# ChlamyCyc a comprehensive database and web-portal centered on Chlamydomonas reinhardtii

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## Overview

The unicellular alga Chlamydomonas reinhardtii is an important eukaryotic model organism for the study of photosynthesis and growth, as well as flagella development and other cellular processes. It has recently attracted substantial interest in the context of bio-fuel and hydrogen production. In the era of modern high-throughput technologies there is an imperative need to integrate large-scale data sets from high-throughput experimental techniques using computational methods and database resources.

ChlamyCyc provides a curated and integrated systems biology repository that will enable and assist in systematic studies of fundamental cellular processes. The ChlamyCyc database and web-portal is freely available: http://chlamycyc.mpimp-golm.mpg.de. It provides comprehensive information about the whole cellular system of an single organism on all levels of molecular organization.

It was assembled using an integrative approach combining the recently published genome sequence, bioinformatics methods such as orthology and paralogy assignments, and experimental data from metabolomics and proteomics experiments such as metabolic profiling. We also analyzed and integrated a combination of primary and secondary database resources, such as existing genome annotations from JGI, EST collections, orthology information, and MapMan [1] classification.



# Metabolomic network analysis and visualization

Based on the adopted MapMan ontology and highthroughput "omics" data, we reconstructed the metabolic network and built a pathway/genome database for Chlamydomonas reinhardtii with Pathway-Tools Software [2] 12.5. It currently features:

- 270 Pathways
- 1395 Reactions, 6919 Enzymatic Reactions
- 14 Regulation
- 1024 Compounds
- 14657 Proteins
- 93 tRNAs, rRNAs, microRNAs

# **Comparative Analysis**

We are mirror for 20 other pathway/genome databases from the BioCyc [3] family. This brings the possibility to compute comparisons across 18 organism, including 12 plants, yeast, mouse and human

#### GoFORSYS - ChlamyCyc Summary Database Blast MapMan GenomeBrowser Search GoFORSYS Downloads ogin (Optional): Why Login Pathway Tools Query Page Create New Account | Help his form provides several different mechanisms for querying Pathway/Genome Databases. Select a dataset: Chlamydomonas reinhardtii 🛛 🗸 19 available GoFORSYS - ChlamyCyc Genome Browser: Chloroplastial chromosome 🗸 Submit UTP--glucose-1-phosphate uridylyltransferase Query All (by name or EC#) Superfamily To retrieve objects by name, first select the type of object you wish to retrieve, then enter the name of the Submit. All objects containing that separating them with commas. iological\_process GoFORSYS - ChlamyCyc nolecular function nsferase activity Browse Ontology: Pathways hosphate uridylyltransferase activ nolecular function Each dataset contains classification ase. Protein involved in cell wall/membrane/envelope biogenesis. Note that th isms from Bifidobacterium, yeast to Arabidopsis is better than between them and compounds, and for genes. Select a anscript is also shorter than the ones in other organisms predicted to be plastidic ICIT ogin (Optional): Why Login' Choose from a list of all Pa . reinhardtii Pathway: sucrose biosynthesi Create New Account | Help Cellular Overview Diagram/ actions More Detail Less Detail Cross-Species Comparison Download Genes BioPAX format Pathway PathwayClass PathwayType AssociatedDisease entose and Links to summary informat pontaneou METABOLIC Summary page for dataset 5.1.3.15 History of updates to this datas PathoLogic Pathway Analysis (n METABOLIC Blast Search Search for sequence ucleotide sugars Nucleotid METABOLIC tarch and Comparative Analysis cytosolic form: phosphoglucomutase: e\_gwW.27.157.1 METABOLIC Generate summary tables that complexity 5.4.2.2 DeltaG Spontaneous Help Advar null lylyltransfe rase ntact: chlamycyc@mpimp-golm.mpg.de ylyltransfe rase nate uridylyltransferase estExt\_GenewiseW\_1.C\_150140 y / Paralogy UDP-D-glucose Description ransferase | chr3:749768-754021 REVERSE fructose-6-phosphatesucrose-phosphate synthase: GTR sucrose-phosphatase 2.4.1.14 fructose-\_ 2.4.1.13 Chire2\_kg.scaffold\_26000101 sucrose-phosphatase estExt\_fgenesh2\_pg.C\_16016 3.1.3.24 H<sub>2</sub>O phosphat egend for Pathway Diagram. hlamycyc@mpimp-golm.mpg.de

