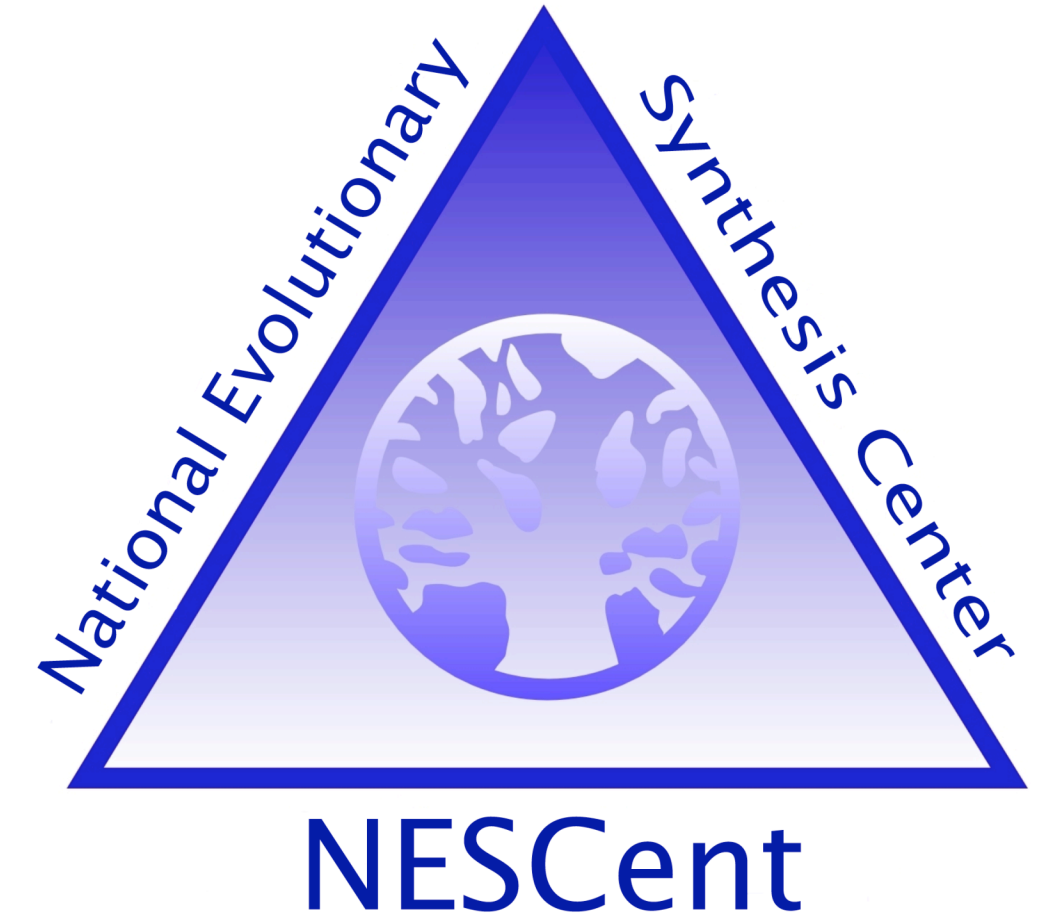




GMOD: Genomics Resources for Emerging Model Organisms

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Abstract

As genomics technologies have become widely available, many emerging model organism communities have accumulated an unprecedented volume of data on sequences, genotypes, expression patterns, etc. Much of this data is from organisms well suited to comparative genomic, evolutionary and ecological studies. More data offers more potential for discovery, but it also makes it is harder to organize, visualize and annotate. GMOD is a collection of interoperable open source software, including tools for managing, annotating and visualizing genomic data. GMOD tools are used in diverse contexts, from genome annotation projects within individual labs to major model organism databases.

