

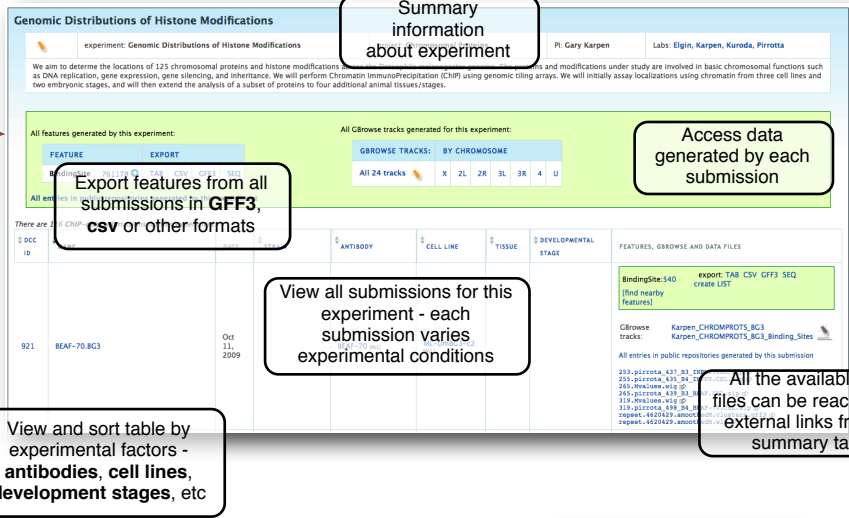
modMine

Accessing modENCODE data

<http://intermine.modencode.org>



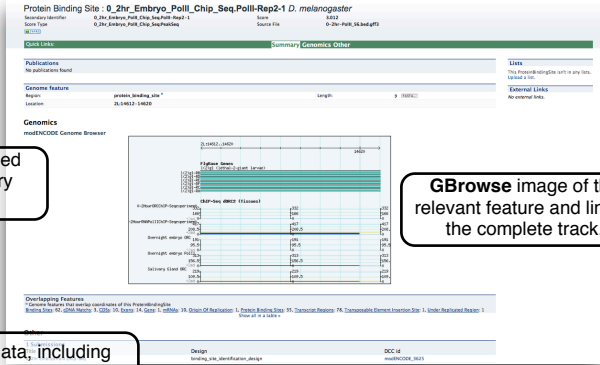
experiment view



submission view



feature view



Web Service API

modMine includes a RESTful web service API allowing you to access data directly from programs you write in Perl, Java, Python or Ruby. See <http://intermine.org/wiki/WebServiceQuickStart>

modENCODE

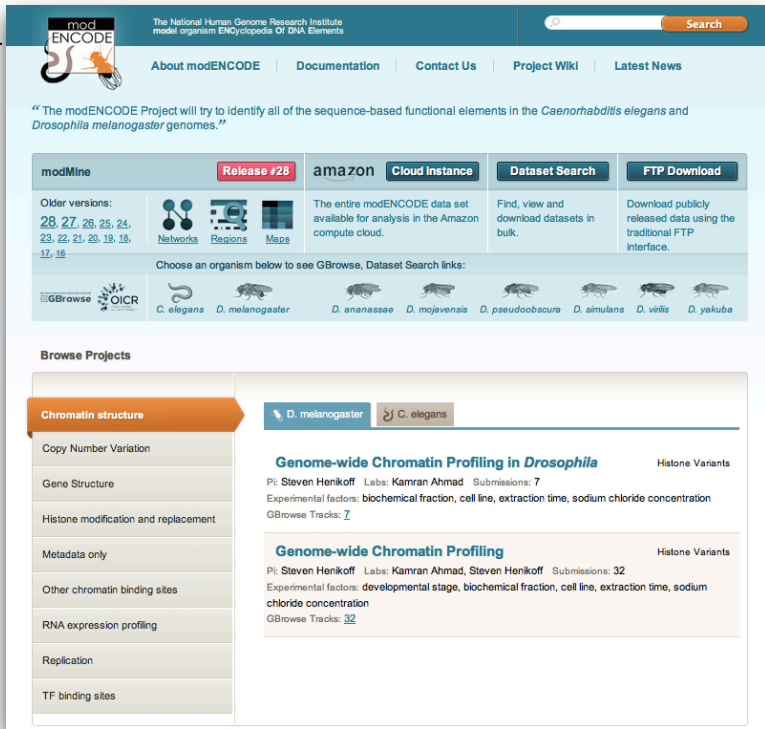
<http://www.modencode.org>
help@modencode.org

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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.

modENCODE portal



- **Faceted dataset search**
- **Sophisticated data mining**
- **GBrowse tracks**
- **Cloud instance**
- **Traditional ftp site**
- **Extensive web service API**
- **Gene networks interactive displays**
- **Expression heatmaps**
- **Project wiki**
- **Blog**
- **Growing set of explanatory documents**
- **Web seminars**
- **Help desk**

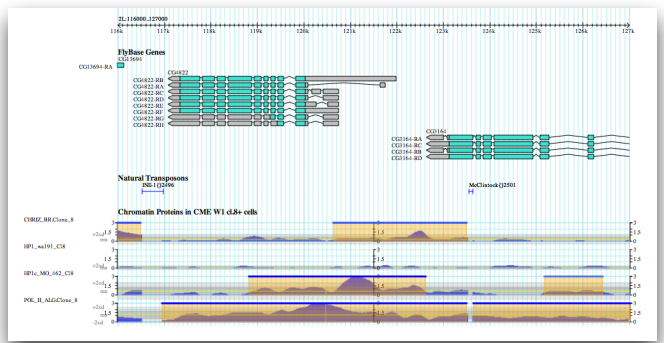
Data Categories

Chromatin structure 4 experiments 50 data submissions
Copy Number Variation 3 experiments 9 data submissions
Gene Structure 18 experiments 128 data submissions
Histone modification and replacement 5 experiments 254 data submissions
Origins of Replication 1 experiment 3 data submissions
Other chromatin binding sites 6 experiments 284 data submissions
Replication Factors 2 experiments 16 data submissions
Replication Timing 2 experiments 4 data submissions
RNA expression profiling 26 experiments 682 data submissions
TF binding sites 3 experiments 390 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.



Dataset Search

<http://data.modencode.org>

The tool make possible to quickly reach the dataset of interest using various **filtering criteria**: organism, category, target element, technique, etc. It then allows to **download** the dataset, **browse** the relevant GBrowse tracks, **view** it in modMine.

