

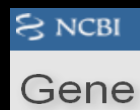
# Data-Mining with InterMine

from queries, to analysis, to display

# InterMine is:

- An integrated data-warehouse
- An optimising and caching query engine
- A set of web services
- **A suite of embeddable widgets**

# You are here



# You are here

*User Scripts and Programs*

*List Widgets*

*Tables*

*Java*

*Perl*

*Python*

*Ruby*

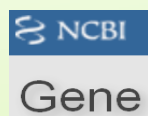
*JS*

*Web-  
Application*

*Web-Services*

*Internal API*

*Object Store*



# Who runs InterMine?

## InterMOD

- SGD (*S. cerevisiae*)
- RGD (*R. norvegicus*)
- ZFIN (*D. rerio*)
- Wormbase (*C. elegans*)
- MGI (*M. musculus*)

- FlyMine (*D. melanogaster*)
- modMine
- metabolicMine
- TargetMine
- mitoMine

*Also: S. pombe, FlyBase, TAIR*

# Goals

- Flexible to do what I want
- Quick to get it done
- Usable for ordinary mortals

# Features

- Queries - predefined and custom
- Saved result lists
- Reports and Analysis
- Flexible export
- API to all features

# Queries

- What are all the genes in the same pathway as my favourite gene, and annotated with a certain ontology term?
- What are the features in this set of regions?



# Templates and Tables

query history: 3 states ▾

Download Get js Code Create / Add to List ▾

Showing 11 to 20 of 1,586 rows Manage Columns

Rows per page: 10 ▾

| Gene > Secondary Identifier | Gene > Symbol | Gene > Proteins > Name | Gene > Exons > DB identifier |
|-----------------------------|---------------|------------------------|------------------------------|
| CG10203                     | x16           |                        | mp163                        |
| CG10203                     | x16           |                        | mp164                        |
| CG10203                     | x16           |                        | mp165                        |
| CG10203                     | x16           |                        | mp162                        |
| CG10203                     | x16           |                        | mp163                        |
| CG10203                     | x16           |                        | mp164                        |
| CG10203                     | x16           |                        | mp165                        |
| CG10268                     | CG10268       |                        | 0032811:1                    |
| CG10268                     | CG10268       |                        | 0032811:2                    |
| CG10399                     | CG10399       |                        | 0031877:1                    |

### All 176 Gene Symbols

Filter values

| Item                              | Count |
|-----------------------------------|-------|
| <input type="checkbox"/> Sam-S    | 171   |
| <input type="checkbox"/> CG5261   | 60    |
| <input type="checkbox"/> Oscillin | 45    |
| <input type="checkbox"/> VhaSFD   | 45    |
| <input type="checkbox"/> Pect     | 40    |
| <input type="checkbox"/> CG9527   | 33    |
| <input type="checkbox"/> GlcAT-S  | 32    |

Filter Reset Select All

Gene ➔ Pathway. ⭐

Show the Pathway identifier(s) and name for the selected gene. (Data Source: KEGG, REACTOME or FlyReactome).

query history: 8 states

Download Get Code Create / Add to List

Showing 1 to 25 of 9,815 rows

Columns Filters

p. 1 Rows per page: 25

| Gene > Pathways ><br>Name          | Gene > Pathways > Genes ><br>Symbol | Gene > Pathways > Genes > GO Annotation ><br>Ontology Term . Name |
|------------------------------------|-------------------------------------|---|
| Activation of Downstream Effectors | Cka                                 | JNK cascade   |
| Activation of Downstream Effectors | Cka                                 | compound eye ph   |
| Activation of Downstream Effectors | Cka                                 | cytoplasm   |
| Activation of Downstream Effectors | Cka                                 | dorsal closure  |
| Activation of Downstream Effectors | Cka                                 | mitotic spindle   |
| Activation of Downstream Effectors | Cka                                 | nucleus   |
| Activation of Downstream Effectors | Cka                                 | phagocytosis, eng   |
| Activation of Downstream Effectors | Cka                                 | positive regulation   |
| Activation of Downstream Effectors | Cka                                 | protein binding   |
| Activation of Downstream Effectors | DAAM                                | Rho GTPase bind   |
| Activation of Downstream Effectors | DAAM                                | actin binding   |
| Activation of Downstream Effectors | DAAM                                | actin cytoskeleton  |
| Activation of Downstream Effectors | DAAM                                | actin filament bund   |
| Activation of Downstream Effectors | DAAM                                | axonal growth con   |

All 33 Ontology Term Names (filtered from 1,179)

