

Tripal: A Construction Toolkit for Online Genomic Databases

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PAG XIII

Poster 931

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 - Marine Genomics Group at the Hollings Marine Lab.

What is Tripal

- Tripal = GMOD Chado + Drupal
 - Chado: database schema for modeling biological data
 - <http://www.gmod.org>
 - Used by many different software tools
 - Unified method of data exchange
 - Open source and community support
 - Drupal: content management
 - <http://www.drupal.org>
 - Simplifies web construction
 - Expandable
 - Well documented, open-source large community support



Sites Using/Slated to Use Tripal

Site developed at CUGI

The screenshot shows the homepage of the Fagaceae Genomics Web. The header includes the site name and a tagline: "genomic tools for chestnut, oak, beech, and other trees." Navigation tabs include Home, Search, BLAST, DNA Libraries, Sequences, Markers, Genetic Maps, and Physical Map. A sidebar on the left lists "Organisms" (American Beech, American Chestnut, Chinese Chestnut, Oak, Red Oak, White Oak) and "Project Information" (Project Background, Project Phases and Objectives, Bioinformatic Methods, Outreach, Progress Reports, Project Team, Publications, Photo Gallery, Links). The main content area features a "Welcome to the Fagaceae Project" section, "Announcements" with a "New Tools & Analysis" sub-section, and a "Conference: Genomics of Forest and Ecosystem Health in the Fagaceae" announcement.

The screenshot shows the homepage of the Marine Genomics Project. The header includes the site name and a tagline: "The Marine Genomics Project". Navigation tabs include Species/Projects, Tools, Search, Contribute, About MG.org, Mailing Lists, and Login. The main content area features a "Welcome to the Marine Genomics Project" section, "Announcements" with a "MG.org Users Mailing List" sub-section, and a "Coming Soon" section. A "Visitor locations" map is also visible.

Sites developed at Washington State U. (Dorrie Main's Lab)

The screenshot shows the homepage of the Citrus Genome Database. The header includes the site name and a tagline: "The Genomics, Genetics and Breeding Resource for Citrus Improvement". Navigation tabs include Home, About, Species, Projects, Maps, Sequences, Tools, Community, and Contact. The main content area features a "Welcome to the Citrus Genome Database" section, "Announcements (3)", and a "Funded by the 2009 USDA CSREES Specialty Crop Research Initiative Program" footer.

The screenshot shows the homepage of the GDR Genome Database for Rosaceae. The header includes the site name and a tagline: "Genomic, Genetic, and Breeding Resources for Rosaceae Crop Improvement". Navigation tabs include Home, General Info, Species, Projects, Maps, Search, Tools, Community, Calendar, and Contact. The main content area features a "Welcome to the Genome Database for Rosaceae" section, "Community News (7)", and a "What's new in GDR?" section.

The screenshot shows the homepage of the Cacao Genome Database. The header includes the site name and a tagline: "The Genomics, Genetics and Breeding Resource for Cacao Improvement". Navigation tabs include Home, About, Events, Groups, Tools, and Contact. The main content area features a "Welcome to the Cacao Genome Project" section, "Announcements (8)", and a "Why Sequence the Cacao Genome?" section.

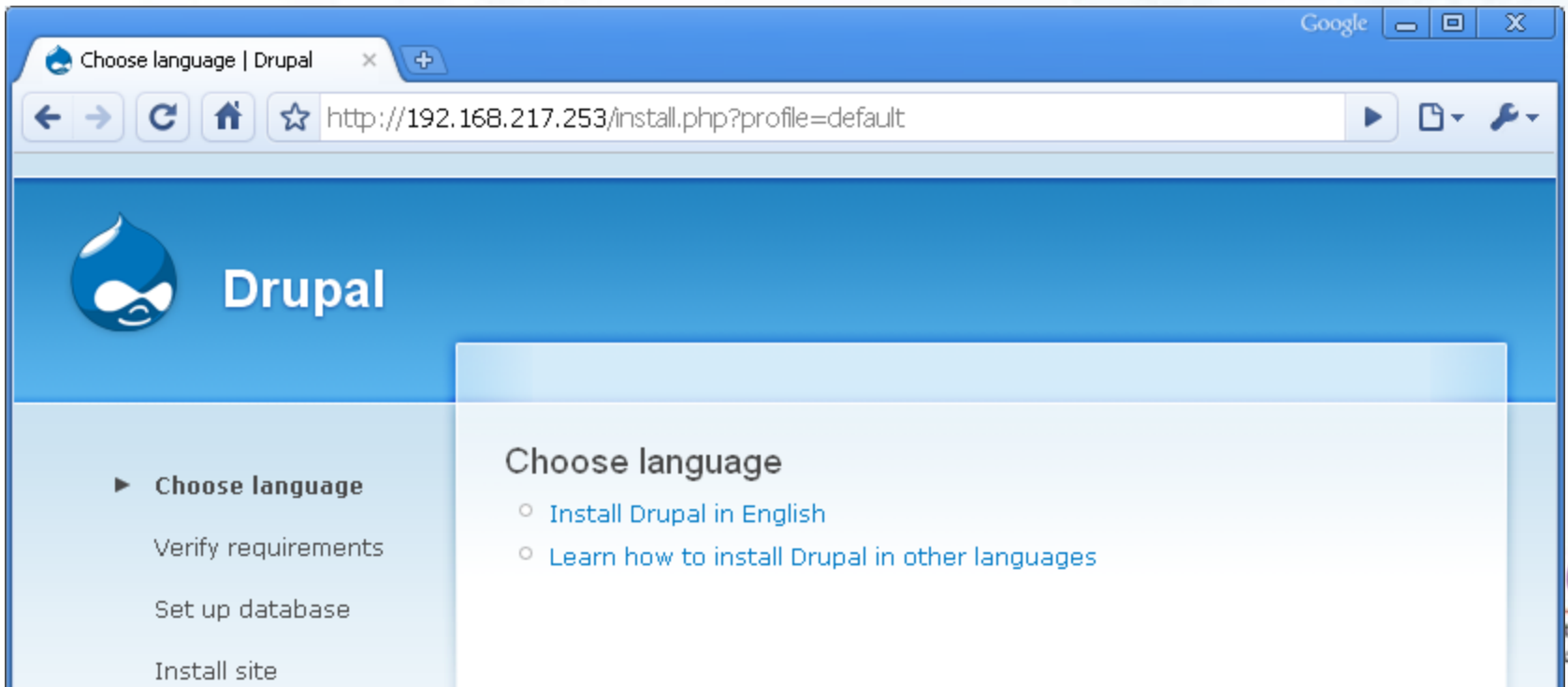
Installation

Prerequisites

- Linux/UNIX
- GMOD Chado
- Drupal / PHP
- Postgres database
 - Two databases (one for Drupal, one for Chado)
 - Login account

Drupal Setup


- Download from <http://www.drupal.org>
- Unpack into web directory
- Create a settings.php file that provides connection info
- Create a 'sites/default/files' directory



The screenshot shows a web browser window with the URL `http://192.168.217.253/install.php?profile=default`. The page features the Drupal logo and the word "Drupal" in a blue header. Below the header, there is a sidebar with a "Choose language" link and a main content area with the heading "Choose language". The main content area contains two radio button options: "Install Drupal in English" and "Learn how to install Drupal in other languages".

Choose language | Drupal

http://192.168.217.253/install.php?profile=default

 **Drupal**

► **Choose language**


Verify requirements

Set up database

Install site

Choose language

- [Install Drupal in English](#)
- [Learn how to install Drupal in other languages](#)





Drupal

- ✓ Choose language
- ✓ Verify requirements
- ✓ Set up database
- ✓ Install site
- ▶ **Configure site**
- Finished

Configure site

All necessary changes to `./sites/default` and `./sites/default/settings.php` have been made. They have been set to read-only for security.

To configure your website, please provide the following information.

Site information

Site name: *

Site e-mail address: *

The *From* address in automated e-mails sent during registration and new password requests, and other notifications. (Use an address ending in your site's domain to help prevent this e-mail being flagged as spam.)

Administrator account

The administrator account has complete access to the site; it will automatically be granted all permissions and can perform any administrative activity. This will be the only account that can perform certain activities, so keep its credentials safe.

Username: *





Tripal Demo

yeast_admin

- [My account](#)
- ▷ [Create content](#)
- ▷ [Administer](#)
- [Log out](#)

Welcome to your new Drupal website!

Please follow these steps to set up and start using your website:

1. Configure your website

Once logged in, visit the [administration section](#), where you can [customize and configure](#) all aspects of your website.

2. Enable additional functionality

Next, visit the [module list](#) and enable features which suit your specific needs. You can find additional modules in the [Drupal modules download section](#).

3. Customize your website design

To change the "look and feel" of your website, visit the [themes section](#). You may choose from one of the included themes or download additional themes from the [Drupal themes download section](#).

4. Start posting content

Finally, you can [create content](#) for your website. This message will disappear once you have promoted a post to the front page.

