show any proteins it has been shown to interact with and for these proteins any regions which have a Pfam domain with a predicted 3-D structure.](#) ➤

Predefined Queries

Predefined Template Queries:

- Show the genes, transcripts and exons located between two points on a chromosome. Give the location of the exons.

This is a template query - edit the values below

Show the genes, transcripts and exons located between two points on a chromosome. Give the location of the exons.

[1] *Show the genes, transcripts and exons located on chromosome:*

Chromosome identifier

[2] *from:*

Organism name

[3] *between base:*

Location start

[4] *and:*

Location end

← Fill in the boxes.



Table-style Results:

Query results

| <input type="checkbox"/> | Chromosome.exons.gene.organismDbId [>][hide] | <input type="checkbox"/> | Chromosome.exons.gene.identifier [<][>][hide] | <input type="checkbox"/> | Chromosome.exons.transcripts.identifier [<][>][hide] | <input type="checkbox"/> | Chromosome.exons.objects.start [<][>][hide] | <input type="checkbox"/> | Chromosome.exons.objects.end [<][>][hide] | <input type="checkbox"/> | Chromosome |
|--------------------------|---|--------------------------|--|--------------------------|---|--------------------------|--|--------------------------|--|--------------------------|------------|
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 13520 | <input type="checkbox"/> | 13625 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 13683 | <input type="checkbox"/> | 14874 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 14933 | <input type="checkbox"/> | 15711 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 19880 | <input type="checkbox"/> | 20020 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 21066 | <input type="checkbox"/> | 21200 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0002121 | <input type="checkbox"/> | CG2671 | <input type="checkbox"/> | CG2671-RF | <input type="checkbox"/> | 21349 | <input type="checkbox"/> | 21372 | <input type="checkbox"/> | -1 |
| <input type="checkbox"/> | FBgn0031208 | <input type="checkbox"/> | CG11023 | <input type="checkbox"/> | CG11023-RA | <input type="checkbox"/> | 7529 | <input type="checkbox"/> | 8116 | <input type="checkbox"/> | 1 |
| <input type="checkbox"/> | FBgn0031208 | <input type="checkbox"/> | CG11023 | <input type="checkbox"/> | CG11023-RA | <input type="checkbox"/> | 8229 | <input type="checkbox"/> | 8589 | <input type="checkbox"/> | 1 |
| <input type="checkbox"/> | FBgn0031208 | <input type="checkbox"/> | CG11023 | <input type="checkbox"/> | CG11023-RA | <input type="checkbox"/> | 8668 | <input type="checkbox"/> | 9491 | <input type="checkbox"/> | 1 |
| <input type="checkbox"/> | FBgn0031209 | <input type="checkbox"/> | CG2657 | <input type="checkbox"/> | CG2657-RA | <input type="checkbox"/> | 21919 | <input type="checkbox"/> | 22687 | <input type="checkbox"/> | -1 |

Displaying 51 to 60 of 86 rows
[First](#) [Previous](#) [Next](#) [Last](#)
Page size 10 [Change](#)

Save and export

in a new bag named

Save

to existing bag

proteinsWithgenes

Add

Export results as comma separated values (suitable for import into Excel)

Export as tab separated values

Export Results

Export Results



Browsing:

- Different queries generate either table-style results or browsable results.
- This template query illustrates the browsing feature of FlyMine.

This is a template query - edit the values below

Find an entry in the database using any identifier or synonym.

[1] Synonym value

Enter any name
or identifier

[View Results](#)

[View Query](#)



Browsable Details Page:

Object details

Summary

Summary for selected Gene

| | |
|--------------|-------------------------|
| identifier | CG1046 |
| organismDbId | FBgn0004053 |
| organism | Drosophila melanogaster |

Fields

| | |
|--------------|-------------|
| organismDbId | FBgn0004053 |
| identifier | CG1046 |
| name | zen |

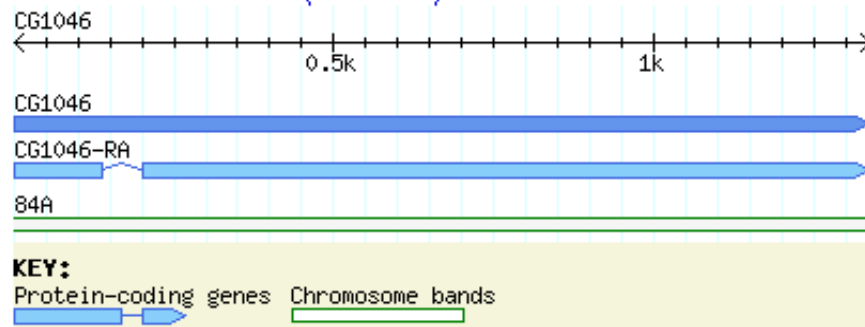
Further information for this Gene

Links to external databases:

