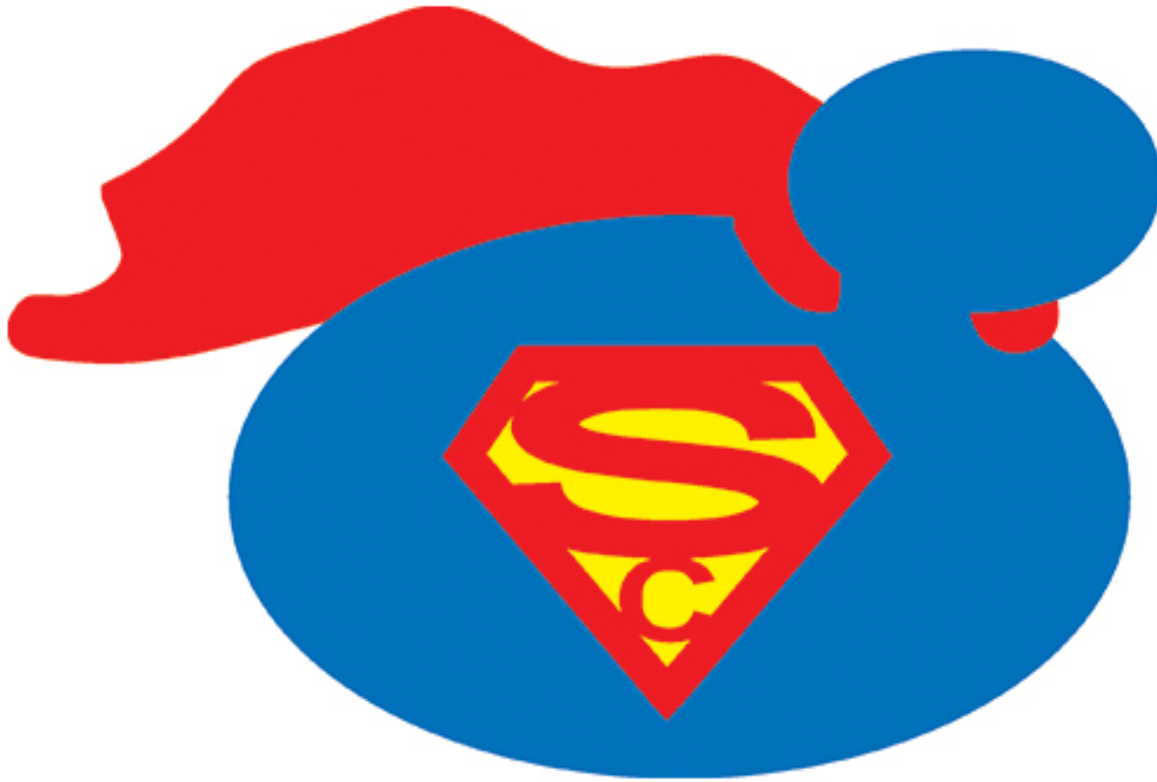


Saccharomyces Genome Database
Workshop
ICYGMB 2019



Slides & Poster PDFs
bit.ly/ICYGMB-2019



SGD Workshop Agenda – ICYGMB 2019

- Introduction (Mike)
- Protein abundance, Disease (Rob)
- Macro-molecular Complexes, Chemical (small molecule) (Edith)
- Transcriptome (Patrick)
- Gene product function at SGD (Suzi)
- Alliance of Genome Resources (Stacia)

SGD website 25th birthday, SGD first online on 8 May 1994

The screenshot shows a web browser window titled "SacchDB Server". The URL bar displays a long, complex URL. The main content area is titled "Class Locus cdc6" and contains a table with gene information. The table has columns for Name, Description, Phenotype, Gene_class, Type, and Molecular_information. The description for cdc6 is "required for initiation of DNA replication". The phenotype is "arrest at initiation of S phase". The gene class is "cdc". The type is "Gene". The molecular information includes a positive clone (6822) and several references, including a 1994 unpublished work by Hieter, P. and a 1985 personal communication by Hilger, F. The page also includes links for "Neighbours", "Link to other classes", and "Bibliography".

Name	Description	Phenotype	Gene_class	Type	Molecular_information
cdc6	required for initiation of DNA replication	arrest at initiation of S phase	cdc	Gene	Positive_clone 6822
					Hieter, P. (1994) Unpublished
					Hilger, F. (1985) Personal Communication
					5926
					Hieter, P. (1994) Unpublished
					Hilger, F. (1985) Personal Communication
					4261
					Hieter, P. (1994) Unpublished
					Hilger, F. (1985) Personal Communication
					Kawasaki, G. (1979) Karyotypic instability and carbon source effects in cell cycle mutants of Saccharomyces cerevisiae. Ph.D Thesis
					cseqX_11
					Dietrich, F., et al. (1994) Consensus sequence generated from GenBank by SGD
					Sequence
					YSCCDC6E (GB)
					YSCCDC6 (GB)
					YSCCDCA (GB)
					SCCDC6 (GB)
					SCCDC6G (GB)
Position	Map	X	-124	0	
Reference					Kawasaki, G. (1979) Karyotypic instability and carbon source effects in cell cycle mutants of Saccharomyces cerevisiae. Ph.D Thesis