For more information, please refer to the [help section](#) or the online [Drupal](#)



Chado Installation

- Chado Tutorial:

[http://gmod.org/wiki/Chado Tutorial](http://gmod.org/wiki/Chado_Tutorial)

- Tripal Tutorial:

[http://gmod.org/wiki/Tripal Tutorial](http://gmod.org/wiki/Tripal_Tutorial)

Tripal Installation

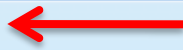
- Current version Tripal v6.x-0.2
 - **To be released next week**
 - Development: GMOD Sourceforge SVN
svn co <https://gmod.svn.sourceforge.net/svnroot/gmod/tripal/trunk>
 - Packages from CUGI:
<http://www.genome.clemson.edu/software/tripal>
- Place Tripal modules in Drupal's 'sites/all/modules' directory
- Place Tripal base theme in Drupal's 'sites/all/themes' directory
- Setup Cron for Tripal tasks.

Site Configuration



Tripal Demo

Home



Primary Menu

Administer

By task

By module

Cron has not run. Please visit the [status report](#) for more information.

Welcome to the administration section. Here you may control how your site functions.

Hide descriptions

Content management
Manage your site's content.

Comments
List and edit site comments and the comment moderation queue.

Content
View, edit, and delete your site's content.

Content types
Manage posts by content type, including default status, front page promotion, etc.

Post settings
Control posting behavior, such as teaser length, requiring previews before posting, and the number of posts on the front page.

RSS publishing
Configure the number of items per feed and whether feeds should be titles/teasers/full-text.

Site building
Control how your site looks and feels.

Blocks
Configure what block content appears in your site's sidebars and other regions.

Menus
Control your site's navigation menu, primary links and secondary links, as well as rename and reorganize menu items.

Modules
Enable or disable add-on modules for your site.

Themes
Change which theme your site uses or allows users to set.



yeast_admin

- My account
- ▷ Create content
- ▼ Administer
 - ▷ Content management
 - ▷ Site building
 - ▷ Site configuration
 - ▷ User management
 - ▷ Reports
 - Help
- Log out



Administration Menu

Site configuration

- o Blocks
- ▷ Menus
- o Modules
- o Themes
- ▷ Site configuration
- ▷ User management
- ▷ Reports
- o Help
- o Log out

To change the appearance of your site, a number of [contributed themes](#) are available.

See the [available updates](#) page for information on installed modules and themes with new versions released.

Screenshot	Name	Version	Enabled	Default	Operations
	Bluemarine Table-based multi-column theme with a marine and ash color scheme.	6.15	<input type="checkbox"/>	<input type="radio"/>	
	Chameleon Minimalist tabled theme with light colors.	6.15	<input type="checkbox"/>	<input type="radio"/>	
	Garland Tableless, recolorable, multi-column, fluid width theme (default).	6.15	<input checked="" type="checkbox"/>	<input checked="" type="radio"/>	configure
	Marvin Boxy tabled theme in all grays.	6.15	<input type="checkbox"/>	<input type="radio"/>	
	Minnelli Tableless, recolorable, multi-column, fixed width theme.	6.15	<input type="checkbox"/>	<input type="radio"/>	



Home » Download

Documentation

Download

Support

Forum

Contribute

Drupal Themes

Online Documentation

Here are a few links:

- [Basic Theme Help](#)
- [Troubleshooting themes](#)
- [Theme guide v5](#)
- [Theme guide v6](#)

IRC Channel, #drupal-themes on freenode.

Mailing list, sign up [here](#).

<!-- If you are looking for a simple fixed theme a suggestion is that you can start with [Pixtute](#), [Wabi](#), or [Twilight](#).--> More advanced themes are table-less, a good example of this is the core Garland theme or the [Tapestry](#) theme. For creating custom themes, the [Zen](#) theme provides a good starting point.

Themes

Themes allow you to change the look and feel of your Drupal site. These contributed themes are not part of any official release and may not work correctly. Only use matching versions of themes with Drupal. Themes released for Drupal 5.x will not work for Drupal 6.x. Many of these themes can also be previewed on the third party site [the Theme Garden](#)

Zen

By [JohnAlbin](#) on the 11th of October, 2006

Zen is the ultimate *starting theme* for Drupal. If you are building your own standards-compliant theme, you will find it much easier to start with Zen than to start with Garland or Bluemarine. This theme has [fantastic online](#)

[documentation](#) and tons of code comments for both the PHP (template.php) and HTML (page.tpl.php, node.tpl.php).

禪 zen
extend and design



“This theme saved me at 2am. Three hours of messing with 1000+ lines of nasty Garland-adapted code later, I abandoned it and recoded the site as a Zen sub-theme in under an hour. Thank you, thank you, thank you.
- Greg

Sort by

- [Title](#)
- [Creation date](#)
- [Last release](#)
- [Recent activity](#)
- [▲ Usage statistics](#)

Search theme

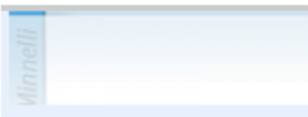




Filter by compatibility

- [4.7.x](#)
- [5.x](#)
- [6.x](#)
- [7.x](#)

User login

Username: *

Password: *

Screenshot	Name	Version	Enabled	Default	Operations
	Minelli Tableless, recolorable, multi-column, fixed width theme.	6.15	<input type="checkbox"/>	<input type="radio"/>	
	Pixture Reloaded Recolorable multi-column liquid/fixed layout theme. Original Design by Pixture Studio, Ported to CSS layout by AdaptiveThemes .	6.x-3.2	<input checked="" type="checkbox"/>	<input checked="" type="radio"/>	configure
	Polpo A Drupal Admin Theme	6.x-1.0	<input checked="" type="checkbox"/>	<input type="radio"/>	configure
	Pushbutton Tabled, multi-column theme in blue and orange tones.	6.15	<input type="checkbox"/>	<input type="radio"/>	
	Tripal Theme A Tripal specific theme for use with any other theme. Requires customization to .info file of the primary theme.	6.x-0.1b	<input checked="" type="checkbox"/>	<input type="radio"/>	



Save configuration Reset to defaults

Tripal Demo

http://192.168.217.253/

yeast_admin

- My account
- Create content
- Administer
- Log out

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Next, visit the [module list](#) and enable features which suit your specific needs. You can find additional modules in the [Drupal modules download section](#).
- 3. Customize your website design**
To change the "look and feel" of your website, visit the [themes section](#). You may choose from one of the included themes or download additional themes from the [Drupal themes download section](#).
- 4. Start posting content**
Finally, you can [create content](#) for your website. This message will disappear once you have promoted a post to the front page.

For more information, please refer to the [help section](#) or the [online Drupal handbook](#).



Tripal Demo

http://192.168.217.253/

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For more information, please refer to the [help section](#), or the [online Drupal handbook](#). You may also post at the [Drupal forum](#), or view the wide range of [other support options](#) available.

Fagaceae Genomics Web
genomic tools for chestnut, oak, beech, and other trees.

Home Search BLAST DNA Libraries Sequences Markers Genetic Maps Physical Map

Organisms

- American Beech
- American Chestnut
- Chinese Chestnut
- Oak
- Red Oak
- White Oak

Project Information

- Project Background
- Project Phases and Objectives
- Bioinformatic Methods
- Outreach
- Progress Reports
- Project Team
- Publications
- Photo Gallery
- Links

Welcome to the Fagaceae Project

The **Fagaceae Genome Web** is the web front-end for a multi-institutional [NSF-funded project](#) dedicated to the development of genomic resources for the *Fagaceae*. This site disseminates data and analyses by providing genetic and physical maps, transcriptomic data, functional analyses, a listing of available resources and data mining tools. Additionally, background and progress information is available.

Announcements

New Tools & Analyses
New analyses and tools are available for contigs of the most recent unigenes. The analyses include annotation of KEGG pathways, Interpro protein motifs & domains and Gene Ontology (GO) terms. GO and KEGG browsers are now available.

Conference: Genomics of Forest and Ecosystem Health in the Fagaceae
A successful international conference on the genomics of forest and ecosystem health in the Fagaceae was held Nov 10th-13th in Raleigh, NC, USA.

The Marine Genomics Project

Species/Projects Tools Search Contribute About MG.org Mailing Lists Login

Welcome to the Marine Genomics Project

MG.org: a web-based interface for public transcriptomic and genomic data and analysis tools.

The Marine Genomics project is an inclusive organization that welcomes all investigators who are interested in applying genomic approaches to furthering our knowledge of marine organisms.

Site Features:

- Species ESTs:** Search annotated ESTs.
- Unigenes:** Search annotated assemblies of ESTs (unigenes).
- Blast:** Blast your sequences against MG.org ESTs and unigenes.
- Mailing List:** Sign up for the MG.org mailing list in your user account preferences.
- Flag Features:** Registered users can flag ESTs/contigs for quick future access.

Coming Soon:

- EST processing pipeline:** Curators can upload their EST sequences for trimming, screening, genbank submission and inclusion onto this site.
- Automatic Updates:** Automatic incorporation of new ESTs from Genbank's dbEST.

Announcements

MG.org Users Mailing List
The MG.org users mailing list has just been improved to allow for easier subscription. To receive notifications about the site please subscribe!

Social Bookmarking
Use common social-networking tools to bookmark or share sequences on the MG.org website. A special link is found at the bottom of each page.

Visitor locations

Acropora coral garden with giant clam, Ragging Horn, Osprey Reef, Coral Sea. Photo obtained from Wiki/Commons. By Richard Ling.

Share / Save



Home » Download

Modules

You can also view an [alphabetical list of projects](#) that includes all projects but only their names.