[Ensembl](#) [CG1046](#)

[FlyBase](#) [FBgn0004053](#)

Genome browser view (GBrowse)



Other Information

| | |
|--------------------------------------|---|
| <input type="checkbox"/> organism | Organism [details...] |
| <input type="checkbox"/> sequence | Sequence [details...] |
| <input type="checkbox"/> chromosome | Chromosome [details...] |
| <input type="checkbox"/> proteins | 1 Protein objects [details...] |
| <input type="checkbox"/> transcripts | 1 Transcript objects [details...] |
| <input type="checkbox"/> objects | 5 Relation objects |
| <input type="checkbox"/> exons | 2 Exon objects |
| <input type="checkbox"/> evidence | 1 Evidence objects [details...] |
| <input type="checkbox"/> subjects | 2 Relation objects |
| <input type="checkbox"/> GOTerms | 6 GOTerm objects |
| <input type="checkbox"/> synonyms | 6 Synonym objects |
| <input type="checkbox"/> orthologues | 1 Orthologue objects [details...] |
| <input type="checkbox"/> annotations | 9 Annotation objects |

Browse for more information

GBrowse Genome Viewer

[Return to results of last query](#)

Browsable Details Page:

Object details

Summary for selected Gene

| | |
|--------------|-------------------------|
| identifier | CG1046 |
| organismDbId | FBgn0004053 |
| organism | Drosophila melanogaster |

Fields

| | |
|--------------|-------------|
| organismDbId | FBgn0004053 |
| identifier | CG1046 |
| name | zen |

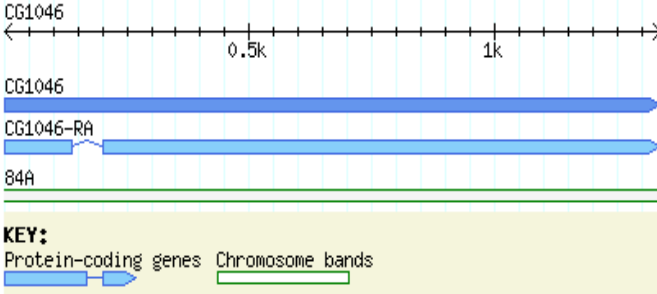
Further information for this Gene

Links to external databases:

[Ensembl](#) [CG1046](#)

[FlyBase](#) [FBgn0004053](#)

[Genome browser view \(GBrowse\)](#)



KEY:
Protein-coding genes Chromosome bands

Other Information

☒ **organism**

Organism [\[details...\]](#)

☒ **sequence**

Sequence [\[details...\]](#)

☒ **chromosome**

Chromosome [\[details...\]](#)

☐ **proteins**

1 Protein objects

| Class | primaryAccession | identifier | organism | | | | |
|---------|------------------|------------|----------|--------------|-----------------|-------------------------|------------------------------|
| | | | taxonId | abbreviation | shortName | name | |
| Protein | P09089 | | 7227 | DM | D. melanogaster | Drosophila melanogaster | [details...] |

☐ **transcripts**

1 Transcript objects

| Class | identifier | organism | | | | |
|------------|------------|----------|--------------|-----------------|-------------------------|------------------------------|
| | | taxonId | abbreviation | shortName | name | |
| Transcript | CG1046-RA | 7227 | DM | D. melanogaster | Drosophila melanogaster | [details...] |

☒ **objects**

5 Relation objects

☒ **exons**

2 Exon objects

☒ **evidence**

1 Evidence objects [\[details...\]](#)

☒ **subjects**

2 Relation objects

☐ **GOTerms**

6 GOTerm objects

| Class | | |
|--------|-------------|------------------------------|
| GOTerm | GO: 0005634 | [details...] |
| GOTerm | GO: 0006355 | [details...] |
| GOTerm | GO: 0007275 | [details...] |
| GOTerm | GO: 0009950 | [details...] |
| GOTerm | GO: 0003677 | [details...] |
| GOTerm | GO: 0003700 | [details...] |

☒ **synonyms**

6 Synonym objects

☒ **orthologues**

1 Orthologue objects [\[details...\]](#)

☒ **annotations**

9 Annotation objects

Expand sections for more information.