Getting Started with GMOD

- Start at GMOD.org
- Download Software
- FAQs and HOWTOS
- Project Events
- Contribute Code! We're open source
- Project News
- GMOD for Biologists
- Contribute Doc! GMOD.org is a Wiki
- Support: Help Desk & mailing lists
- Popular GMOD Components

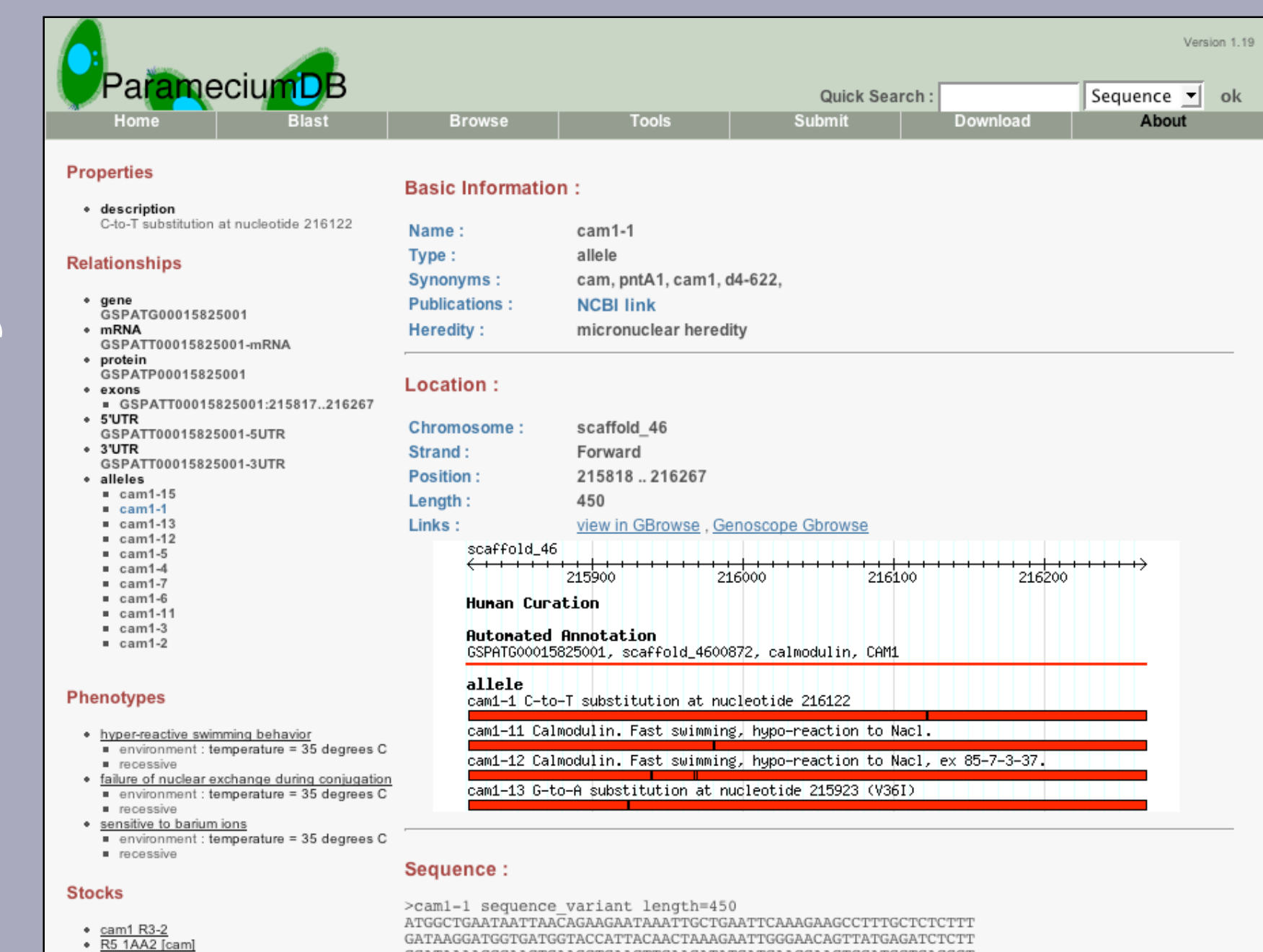
<http://gmod.org>

What Can GMOD Do?

If you have	& you need to	then GMOD can help with
Genomic Sequence	View Annotate Organize	GBrowse Apollo Chado Sequence Module
Comparative, Synteny	View Annotate Organize	CMap, SynView, SynBrowse, Sybil Sybil Chado Map Module
Phylogenetic Trees	Organize View	Chado Organism, Phylogeny modules GMODWeb
Phenotype, Genotype	Organize View	Chado Genetics Module GMODWeb
Microarray and Expression	View Organize	Java TreeView, Caryoscope, GeneXplorer Chado Mage, Expression Modules
Ontologies	Curate View	Chado CV module GO Term Viewer
Pathways	View, predict, organize	Pathway Tools
Publications	Curate/search Organize	TextPresso, PubSearch Chado Publication Module

