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

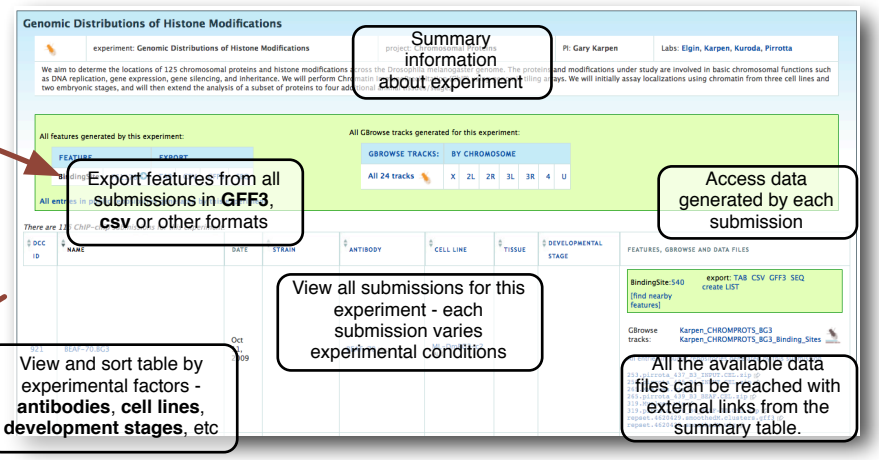
Expressions **heatmap** for a list of selected genes

Interactive exploratory interface of the **regulatory regions**

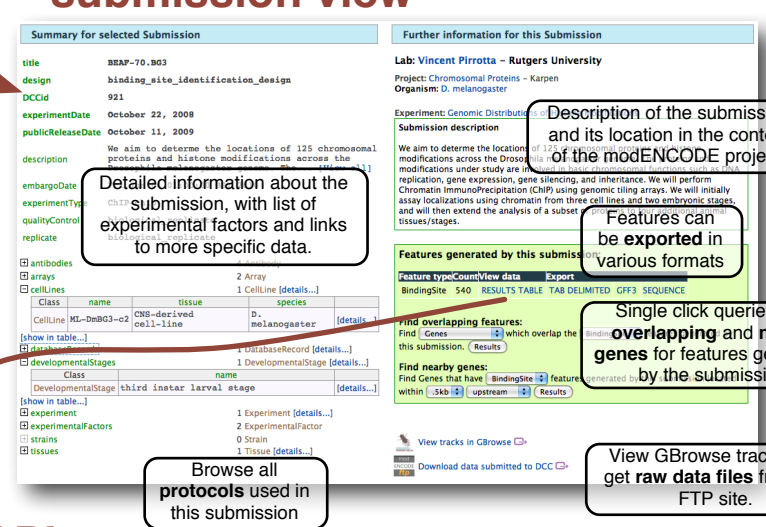
modMine...

- 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.