1994

The screenshot shows the SGD website interface. The top navigation bar includes links for "About", "Blog", "Download", "Help", "YeastMine", and social media icons. The main content area is titled "CDC4 / YFL009W Overview". It provides a summary of the gene, including its standard name (CDC4), systematic name (YFL009W), SGD ID (SGD:S000001885), feature type (ORF, Verified), and description (F-box protein required for both the G1/S and G2/M phase transitions; modular substrate specificity factor which associates with core SCF (Cdc53p, Skp1p and Hrt1p/Rbx1p) to form the SCFCdc4 complex; SCFCdc4 acts as a ubiquitin-protein ligase directing ubiquitination of cyclin-dependent kinase (CDK) phosphorylated substrates, such as Sic1p, Far1p, Cdc6p, Clb6p, and Cln3p). The page also includes a "Sequence" section with a "Download (fsa)" button and a "View in: JBrowse" button. The JBrowse view shows the CDC4 location on Chromosome VI (116145..118484) and a genomic map with various features like HXT30, CDC4, SMC1, and WWM1. The genetic position is -9 cM. The subfeatures section shows the CDC4 CDS (coding sequence) with a scale from 116200 to 118400.

2019

On May 1994 there were a total of only 2000 websites

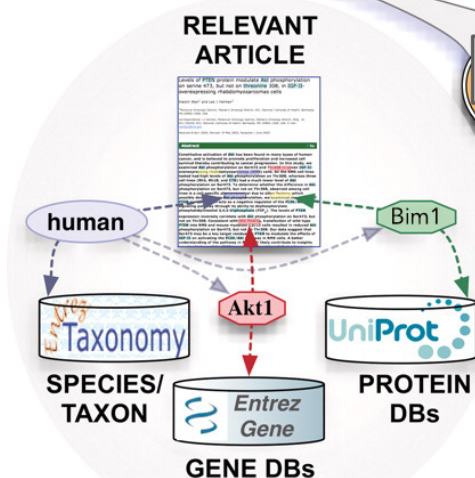
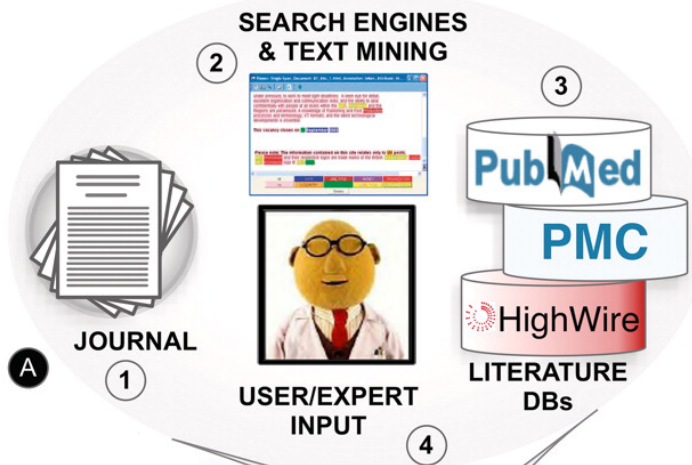
This image is a dense collage of scientific and technical information, primarily related to genetics, molecular biology, and genomics. It includes:

- Genomic Data and Visualizations:** Circular genome maps (e.g., CASAVA, Pileup), heatmaps, and scatter plots showing genomic data. A large circular diagram at the top left shows a genome map with various genes labeled (HSP12, YGR043, POC1, YLL044, YGP1, YPL142, PDR5, POK1).
- Scientific Publications and Abstracts:**
 - Structure of the 30S ribosomal subunit:** A paper by PLOS ONE, dated 11 September 2008, discussing the influence of physical and physiological cues on atomic force microscopy-based cell stiffness assessment.
 - The Yeast Type I Topoisomerase Top3 Interacts with Sgs1, a DNA Helicase Homolog:** A paper by SERGE GANLOFF, JOHN P. McDONALD, CHRISTIAN BENDIX, LANE ARTHUR, and RODNEY KOTHEIN, published in Molecular and Cellular Biology, Dec 1994, p. 8391-8398.
 - Intrinsic Suppressors of Mutant DNA Topoisomerase I-induced Lethality Diminish Enzyme Binding of DNA:** A paper by Christine L. Hann, Alyssa L. Carlborg, and Mary-Ann Hresch, published in PNAS, February 1997.
 - Genetic Control of the Cell-Division Cycle in Yeast, I. Detection of Mutants:** A paper by Leland H. Hartwell, Joseph Culotti, and Brian Reid, published in the Department of Genetics, University of Washington, Seattle, March 27, 1970.
 - Two protein tyrosine phosphatases, Ptp2 and Ptp3, modulate the subcellular localization of the Hog1 MAP kinase in yeast:** A paper by Christopher P. Mattison and Irene M. Ota, published in the Department of Chemistry and Biochemistry, University of Colorado, Boulder, Colorado 80509-0315 USA.
- Biological Diagrams and Schematics:**
 - A diagram of the cell cycle showing the progression from G1 to S to G2 to M.
 - A diagram of the DNA replication fork showing the leading and lagging strands.
 - A diagram of the cell division process showing the separation of chromosomes.
- Technical and Computational Data:**
 - A large table of data, possibly a gene expression matrix, with columns for various genes and rows for different conditions.
 - A diagram of a cell showing various organelles and their functions.
 - A diagram of a cell showing the localization of various proteins.