Click on details to go to the details page for that object.

[Return to results of last query](#)

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[\[help...\]](#)

Genomics

[Chromosome](#), [ChromosomeBand](#), [Gene](#), [Transcript](#), [Exon](#), [TRNA](#), [NcRNA](#), [Orthologue](#), [Paralogue](#), [GOTerm](#), [Phenotype](#), [RNAiExperiment](#)
or [view related template queries...](#)

[Create a bag of identifiers](#) ➔
[List all classes](#) ➔
[Browse model](#) ➔

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[Transcript](#)

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[Protein](#), [ProteinInteraction](#), [ProteinInteractionExperiment](#), [ProteinStructure](#)
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[AnalysisResult](#), [Experiment](#), [InfoSource](#), [Database](#), [Publication](#)

Others

[Organism](#)

Query Builder

Browse

[\[help...\]](#)

Browse
Enter an identifier or synonym (e.g. 'timeout')

Browse Mode

Predefined template queries

[\[help...\]](#)

Genomics

Find an entry in the database using any identifier or synonym. ➔

Show the GO annotations for a particular gene ➔

For a particular genome database identifier, show all other identifiers and synonyms in FlyMine. ➔

Show the genes, transcripts and exons located between two points on a chromosome. Give the location of the exons. ➔

Show the chromosome location of the exons for a particular gene ➔

Show the predicted orthologues between two organisms. ➔

Show genes from *Drosophila* annotated with GO term. ➔

Show the predicted transcripts and the number of exons for a particular gene ➔

Show genes located on a particular chromosome. ➔

Proteomics

For the protein product of a particular gene, show any proteins it has been shown to interact with and for these proteins any regions which have a Pfam domain with a predicted 3-D structure. ➔

Predefined Queries

The Query Builder:

Build your query using this page

[help...]

Model browser ?

Browse through the results

1. The Model browser: browse and select data required.

Gene ?

CONSTRAIN

Identifier ?

SHOW

CONSTRAIN

name ?

SHOW

CONSTRAIN

organismDbId ?

SHOW

CONSTRAIN

+ annotations Annotation ? collection

SHOW

CONSTRAIN

+ CDSs CDS ? collection

SHOW

CONSTRAIN

+ chromosome Chromosome ?

SHOW

CONSTRAIN

+ evidence Evidence ? collection

SHOW

CONSTRAIN

+ exons Exon ? collection

SHOW

CONSTRAIN

+ GOTerms GOTerm ? collection

SHOW

CONSTRAIN

+ objects Relation ? collection

SHOW

CONSTRAIN

+ organism Organism ?

SHOW

CONSTRAIN

+ orthologues Orthologue ? collection

SHOW

CONSTRAIN

+ phenotypes Phenotype ? collection

SHOW

CONSTRAIN

+ proteins Protein collection

SHOW

CONSTRAIN

+ regulatoryRegions RegulatoryRegion ? collection

SHOW

CONSTRAIN

+ sequence Sequence

SHOW

CONSTRAIN

+ subjects Relation ? collection

SHOW

CONSTRAIN

+ synonyms Synonym ? collection

SHOW

CONSTRAIN

+ transcripts Transcript ? collection

SHOW

CONSTRAIN

+ UTRs UTR collection

SHOW

CONSTRAIN

Constraints on the current query ?

Click on a class name to view its fields in the left-hand pane

Gene

name

= zen

2. The Constraints list: add constraints to select subsets of data.

Fields selected for output ?

Gene
Gene
[x]

3. The Output Fields list: select what you want to see in your results.

Show results

Actions ?

Save query

The Query Builder:

Build your query using this page

[\[help...\]](#)

Model browser ?

