Yeast Genetics
Meeting

Looking at Loci with SGD

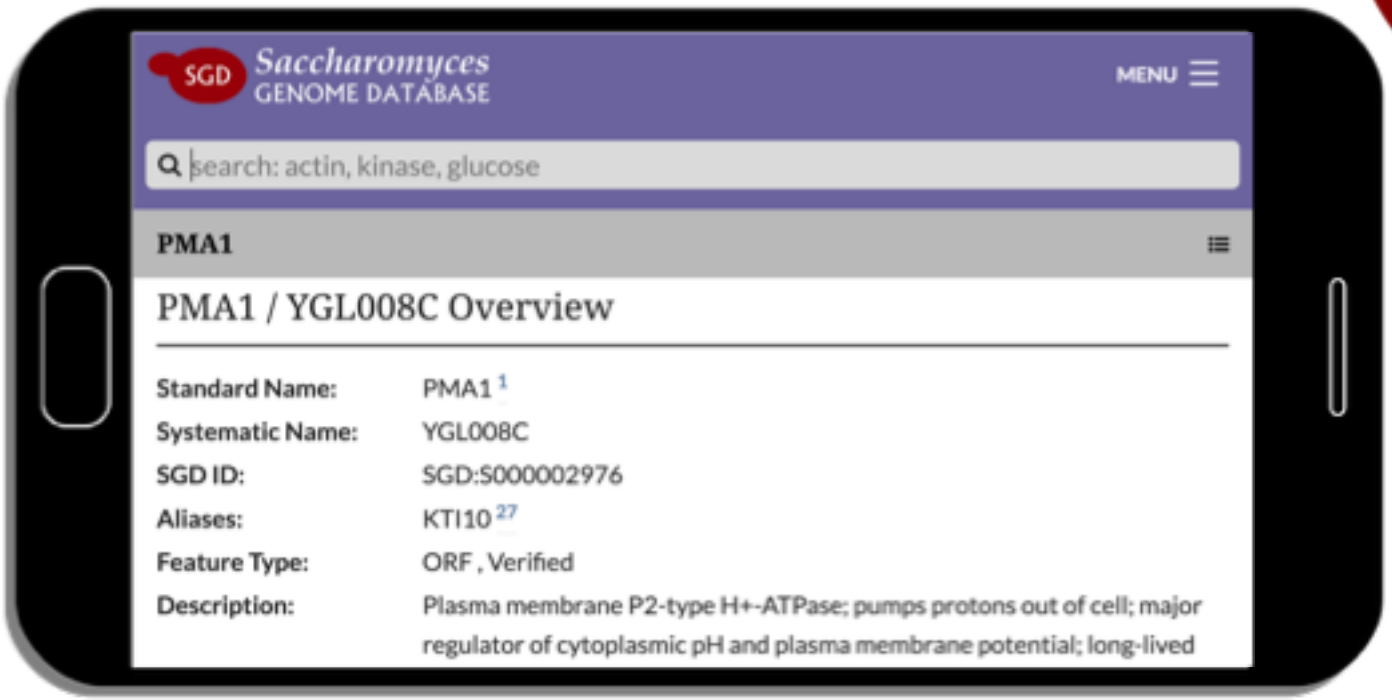
#Yeast18 – Stanford University

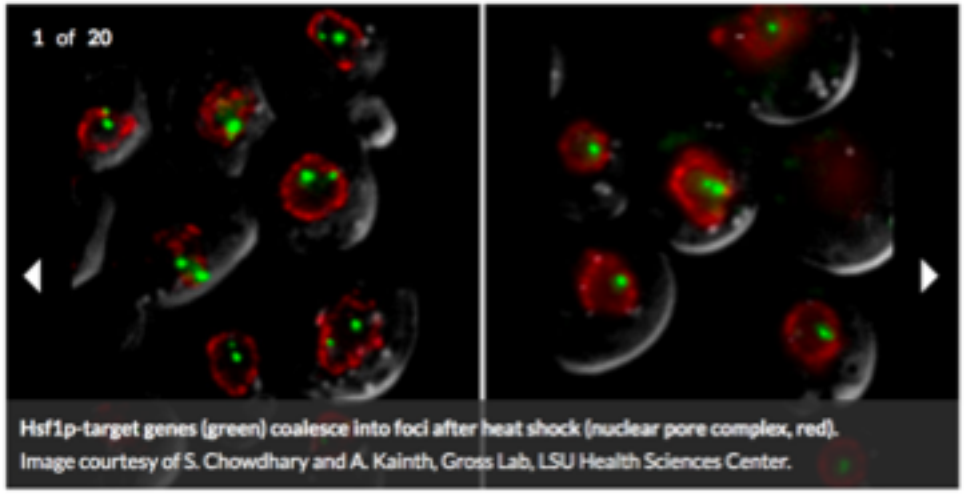
#APOYG – Awesome Power of Yeast Genetics

