

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 Project News Log in / create account **GMOD** for Biologists Download Software Contribute Doc! FAQs and HOWTOs GMOD.org is a Wiki GBrowse Tutorial at PAG XVI Support: Help Desk GMOD News • Biopackages HOWTO **Project Events** & mailing lists Contribute Code! Popular GMOD We're open source Components

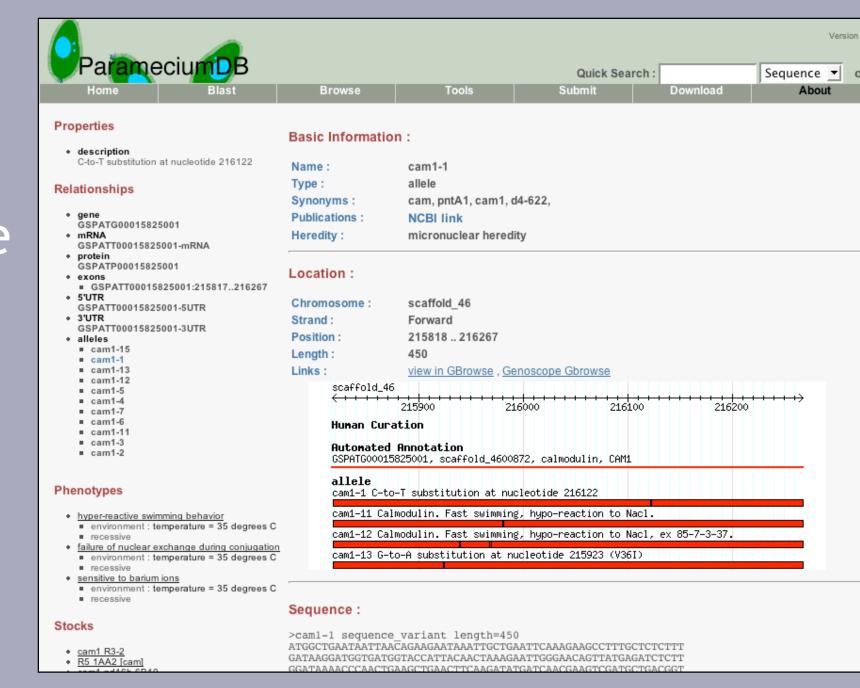
http://gmod.org

What Can GMOD Do?

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

Behavior and Phenotype in GMOD

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 ParameciumDB showing phenotype information integrated with sequence, genetic, and stock data.

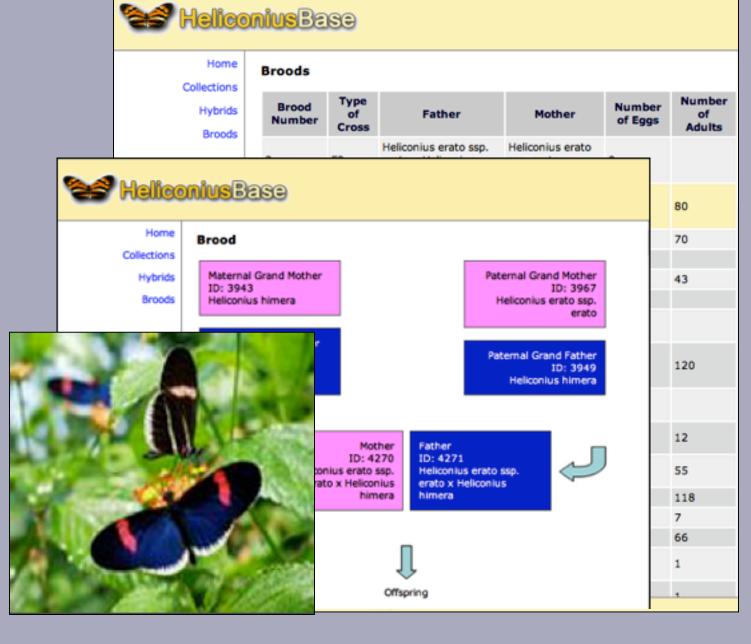
GBrowse Genome Browser

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.

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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.

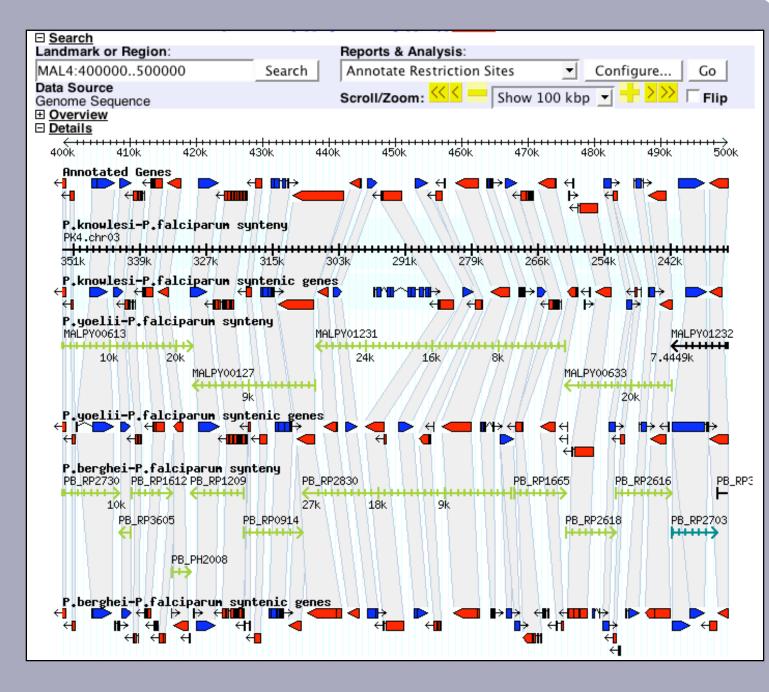
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Apollo Genome Editor

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.





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