# Gene report pages

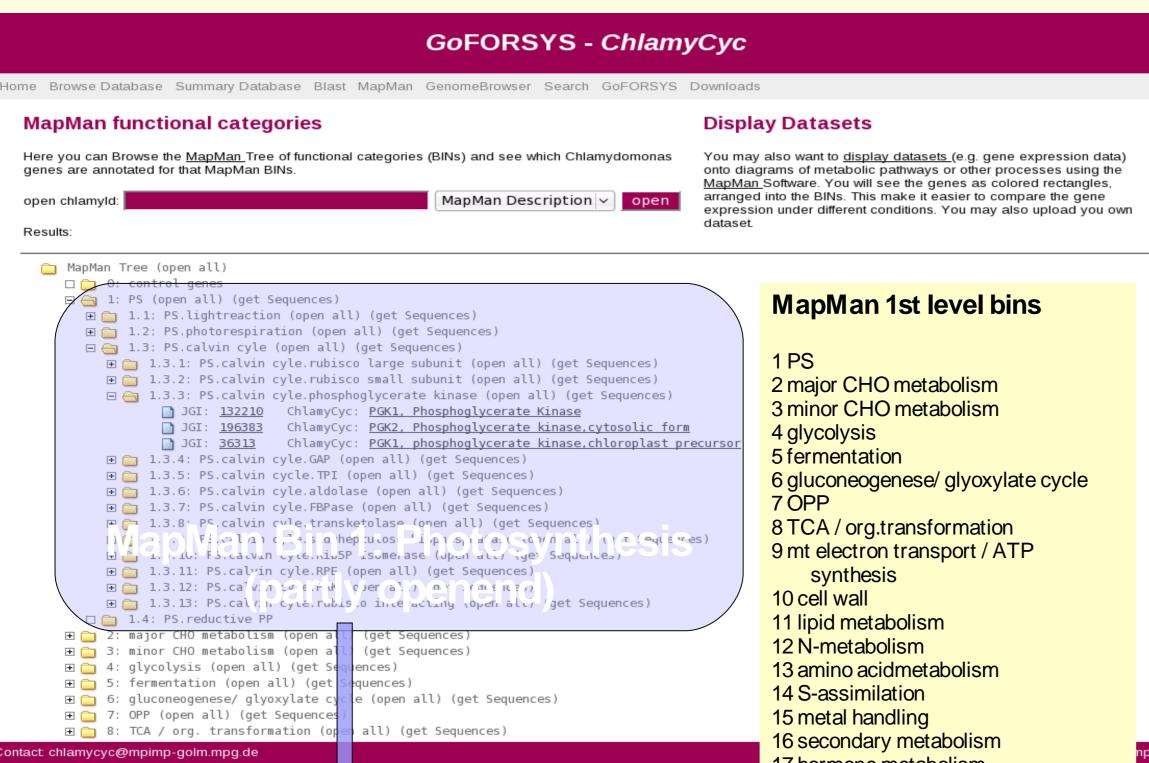
In addition to to pathway information, comprehensive gene-based annotation including sequence data, domain annotation, MapMan annotation, orthology and paralogy information, reactions, peptide support, links to genome browser, primer information and external databases is provided by gene centered report pages.

#### MapMan annotation

MapMan is an ontology developed to capture the functional capabilities of plants.

We could annotate 5.277 proteins (including 76 organelleencoded) into 681 non-trivial MapMan classification bins.

The visualization of *Chlamydomonas* gene expression experiments with MapManWeb is directly linked.



#### **Genome Browser**

We have implemented a Chlamydomonas *reinhardtii* specific genome browser based on the GBrowse Software package [4] to provide a detailed view of the nuclear, plastid and mitochondrial genomes.

The GBrowse window can be used to display user defined combinations of 30 tracks including gene and protein annotation, various RNA-species as well as the EST and peptide coverage from inhouse proteomics experiments and external annotations.