Browse through the classes and attributes. Click on "show" links to add fields to the results table or on the arrows to constrain a value in the query

Gene ? [SHOW](#) [CONSTRAIN](#)

- identifier ? [SHOW](#) [CONSTRAIN](#)
- name ? [SHOW](#) [CONSTRAIN](#)
- organismDbId ? [SHOW](#) [CONSTRAIN](#)
- + annotations Annotation ? collection [SHOW](#) [CONSTRAIN](#)
- + chromosome Chromosome ? [SHOW](#) [CONSTRAIN](#)
- + evidence Evidence ? collection [SHOW](#) [CONSTRAIN](#)
- + exons Exon ? collection [SHOW](#) [CONSTRAIN](#)
- + GO Terms GO Term ? collection [SHOW](#) [CONSTRAIN](#)
- + objects Relation ? collection [SHOW](#) [CONSTRAIN](#)
- + organism Organism ? [SHOW](#) [CONSTRAIN](#)
- + orthologues Orthologue ? collection [SHOW](#) [CONSTRAIN](#)
- + phenotypes Phenotype ? collection [SHOW](#) [CONSTRAIN](#)
- + proteins Protein collection [SHOW](#) [CONSTRAIN](#)
- + regulatoryRegions RegulatoryRegion ? collection [SHOW](#) [CONSTRAIN](#)
- + sequence Sequence [SHOW](#) [CONSTRAIN](#)
- + subjects Relation ? collection [SHOW](#) [CONSTRAIN](#)
- + synonyms Synonym ? collection [SHOW](#) [CONSTRAIN](#)
- + transcripts Transcript ? collection [SHOW](#) [CONSTRAIN](#)
 - exonCount [SHOW](#) [CONSTRAIN](#)
 - identifier [SHOW](#) [CONSTRAIN](#)
 - + annotations Annotation ? collection [SHOW](#) [CONSTRAIN](#)
 - + chromosome Chromosome ? [SHOW](#) [CONSTRAIN](#)
 - + evidence Evidence ? collection [SHOW](#) [CONSTRAIN](#)
 - + exons Exon ? collection [SHOW](#) [CONSTRAIN](#)
 - + gene Gene ? [SHOW](#) [CONSTRAIN](#)
 - + objects Relation ? collection [SHOW](#) [CONSTRAIN](#)
 - + organism Organism ? [SHOW](#) [CONSTRAIN](#)
 - + protein Protein [SHOW](#) [CONSTRAIN](#)
 - + sequence Sequence [SHOW](#) [CONSTRAIN](#)
 - + subjects Relation ? collection [SHOW](#) [CONSTRAIN](#)
 - + synonyms Synonym ? collection [SHOW](#) [CONSTRAIN](#)

Constraints on the current query ?

Click on a class name to view its fields in the left-hand pane

No fields constrained

Expand a field to show attributes for that class and the links to other classes.

Fields selected for output ?

No fields selected for output - click on the "show" links to add fields to the results table

The Query Builder:

Build your query using this page

[\[help...\]](#)

Model browser ?

Browse through the classes and attributes. Click on "show" links to add fields to the results table or on the arrows to constrain a value in the query

Gene ? [SHOW](#) [CONSTRAIN](#)

 identifier ? [SHOW](#) [CONSTRAIN](#)

 name ? [SHOW](#) [CONSTRAIN](#)

 organismDbId ? [SHOW](#) [CONSTRAIN](#)

 + annotations Annotation ? collection [SHOW](#) [CONSTRAIN](#)

 + chromosome Chromosome ? [SHOW](#) [CONSTRAIN](#)

 + evidence Evidence ? collection [SHOW](#) [CONSTRAIN](#)

 + exons Exon ? collection [SHOW](#) [CONSTRAIN](#)

 + GO Terms GO Term ? collection [SHOW](#) [CONSTRAIN](#)

 + objects Relation ? collection [SHOW](#) [CONSTRAIN](#)

 - organism Organism ? [SHOW](#) [CONSTRAIN](#)

 abbreviation [SHOW](#) [CONSTRAIN](#)

 genus [SHOW](#) [CONSTRAIN](#)

 name [SHOW](#) [CONSTRAIN](#)

 shortName [SHOW](#) [CONSTRAIN](#)

 species [SHOW](#) [CONSTRAIN](#)

 taxonId [SHOW](#) [CONSTRAIN](#)

 + orthologues Orthologue ? collection [SHOW](#) [CONSTRAIN](#)

 + phenotypes Phenotype ? collection [SHOW](#) [CONSTRAIN](#)

 + proteins Protein collection [SHOW](#) [CONSTRAIN](#)

 + regulatoryRegions RegulatoryRegion ? collection [SHOW](#) [CONSTRAIN](#)

 + sequence Sequence [SHOW](#) [CONSTRAIN](#)

 + subjects Relation ? collection [SHOW](#) [CONSTRAIN](#)

 + synonyms Synonym ? collection [SHOW](#) [CONSTRAIN](#)

 + transcripts Transcript ? collection [SHOW](#) [CONSTRAIN](#)

Constraints on the current query ?