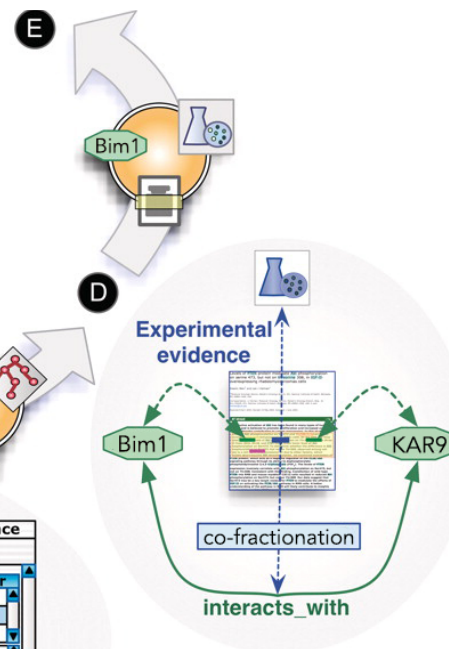
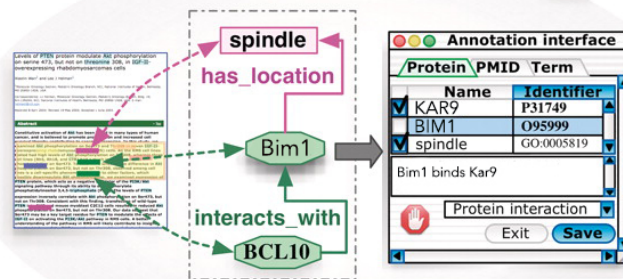
Literature
selection &
triage