Contributed (contrib) modules are plugins for Drupal that extend, build or enhance Drupal core functionality. Use matching [versions](#) (modules released for Drupal 5.x will not work for Drupal 6.x). Contributed modules are not part of Drupal core releases and may or may not have optimized code/functionality. If a module solves your needs please consider [joining forces](#) and helping the maintainer. You can [view module usage statistics](#) for all modules to view the most popular modules used by the Drupal community.

Views

By [merlinofchaos](#) on the 25th of November, 2005

The Views module provides a flexible method for Drupal site designers to control how lists and tables of content (nodes in Views 1, almost anything in Views 2) are presented. Traditionally, Drupal has hard-coded most of this, particularly in how taxonomy and tracker lists are formatted.

This tool is essentially a smart query builder that, given enough information, can build the proper query, execute it, and display the results. It has four modes, plus a special mode, and provides an impressive amount of functionality from these modes.

Among other things, Views can be used to generate reports, create summaries, and display collections of images and other content.

Version	Date	Links	Status
7.x-3.x-dev	2010-Jan-07	Download · Release notes	Development snapshot ✘
6.x-2.8	2009-Dec-03	Download · Release notes	Recommended for 6.x ✔
5.x-1.6	2007-1-1-14	Download · Release notes	Recommended for 5.x ✔

Sort by

- Title
- Creation date
- Last release
- Recent activity
- ▲ Usage statistics

Search modules

Submit

Filter by compatibility

- 4.7.x
- 5.x
- (-) 6.x
- 7.x

Projects

- Utility (650)
- Content (614)
- Content display (5)
- Third-party integra (569)

Tripal Modules

Tripal Core

- Jobs management
- Generic support for CVterms
- Materialized views management
- Generic theming

Organism

Feature

CV

DB

Library

Chado Tables Managed by Tripal:

organism, feature, library, featureprop, featureloc, libraryprop, cv, cvterm, cvterm_dbxref, cvtermpath, cvtermprop, db, dbxref, feature_cvterm, feature_dbxref, library, libraryprop,

Analysis Core

BLAST

KEGG

GO

Unigene

Interpro

Chado Tables Managed by Tripal:

analysis, analysisprop, analysisfeature, analysisfeatureprop

Core - Required

Tripal

Enabled	Name	Version	Description
<input type="checkbox"/>	Tripal Analysis	6.x-0.2b-m0.2	<p>A module that controls the display of all analysis sub-modules. This module also interfaces the GMOD chado database with Drupal, providing viewing, inserting and editing of chado analyses.</p> <p>Depends on: Tripal Core (disabled), Tripal Chado Feature (disabled), Tripal Chado Organism (disabled), Search (disabled), Path (disabled), Tripal CV (disabled), Tripal DB (disabled)</p> <p>Required by: Tripal Blast (disabled), Tripal GO (disabled), Tripal Interpro (disabled), Tripal Kegg (disabled), Tripal Unigene (disabled)</p>
<input type="checkbox"/>	Tripal Blast	6.x-0.2b-m0.2	<p>An analysis sub-module for adding, editing, and displaying blast analysis results.</p> <p>Depends on: Tripal Core (disabled), Tripal Chado Feature (disabled), Tripal Analysis (disabled), Tripal Chado Organism (disabled), Search (disabled), Path (disabled), Tripal CV (disabled), Tripal DB (disabled)</p>
<input type="checkbox"/>	Tripal Chado Feature	6.x-0.2b-m0.2	<p>A module for interfacing the GMOD chado database with Drupal, providing viewing, inserting and editing of chado features.</p> <p>Depends on: Tripal Core (disabled), Tripal Chado Organism (disabled), Search (disabled), Path (disabled), Tripal CV (disabled), Tripal DB (disabled)</p> <p>Required by: Tripal Analysis (disabled), Tripal Blast (disabled), Tripal GO (disabled), Tripal Interpro (disabled), Tripal Kegg (disabled), Tripal Unigene (disabled), Tripal Search (disabled)</p>
<input type="checkbox"/>	Tripal Chado Library	6.x-0.2b-m0.2	<p>A module for interfacing the GMOD chado database with Drupal, providing viewing, inserting and editing of libraries.</p> <p>Depends on: Tripal Core (disabled), Tripal Chado Organism (disabled), Search (disabled), Path (disabled)</p>
<input type="checkbox"/>	Tripal Chado Organism	6.x-0.2b-m0.2	<p>A module for interfacing the GMOD chado database with Drupal, providing viewing, inserting and editing of organisms.</p> <p>Depends on: Tripal Core (disabled), Search (disabled), Path (disabled)</p> <p>Required by: Tripal GO (disabled), Tripal Chado Feature (disabled), Tripal Chado Library (disabled), Tripal Analysis (disabled), Tripal Blast (disabled), Tripal Interpro (disabled), Tripal Kegg (disabled), Tripal Unigene (disabled).</p>

For this example enable:

1. Tripal Core
2. Tripal DB
3. Tripal CV
4. Tripal Organism
5. Tripal Feature
6. Tripal Analysis
7. Tripal Blast
8. Tripal KEGG
9. Tripal Interpro
10. Tripal GO
11. Tripal Search



Tripal Demo

[Analyses](#)

[Organisms](#)

New Menu Items ←

- yeast_admin
 - My account
 - Create content
 - ▼ Administer
 - Content management
 - Site building
 - Site configuration
 - ▼ Tripal Management
 - Analyses
 - CV
 - DB
 - Features
 - Jobs
 - Materialized Views
 - Organisms
 - User management
 - Reports
 - Help
 - Log out

Home » [Administer](#)

Tripal Management

Analyses

Settings for the displays of analysis results.

CV

Manage integration of Chado controlled vocabularies

DB

Manage External Databases

Features

Settings for Chado Features

Jobs

Jobs managed by Tripal

Materialized Views

Materialized views are used to improve speed of large or complex queries.

Organisms

Manage integration of Chado organisms including associated features

New Admin Functions

Organisms



Tripal Demo

[Analyses](#)

[Organisms](#)

yeast_admin

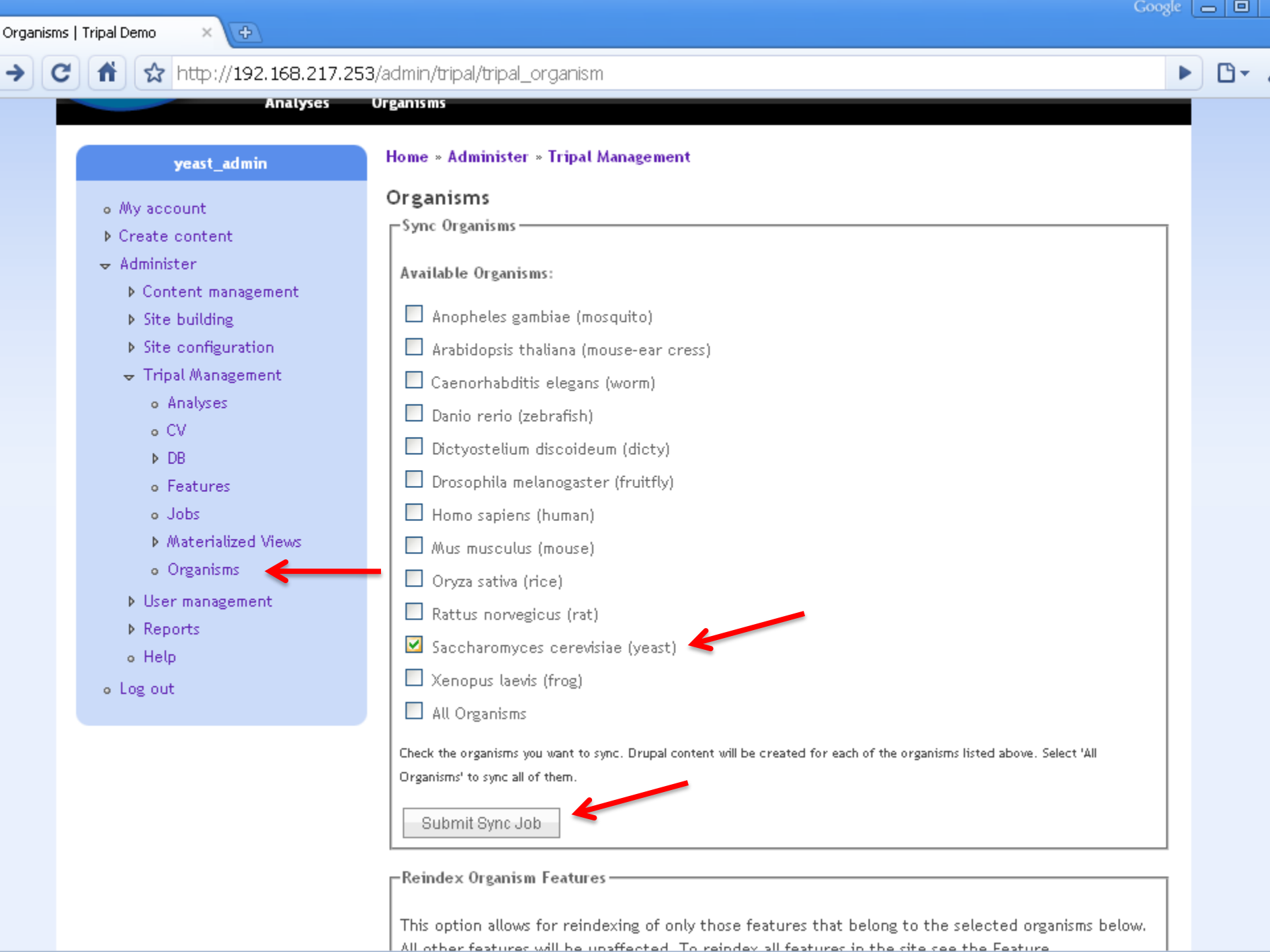
- [My account](#)
- ▶ [Create content](#)
- ▶ [Administer](#)
- [Log out](#)

[Home](#)

Organisms

No organism exists. Please contact administrators to synchronize organisms.





