

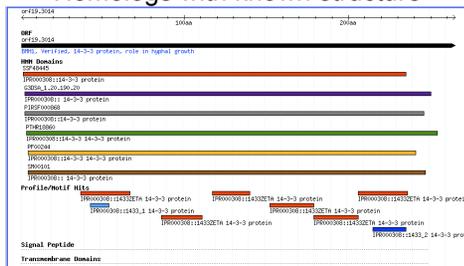
## View Protein Properties, Orthologs, & Pathways

### Protein Information

#### “Protein” tab on Locus Summary

Find basic information about a protein, links to detailed data and predictions, and protein-specific tools, including:

- Sequence
- Protein domains & motifs
- Transmembrane domains
- Signal peptide cleavage sites
- Homologs with known structure



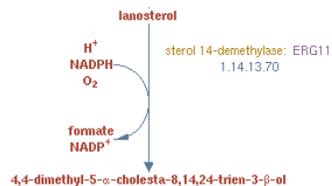
### Orthologs

Links on Locus Summary pages lead to:

- S. cerevisiae* and *C. dubliniensis* orthologs
- S. cerevisiae* best hits
- Orthologs from more species coming soon!

### Biochemical Pathways

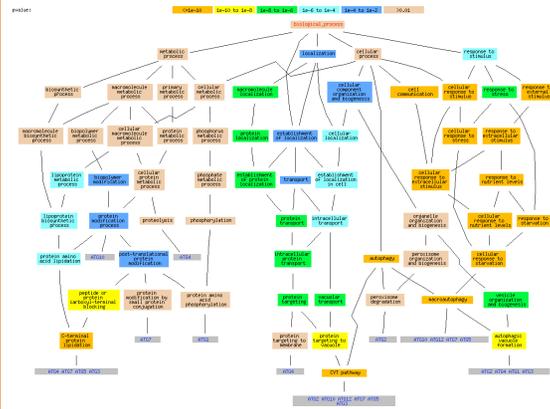
Explore *Candida* biochemistry with this dynamic display of curated enzymatic pathways. Browse or search by gene/protein, pathway name, compound, or E.C. number.



## Get an Overview of Gene Sets or the Genome

### GO Term Finder

Using a list of genes, find shared functions, processes, or locations.



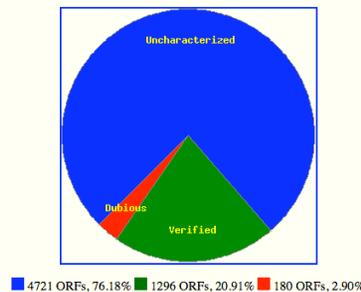
### GO Slim Mapper

Map genes to the Candida GO Slim: broad functional categories that represent the major biological processes, functions, and cellular components in *C. albicans*

### Genome Snapshot

Genome-wide summaries of sequence and functional annotations, updated daily

Graphical View of Protein Coding Genes (as of Mar 09, 2010)



## Quick Resource Guide

March 2010

Find & View  
Chromosomal Features

Retrieve Sets of Genes  
or Papers

Investigate Mutant  
Phenotypes

View Protein  
Properties, Orthologs,  
& Pathways

Get an Overview of  
Gene Sets or the  
Genome

[www.candidagenome.org](http://www.candidagenome.org)  
[candida-curator@genome.stanford.edu](mailto:candida-curator@genome.stanford.edu)

# Find & View Chromosomal Features

## Quick Search



Use a keyword to simultaneously search 10 major categories of information in CGD.