Click on a class name to view its fields in the left-hand pane

Gene   Organism 

 organism  name 

Constrain ?

name

=  Drosophila melanogaster  [Add to query](#)

☒ NULL ☐ Not NULL [Add to query](#)

Clicking on a constrain button brings up a box where you specify your constraint.

Fields selected for output ?

No fields selected for output - click on the "show" links to add fields to the results table

The Query Builder:

Build your query using this page

[\[help...\]](#)

Model browser ?

Browse through the classes and attributes. Click on "show" links to add fields to the results table or on the arrows to constrain a value in the query.

- Gene ? [SHOW](#) [CONSTRAIN](#)
- [identifier](#) ? [CONSTRAIN](#)
- [name](#) ? [CONSTRAIN](#)
- [organismDbId](#) ? [SHOW](#) [CONSTRAIN](#)
- ☒ [annotations](#) Annotation ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [chromosome](#) Chromosome ? [SHOW](#) [CONSTRAIN](#)
- ☒ [evidence](#) Evidence ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [exons](#) Exon ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [GO Terms](#) GO Term ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [objects](#) Relation ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [organism](#) Organism ? [SHOW](#) [CONSTRAIN](#)
- [abbreviation](#) [SHOW](#) [CONSTRAIN](#)
- [genus](#) [SHOW](#) [CONSTRAIN](#)
- [name](#) [SHOW](#) [CONSTRAIN](#)
- [shortName](#) [SHOW](#) [CONSTRAIN](#)
- [species](#) [SHOW](#) [CONSTRAIN](#)
- [taxonId](#) [SHOW](#) [CONSTRAIN](#)
- ☒ [orthologues](#) Orthologue ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [phenotypes](#) Phenotype ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [proteins](#) Protein collection [SHOW](#) [CONSTRAIN](#)
- ☒ [regulatoryRegions](#) RegulatoryRegion ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [sequence](#) Sequence [SHOW](#) [CONSTRAIN](#)
- ☒ [subjects](#) Relation ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [synonyms](#) Synonym ? collection [SHOW](#) [CONSTRAIN](#)
- ☒ [transcripts](#) Transcript ? collection [SHOW](#) [CONSTRAIN](#)

Constraints on the current query ?

Click on a class name to view its fields in the left-hand pane

Gene ☒ [organism](#) ☒ Organism ☒
 [name](#) ☒
 = *Drosophila melanogaster* ☒

Clicking on a show button next to a field or attribute, adds it to the 'fields selected for output', meaning that it will be shown in your results.

Fields selected for output ?

Use "<" and ">" to choose the output column order

Gene > identifier
String
[>][x]

Gene > name
String
[<][x]

Show results

Actions ?

Save query

Integrating Protein interactions with 3-D structure:

- For the protein product of a particular gene, show any proteins it has been shown to interact with, the Pfam domains of these proteins and any predicted structure for the domains.

This is a template query - edit the values below

For the protein product of a particular gene, show any proteins it has been shown to interact with and for these proteins any regions which have a Pfam domain with a predicted 3-D structure.

[1] *Show protein interactions and Pfam domains with predicted 3-D structures for the protein product of gene:*

Synonym value = 128up

[View Results](#) [View Query](#)



Results Table (subset):

Bait Protein

Pfam Domains

Link to
modelled
structure

S

Query results

| <input type="checkbox"/> Synonym.subject.proteins.interactions.bait.primaryAccession [>] hide | <input type="checkbox"/> Synonym.subject.proteins.interactions.bait.regions.sequenceFamily.name [<] [>] hide | <input type="checkbox"/> Synonym.subject.proteins.interactions.bait.regions.structures [<] [>] hide | <input type="checkbox"/> |
|--|--|---|--------------------------|
| <input type="checkbox"/> P32234 | <input type="checkbox"/> PF01018 | <input type="checkbox"/> ModelledProteinStructure [details...] | <input type="checkbox"/> |
| <input type="checkbox"/> P32234 | <input type="checkbox"/> PF02824 | <input type="checkbox"/> ModelledProteinStructure [details...] | <input type="checkbox"/> |