- yeast_admin
 - My account
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 - Analyses
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 - User management
 - Reports
 - Help
 - Log out

Home » Administer » Tripal Management

Organisms

Sync Organisms

Available Organisms:

- Anopheles gambiae (mosquito)
- Arabidopsis thaliana (mouse-ear cress)
- Caenorhabditis elegans (worm)
- Danio rerio (zebrafish)
- Dictyostelium discoideum (dicty)
- Drosophila melanogaster (fruitfly)
- Homo sapiens (human)
- Mus musculus (mouse)
- Oryza sativa (rice)
- Rattus norvegicus (rat)
- Saccharomyces cerevisiae (yeast)
- Xenopus laevis (frog)
- All Organisms

Check the organisms you want to sync. Drupal content will be created for each of the organisms listed above. Select 'All Organisms' to sync all of them.

Submit Sync Job

Reindex Organism Features

This option allows for reindexing of only those features that belong to the selected organisms below. All other features will be unaffected. To reindex all features in the site see the Feature



- yeast_admin
 - o My account
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 - o Jobs ←
 - Materialized Views
 - o Organisms
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 - o Log out

Home » Administer » Tripal Management

Jobs

Waiting jobs are executed first by priority level (the lower the number the higher the priority) and second by the order they were entered

Job ID	Job Name	Dates	Priority	Progress	Status
2	Sync organism: Saccharomyces cerevisiae	Submit Date: Mon, 01/11/2010 - 14:51 Start Time: Not Yet Started End Time:	10	0%	Waiting
1	Update materialized view 'organism_feature_count'	Submit Date: Mon, 01/11/2010 - 14:44 Start Time: Not Yet Started End Time:	10	0%	Waiting



Tripal Demo

[Analyses](#)

[Organisms](#)

yeast_admin

- My account
- ▶ Create content
- ▶ Administer
- Log out

[Home](#)

Organisms

[\[-\] Collapse All](#)

yeast	
Name: yeast	
Genus: Saccharomyces	
Species: cerevisiae	
Description:	





yeast_admin

- My account
- ▶ Create content
- ▶ Administer
- Log out

Home

Saccharomyces cerevisiae

[View](#)

[Edit](#)



Anonymous - Posted on 11 January 2010



Details

Common Name	yeast
Genus	Saccharomyces
Species	cerevisiae

Gene Ontology Summary 

There are currently no Gene Ontology (GO) reports for this organism

[Show on menu](#)

KEGG Analysis Results 

Select a KEGG report to view:

Any analysis with KEGG results related to this organism are available for viewing. For further information, see the

- ▶ Administer
- Log out

— ▶ Menu settings

Genus: *

Saccharomyces

Species: *

cerevisiae

Abbreviation: *

S.cerevisiae

Common Name: *

yeast

Description: *

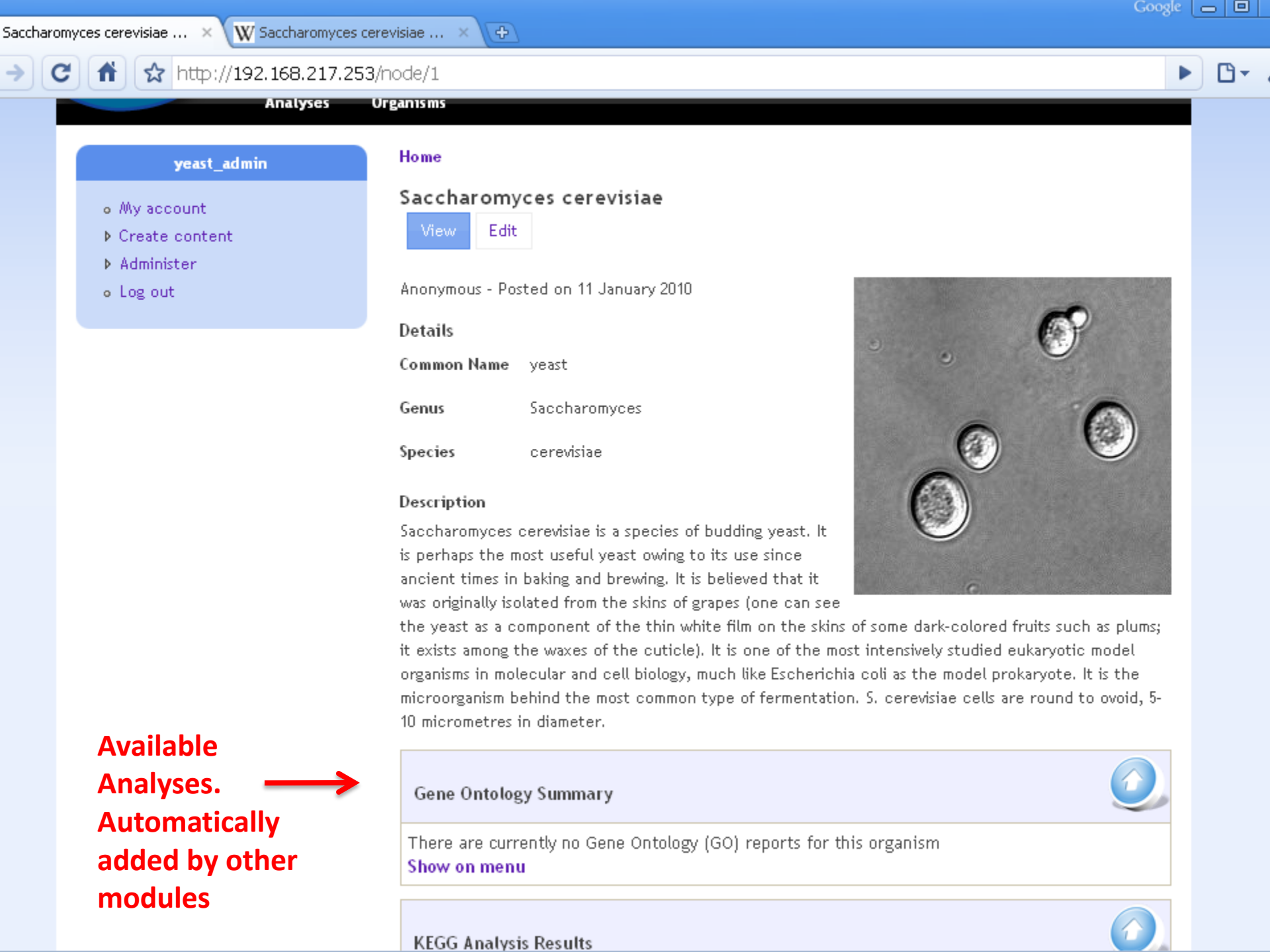
Saccharomyces cerevisiae is a species of budding yeast. It is perhaps the most useful yeast owing to its use since ancient times in baking and brewing. It is believed that it was originally isolated from the skins of grapes (one can see the yeast as a component of the thin white film on the skins of some dark-colored fruits such as plums; it exists among the waxes of the cuticle). It is one of the most intensively studied eukaryotic model organisms in molecular and cell biology, much like Escherichia coli as the model prokaryote. It is the microorganism behind the most common type of fermentation. S. cerevisiae cells are round to ovoid, 5-10 micrometres in diameter.

Add a description →

Add a picture for the organism →

Organism Image:

Choose File yeast.jpg



yeast_admin

- My account
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Home

Saccharomyces cerevisiae

[View](#) [Edit](#)

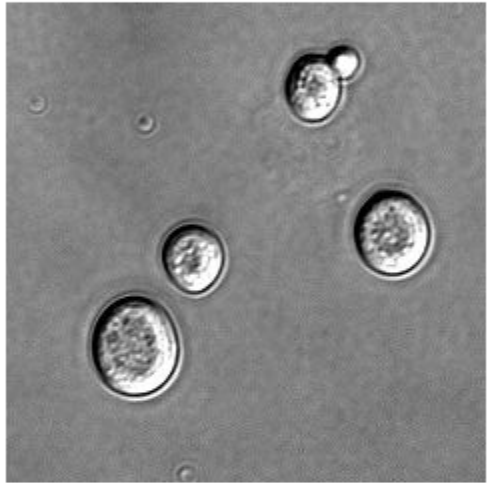
Anonymous - Posted on 11 January 2010

Details

Common Name	yeast
Genus	Saccharomyces
Species	cerevisiae

Description

Saccharomyces cerevisiae is a species of budding yeast. It is perhaps the most useful yeast owing to its use since ancient times in baking and brewing. It is believed that it was originally isolated from the skins of grapes (one can see the yeast as a component of the thin white film on the skins of some dark-colored fruits such as plums; it exists among the waxes of the cuticle). It is one of the most intensively studied eukaryotic model organisms in molecular and cell biology, much like Escherichia coli as the model prokaryote. It is the microorganism behind the most common type of fermentation. S. cerevisiae cells are round to ovoid, 5-10 micrometres in diameter.