SGD Curation Pipeline Literature to Integrated Annotations

Biological
object
identification



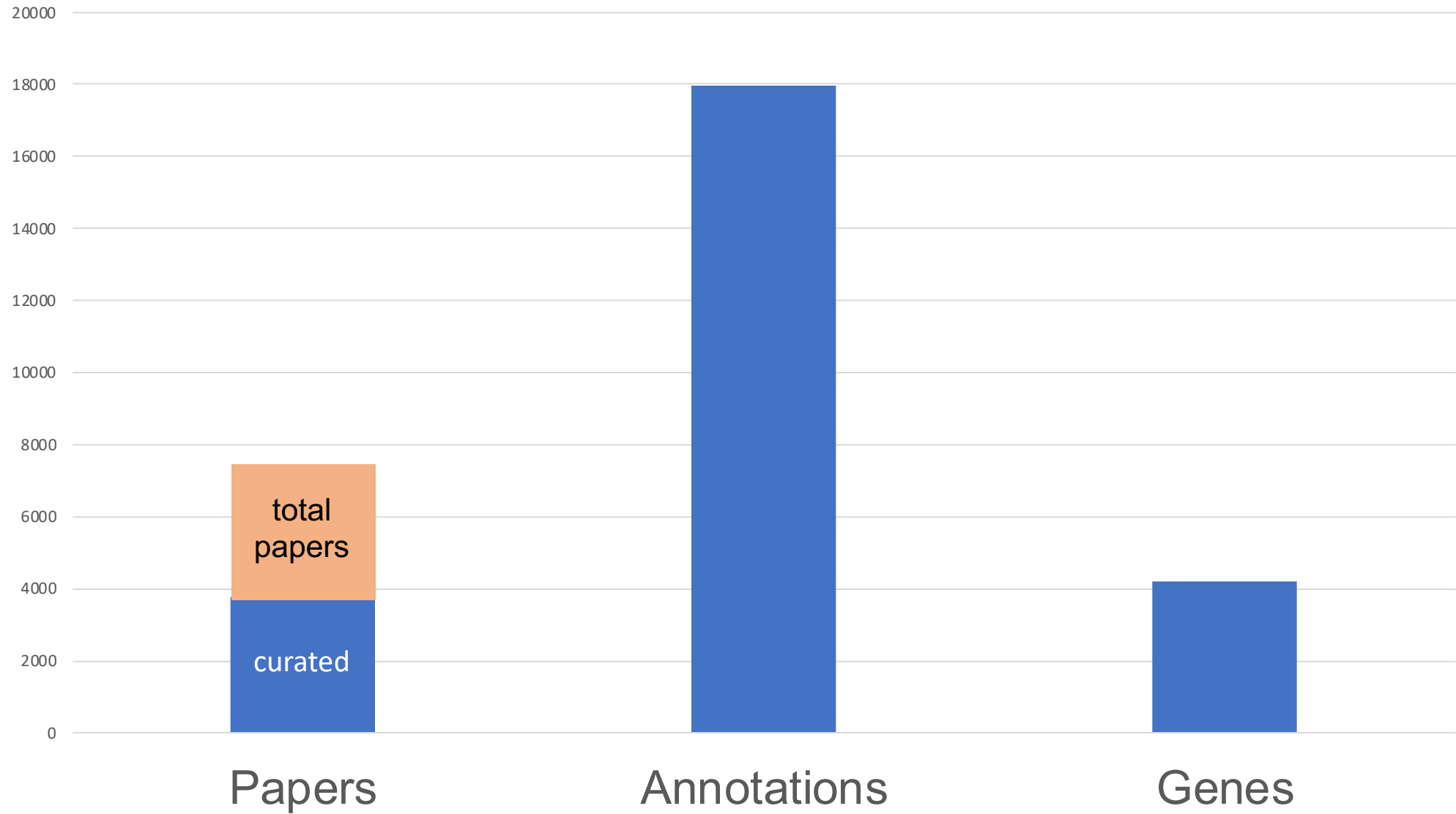
Bio-entity
mapping



Evidence
evaluation

SGD Curators are busy

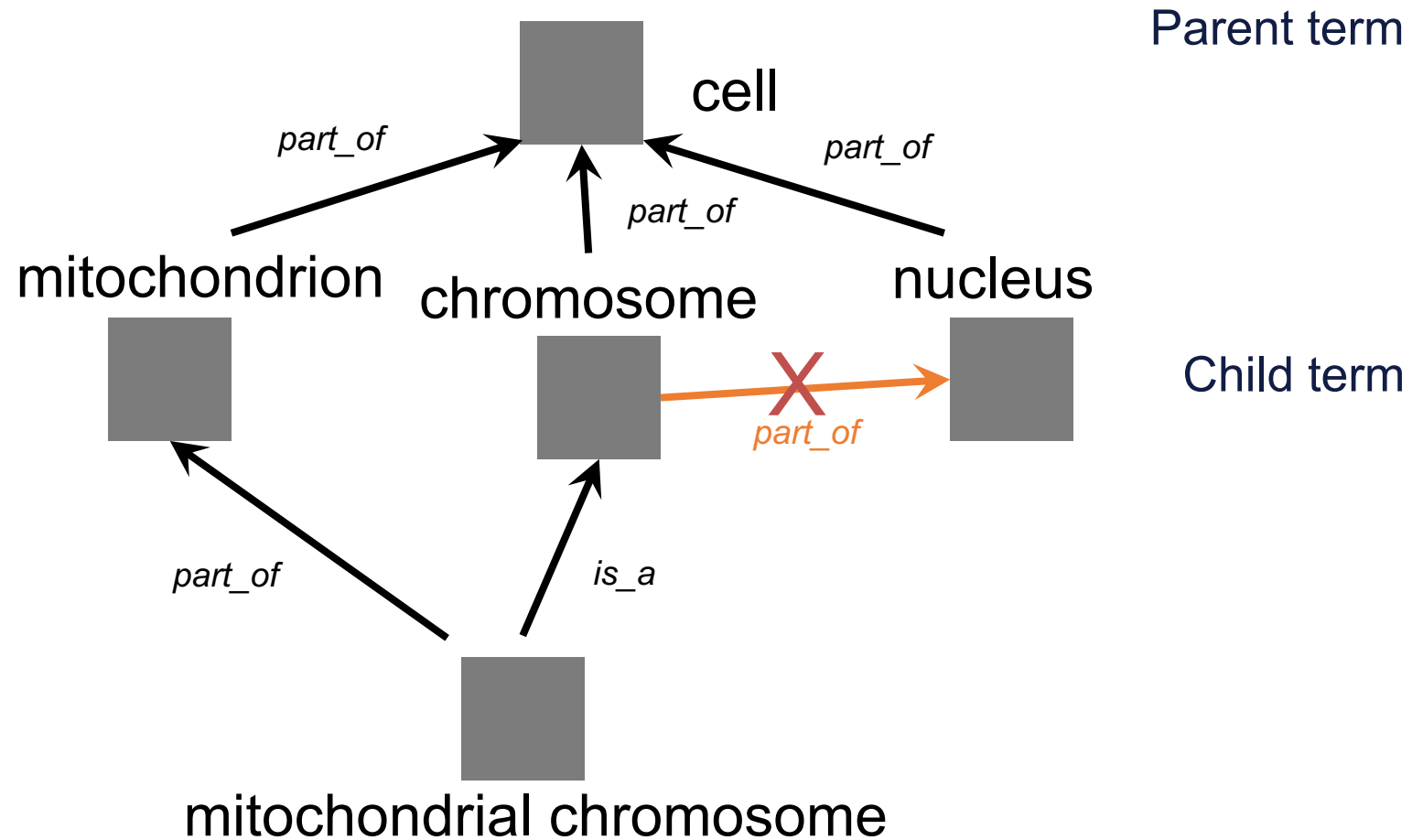
Number for 2018



An ontology is a set of words...

.. with different types of relationships to each other.

All relationships must be true.



