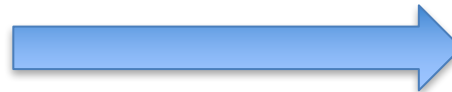
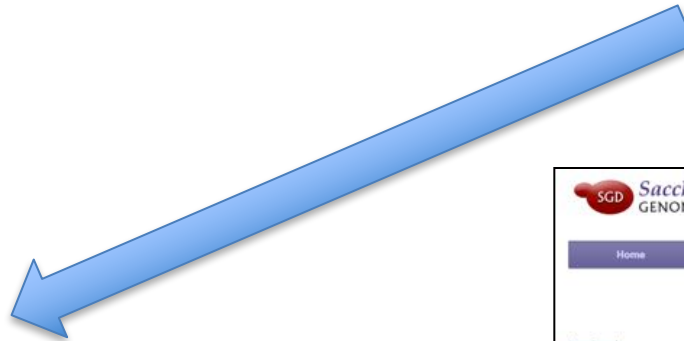
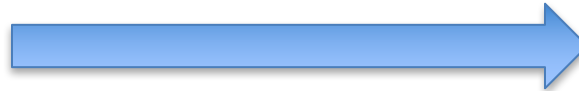




Gene and Protein Expression Data at the *Saccharomyces* Genome Database

International Biocuration Conference
April 08-11 2018
Shanghai, China

Gene expression data



SGD Saccharomyces GENOME DATABASE

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YeastMine: Batch Analysis or Advanced Search

Home Analyze Sequence Function Literature Community

SPELL - *S. cerevisiae*

SPELL (Yeast)

Gene Name(s): # Results: 239 Search

Options for Filtering Results by Dataset Tags™

New Search
Dataset Listing
Show Expression Levels
Download Expression Data
About the Website
SPELL Version 2.0.3

SPELL (Serial Pattern of Expression Levels Locator) is a query-driven search engine for large gene expression microarray compendia. Given a small set of query genes, SPELL identifies which datasets are most informative for these genes, then within those datasets additional genes are identified with expression profiles most similar to the query set. This instance of SPELL currently contains 537 datasets representing 11449 total arrays from 386 published studies.

To use SPELL, simply enter a set of *S. cerevisiae* gene names (defined by SGD) into the text box above and then click the "Search" button.

Please note that the "Filtering Results by Dataset Tags" feature simply filters the datasets for display purposes. It does not affect the SPELL search algorithm.

Need help getting started with SPELL? Check out the video tutorial. Additional help may be obtained by hovering over the help icon whenever you see it.

To access SPELL version 1.0 with the original datasets, please visit spell1.princeton.edu.

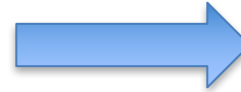
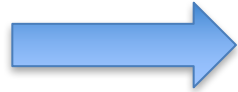
SPELL Version 2.0.3: Hilke MA, Hase DC, Myers CL, Hutterhower C, Li X and Tziporin DG (2007) Exploring the functional landscapes of gene expression: directed search of large microarray compendia. *Bioinformatics* 23: 2982-9
Contact: sgdhelpdesk@lists.stanford.edu

Stanford University

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GENETICS

Collection of GEO metadata



Automated

- Dataset GEO ID
- Dataset title
- Dataset description
- Assay type (RNA-seq, microarray, etc)
- Channel information
- Lab location
- Pubmed ID
- Date submitted
- Data sample GEO IDs
- Data sample titles
- Data sample types (RNA, DNA)
- Taxon
- Strain background

Manual

- Category terms
- Taxon
- Lab location
- Assay type
- Strain background

Similar datasets

 **Saccharomyces**
GENOME DATABASE

Analyte • Sequence • Function • Literature • Community •

 search: actin, kinase, glucose

Keyword:
fermentation

Overview

Datasets

Additional
Keywords

Keyword: fermentation

Description: The conversion of carbohydrates to carbon dioxide and alcohol under low oxygen or anaerobic conditions.