Available Analyses. Automatically added by other modules →

Gene Ontology Summary 

There are currently no Gene Ontology (GO) reports for this organism

[Show on menu](#)

KEGG Analysis Results 

Genomic Features



Tripal Demo

Analyses Organisms

yeast_admin

- My account
- Create content
- ▼ Administer
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 - Site building
 - Site configuration
 - ▼ Tripal Management
 - Analyses
 - CV
 - DB
 - **Features**
 - Jobs
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 - User management
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Home » Administer » Tripal Management

Features

Accession Prefix: *

Accession numbers for features consist of the chado feature_id and a site specific prefix. Set the prefix that will be incorporated in front of each feature_id to form a unique accession number for this site.

Feature Types: *

Content only for features of these types will be generated

Enter the names of the sequence types that the "site will support with independent pages. Pages for these data "types will be built automatically for features that exist in the "chado database. The names listed here should be separated by "spaces or entered separately on new lines. The names must match "exactly (spelling and case) with terms in the sequence ontology

Feature Browser

Feature Browser on Organism Page:

- Show the feature browser on the organism page. The browser loads when page loads. This may be slow for large sites.
- Hide the feature browser on the organism page. Disables the feature browser completely.

A feature browser can be added to an organism page to allow users to quickly access a feature. This will most likely not be the ideal mechanism for accessing feature information, especially for large sites, but it will allow users exploring the site (such as

Sync Features

Click the 'Sync all Features' button to create Drupal content for features in chado. Only features of the types listed above in the Feature Types box will be synced. Depending on the number of features in the chado database this may take a long time to complete.

Only features for the following organisms will be synced: *Saccharomyces cerevisiae*,



Set Taxonomy

Drupal allows for assignment of "taxonomy" or catagorical terms to nodes. These terms allow for advanced filtering during searching.

Available Taxonomic Classes:

- Organism name
- Feature Type (e.g. EST, mRNA, etc.)
- Analysis Name
- Library Name

Please select the class of terms to assign to chado features



Reindex

Reindexing of nodes is important when content for nodes is updated external to drupal, such as external uploads to chado. Features need to be reindexed to ensure that updates to features are searchable. Depending on the number of features this may take quite a while. Click the button below to begin reindexing of features.



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Jobs

Waiting jobs are executed first by priority level (the lower the number the higher the priority) and second by the order they were entered

Job ID	Job Name	Dates	Priority	Progress	Status
7	Set all feature taxonomy	Submit Date: Mon, 01/11/2010 - 20:47 Start Time: Mon, 01/11/2010 - 20:48 End Time:	10	32%	Running
6	Sync all features	Submit Date: Mon, 01/11/2010 - 17:56 Start Time: Mon, 01/11/2010 - 17:56 End Time: Mon, 01/11/2010 - 20:36	10	100%	Completed
5	Reindex all features	Submit Date: Mon, 01/11/2010 - 17:47 Start Time: Mon, 01/11/2010 - 17:47 End Time: Mon, 01/11/2010 - 17:47	10	100%	Completed
4	Set all feature taxonomy	Submit Date: Mon, 01/11/2010 - 17:47 Start Time: Mon, 01/11/2010 - 17:47 End Time: Mon, 01/11/2010 - 17:47	10	100%	Completed
3	Sync all features	Submit Date: Mon, 01/11/2010 - 17:46 Start Time: Mon, 01/11/2010 - 17:47 End Time: Mon, 01/11/2010 - 17:47	10	100%	Completed
2	Sync organism: Saccharomyces cerevisiae	Submit Date: Mon, 01/11/2010 - 14:51 Start Time: Mon, 01/11/2010 - 14:52 End Time: Mon, 01/11/2010 - 14:52	10	100%	Completed
		Submit Date: Mon, 01/11/2010 - 14:44			



- ▶ Create content
- ▶ Administer
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[View](#) [Edit](#)

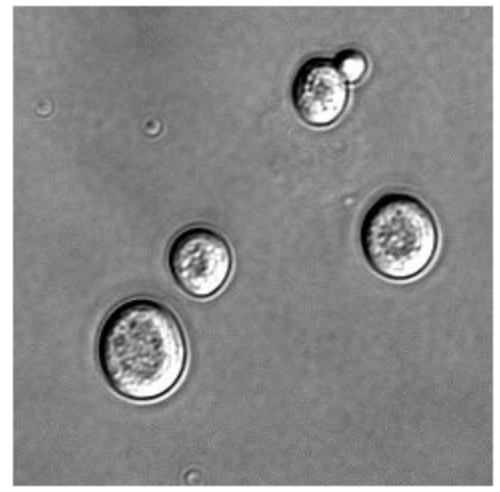
Anonymous - Posted on 11 January 2010

Details

Common Name yeast

Genus Saccharomyces

Species cerevisiae



Description

Saccharomyces cerevisiae is a species of budding yeast. It is perhaps the most useful yeast owing to its use since ancient times in baking and brewing. It is believed that it was originally isolated from the skins of grapes (one can see the yeast as a component of the thin white film on the skins of some dark-colored fruits such as plums; it exists among the waxes of the cuticle). It is one of the most intensively studied eukaryotic model organisms in molecular and cell biology, much like Escherichia coli as the model prokaryote. It is the microorganism behind the most common type of fermentation. S. cerevisiae cells are round to ovoid, 5-10 micrometres in diameter.

Synced 'genes' now appear here For easy browsing (optional) →

Browse Features

Below are the features associated with this organism.

Feature Name	Type
YAL069W	gene
YAL068W-A	gene
YAL068C	gene
YAL067W-A	gene
YAL067C	gene



Tripal Demo

Analyses

Organisms

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Home » Administer » Tripal Management

Materialized Views

	Name	Last_Update	
View Update	cv_root_mview	Not yet populated	Delete
View Update	go_count_analysis	Not yet populated	Delete
View Update	go_count_organism	Not yet populated	Delete
View Update	kegg_by_organism	Not yet populated	Delete
View Update	organism_feature_count	Mon, 01/11/2010 - 14:52	Delete



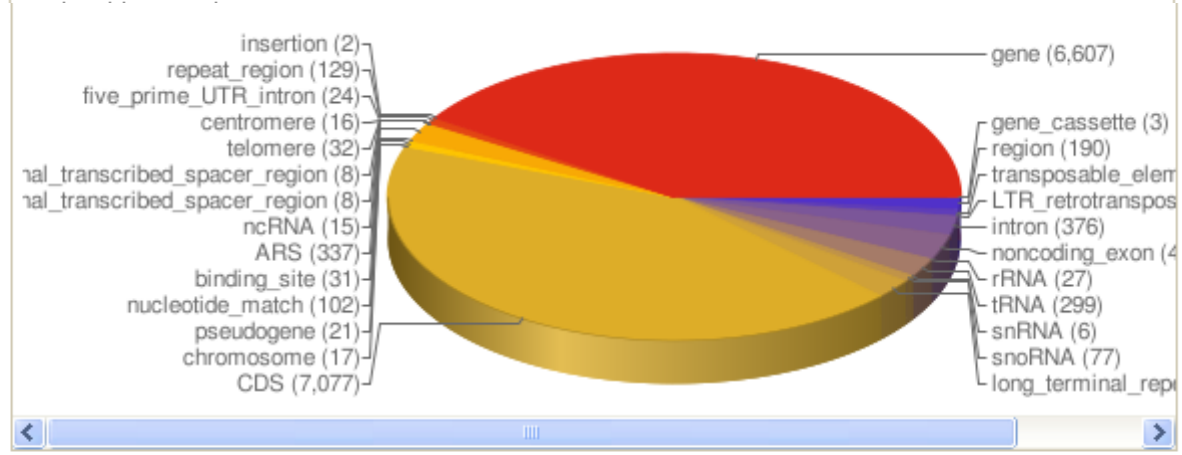
Create a new materialized view.

microorganism behind the most common type of fermentation. *S. cerevisiae* cells are round to ovoid, 5-10 micrometres in diameter.