Yeast Genetics Meeting

yeastgenome.org

SGD





Hsf1p-target genes (green) coalesce into foci after heat shock (nuclear pore complex, red).
Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LSU Health Sciences Center.

About SGD

The *Saccharomyces* Genome Database (SGD) provides comprehensive integrated biological information for the budding yeast *Saccharomyces cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms.

Try this?

Meetings

Yeast Genetics Meeting
August 22 to August 26, 2018 -
Stanford University, Stanford, California

13th International Meeting on Yeast Ageing and Apoptosis
August 26 to August 30, 2018 -
Leuven, Belgium

Small Meeting on Yeast Transport and Energetics (SMYTE 36th)
September 06, 2018 -

New & Noteworthy

(Almost) All Hands on Deck for Calcineurin - **July 31, 2018**
If there was a World Cup soccer championship for cellular proteins, it's a pretty sure bet that calcineurin wouldn't make the team. That's because this protein is one of those players that just can't help but use their hands! And as pretty much everyone knows, that's a big no-no for soccer players (except goalies, of [...]
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New and Improved Gene/Sequence Resources -

Tweets by @yeastgenome

SGD Project
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Congrats to @YeastCourseCSHL, winners of the @cshl plate race
23h

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@yeastgenome
Want to get more out of SGD? Come to our workshop at #Yeast18! Register here: bit.ly/GSAyeast18

