Tripal:
A Construction Toolkit for Online Genomic Databases

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PAG XIII
Poster 931
Acknowledgments

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  – Chun-Huai Cheng

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What is Tripal

• Tripal = GMOD Chado + Drupal
  – Chado: database schema for modeling biological data
    • [http://www.gmod.org](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](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

Sites developed at Washington State U. (Dorrie Main’s Lab)
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](http://www.drupal.org)
- Unpack into web directory
- Create a settings.php file that provides connection info
- Create a ‘sites/default/files’ directory
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: *
Tripal Demo

Site e-mail address: *
ficklin@clemson.edu
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: *
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.
Chado Installation

• Chado Tutorial:
  http://gmod.org/wiki/Chado_Tutorial

• 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

Administration Menu

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

Primary Menu

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.
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.

<table>
<thead>
<tr>
<th>Screenshot</th>
<th>Name</th>
<th>Version</th>
<th>Enabled</th>
<th>Default</th>
<th>Operations</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Drupal" /></td>
<td><strong>Bluemarine</strong> Table-based multi-column theme with a marine and ash color scheme.</td>
<td>6.15</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><img src="image" alt="Chameleon" /></td>
<td><strong>Chameleon</strong> Minimalist tabled theme with light colors.</td>
<td>6.15</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><img src="image" alt="Garland" /></td>
<td><strong>Garland</strong> Tableless, recolorable, multi-column, fluid width theme (default).</td>
<td>6.15</td>
<td></td>
<td></td>
<td>configure</td>
</tr>
<tr>
<td><img src="image" alt="Marvin" /></td>
<td><strong>Marvin</strong> Boxy tabled theme in all grays.</td>
<td>6.15</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><img src="image" alt="Minnelli" /></td>
<td><strong>Minnelli</strong> Tableless, recolorable, multi-column, fixed width theme.</td>
<td>6.15</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
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).

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
<table>
<thead>
<tr>
<th>Screenshot</th>
<th>Name</th>
<th>Version</th>
<th>Enabled</th>
<th>Default</th>
<th>Operations</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="https://via.placeholder.com/150" alt="Screenshot" /></td>
<td>Tableless, recolorable, multi-column, fixed width theme.</td>
<td>6.1b</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><img src="https://via.placeholder.com/150" alt="Screenshot" /></td>
<td>Pixture Reloaded</td>
<td>6.x-3.2</td>
<td></td>
<td></td>
<td><img src="https://via.placeholder.com/150" alt="Configure" /></td>
</tr>
<tr>
<td><img src="https://via.placeholder.com/150" alt="Screenshot" /></td>
<td>Polpo</td>
<td>6.x-1.0</td>
<td><img src="https://via.placeholder.com/150" alt="Enabled" /></td>
<td><img src="https://via.placeholder.com/150" alt="Default" /></td>
<td><img src="https://via.placeholder.com/150" alt="Configure" /></td>
</tr>
<tr>
<td><img src="https://via.placeholder.com/150" alt="Screenshot" /></td>
<td>Pushbutton</td>
<td>6.15</td>
<td><img src="https://via.placeholder.com/150" alt="Enabled" /></td>
<td><img src="https://via.placeholder.com/150" alt="Default" /></td>
<td><img src="https://via.placeholder.com/150" alt="Configure" /></td>
</tr>
<tr>
<td><img src="https://via.placeholder.com/150" alt="Screenshot" /></td>
<td>Tripal Theme</td>
<td>6.x-0.1b</td>
<td><img src="https://via.placeholder.com/150" alt="Enabled" /></td>
<td><img src="https://via.placeholder.com/150" alt="Default" /></td>
<td><img src="https://via.placeholder.com/150" alt="Configure" /></td>
</tr>
</tbody>
</table>

**Tripal Theme**
A Tripal specific theme for use with any other theme. Requires customization to info file of the primary theme.

Save configuration  Reset to defaults
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
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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. You may also post at the Drupal forum, or view the wide range of other support options available.
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.
Tripal Modules

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,

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

Analysis Core

Chado Tables Managed by Tripal:
- analysis, analysisprop, analysisfeature, analysisfeatureprop

BLAST
KEGG
GO
Unigene
Interpro
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
New Menu Items

New Admin Functions

Tripal Demo

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
Organisms
Organisms

Home

Organisms
No organism exists. Please contact administrators to synchronize organisms.
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

<table>
<thead>
<tr>
<th>Job ID</th>
<th>Job Name</th>
<th>Dates</th>
<th>Priority</th>
<th>Progress</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Sync organism: Saccharomyces cerevisiae</td>
<td>Submit Date: Mon, 01/11/2010 - 14:51</td>
<td>10</td>
<td>0%</td>
<td>Waiting</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Start Time: Not Yet Started</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Update materialized view 'organism_feature_count'</td>
<td>Submit Date: Mon, 01/11/2010 - 14:44</td>
<td>10</td>
<td>0%</td>
<td>Waiting</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Start Time: Not Yet Started</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Organisms</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>--------------------</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yeast</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Name: <strong>yeast</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genus: <strong>Saccharomyces</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Species: <strong>cerevisiae</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Description:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Saccharomyces cerevisiae

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 documentation.
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.
Genomic Features
Content only for features of these types will be generated
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 categorical 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

Set/Reset Taxonomy for all feature nodes

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.