Feature Summary

Type	Number
CDS	7,077
gene	6,607
noncoding_exon	480
long_terminal_repeat	383
intron	376
ARS	337
tRNA	299
region	190
repeat_region	129

Feature summary for the organism (optional) →



- yeast_admin**
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Home

YAL068W-A

[View](#) [Edit](#)

Anonymous - Posted on 11 January 2010

Name YAL068W-A

Accession YDBID10

Sequence

```

ATGCACGGCACTTGCCTCAGCGGTCTATACCCTGTGCCATTTACCCATAA
CGCCCATCATTATCCACATTTTGATATCTATATCTCATTGCGCGGTCCCA
AATATTGTATAACTGCCCTTAATACATACGTTATACCACTTTTGCACCAT
ATACTTACCACTCCATTTATATACACTTATGTCAATATTACAGAAAAATC
CCCACAAAAATCACCTAAACATAAAAAATTTCTACTTTTCAACAATAATA
CATAA

```

Length 255

Type gene

Organism yeast

[\[-\] Collapse All](#)

References 

Dababase	Accession
SGD	S000028594
GFF_source	SGD

Analyses

yeast_admin

- o My account
- ▼ Create content
 - o Analysis
 - o Analysis: Blast
 - o Analysis: Interpro
 - o Analysis: KEGG
 - o Feature
 - o Organism
 - o Page
 - o Story
- ▶ Administer
- o Log out



Home » Create content

Create Analysis: Interpro

- ▶ Menu settings

Analysis Name:

Saccharomyces cerevisiae interpro

Program: *

InterproScan

Program Version: *

2

Algorithm:

Source Name:

Source Version:

Source URI:

Time Executed: *

Dec 12 2009

Description and/or Program Settings:

Analysis performed to annotate Saccharomyces cerevisiae genes with protein domains and motifs

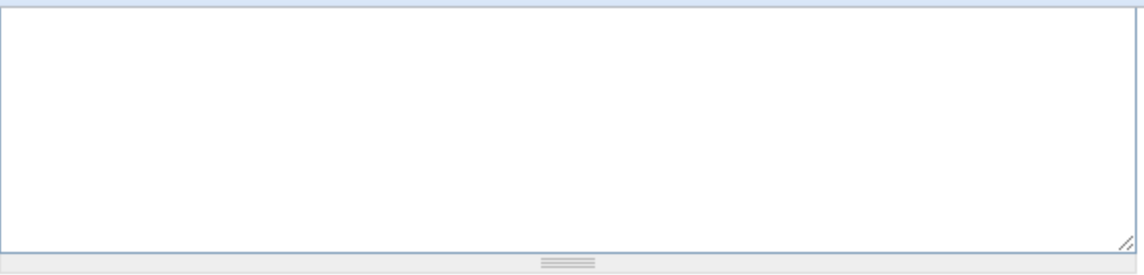
Specify the .html output



Indicate the File should be parsed for display on the website



Indicate the GO terms should be extracted



▼ Interpro Settings

Specific Settings for Interpro Analysis.

Interproscan Output File (in html format):

/var/www/sites/default/files/iprscan-20091208-16345492.html

The html output file generated by Interproscan in full path.

Submit a job to parse the Interpro html output

Note: features associated with the interpro results must exist in chado before parsing the file. Otherwise, interpro results that cannot be linked to a feature will be discarded. Also, Triapl Interpro module needs to be enabled.

Load GO terms to the database

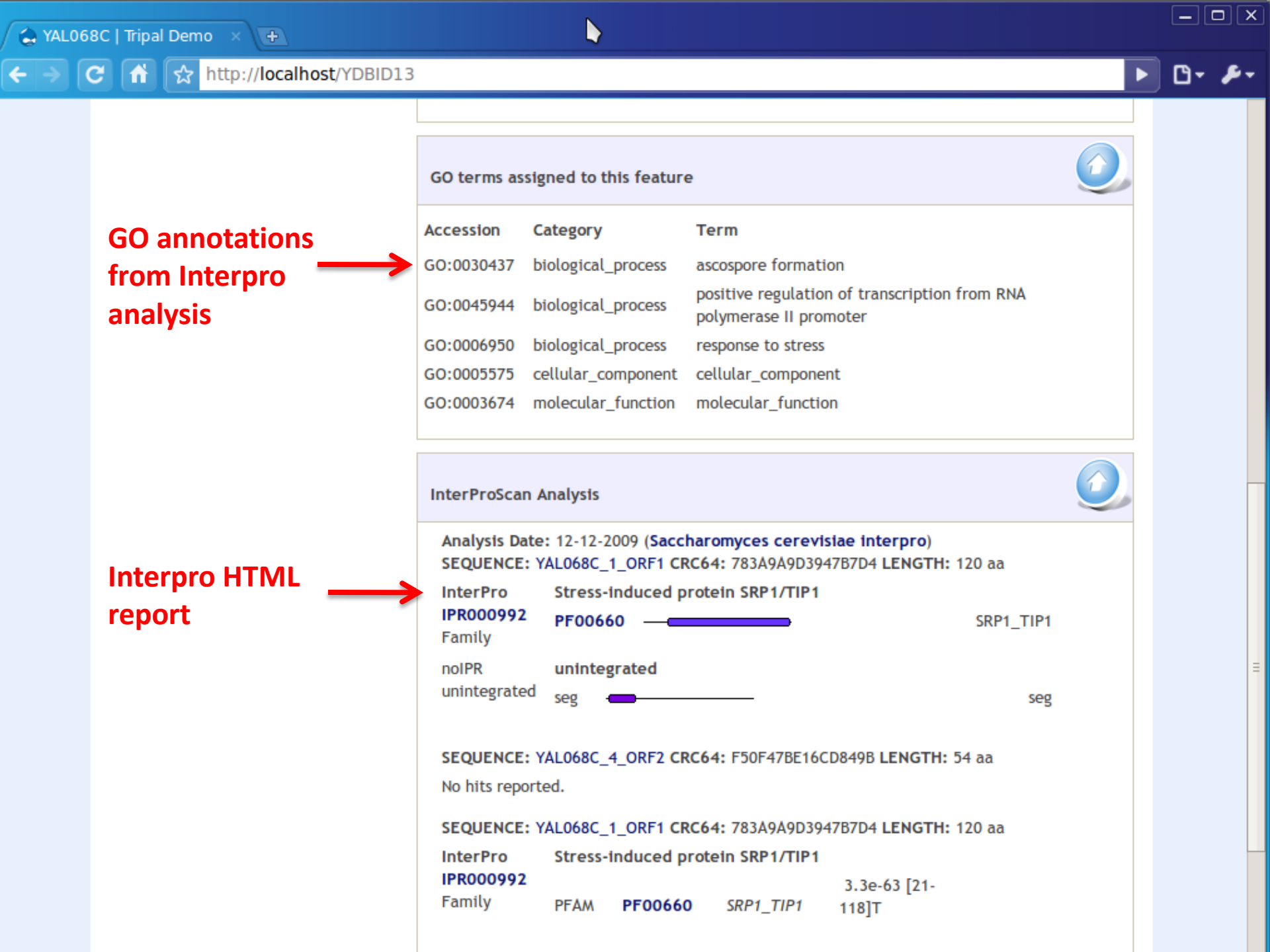
Check the box to load GO terms to chado database

Parameters:

iprscan -cli -i yeast.fasta -o yeast.interpro.html -format html -goterms -ipr

The parameters for running the interpro analysis.

- ▶ Revision information
- ▶ URL path settings
- ▶ Comment settings
- ▶ Authoring information
- ▶ Publishing options



GO terms assigned to this feature

Accession	Category	Term
GO:0030437	biological_process	ascospore formation
GO:0045944	biological_process	positive regulation of transcription from RNA polymerase II promoter
GO:0006950	biological_process	response to stress
GO:0005575	cellular_component	cellular_component
GO:0003674	molecular_function	molecular_function

GO annotations from Interpro analysis



InterProScan Analysis

Analysis Date: 12-12-2009 (*Saccharomyces cerevisiae* interpro)

SEQUENCE: YAL068C_1_ORF1 CRC64: 783A9A9D3947B7D4 LENGTH: 120 aa

InterPro	Stress-induced protein SRP1/TIP1	
IPR000992	PF00660	SRP1_TIP1
Family		
noIPR	unintegrated	
unintegrated	seg	seg

Interpro HTML report



SEQUENCE: YAL068C_4_ORF2 CRC64: F50F47BE16CD849B LENGTH: 54 aa

No hits reported.

SEQUENCE: YAL068C_1_ORF1 CRC64: 783A9A9D3947B7D4 LENGTH: 120 aa

InterPro	Stress-induced protein SRP1/TIP1	
IPR000992		3.3e-63 [21-118]T
Family	PFAM PF00660	SRP1_TIP1

Select a GO report to view:

Saccharomyces cerevisiae interpro

Select the GO analysis to view

Any analysis with GO results related to this organism are available for viewing. For further information, see the analysis information page.

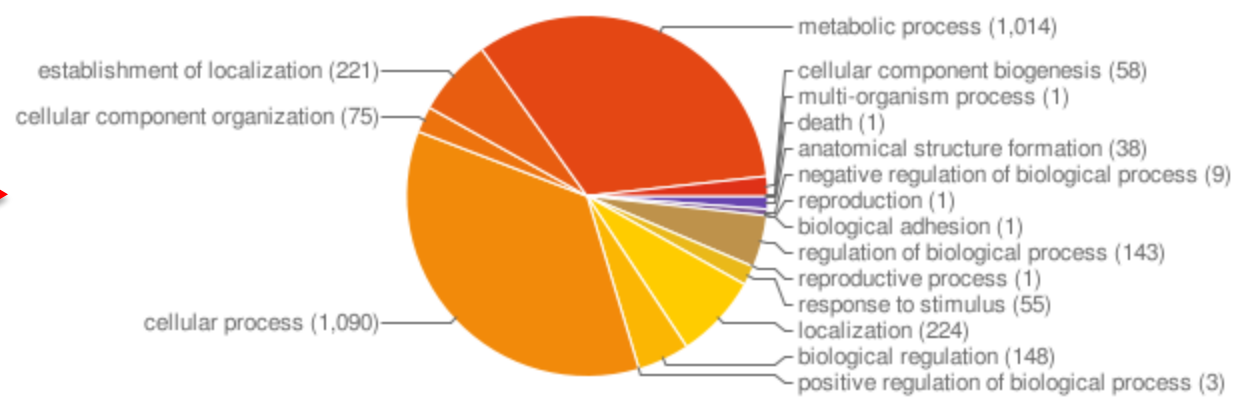
Biological Process

Expand the tree to browse term counts. Click a term to view term details.