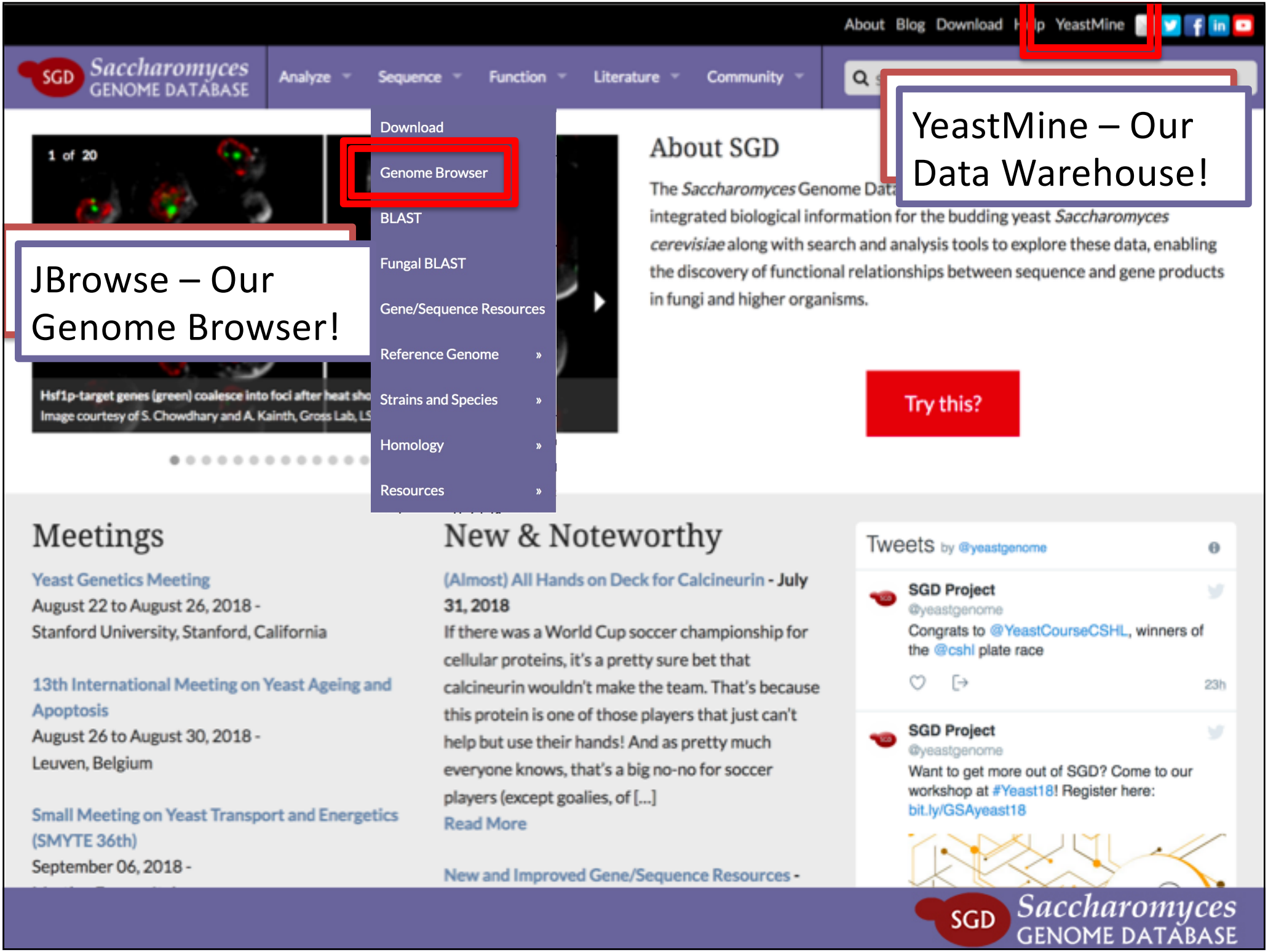
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Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LS
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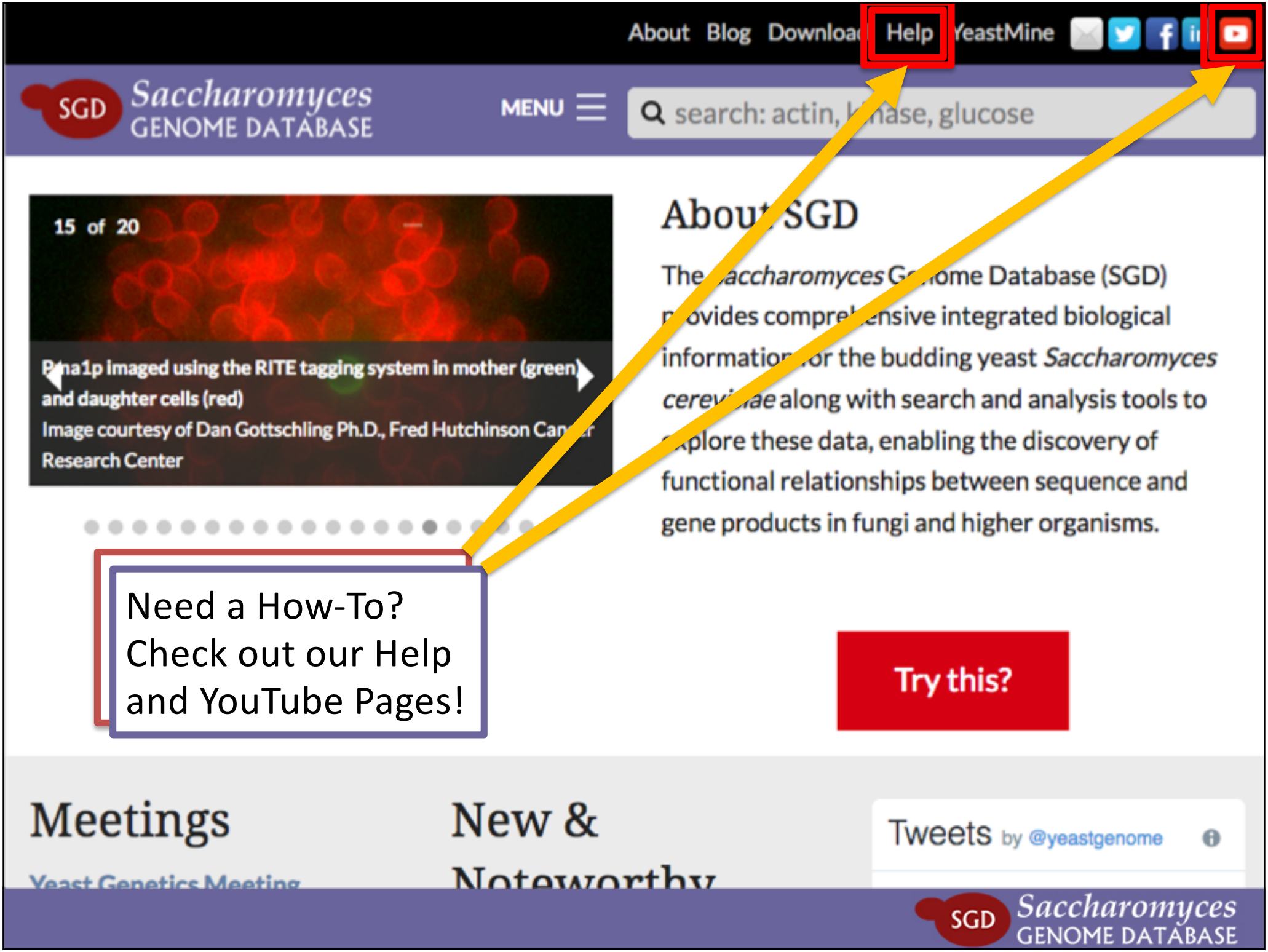