Gene Ontology Term Name, ID, **Definition** and Synonyms

Term name	ID	Definition	Synonyms
nucleus	GO:0005634	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.	cell nucleus
mitochondrion	GO:0005739	A semiautonomous, self replicating organelle that occurs in varying numbers, shapes, and sizes in the cytoplasm of virtually all eukaryotic cells. It is notably the site of tissue respiration.	mitochondria
chromosome	GO:0005694	A structure composed of a very long molecule of DNA and associated proteins (e.g. histones) that carries hereditary information.	Chromatid interphase chromosome prophase chromosome

Saccharomyces Genome Data: X +

yeastgenome.org

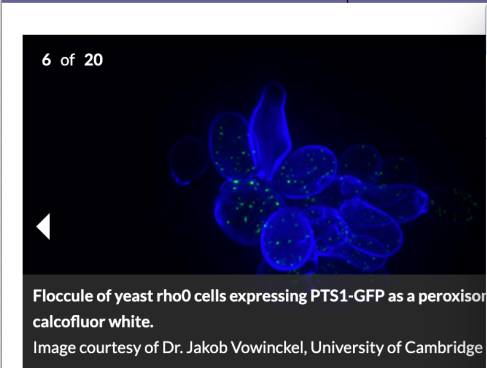
Apps NCAA NWS News SU Map Hoshnasi Ham KFS WebSDR FM-Radio 92 Code FCC Search baofeng bf-f8hp

About Blog Download Help YeastMine

SGD *Saccharomyces* GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu



Meetings

37th Small Meeting on Yeast Transport and Energetics (SMYTE)
September 11 to September 15, 2019 - Nove Hradý, Czechia

35th International Specialised Symposium on Yeasts (ISSY)

YeastMine: Home

Search and retrieve S. cerevisiae data

Data Updated on: Aug 1, 2019

Home Templates Lists QueryBuilder

Search

Search YeastMine. Enter name, identifier or keyword for genes, proteins, ontology terms, authors, abstract etc. (e.g. rad54, Act1p, DNA binding, Betel D).

e.g. act1

SEARCH

GENOME PROTEINS FUNCTION PHENOTYPES

[Read more](#)

Query for genome:

- Chromosomal Region ➔ All genes
- Gene ➔ Flanking features within a specific distance
- Gene ➔ Protein Sequence
- Feature Type ➔ Features of a selected feature Type
- Gene ➔ Non-Fungal and S. cerevisiae Homologs
- Gene ➔ Transcripts

Saccharomyces cerevisiae met X +

pathway.yeastgenome.org/YEAST/NEW-IMAGE?type=PATHWAY&object=PWY30-64&detail-level=3

Enter a gene, protein, metabolite or pathway... Quick Search Gene Search

Home Search Genome Metabolism Analysis Help

Saccharomyces cerevisiae Pathway: methionine salvage pathway

Show Predicted Enzymes More Detail Less Detail

The diagram illustrates the methionine salvage pathway in *Saccharomyces cerevisiae*. It begins with S-methyl-5-thioadenosine, which is converted to S-methyl-5-thio-D-ribose 1-phosphate by the enzyme 5'-methylthioadenosine phosphorylase (MEU1, EC 2.4.2.28). This step releases phosphate and adenine. S-methyl-5-thio-D-ribose 1-phosphate is then converted to 5-(methylsulfanyl)-ribitol 1-phosphate by methylthioribose-1-phosphate isomerase (MRI1, EC 5.3.1.23). 5-(methylsulfanyl)-ribitol 1-phosphate is converted to 5-(methylsulfanyl)-2,3-dioxopentyl 1-phosphate by methylthioribulose-1-phosphate dehydratase (MDE1, EC 4.2.1.109), releasing water. 5-(methylsulfanyl)-2,3-dioxopentyl 1-phosphate is converted to 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one by 2,3-dioxomethylpentane-1-phosphate enolase/phosphatase (UTR4, EC 3.1.3.77), releasing phosphate and H+. 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one is converted to 4-(methylsulfanyl)-2-oxobutanoate by spontaneous acireductone dioxxygenase (ADI1, EC 1.13.11.54), consuming oxygen and releasing formate and H+. 4-(methylsulfanyl)-2-oxobutanoate is then converted to 4-methylthio-2-oxobutanoate.

Compound: 5-(methylsulfanyl)-ribulose 1-phosphate
ID: CPD-1063
Synonyms: 5-methylthio-5-deoxy-D-ribulose 1-phosphate, 1-phosphomethylthioribulose, methylthioribulose 1-phosphate, MTRU-1-P, 1PMT-ribulose, 1-phospho-5-S-methylthioribulose, 5-(methylthio)ribulose 1-phosphate

Suzi Aleksander
Gene Ontology

Patrick Ng
Transcriptome

Gene Ontology Slim Term Mapper

The GO Slim Mapper maps annotations of a group of genes to more general terms and/or bins them into broad categories, i.e. [GO Slim](#) terms.