Behavior and Phenotype in GMOD

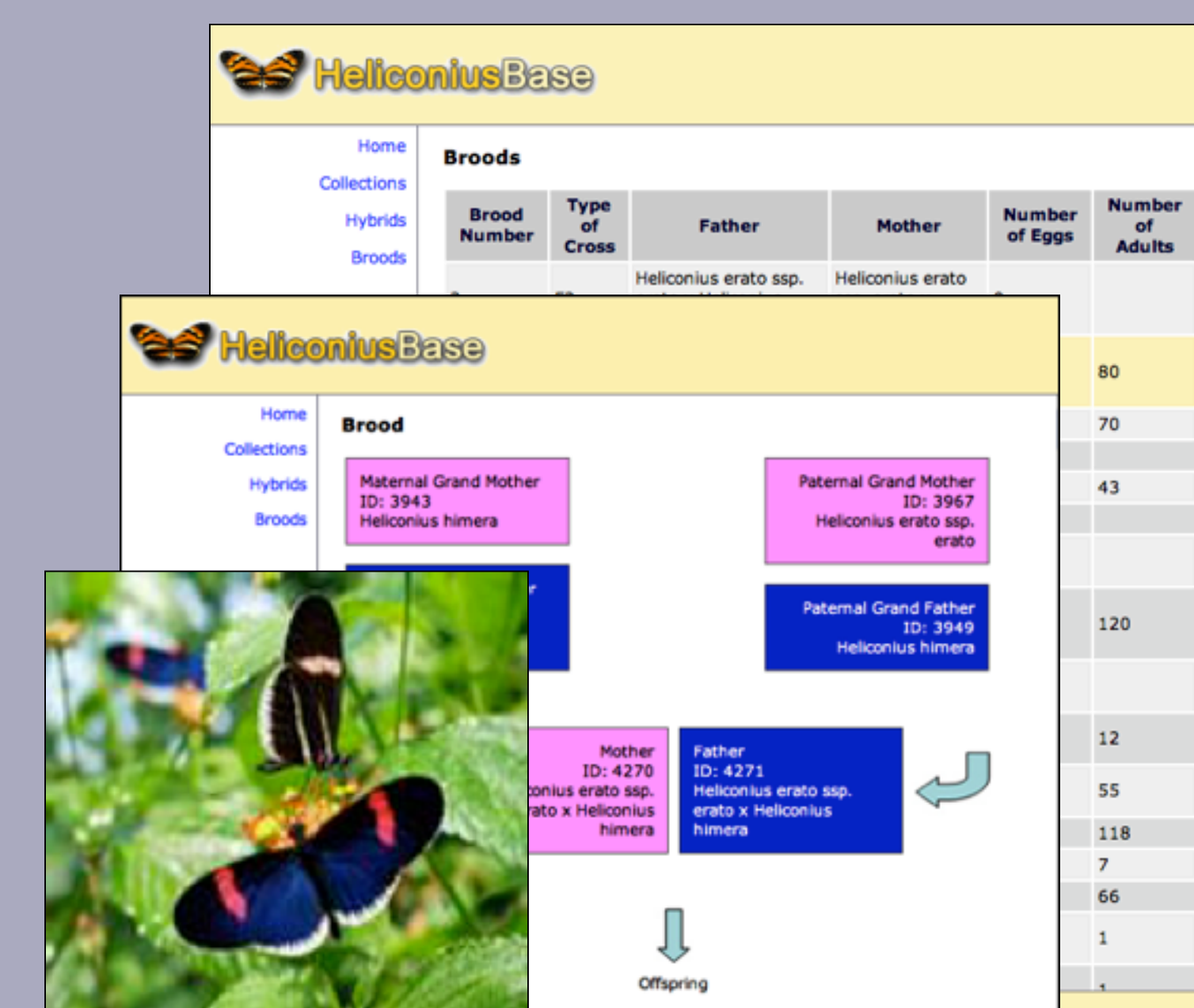
GMOD records behaviors as phenotypes by combining ontologies such as GO and PATO (the Gene and Phenotype ontologies) in Chado, GMOD's database schema. These can then be displayed or queried. You can also use (or create) more specific ontologies such as the Social Insect Behavior Ontology (SIBO) or anatomy ontologies for specific organisms.