Datasets 329 datasets for 63 references

Dataset	Description	Keywords	Number of Conditions	Reference
A combined genetic and genomic approach uncovers molecular basis of wine yeast fermentation traits	Industrial wine yeast strains possess specific abilities to ferment under stressing conditions and give a suitable aromatic outcome	fermentation, nitrogen utilization	40	Arribas C, et al. (2011) PMID: 21843386
A genetic approach of wine yeast fermentation capacity in nitrogen-starvation reveals the key role of nitrogen signaling	In conditions of nitrogen limitation, <i>Saccharomyces cerevisiae</i> strains differ in their fermentation capacities, due to differences in their nitrogen requirements	nitrogen utilization, fermentation	8	
A <i>Saccharomyces cerevisiae</i> strain widely used in bioethanol production	In the search for renewable sources of energy, bioethanol stands out as a benchmark biofuel because its production is based on a proven technological platform	fermentation, oxidative stress, heat shock	3	Argueso JL, et al. (2009) PMID: 19363398
A transcriptomic analysis of the response of <i>S. cerevisiae</i> EC1118 to nitrogen supplementation during the stationary phase of four-stages continuous fermentation (FSCF)	The first aim was to investigate the suitability of FSCF to analyze yeast physiology during the stationary phase of wine making	fermentation, stationary phase	16	
Adaptation of <i>S. cerevisiae</i> to fermentative conditions	The capacity of respiring cultures of <i>Saccharomyces cerevisiae</i> to instantaneously switch to fast alcoholic fermentation upon a transfer to anaerobic sugar-excess conditions is a key characteristic of <i>Saccharomyces cerevisiae</i> in many of its industrial applications	carbon utilization, fermentation, oxygen level alteration, respiration	13	van den Brink J, et al. (2008) PMID: 18556356

References and datasets

SGD

Saccharomyces
GENOME DATABASE

MENU

Q search: actin, kinase, glucose

Reference:
Slavov N, et al.
(2014)

Abstract

Expression
Datasets

Reference: **Slavov N, et al. (2014)** Constant growth rate can be supported by decreasing energy flux and increasing aerobic glycolysis. *Cell Rep* 7(3):705-14

Abstract

Fermenting glucose in the presence of enough oxygen to support respiration, known as aerobic glycolysis, is believed to maximize growth rate. We observed increasing aerobic glycolysis during exponential growth, suggesting additional physiological roles for aerobic glycolysis. We investigated such roles in yeast batch cultures by quantifying O₂ consumption, CO₂ production, amino acids, mRNAs, proteins, posttranslational modifications, and stress sensitivity in the course of nine doublings at constant rate. During this course, the cells support a constant biomass-production rate with decreasing rates of respiration and ATP production but also decrease their stress resistance. As the respiration rate decreases, so do the levels of enzymes catalyzing rate-determining reactions of the tricarboxylic-acid cycle (providing NADH for respiration) and of mitochondrial folate-mediated NADPH production (required for oxidative defense). The findings demonstrate that exponential growth can represent not a single metabolic/physiological state but a continuum of changing states and that aerobic glycolysis can reduce the energy demands associated with respiratory metabolism and stress survival.

PMID: 24767987 DOI full text: P PMC full text: P PubMed: P

Download Citation (.nbib)

Reference Type: Journal Article | Research Support, N.I.H., Extramural | Research Support, Non-U.S. Gov't

Authors: Slavov N, Budnik BA, Schwab D, Alroidi EM, van Oudenaarden A

Additional Lit For: AFT1, APT2, ARG81, CAT2, CYC1, DFR1, FHL1, GCN4, GPH1, GRX3, GRX4, ... Show all

Expression Datasets 1 dataset for 1 reference

Dataset	Description	Keywords	Number of Conditions
Expression time course of yeast grown in a minimal medium	Time course of exponentially growing yeast cells Fermenting glucose in the presence of enough oxygen to support respiration, known as aerobic glycolysis, is believed to maximize growth rate	fermentation, nutrient utilization	8