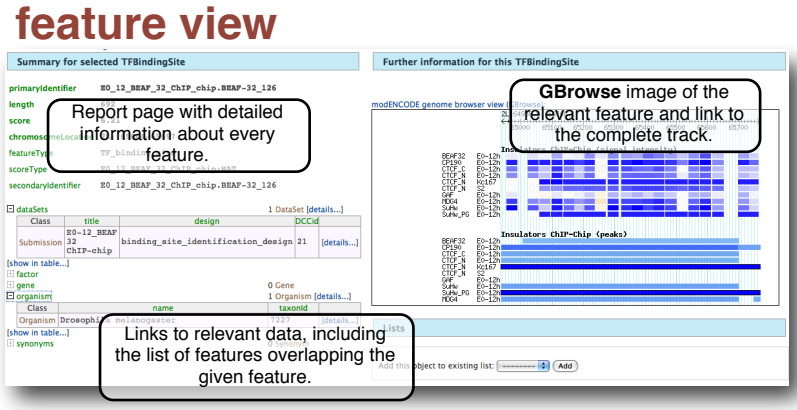
experiment view



submission view



feature view



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

modENCODE

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

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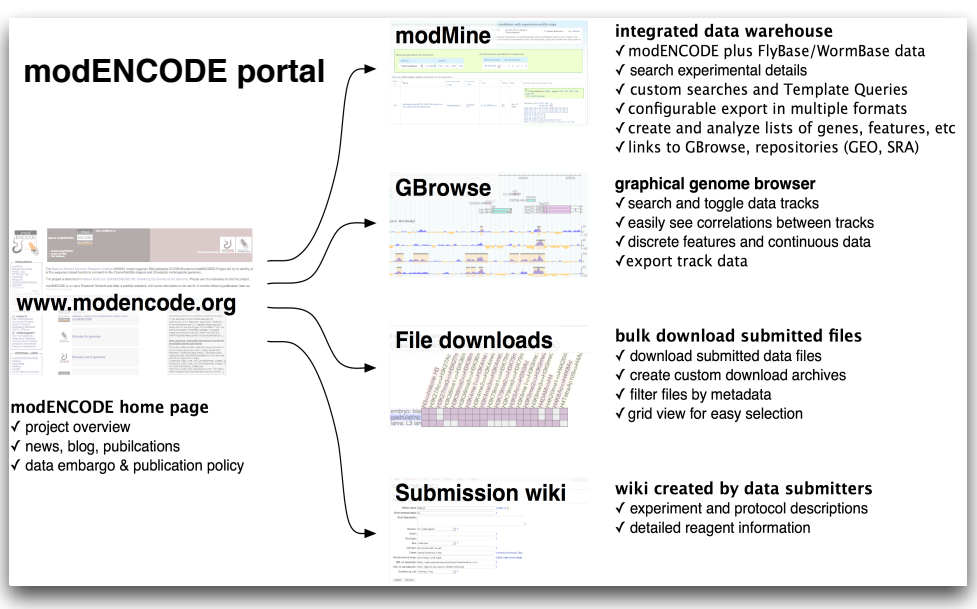
- a comprehensive **encyclopedia of genomic functional elements** in the model organisms C. elegans and D. melanogaster
- a consortium of 11 primary projects, divided between worm and fly, spanning the various domains (see data categories).
- extensive collection of metadata, enabling fine-grained control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

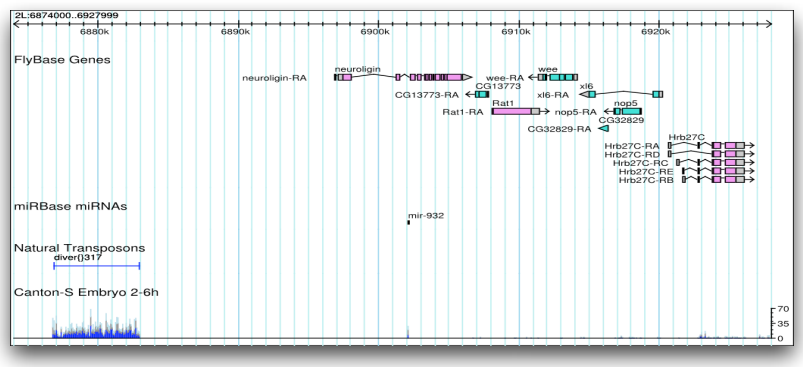
Data Categories

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*

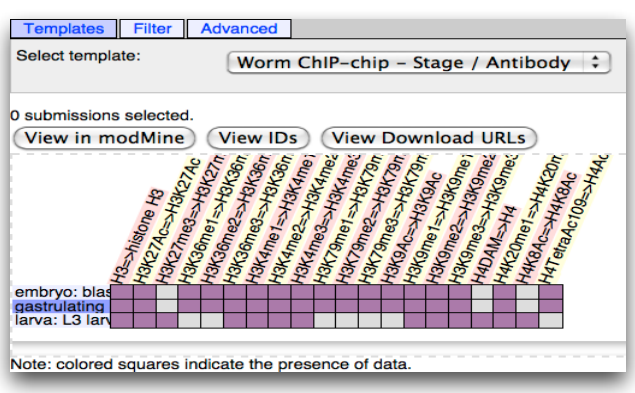


GBrowse

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.