An allele page at ParamoeciumDB showing phenotype information integrated with sequence, genetic, and stock data.

Natural Diversity in GMOD

Chado has recently been extended with the Natural Diversity module, which supports stocks, individuals, pedigrees, crosses, geolocations, and phenotype and genotype experiments. Taxonomy and phylogenetic trees in Chado's core modules have also been rationalized.

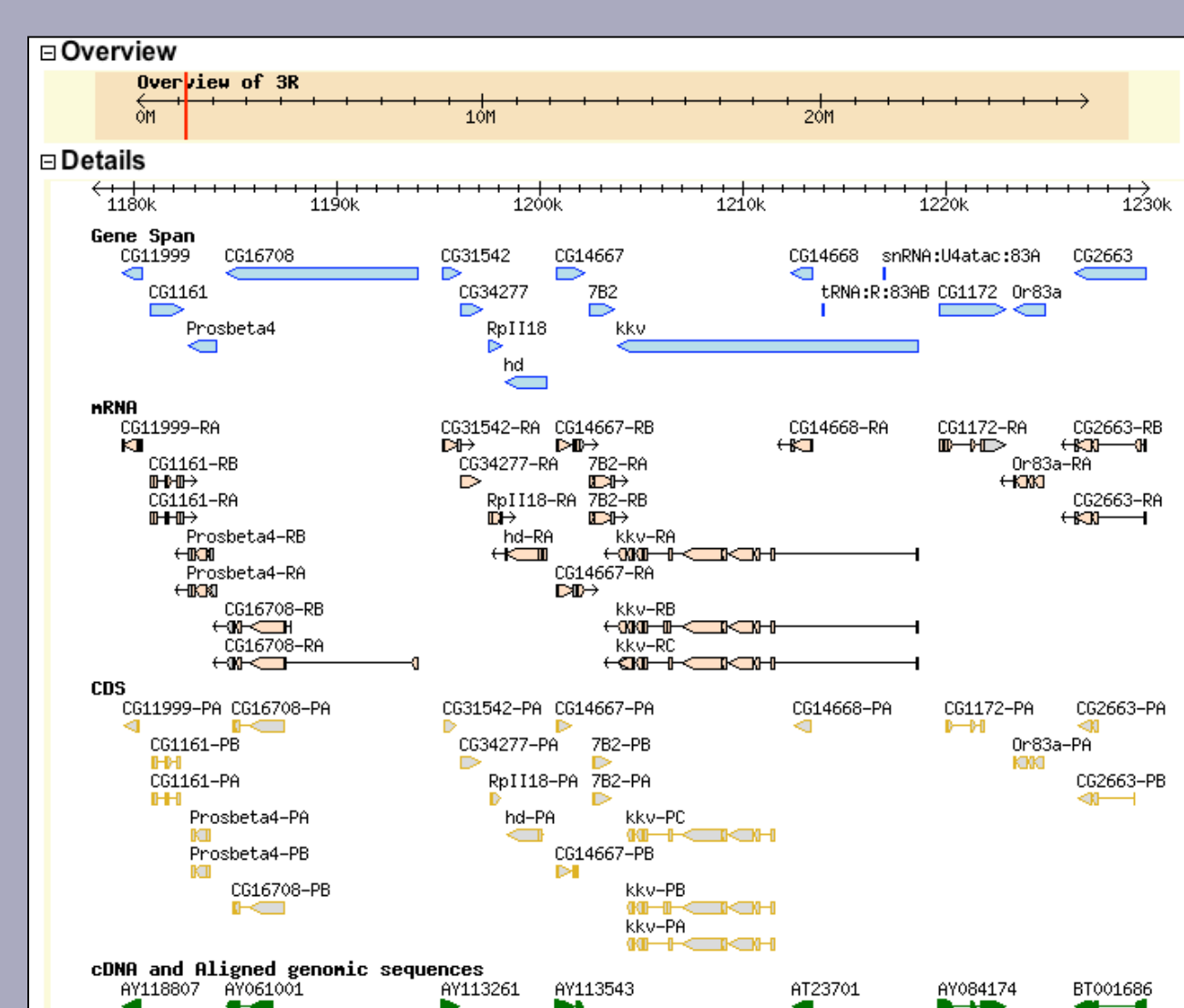


Chado Database Schema

Chado is the unifying data model for GMOD. It is a modular and extensible database design for biological data. Chado supports sequence, genetic, phenotypic, ontology, gene expression, and many other datatypes.