Showing 1 to 1 of 1 entries 10 records per page 1

Download (.txt)

Dataset pages



Analyze - Sequence - Function - Literature - Community -

search: actin, kinase, glui

Dataset:
Expression
time course of
yeast grown in
a minimal
medium

Overview

Summary

Conditions

Resources

Dataset: Expression time course of yeast grown in a minimal medium

GEO ID:

GSE56773 [↗](#)

Reference:

Slavov N, et al. (2014)

Channels:

2

Conditions:

8

Description:

Time course of exponentially growing yeast cells Fermenting glucose in the presence of enough oxygen to support respiration, known as aerobic glycolysis, is believed to maximize growth rate

Categories:

[fermentation](#), [nutrient utilization](#)

Conditions

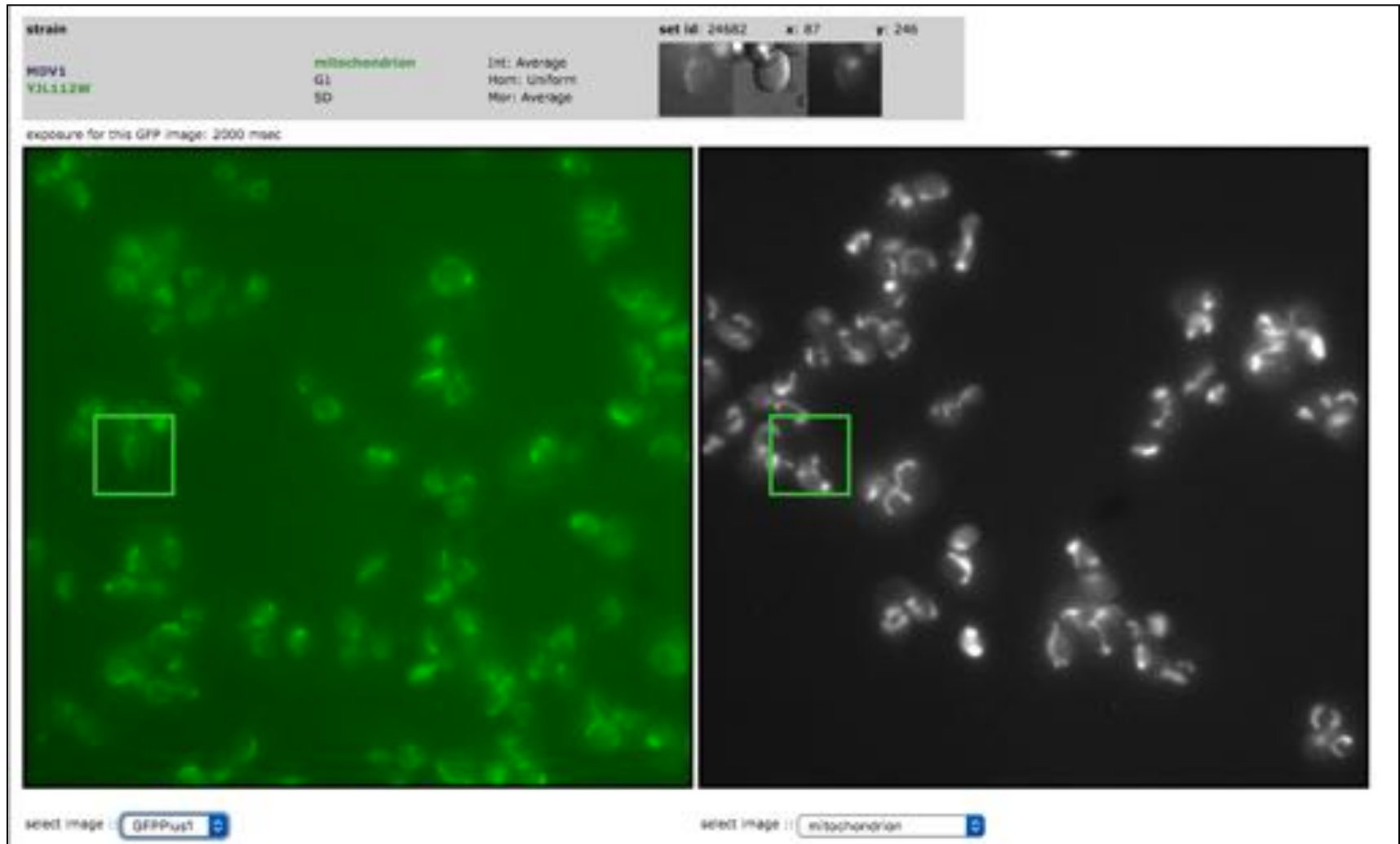
Condition	GEO ID
23 h	GSM1368904 ↗
22 h	GSM1368903 ↗
16 h	GSM1368898 ↗
17 h	GSM1368899 ↗
19 h	GSM1368900 ↗
20 h	GSM1368901 ↗
21 h	GSM1368902 ↗
24 h	GSM1368905 ↗