- biological_process

Browseable tree of all terms

Number of Biological Process Terms From Saccharomyces cerevisiae interpro Analysis



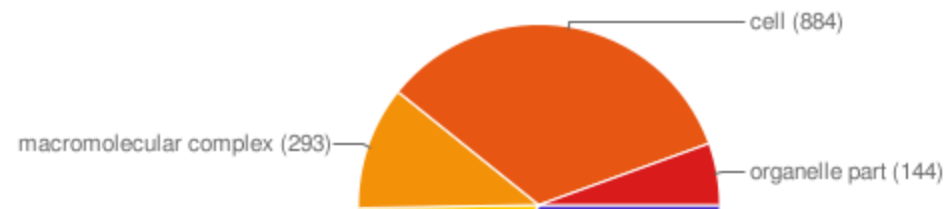
Pie charts summarizing top level ontology terms

Cellular Component

Expand the tree to browse term counts. Click a term to view term details.

- cellular_component

Number of Cellular Component Terms From Saccharomyces cerevisiae interpro Analysis



- + multicellular organismal process
- + multi-organism process (1 Features)
- + negative regulation of biological process (9 Features)
- + pigmentation
- + positive regulation of biological process (3 Features)
- + regulation of biological process (143 Features)
- + reproduction (1 Features)
- + **reproductive process (1 Features)**

Click to see term information

Close [X]

Term Information

Term reproductive process

Accession 0022414

Ontology biological_process

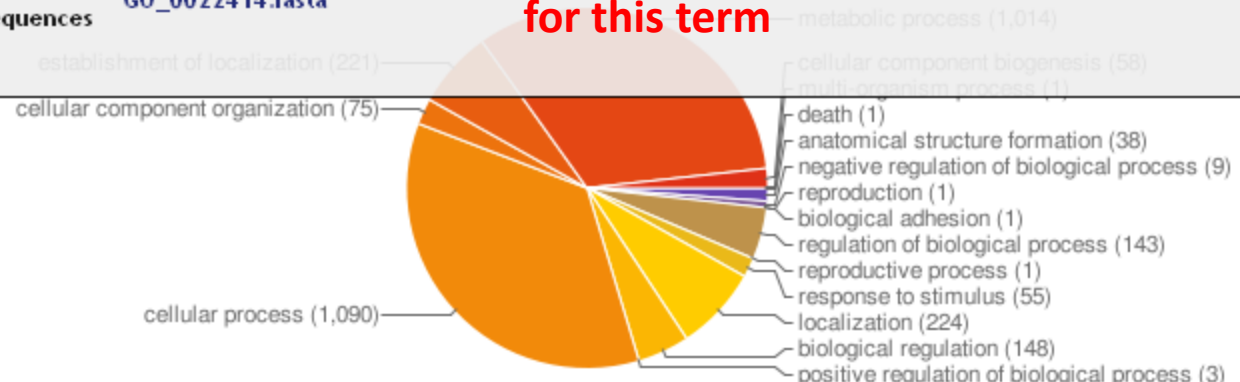
Definition A biological process that directly contributes to the process of producing new individuals by one or two organisms. The new individuals inherit some proportion of their genetic material from the parent or parents.

Synonyms

Internal ID 15342

Download sequences [GO_0022414.fasta](#)

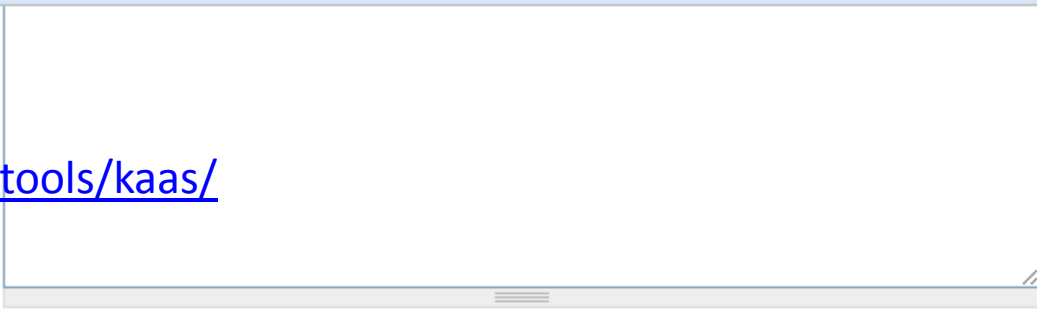
Download FASTA file of features for this term



KAAS Server

<http://www.genome.jp/tools/kaas/>

Provide the directory containing KAAS/KEGG result files



▼ **KEGG Settings**

Specific Settings for KEGG Analysis.

KAAS hier.tar.gz Output File:

The full path to the hier.tar.gz file generated by KAAS. Alternatively, you can input the full path to the directory that contains decompressed kegg files.

Submit a job to parse the kegg output into analysisfeatureprop table

Note: features associated with the KAAS results must exist in chado before parsing the file. Otherwise, KEGG results that cannot be linked to a feature will be discarded.

- ▶ **Revision information**
- ▶ **URL path settings**
- ▶ **Comment settings**
- ▶ **Authoring information**
- ▶ **Publishing options**

Save Preview

YJL196C | Tripal Demo

http://184.48.85.77/YDBID8085

GO terms assigned to this feature

Accession	Category	Term
GO:0019368	biological_process	fatty acid elongation, unsaturated fatty acid
GO:0016020	cellular_component	membrane
GO:0009922	molecular_function	fatty acid elongase activity

KEGG Analysis

Analysis Date: 01-12-2010 (**Saccharomyces cerevisiae KEGG**)

K10245 ELO2; fatty acid elongase 2 [EC:2.3.1.-]

InterProScan Analysis

Analysis Date: 12-12-2009 (**Saccharomyces cerevisiae interpro**)

SEQUENCE: YJL196C_1_ORF1 **CRC64:** 051D5369976BF48F **LENGTH:** 310 aa
No hits reported.

SEQUENCE: YJL196C_2_ORF2 **CRC64:** 983F4783367CCD56 **LENGTH:** 64 aa
noIPR **unintegrated**
unintegrated seg seg

SEQUENCE: YJL196C_4_ORF2 **CRC64:** B458AAE7607F48AF **LENGTH:** 84 aa
No hits reported.

SEQUENCE: YJL196C_5_ORF2 **CRC64:** 88F62F369ABD9D6E **LENGTH:** 52 aa
No hits reported.

cmd.rlh.snd.wayport.net...

KEGG results on feature page





ORTHOLOGY: K10245

[Help](#)

Entry	K10245 KO
Name	ELO2
Definition	fatty acid elongase 2 [EC:2.3.1.-]
Class	Metabolism; Lipid Metabolism; Biosynthesis of unsaturated fatty acids [PATH:ko01040] Metabolism; Lipid Metabolism; Lipid biosynthesis proteins [BR:ko01004] BRITE hierarchy
Other DBs	RN: R07758 GO: 0009922
Genes	SCE: YCR034W(FEN1) YJL196C(ELO1) AGO: AGOS_AFR624W KLA: KLLA0C03542g DHA: DEHA0G10912g PIC: PICST_34675(ELO2) VPO: Kpol_2001p51 CAL: CaO19.13699(FEN1) CGR: CAGL0L08184g YLI: YALI0B20196g SSL: SS1G_01397 Taxonomy KOALA
Reference	PMID:8702485
Authors	Toke DA, Martin CE
Title	Isolation and characterization of a gene affecting fatty acid elongation in <i>Saccharomyces cerevisiae</i> .
Journal	J Biol Chem 271:18413-22 (1996)
Reference	PMID:9211877
Authors	Oh CS, Toke DA, Mandala S, Martin CE
Title	ELO2 and ELO3, homologues of the <i>Saccharomyces cerevisiae</i> ELO1 gene, function in fatty acid elongation and are required for sphingolipid formation.