cyto

Item

☐ cytoplasm

☐ phagocytosis, engulfment

☐ actin cytoskeleton organization

☐ cytokinesis

☐ immune response-regulating cell surface receptor sig

☐ microtubule cytoskeleton organization involved in est

☐ cytoskeleton organization

Filter Reset Select All

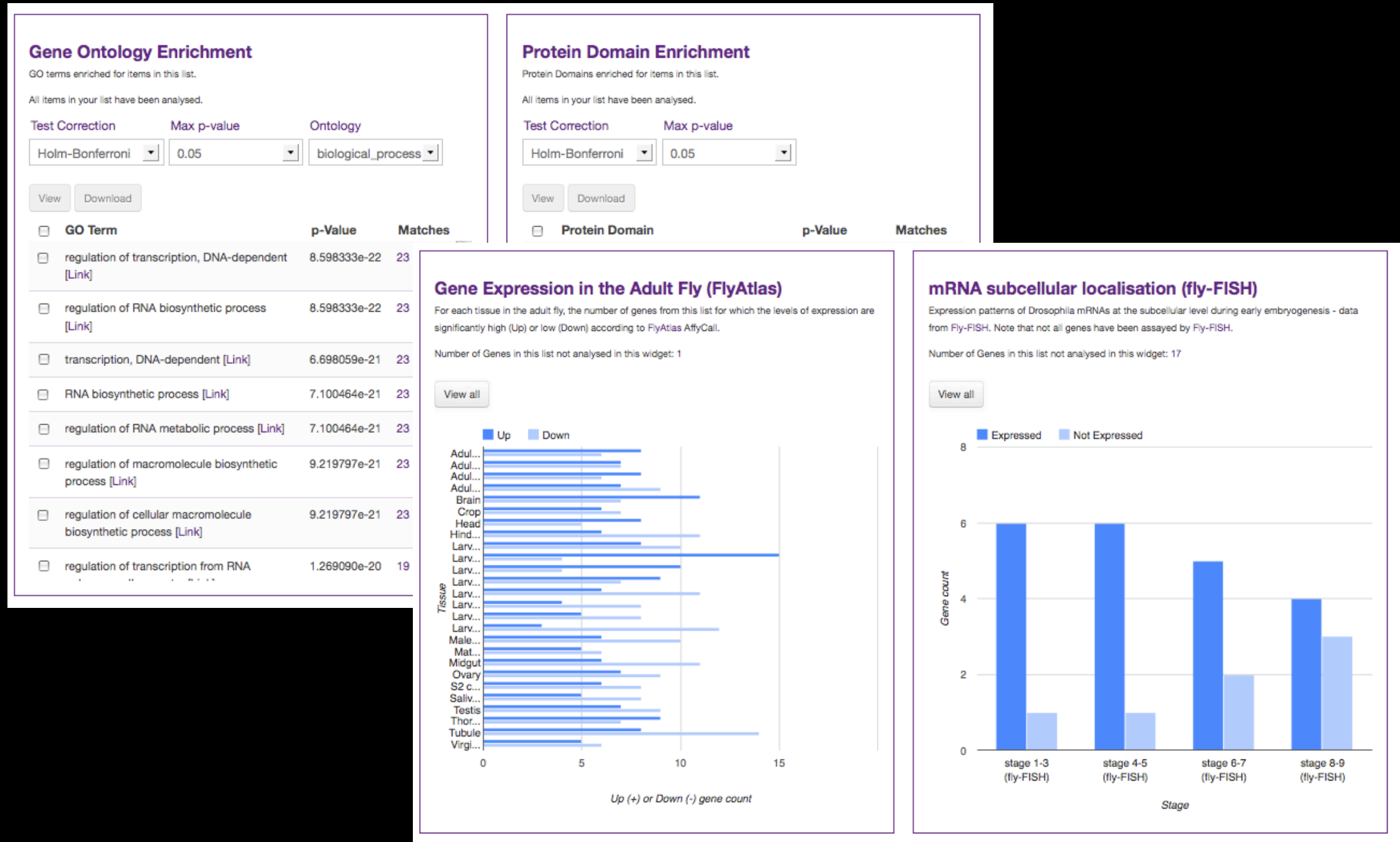
# Lists

- I have found a list of genes - can I
  - query over all of them at once?
  - See what characterises them?
  - See which are present in another list?

# Reports and Analysis

- For individual items: its properties and connections
- For groups of items: What is most significantly associated with these items, as a group.

# Analysis Widgets



# APIs and Libraries

- Support for:
  - ✓ Python
  - ✓ Perl
  - ✓ Ruby
  - ✓ Java
  - ✓ JavaScript (cross-browser & node.js)

```
from intermine.webservice import Service
s = Service('www.flymine.org/query')
q = s.model.Gene.select('*', 'proteins.proteinDomains.*')\
    .where('pathways', 'LOOKUP', 'pentose*')

for gene in q:
    print gene.symbol
    for protein in gene.proteins:
        for domain in protein.proteinDomains:
            print domain.name
```

```
from intermine.webservice import Service
s = Service('www.flymine.org/query')
q = s.model.Gene.select('*', 'proteins.proteinDomains.*')\
    .where('pathways', 'LOOKUP', 'pentose*')

for row in q.rows():
    print row['name'], row['proteins.proteinDomains.name']
```



# Over to You

- [www.flymine.org](http://www.flymine.org)
- [yeastmine.yeastgenome.org](http://yeastmine.yeastgenome.org)
- [ratmine.mcw.edu](http://ratmine.mcw.edu)
- [intermine.modencode.org](http://intermine.modencode.org)



# Toolkit



**Bootstrap**

UNDERSCORE.JS

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BACKBONE.JS

# One stop shop:

- All files served from [cdn.intermine.org](http://cdn.intermine.org)
  - ➡ *Dependencies (jquery, backbone, bootstrap)*
  - ➡ `im.js`
  - ➡ `im-tables.js`
  - ➡ `widgets.js`



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