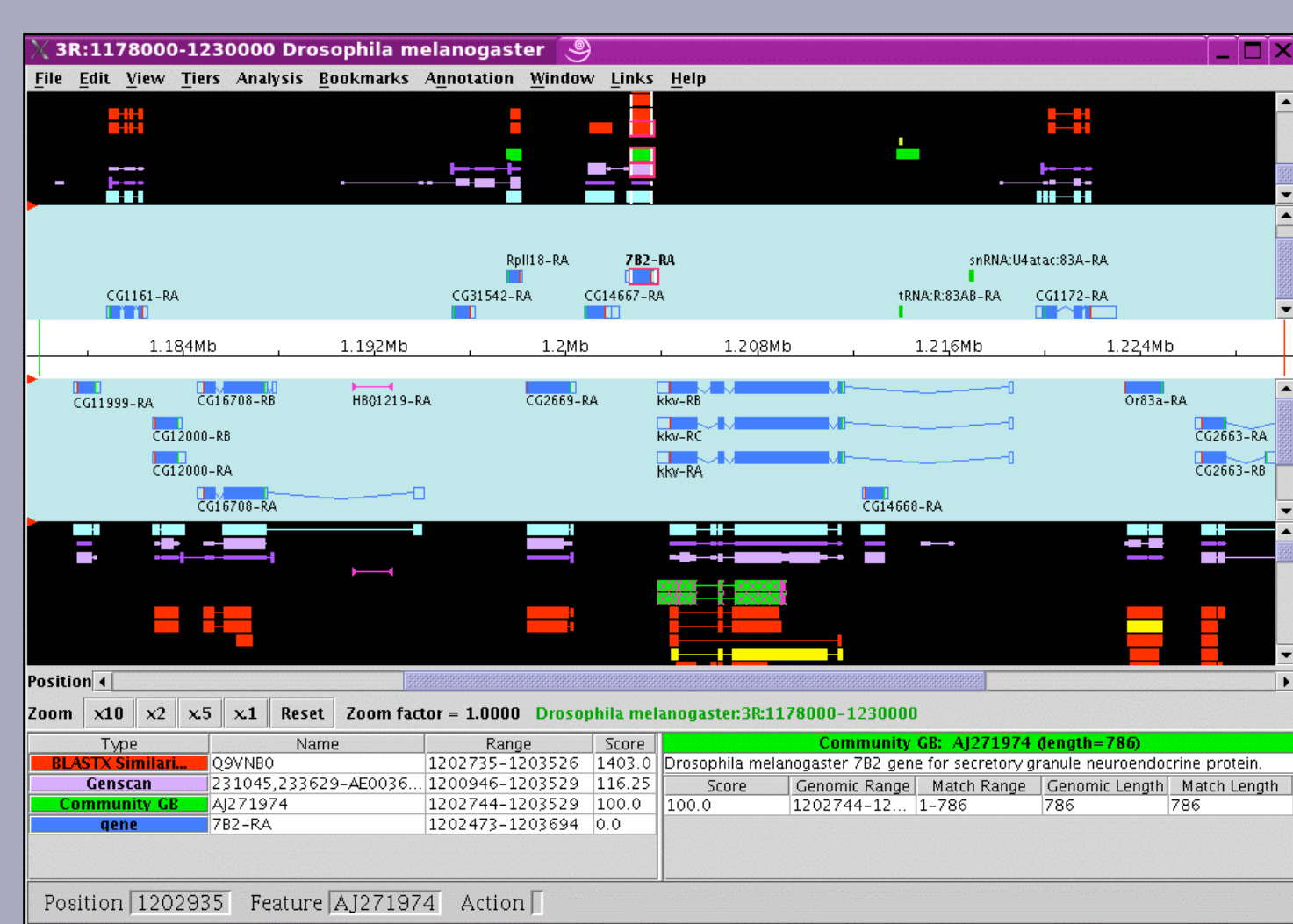
GBrowse Genome Browser

GBrowse is a web-based viewer for displaying genomes and their annotation. It is highly configurable by end-users and site administrators. If you have sequence and/or genomic annotation, GBrowse can show it.