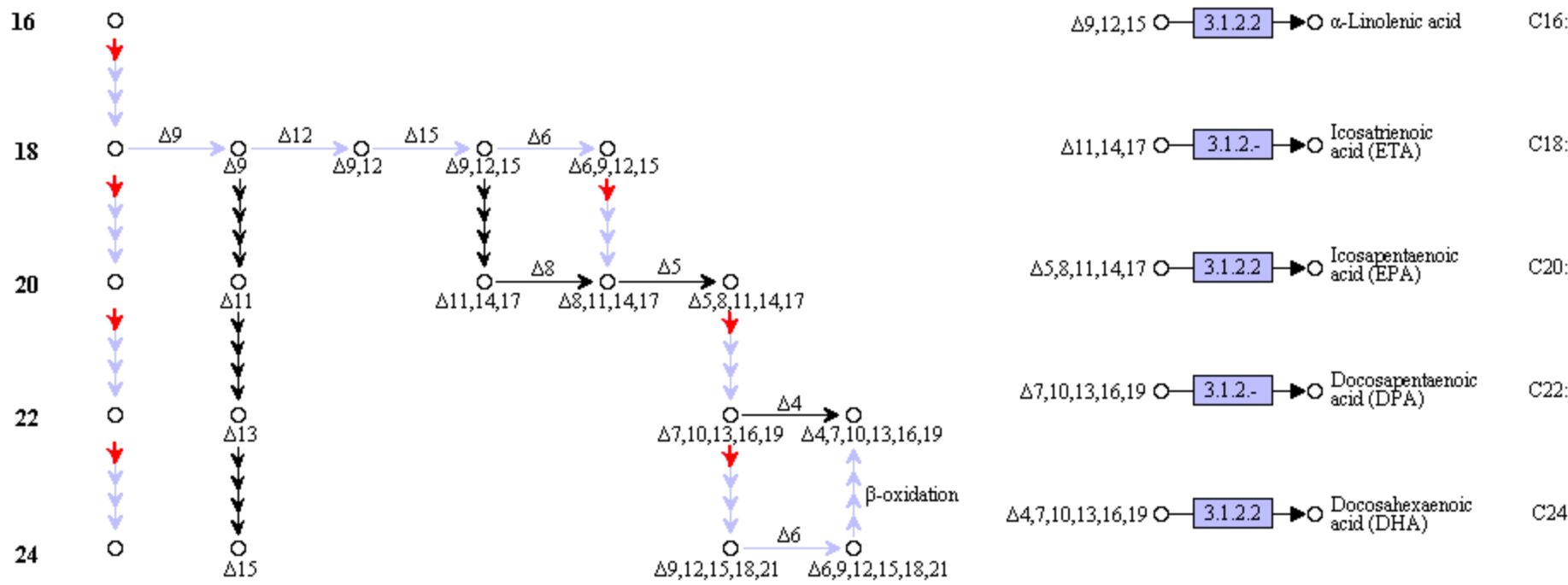
All links

Ontology (4)
 KEGG BRITE (3)
 GO (1)
 Pathway (12)
 KEGG PATHWAY (12)
 Chemical reaction (2)
 KEGG ENZYME (1)
 KEGG REACTION (1)
 Gene (33)
 KEGG GENES (11)
 KEGG DGENES (7)
 KEGG EGENES (15)
 Literature (2)
 PubMed (2)
 All databases (53)

BIOSYNTHESIS OF UNSATURATED FATTY ACIDS

0 1 2 3 4 5 6

n-3 family



Saccharomyces cerevisiae KEGG

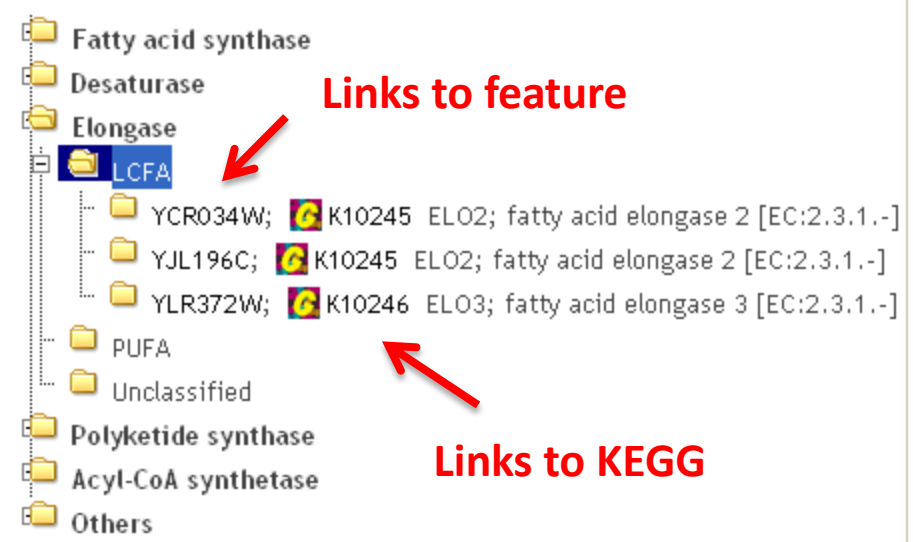
Any analysis with KEGG results related to this organism are available for viewing. For further information, see the analysis information page.

Analysis Results

KEGG BRITE

- Cellular antigens
- Lipid biosynthesis proteins
- SNAREs
- Glycan Binding Proteins
- Translation factors
- Proteoglycans
- Cancer stage
- Cytochrome P450
- Photosynthesis proteins
- Lipopolysaccharide biosynthesis proteins
- Bacterial toxins
- Two-component system
- Bacterial motility proteins
- GTP-binding proteins
- Cytoskeleton proteins
- Secretion system proteins

Hierarchy: Lipid biosynthesis proteins



Browseable KEGG results from analysis on organism page



Links to feature






Links to KEGG



**BLAST results
on feature page**

ExpASy Swissprot 

Analysis Date: 01-12-2010 (**Blast Saccharomyces cerevisiae vs Uniprot Sprot**)
 Query: YJL196C ELO1 SGDID:S000003732, Chr X from 68781-67849, reverse complement, Verified ORF, "Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids"
 Best 10 Hits Shown | [Show Best 25 Hits](#) | [Show All Hits](#)
 Note: Click a description for more details.

Match Name	E value	Identity
 ELO1_YEAST	0	100.00%
Elongation of fatty acids protein 1 OS=Saccharomyces cerevisiae GN=ELO1 PE=1 SV=1		
 ELO2_YEAST	5.07277e-105	59.04%
Elongation of fatty acids protein 2 OS=Saccharomyces cerevisiae GN=ELO2 PE=1 SV=1		
 ELO3_YEAST	9.63362e-80	48.47%
Elongation of fatty acids protein 3 OS=Saccharomyces cerevisiae GN=ELO3 PE=1 SV=1		

```

HSP 1

Score: 296.975 bits (759), Expect = 9.63362e-80
Identity = 143/295 (48.47%), Postives = 203/295 (68.81%), Query Frame = 1

Query:   52 PTIDRPFNFNIYLWDYFNRAVGWATAGRFQPKDFEFTVGKQPLSEPRPVLFFIAMYYVVFVGGGRSLV
KS--CKPLKLRFISQVHNLMLTSVSFLWLILMVEQMLPIVYRHGLYFAVCNVESWTQPMETLYYLNMYMTKFVEFADTV
LMVLKHRKLTFLHTYHHGATALLCYNQLVGYTAVTWVPVTLNLAVHVLVWYMYWYFLSASGIRVWVKAWVTRLQIVQFML
DLIVVYVLYQKIVAAYFKNACTPQCEDCLGSMTAIAAGAAILTSYLFILFISFYIEVYKRGSSASGKKKINKNN 930
          P+I+ PF  I LW  F++  + +  + + FEF  K  L+  +  I +Y++IFGG++++
++   PLK + + +++HNL LTS+S +  +LM+EQ++P+VY +GL++++C+ E++  + TLYYLN+TKFVE  DTV
  +VL+ +KL FLHTYHHGATALLCY QL+G T+V WV + LNL VHV+MYWYFLS+ GIRVWVK WVTR QI+QF++
DL+ VY+ Y   A  + +  P   C G+  A A G  ILTSYL LFISFYI+ YK+G   GKK + K +
Sbjct:  32 PSIENPF--GIELWPIFSKVFEYFSG--YPAEQFEFIHNKTFLANGYHAVSIIIVYIIIFGGQAIL
RALNASPLKFKLLFEIHNLFLTSLVLLMLLEQLVPMVYHNGLFWSICSKEAFAPKLVTLTYLNYLTKFVELIDTV
FLVLRKKLLFLHTYHHGATALLCYTQLIGRTSVEWVVILLNLGVHVIMYWYFLLSSCGIRVWVKQWVTRFQIIQFLI
    
```

yeast_admin

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Home » Search

Search

Enter your keywords:

[Download features \(multi-FASTA format\)](#)

[Advanced search](#)

Any term of Interest (Full text searching)



Search results



Search results

YGR130C

... InterPro IPR001747 Domain **Lipid** transport protein, N-terminal PF01347 ... InterPro IPR001747 Domain transport protein, N-terminal PFAM PF01347 ...

Feature - Anonymous - 01/11/2010 - 20:32 - 0 comments

YDR284C

... phosphatase, zinc-regulated vacuolar membrane-associated **lipid** phosphatase, dephosphorylates DG phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in **lipid** signaling and cell metabolism" Be Shown | Show Best 25 ...

Feature - Anonymous - 01/11/2010 - 20:31 - 0 comments

YDR503C

... from 1455859-1455035, reverse complement, Verified ORF, "**Lipid** phosphate phosphatase, catalyzes independent dephosphorylation of ... LPP1_YEAST 9.16152e-161 100.00% **Lipid** phosphate phosphatase 1 OS=Saccharomyces cerevisiae GN=LPP1 PE=1 SV=1 ...

Feature - Anonymous - 01/11/2010 - 20:31 - 0 comments

User Contributions

- Drupal API
- Tripal API
 - Jobs
 - Materialized Views
 - CVTerms
 - Trees
 - Charts
 - Analysis Management
- CUGI will host user contributed modules to share with Tripal

Thank You

Mailing list: <https://lists.sourceforge.net/lists/listinfo/gmod-tripal>