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search: actin, kinase, glucose
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Pma1p imaged using the RITE tagging system in mother (green) and daughter cells (red)
Image courtesy of Dan Gottschling Ph.D., Fred Hutchinson Cancer Research Center
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Need a How-To? Check out our Help and YouTube Pages!
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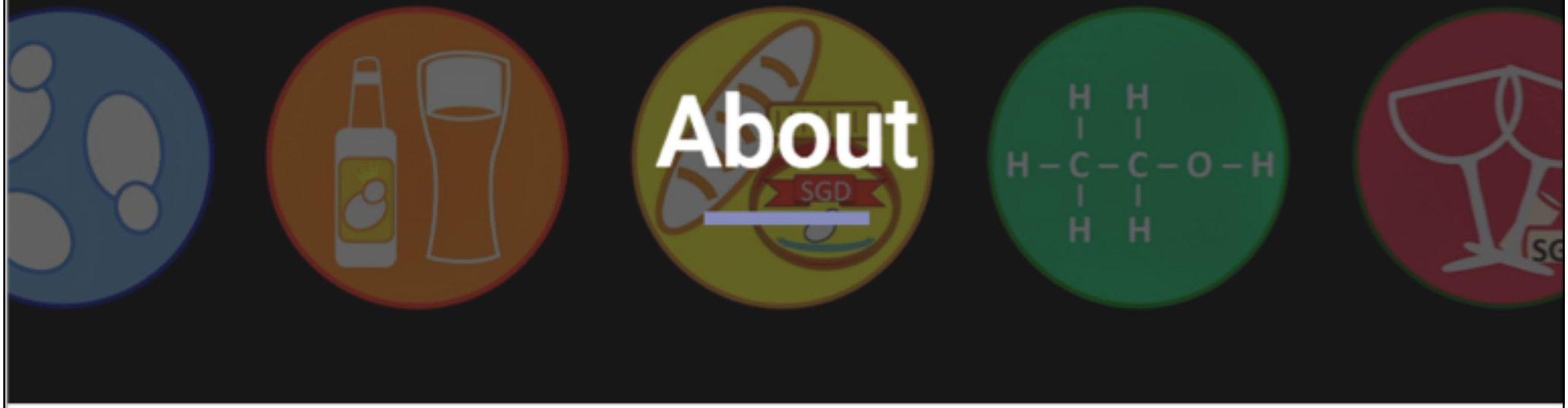
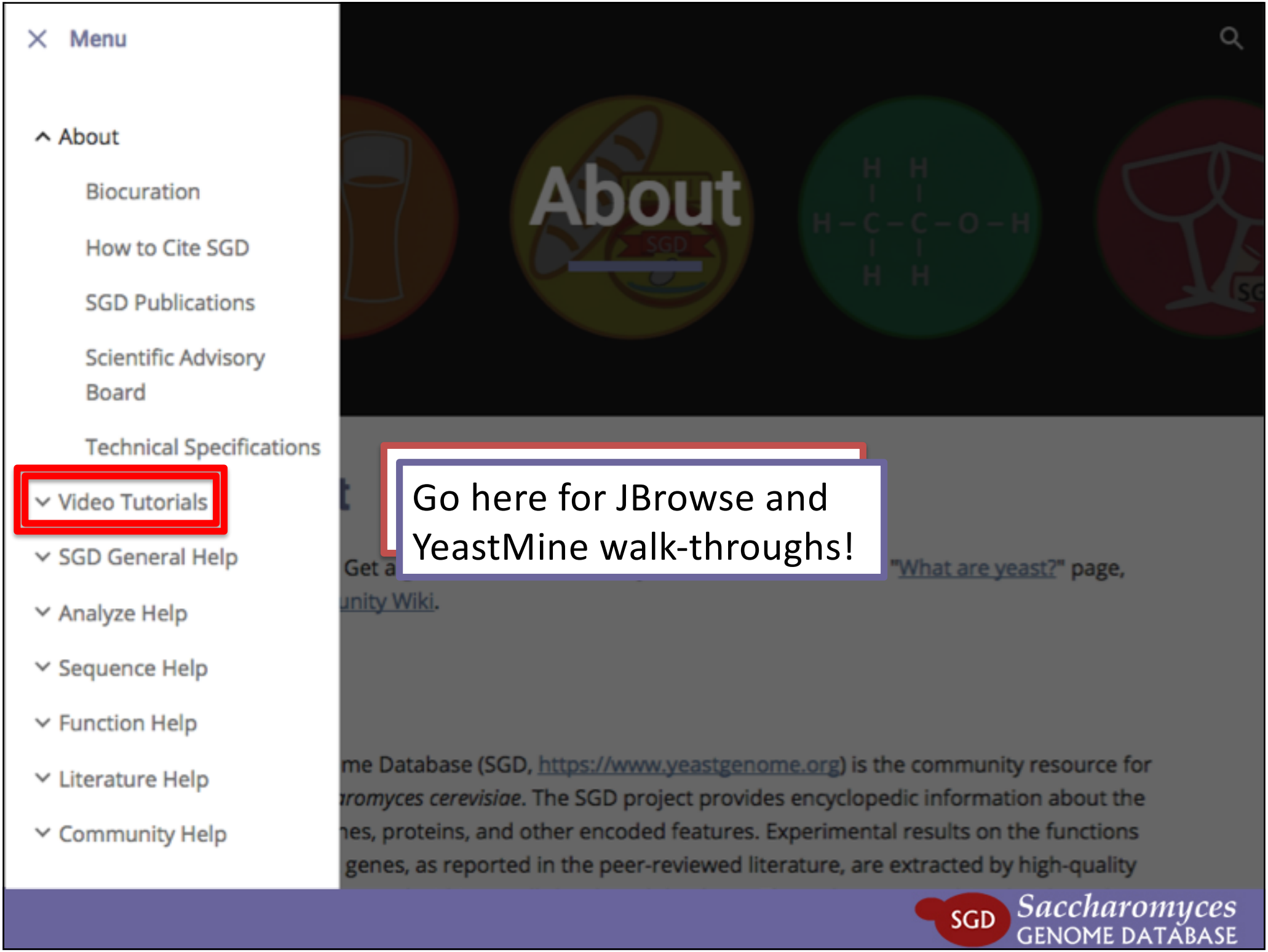