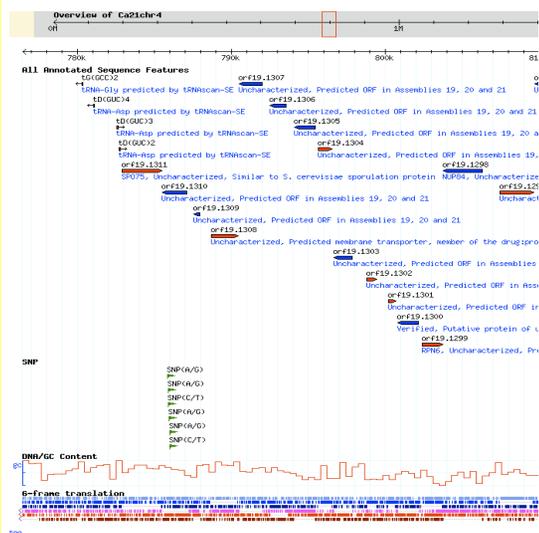
## Advanced Search

Use multiple search criteria.

Select features (e.g. ORF, tRNA, etc.)  
Narrow results by sequence & annotations; chromosome; function, process, or localization; or any desired GO term

## GBrowse Genome Browser

View the genome with this customizable, dynamic map where annotated features or your own annotations are displayed on multiple “tracks”.



# Retrieve Sets of Genes or Papers

## Batch Download

Retrieve various types of data for a list of genes or for all genes in a specified region:

- Nucleotide or protein sequences
- Chromosomal feature information (gene names, descriptions, coordinates)
- Gene Ontology annotations
- Mutant phenotypes
- Ortholog information

## Download Data

Download genome-wide data files:

- Sequences (A19, A21)
- Chromosomal feature information
- Functional information (literature curation)
- Biochemical pathway information
- Mapping files (correspondence between names in historical assemblies; mapping to external identifiers)
- Ortholog and best hit mappings
- Large-scale datasets
- Community-contributed datasets

## Textpresso

Search the full text of almost 20,000 *Candida*-related articles.



Enter one or more search keyword(s) in the box (e.g., 'glabrata' or 'azole'). You may also limit the fields searched, specify case sensitivity, and/or require an exact match to your keywords. Additional options are described in the User Guide.

**Keywords**

Separate multiple, *required* keywords by white spaces (Boolean 'and').

Separate multiple, *alternative* keywords by a comma with no white spaces (Boolean 'or').

Enter phrases in double quotes, and put a '-' sign in front of words which are to be excluded.

**Keyword Specification**

 Exact match

**Fields**

 abstract  
 author  
 body  
 title  
 year

**Search Scope**

**Search Mode**

**Sort by**

# Investigate Mutant Phenotypes

## Browse Phenotypes

- Find mutant phenotypes associated with a gene
- Find all genes with a specific mutant phenotype (e.g., affecting *virulence*)

Single Mutant Phenotype(s) for <i>virulence</i>									
Gene Name	Experiment Type	Mutant Information	Strain background	Phenotype	Details	Virulence Model	References	All phenotypes	
ASH1orf19.5343	heterozygous diploid, classical genetics	Description: null	Not recorded	virulence: decreased	Details: virulence is intermediate between that of the heterozygous null mutant and wild type	mouse intravenous infection	Ingle DO and Johnson AD (2002) Ash1 protein, an asymmetrically localized transcriptional regulator controls filamentous growth and virulence of <i>Candida albicans</i> . <i>Mol Cell Biol</i> 22(24):8669-80 <a href="#">PubMed</a> <a href="#">PMCID</a>	ASH1 phenotypes	
ATC1orf19.6214	heterozygous diploid, classical genetics	Description: null	Not recorded	virulence: decreased		mouse intravenous infection	Prefers Y, et al. (2007) Disruption of the <i>Candida albicans</i> ATC1 gene encoding a cell-linked acid phosphatase decreases hyphae formation and infectivity without affecting resistance to oxidative stress. <i>Microbiology</i> 153(Pt 5):1372-81 <a href="#">PubMed</a> <a href="#">PMCID</a>	ATC1 phenotypes	

## Search Phenotypes

Quick Search: *looks at major phenotype terms*  
Expanded Phenotype Search: *looks at all text associated with phenotype annotations*

## Phenotype Viewer software

Downloadable application to view and search phenotype data from Homann et al. (2009) A phenotypic profile of the *Candida albicans* regulatory network. *PLoS Genet* 5(12):e1000783