Reindex all feature nodes
### 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.

<table>
<thead>
<tr>
<th>Job ID</th>
<th>Job Name</th>
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<th>Priority</th>
<th>Progress</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>Set all feature taxonomy</td>
<td>Start Date: Mon, 01/11/2010 - 20:48</td>
<td>10</td>
<td>32%</td>
<td>Running</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>Sync all features</td>
<td>Start Date: Mon, 01/11/2010 - 17:56</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Reindex all features</td>
<td>Start Date: Mon, 01/11/2010 - 17:47</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Set all feature taxonomy</td>
<td>Start Date: Mon, 01/11/2010 - 17:47</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Sync all features</td>
<td>Start Date: Mon, 01/11/2010 - 17:47</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Saccharomyces cerevisiae</td>
<td>Start Date: Mon, 01/11/2010 - 14:51</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sync organism:</td>
<td>Start Date: Mon, 01/11/2010 - 14:52</td>
<td>10</td>
<td>100%</td>
<td>Completed</td>
</tr>
<tr>
<td></td>
<td></td>
<td>End Time:</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
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.
<table>
<thead>
<tr>
<th>View Update</th>
<th>Name</th>
<th>Last_Update</th>
<th>Delete</th>
</tr>
</thead>
<tbody>
<tr>
<td>View Update</td>
<td>cv_root_mview</td>
<td>Not yet populated</td>
<td>Delete</td>
</tr>
<tr>
<td>View Update</td>
<td>go_count_analysis</td>
<td>Not yet populated</td>
<td>Delete</td>
</tr>
<tr>
<td>View Update</td>
<td>go_count_organism</td>
<td>Not yet populated</td>
<td>Delete</td>
</tr>
<tr>
<td>View Update</td>
<td>kegg_by_organism</td>
<td>Not yet populated</td>
<td>Delete</td>
</tr>
<tr>
<td>View Update</td>
<td>organism_feature_count</td>
<td>Mon, 01/11/2010 - 14:52</td>
<td>Delete</td>
</tr>
</tbody>
</table>

Create a new materialized view.
Feature summary for the organism (optional)

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

<table>
<thead>
<tr>
<th>Type</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>CDS</td>
<td>7,077</td>
</tr>
<tr>
<td>gene</td>
<td>6,607</td>
</tr>
<tr>
<td>noncoding_exon</td>
<td>480</td>
</tr>
<tr>
<td>long_terminal_repeat</td>
<td>383</td>
</tr>
<tr>
<td>intron</td>
<td>376</td>
</tr>
<tr>
<td>ARS</td>
<td>337</td>
</tr>
<tr>
<td>tRNA</td>
<td>299</td>
</tr>
<tr>
<td>region</td>
<td>190</td>
</tr>
<tr>
<td>repeat_region</td>
<td>129</td>
</tr>
<tr>
<td>insertion</td>
<td>2</td>
</tr>
<tr>
<td>repeat_region (129)</td>
<td></td>
</tr>
<tr>
<td>five_prime_UTR_intron</td>
<td>24</td>
</tr>
<tr>
<td>centromere</td>
<td>16</td>
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<tr>
<td>telomere</td>
<td>32</td>
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<tr>
<td>ral_transcribed_spacer_region</td>
<td>8</td>
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<tr>
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<td>8</td>
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<td>noRNA (15)</td>
<td></td>
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<td>ARS (337)</td>
<td></td>
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<td>binding_site (31)</td>
<td></td>
</tr>
<tr>
<td>nucleotide_match (102)</td>
<td></td>
</tr>
<tr>
<td>pseudogene (21)</td>
<td></td>
</tr>
<tr>
<td>chromosome (17)</td>
<td></td>
</tr>
<tr>
<td>CDS (7,077)</td>
<td></td>
</tr>
</tbody>
</table>
YAL068W-A

Name: YAL068W-A

Accession: YDBID10

Sequence:
ATGCACGGCACTTGGCTCAGCGGTCTATACCCCTGTGCCATTTACCATAA
CCGCCATCAAATCCACATTTTGGATATCTATATCTCATATCCGGGTTCTCCA
AACTTTGTTGTAACTGGCCTTAATACTACGTTATACCATCTACCACTTTTGACCAT
ATACCTACCACTCCATTTATATACACTTTATGCTAATATTATAAGAAAAATC
CCCACAAAAATCACCATAACAGAATATTTCTACTTTTCACAATATAAT

Length: 255

Type: gene

Organism: yeast

References:

<table>
<thead>
<tr>
<th>Database</th>
<th>Accession</th>
</tr>
</thead>
<tbody>
<tr>
<td>SGD</td>
<td>S000028594</td>
</tr>
<tr>
<td>GFF_source</td>
<td>SGD</td>
</tr>
</tbody>
</table>
Analyses
Create Analysis: Interpro

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
GO annotations from Interpro analysis

Interpro HTML report

GO terms assigned to this feature

<table>
<thead>
<tr>
<th>Accession</th>
<th>Category</th>
<th>Term</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0030437</td>
<td>biological_process</td>
<td>ascospore formation</td>
</tr>
<tr>
<td>GO:0045944</td>
<td>biological_process</td>
<td>positive regulation of transcription from RNA polymerase II promoter</td>
</tr>
<tr>
<td>GO:0066950</td>
<td>biological_process</td>
<td>response to stress</td>
</tr>
<tr>
<td>GO:0005575</td>
<td>cellular_component</td>
<td>cellular_component</td>
</tr>
<tr>
<td>GO:0003674</td>
<td>molecular_function</td>
<td>molecular_function</td>
</tr>
</tbody>
</table>

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
Family

IPR000992

No hits reported.

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   PFAM   PF00660   SRP1_TIP1
Family

3.3e-63 [21-118]T
Select a GO report 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.

- metabolic process (1,014)
- cellular component biogenesis (58)
- multi-organism process (1)
- death (1)
- anatomical structure formation (38)
- negative regulation of biological process (9)
- reproduction (1)
- biological adhesion (1)
- regulation of biological process (143)
- reproductive process (1)
- response to stimulus (55)
- localization (224)
- biological regulation (148)
- positive regulation of biological process (3)

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

- cell (884)
- macromolecular complex (293)
- organelle part (144)
KAAS Server
http://www.genome.jp/tools/kaas/

Provide the directory containing KAAS/KEGG result files
KEGG results on feature page

<table>
<thead>
<tr>
<th>Accession</th>
<th>Category</th>
<th>Term</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0019368</td>
<td>biological_process</td>
<td>fatty acid elongation, unsaturated fatty acid</td>
</tr>
<tr>
<td>GO:0016020</td>
<td>cellular_component</td>
<td>membrane</td>
</tr>
<tr>
<td>GO:0009922</td>
<td>molecular_function</td>
<td>fatty acid elongase activity</td>
</tr>
</tbody>
</table>

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

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

SEQUENCE: YJL196C_5_ORF2 CRC64: 88F62F369ABD9D6E LENGTH: 52 aa
No hits reported.
## ORTHOLOGY: K10245

<table>
<thead>
<tr>
<th>Entry</th>
<th>K10245</th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
<td>ELO2</td>
</tr>
<tr>
<td>Definition</td>
<td>fatty acid elongase 2 [EC:2.3.1.-]</td>
</tr>
</tbody>
</table>
| Class   | Metabolism; Lipid Metabolism; Biosynthesis of unsaturated fatty acids [PATH:ko01040]  
          | Metabolism; Lipid Metabolism; Lipid biosynthesis proteins [BR:ko01004] |
| Other DBs | RN: R07758  
       | GO: 0009922 |
| Genes   | YCR034W(FEN1)  
          | YJL196C(EL01)  
          | AGO: AG010424W  
          | KLA: KLLA0C03542g  
          | DHA: DEHA0G10912g  
          | PIC: PICST_34675(ELO2)  
          | VPO: Kpol_2001p51  
          | CAL: CaO19.13699(FEN1)  
          | CGR: CAGL0L08184g  
          | YLI: YALI0B20196g  
          | SSL: SS1G_01397 |

### Reference Authors Title
- PMID: 8702485  
  Toke DA, Martin CE  
  Isolation and characterization of a gene affecting fatty acid elongation in Saccharomyces cerevisiae.  
- PMID: 9211877  
  Oh CS, Toke DA, Mandala S, Martin CE  
  ELO2 and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene, function in fatty acid elongation and are required for sphingolipid formation.
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:S00003732, 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.

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

HSP 1

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


Subject: 32 PSISEPF-GIELWPIFSKVFHYFSF--YPAEQFEPFIHNTFLANGYHAYSVIIIYIIIFGQAIR ALNASPLKFKLMLFEIHNLFLTSISLVLLWMLMLEQLVPMVHYNLGFSICSKEAFAPKLTLYLYNLTYLFKEVLIDTV FLVLRKLLKFHHTYHGATALLCYTQLIGTRAISVAVVILLNLGVHIMMYWYFLSSCGIRwWkQwVTRFQIIQFLI
Any term of Interest (Full text searching)

Search results

YGR130C
... InterPro IPR001747 Domain Lipid transport protein, N-terminal PF01347 ... InterPro IPR001747 Domain Lipid 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 DAG phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism" Best 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 A independent dephosphorylation of ... LPP1_YEAST 9.16152e-161 100.00% Lipid phosphate phosphatase 2 ... 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
  – Matrialized 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