Resources

Download data [↗](#) | GEO [↗](#) | GEO supplementary data



Protein expression



Protein abundance and half-life

**Saccharomyces**
GENOME DATABASE

MENU

Summary Sequence **Protein** Gene Ontology Phenotype Interactions Regulation Expression Literature

MDV1 / YJL112W

Protein Overview

Experimental Data

Domains and Classification

Sequence

External Identifiers

Resources

MDV1 / YJL112W Protein [Protein Help](#)

Aliases: NET2⁶, FIS2⁷, GAG3²

Feature Type: ORF, Verified

Description: Peripheral protein of cytosolic face of mitochondrial outer membrane; required for mitochondrial fission; interacts with Fis1p and with the self-assembled oligomeric form of the dynamin-related GTPase Dnm1p; contains WD repeats; MDV1 has a paralog, CAF4, that arose from the whole genome duplication^{1 2 3 4 5}

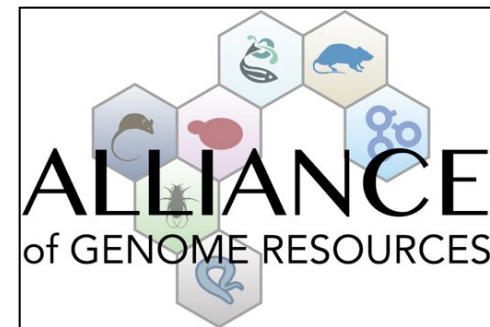
Paralog: CAF4⁴

Experimental Data

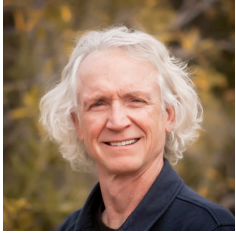
[Filter table](#)

Experiment	Result	Reference
abundance	3730 molecules/cell	Ghaemmaghami S, et al. (2003)
abundance	101 arbitrary fluorescence units	Newman JR, et al. (2006)
abundance	446 molecules/cell	Kulak NA, et al. (2014)
abundance	72 arbitrary fluorescence units	Chong YT, et al. (2015)
half-life	7.3 hr	Christiano R, et al. (2014)

[Download \(.txt\)](#)



Acknowledgements



J. Michael Cherry



Stacia Engel



Rob Nash



Marek Skrzypek



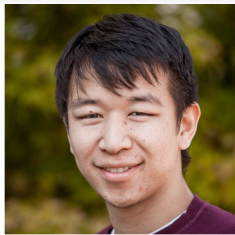
Barbara Dunn



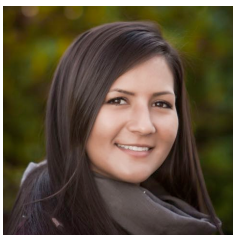
Sage Hellerstedt



Kevin MacPherson



Patrick Ng



Suzi Aleksander



Olivia Lang



Terry Jackson



Gail Binkley



Travis Sheppard



Shuai Weng



Kalpana Karra



Felix Gondwe



Ajay Prathivadhiba



Matt Simison



Stuart Miyasato

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