Three GO Slim sets are available at SGD:

- Yeast GO-Slim: broad, high level GO terms from the Biological Process, Molecular Function and Cellular Component ontologies maintained by the Saccharomyces Genome Database (SGD)
- Generic GO-Slim: broad, high level GO terms from the Biological Process, Molecular Function and Cellular Component ontologies maintained by the Gene Ontology Consortium (GOC)
- Macromolecular complex terms: protein complex terms from the Cellular Component ontology

Query Set (Your Input)

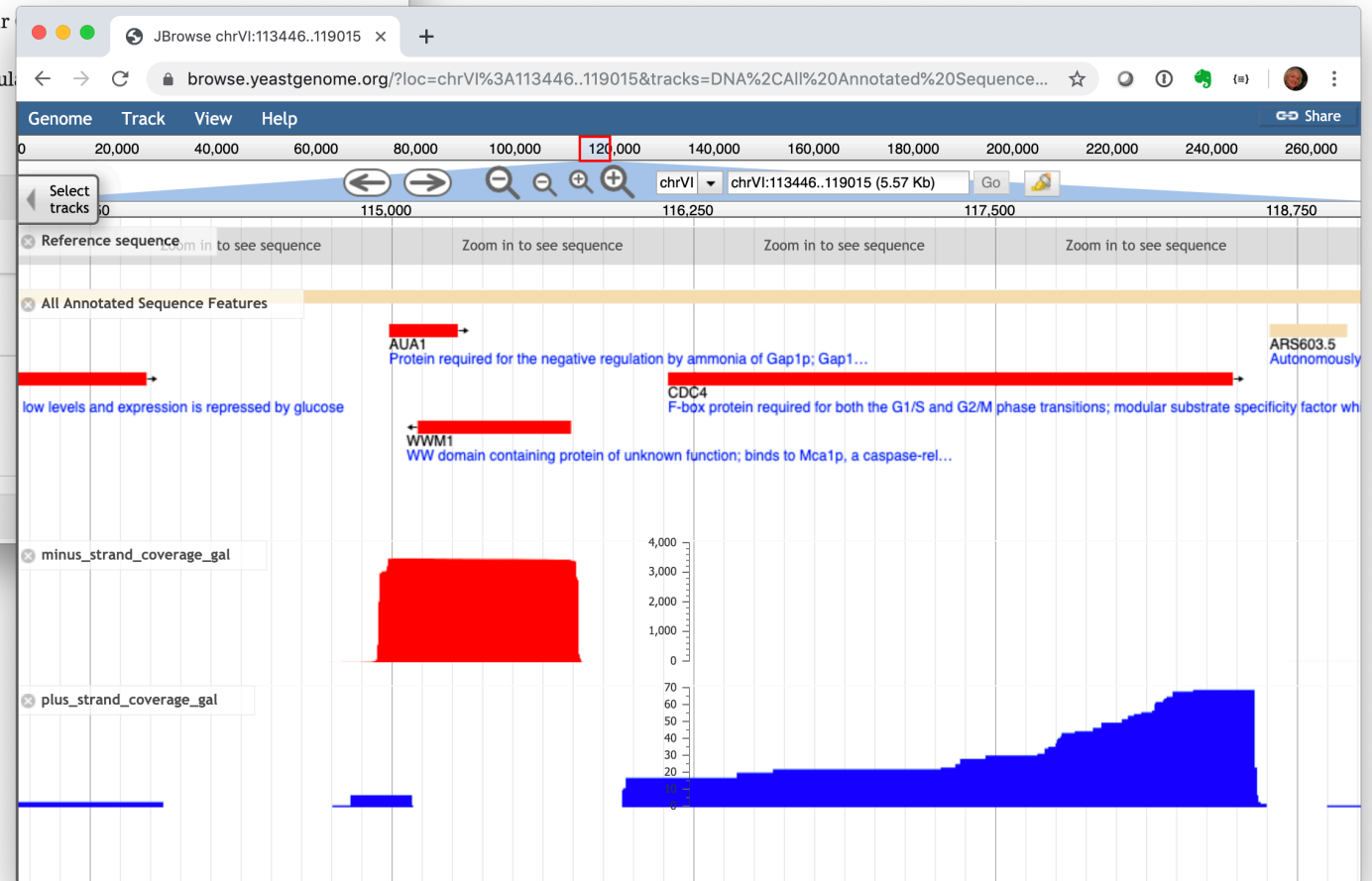
Enter Gene/ORF names (separated by a return or a space):

Note: If you have a big gene list (>100), save it as a file and upload it below.

OR Upload a file of Gene/ORF names (.txt or .tab format):

Choose File No file chosen

Specify your Slim Terms



MSH2 | SGD

yeastgenome.org/locus/S000005450

Apps NCAA NWS News SU Map Hoshnasi Ham KFS WebSDR FM-Radio 92 Code FCC Search baofeng bf-f8hp

About Blog Download Help YeastMine

SGD *Saccharomyces* GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu

Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Regulation Expression Literature

Rob Nash
Disease Annotation

MSH2 / YOL090W

Locus Overview
Sequence
Protein
Gene Ontology
Complex
Phenotype
Disease
Interaction
Regulation
Expression
Summary Paragraph
Literature
History
References

Standard Name: MSH2
Systematic Name: YOL090W
SGD ID: SGD:S000005450
Aliases: PMS5
Feature Type: ORF, Ve
Description: Protein mismatch activity
Name Description: MutS Homolog
Comparative Info: Integrat

Sequence

Download (.fsa)

MSH2 Location: Chromosome

MSH2 Disease | SGD

yeastgenome.org/locus/S000005450/disease

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SGD *Saccharomyces* GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu

Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Regulation Expression Literature