## **BLAST** search

We have implemented a web version of the standard BLAST [5] software to search against more than 40 sequence databases including those browseable with the genome browser.

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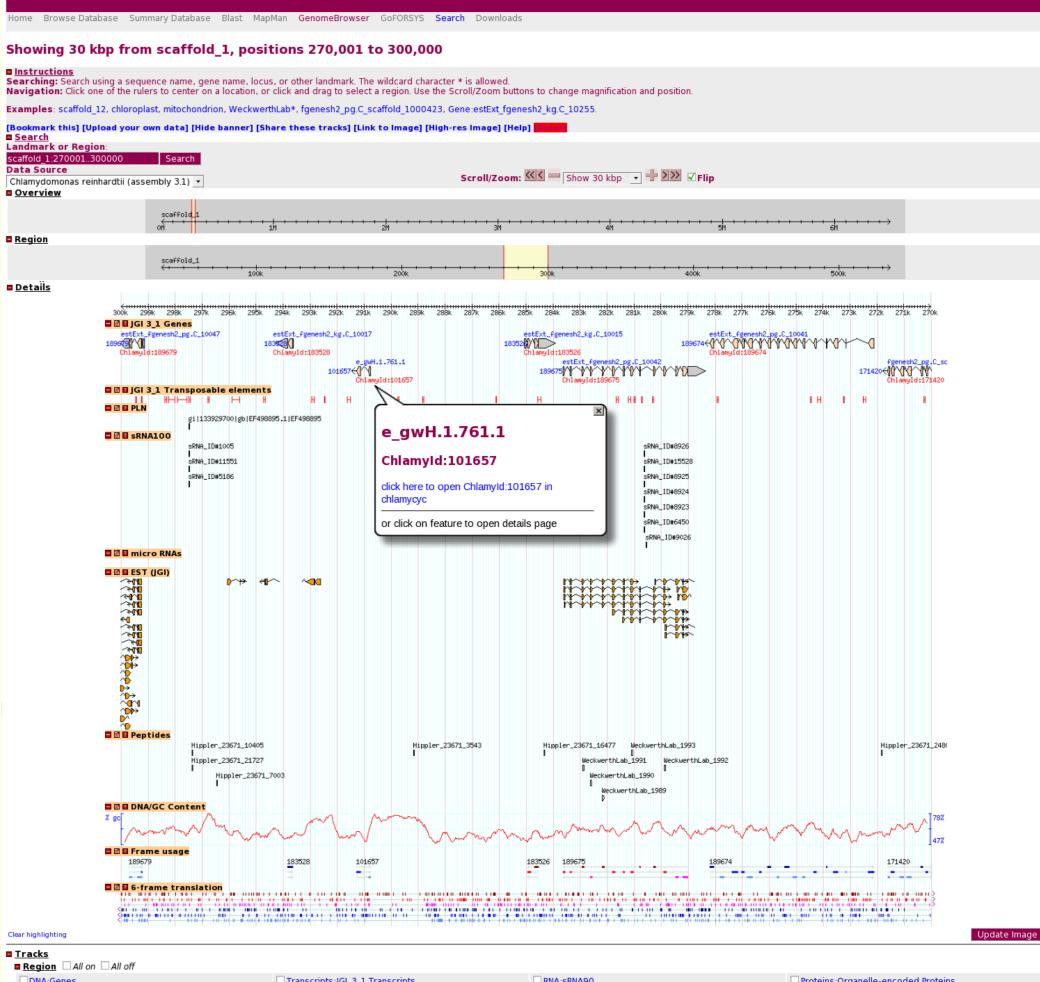
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We present an integrated analysis of the molecular repertoire of *Chlamydomonas reinhardtii*. Bioinformatics annotation methods combined with GCxGC/MS-based metabolomics and LC/MS-based shotgun proteomics profiling technologies have been applied to characterize abundant proteins and metabolites. Based on the adopted MapMan annotation and highthroughput "Omics" data we reconstructed the metabolic network and built the pathway/genome database ChlamyCyc. The web resource combines network analysis and visualization, sequence analysis, and genome annotation.

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