Displaying 1 to 2 of 2 rows

Page size [Change](#)

Save and export

- ♦ in a new bag named [Save](#)
- ♦ to existing bag [Add](#)
- ♦ [Export results as comma separated values \(suitable for import into Excel\)](#)
- ♦ [Export as tab separated values](#)



Jmol Structural Viewer:

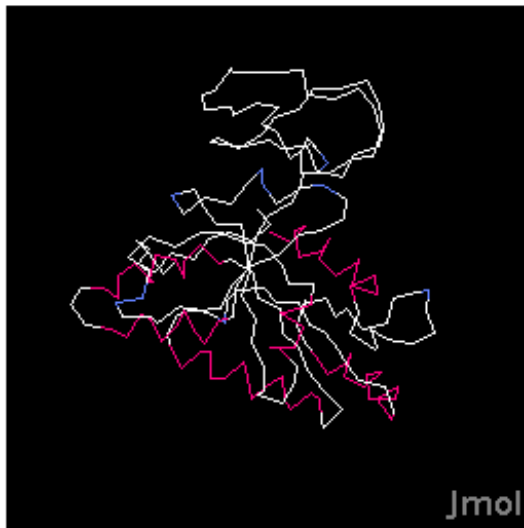
Object details

Summary for selected ModelledProteinStructure

Fields

atm EXPDTA MODEL, MODELLER Version 6v2 2004/04/22 11:47:18. ...
ZScore -3.03
QScore -0.55

Further information for this ModelledProteinStructure



[Return to results of last query](#)



Other Features:

Saved bags

| | Bag name | Number of objects |
|--------------------------|-------------------------------------|-------------------|
| <input type="checkbox"/> | proteinsWithgenes | 30333 |
| <input type="checkbox"/> | proteinsWithGenesDM | 21068 |
| <input type="checkbox"/> | bag1 | 3 |
| <input type="checkbox"/> | proteinsWithGenes2 | 30333 |

Saved Bags

Delete Union Intersect

Logical Operations

Saved queries

| | Query name | Approx rows |
|--------------------------|--|-------------|
| <input type="checkbox"/> | Gene2ProteinInteractions2structure | |
| <input type="checkbox"/> | testInterologs2_18_11_04 | |
| <input type="checkbox"/> | synonymGene2exonChromosomeLocations1 | |
| <input type="checkbox"/> | synonym2proteinInteractionsWithGO1 | |
| <input type="checkbox"/> | Genes2proteinStructure1 | |
| <input type="checkbox"/> | test | |
| <input type="checkbox"/> | testInterologs1_18_11_04 | |
| <input type="checkbox"/> | query_1 | |
| <input type="checkbox"/> | GOidentifier2proteinInteractions1 | |
| <input type="checkbox"/> | Gene2Transcripts1 | |
| <input type="checkbox"/> | Genes2chromosome1 | |
| <input type="checkbox"/> | Gene2GO1 | |
| <input type="checkbox"/> | testInterologs3_19_11_04 | |
| <input type="checkbox"/> | Orthologues1 | |
| <input type="checkbox"/> | query_4 | |
| <input type="checkbox"/> | query_2 | |
| <input type="checkbox"/> | ChromosomeLocation2genes1 | |
| <input type="checkbox"/> | Genes2proteinStructure2 | |
| <input type="checkbox"/> | synonym2proteinInteractions1 | |
| <input type="checkbox"/> | Gene2proteinStructure2.1 | |
| <input type="checkbox"/> | test1_18_11_04 | |
| <input type="checkbox"/> | query_6 | |
| <input type="checkbox"/> | synonymGene2exonChromosomeLocations2 | |
| <input type="checkbox"/> | query_3 | |
| <input type="checkbox"/> | Pfam2proteinStructure1 | |

Saved Queries



Further Information, Help and Feedback

- FlyMine website: www.flymine.org: **release-2.0 Now Available.**
- On-line documentation: manual, tutorials, quick-start guide.
- Please give us feedback: Comments, suggestions, queries and data.
- Contact: email info@flymine.org / use the feedback form on the web site / contact Rachel Lyne: +44 1223 333377.
- Mailing list for announcements from the FlyMine web site.
- Drop-in for a tutorial/demonstration during the conference.



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More information at www.flymine.org



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FlyMine