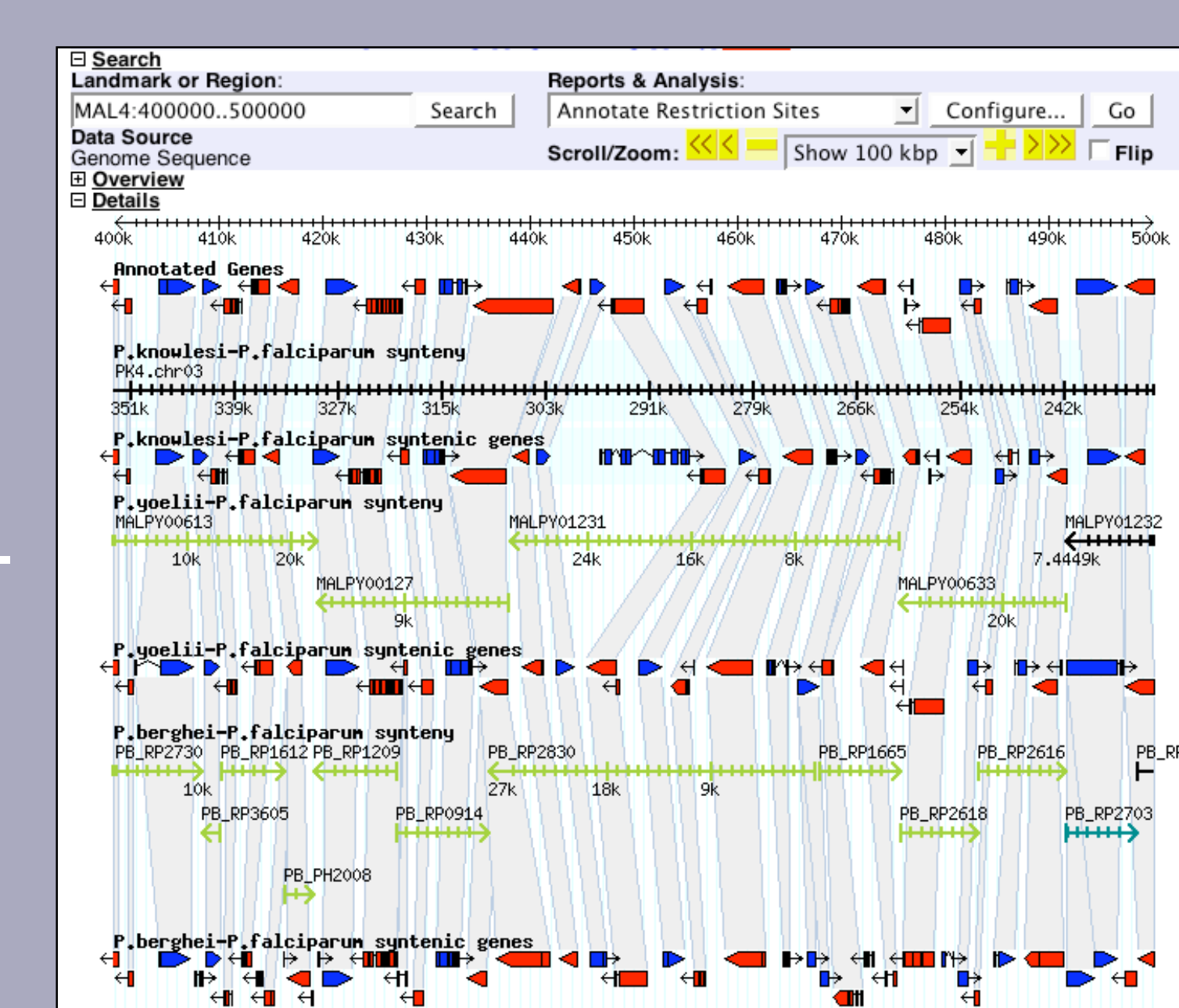
Apollo Genome Editor

The Apollo genome editor is used to annotate genomic sequences. Apollo supports adding new annotations and refining computational annotations. It is used in several community annotation efforts.



Comparative Genomics

GMOD supports visualizing comparative genomics data. Sybil displays syntenic regions and whole genome comparisons. CMap shows comparative maps of any type (genetic, physical, sequence, ...). SynView, GBrowse_syn and SynBrowse are GBrowse-based synteny browsers.



The GMOD Help Desk is hosted by NESCent and is funded by National Institutes of Health grants to Ian Holmes at UC Berkeley and James Hu at Texas A&M.