MSH2 / YOL090W Disease

Summary: Yeast MSH2 is homologous to human MSH2, and has been used to study Lynch syndrome, breast cancer, and ovarian cancer

Download All Annotations (.txt)

Manually Curated 4 entries for 4 Disease

Disease Ontology Term	Qualifier	Evidence
cancer		ISS w
breast cancer		ISS w
ovarian cancer		ISS w
Lynch syndrome		ISS w

Edith Wong
Macromolecular
Complexes

CNA1 | SGD

yeastgenome.org/locus/S000004425#complex

Apps NCAA NWS News SU Map Hoshnasi Ham KFS WebSDR FM-Radio 92 Code FCC Search baofeng bf-f8hp

About Blog Download Help YeastMine

SGD *Saccharomyces* GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu

Summary Sequence Protein Gene Ontology Phenotype Complex Interaction Regulation Expression Literature

Complex

- Calcineurin complex variant 1

Phenotype

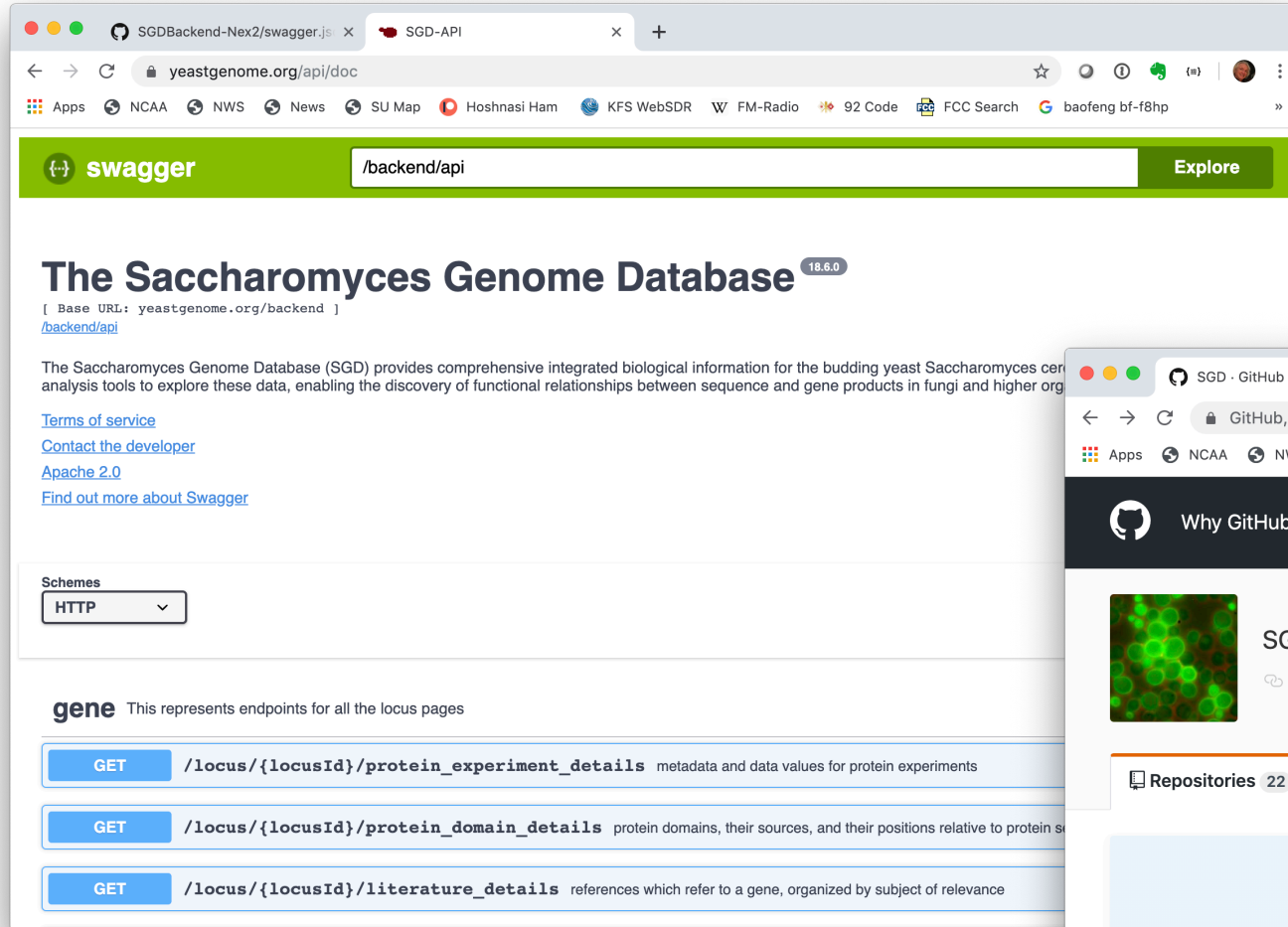
Summary: Non-essential gene; null mutant accumulates increased amounts of calcium and shows increased resistance to cyclosporin A

Classical Genetics

null:

