

modMine

<http://intermine.modencode.org>

Accessing modENCODE data

Links to summary of all experiments and data generated...

Keyword Search: ordered faceted results

Genome Region Search: find features in user assigned genomic regions

Interactive exploratory interface of the regulatory regions

Expressions heatmap for a list of selected genes

Upload Lists

Use Template Queries

Analyze Lists of Data

feature view

Report page with detailed information about every feature.

GBrowse image of the relevant feature and link to the complete track.

Links to relevant data, including the list of features overlapping the given feature.

modENCODE

<http://www.modencode.org>
help@modencode.org

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- a comprehensive **encyclopedia of genomic functional elements** in the model organisms *C. elegans* and *D. melanogaster*
- a consortium of 11 primary projects, divided between worm and fly, spanning the various domains (see data categories).
- extensive collection of metadata, enabling fine-grained control over presentation and queries.
- a **portal** (www.modencode.org) to access the data.

Data Categories

Chromatin structure 3 experiments 43 data submissions
Copy Number Variation 2 experiments 5 data submissions
Gene Structure 4 experiments 132 data submissions
Histone modification and replacement 4 experiments 224 data submissions
Origins of Replication 1 experiment 3 data submissions
Other chromatin binding sites 5 experiments 332 data submissions
Replication Factors 2 experiments 13 data submissions
Replication Timing 1 experiment 3 data submissions
RNA expression profiling 21 experiments 436 data submissions
TF binding sites 1 experiment 43 data submissions

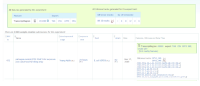
modENCODE portal



www.modencode.org

modENCODE home page
✓ project overview
✓ news, blog, publications
✓ data embargo & publication policy

modMine



integrated data warehouse

- ✓ modENCODE plus FlyBase/WormBase data
- ✓ search experimental details
- ✓ custom searches and Template Queries
- ✓ configurable export in multiple formats
- ✓ create and analyze lists of genes, features, etc
- ✓ links to GBrowse, repositories (GEO, SRA)

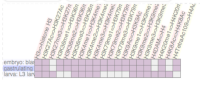
GBrowse



graphical genome browser

- ✓ search and toggle data tracks
- ✓ easily see correlations between tracks
- ✓ discrete features and continuous data
- ✓ export track data

File downloads



bulk download submitted files

- ✓ download submitted data files
- ✓ create custom download archives
- ✓ filter files by metadata
- ✓ grid view for easy selection

Submission wiki



wiki created by data submitters

- ✓ experiment and protocol descriptions
- ✓ detailed reagent information

modMine...

- is a **data warehouse** that integrates modENCODE results with data from **FlyBase**, **WormBase** and other sources.
- provides **easy navigation** through modENCODE experiments to view and **export data** that have been submitted and vetted in the project.
- includes a library of pre-defined **template queries** to mine modENCODE
- allows you to create and **analyse lists of data** and upload your own lists
- is based on the **InterMine** data warehousing system.

experiment view

Summary information about experiment

Export features from all submissions in GFF3, csv or other formats

Access data generated by each submission

View all submissions for this experiment - each submission varies experimental conditions

View and sort table by experimental factors - antibodies, cell lines, development stages, etc

All the available data files can be reached with external links from the summary table.

submission view

Detailed information about the submission, with list of experimental factors and links to more specific data.

Description of the submission and its location in the context of the modENCODE project.

Features can be exported in various formats

Single click queries find overlapping and nearby genes for features generated by the submission.

Browse all protocols used in this submission

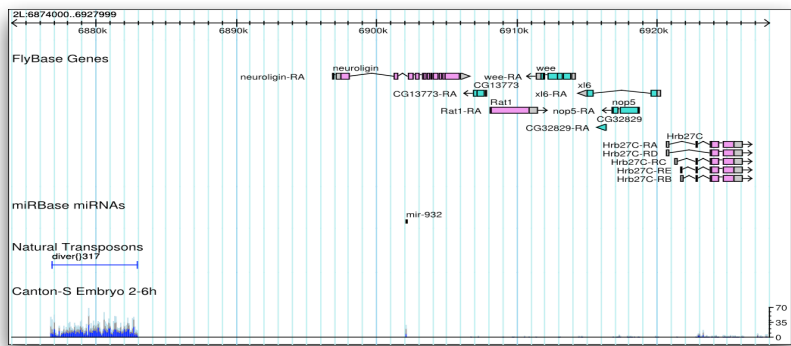
View GBrowse tracks and get raw data files from the FTP site.

query API

modMine includes a RESTful web service API allowing you to access data directly from programs you write in Perl or Java. See <http://blog.modencode.org/modmine/help>

GBrowse

Data are shown as a series of **graphical tracks** spanning the worm and fly genomes, alongside core datasets from WormBase and FlyBase. GBrowse is able to show **correlations** among diverse modENCODE data sets. For example, the stage-specific binding of a transcription factor can be visually correlated with stage-specific changes in that factor's putative target genes. GBrowse can visualize both **continuous quantitative data**, such as ChIP signal plots, and **discrete features** such as gene models and inferred binding sites. When appropriate, the two types of data can be shown simultaneously, for example called transcription factor binding sites superimposed on top of the underlying signal data.



Graphical Submission Filtering Tool

http://submit.modencode.org/submit/bulk_download

An easy-to-navigate **matrix** for the download of submission data.

The matrix is created by intersecting two submission categories. We provide **preset template** matrices such as ChIP-chip experiments displayed as a table of sample stage vs. antibody. Users can also create **custom tables** based on any of the large experiment groupings, such as cell line, tissue, stage, antibody, array platform. **Submissions** are selected by clicking on the matrix position at the intersection of the categories, providing access to the original raw submission files.