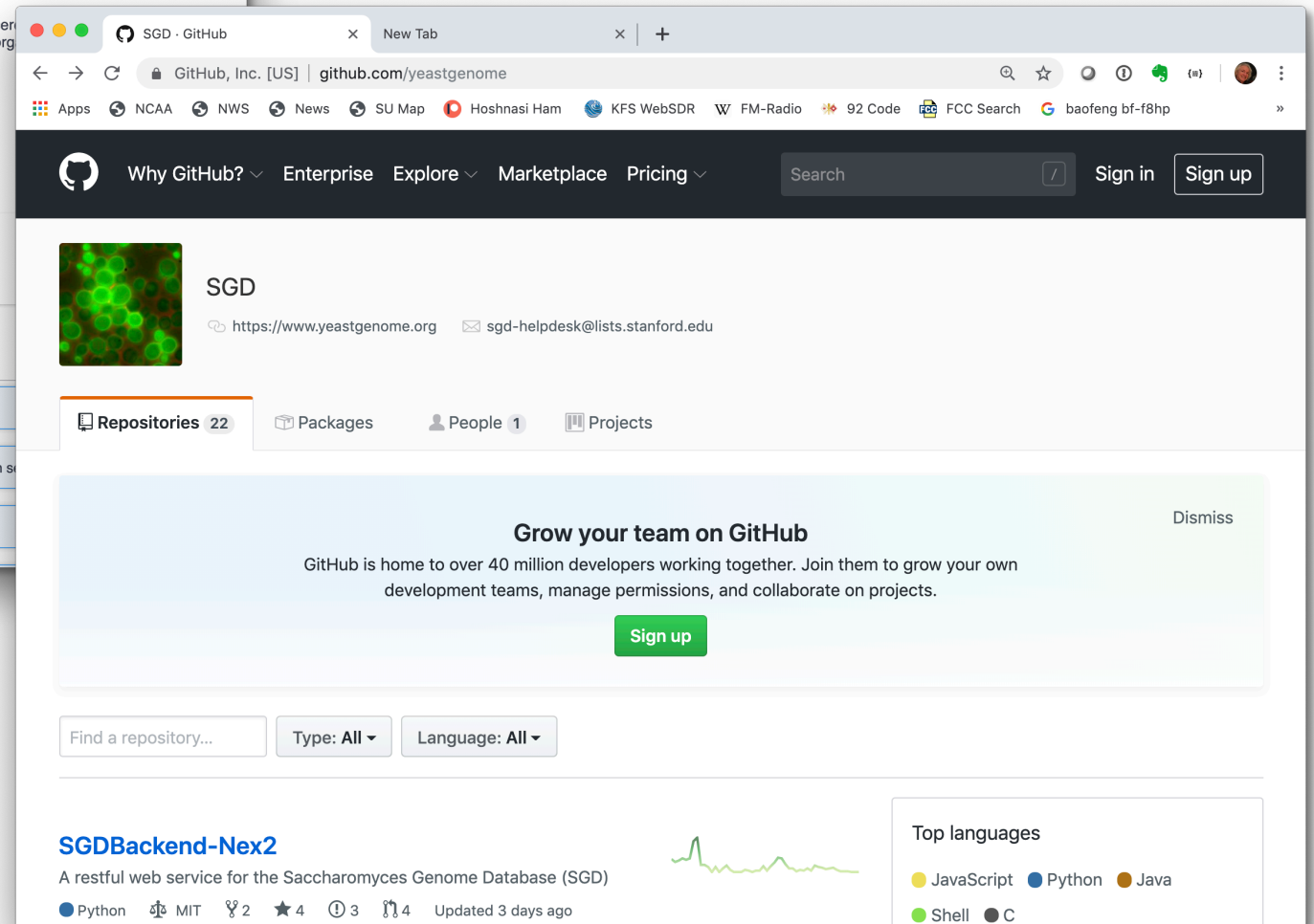
- chemical compound accumulation: increased
- recovery from pheromone-induced cell cycle arrest: normal
- resistance to chemicals: decreased

Felix Gondwe Open Source Software API



Swagger

<https://www.yeastgenome.org/api/doc>



GitHub

<https://github.com/yeastgenome>

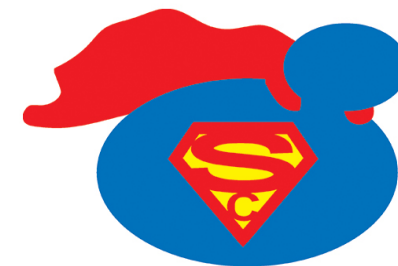
Leadership Team



Mike Cherry, PhD



Stacia Engel, PhD



Biocuration Scientists



Rob Nash, PhD



Edith Wong, PhD



Marek Skrzypek, PhD



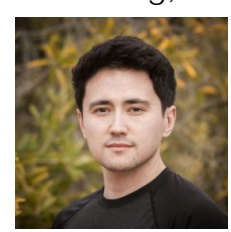
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Joanna Argasinska, PhD



Suzi Aleksander



Kevin MacPherson, MS



Patrick Ng, MS



Department of Genetics,
Stanford University

Software Developers



Shuai Weng, PhD



Kalpana Karra, MS



Felix Gondwe



Sagar Jha, MS

System Administrators (Dev/Ops)



Stuart Miyasato



Matt Simison

<https://cherrylab.stanford.edu/people/SGD/grid>



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GOC : U41 HG002273