About Yeast

What are yeast, anyway? Get a general introduction to yeast and its uses on our "What are yeast?" page, found in the SGD Community Wiki.

About SGD

The *Saccharomyces* Genome Database (SGD, https://www.yeastgenome.org) is the community resource for the budding yeast *Saccharomyces cerevisiae*. The SGD project provides encyclopedic information about the yeast genome and its genes, proteins, and other encoded features. Experimental results on the functions and interactions of yeast genes, as reported in the peer-reviewed literature, are extracted by high-quality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"What are yeast?" page,
unity Wiki.
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Saccharomyces
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Video Tutorials

SGD has created short video tutorials that describe specific aspects of tools and features at SGD. Click on the name of a tool or feature below to find associated video tutorials describing its use.

Basic Navigation

Biochemical Pathways

Expression: Expression

Genome Browser

Our JBrowse Tutorials!

Interactions: Interactions Overview | Interaction Network

Phenotypes

YeastMine

Our YeastMine Tutorials!

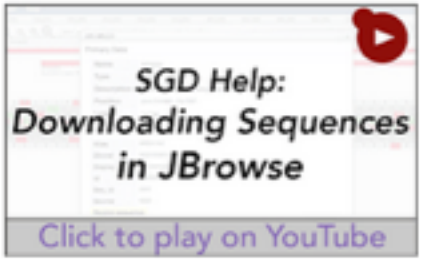
Overview & Navigation Basics

browse.yeastgenome.org

Get started using JBrowse and learn the different ways of exploring the genome. (3:53;*created 3/24/16*)

Learn the different ways of finding and displaying data tracks from various published data sets. (3:41; *created 4/1/16*)

Downloading & Uploading Information



A tutorial on how to download the sequence information on JBrowse. (1:02; *created 3/30/16*)

Find out how to download data tracks and upload your own in JBrowse. (1:56; *created 5/10/16*)

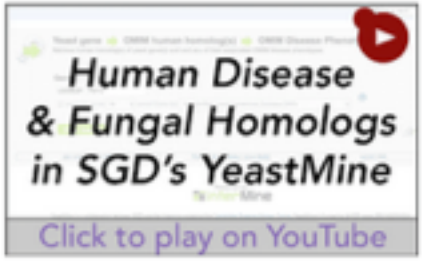
Overviews & Navigation

yeastmine.yeastgenome.org

A quick sampling of 3 cool features in YeastMine. (1:07; *created 1/29/14*)

An overview of YeastMine's major features. (3:21; *created 7/17/14*)

Data Types



Search the OMIM-based human-to-fungal or fungal-to-human homologs in YeastMine. (2:28; *created 3/5/14*)

Fungal Homolog data for 25 different fungal species has been loaded into YeastMine. (2:13;*created 9/15/14*)

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Saccharomyces Genome Database

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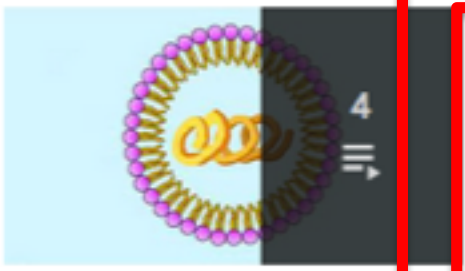
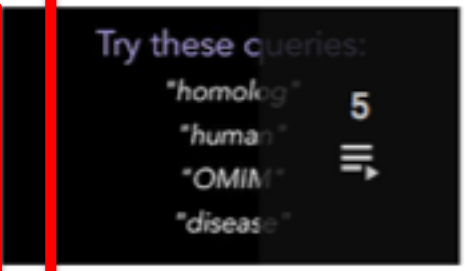


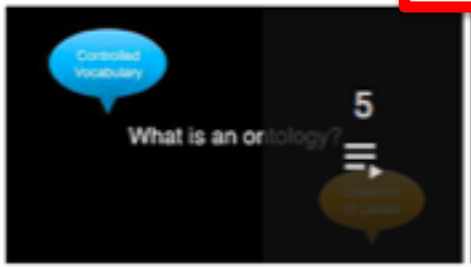
Research Spotlights

Genome Browser (JBrowse)

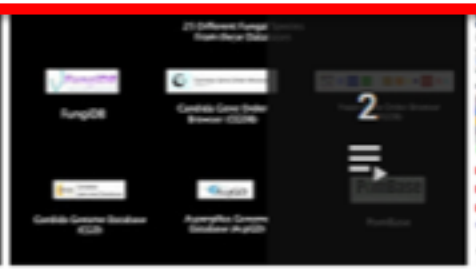


Human Disease and Homol...

SGD Webinar Series

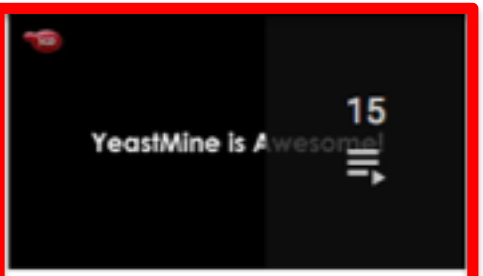


Gene Ontology (GO)



Fungal Homology

Tools at SGD



YeastMine: Getting Started

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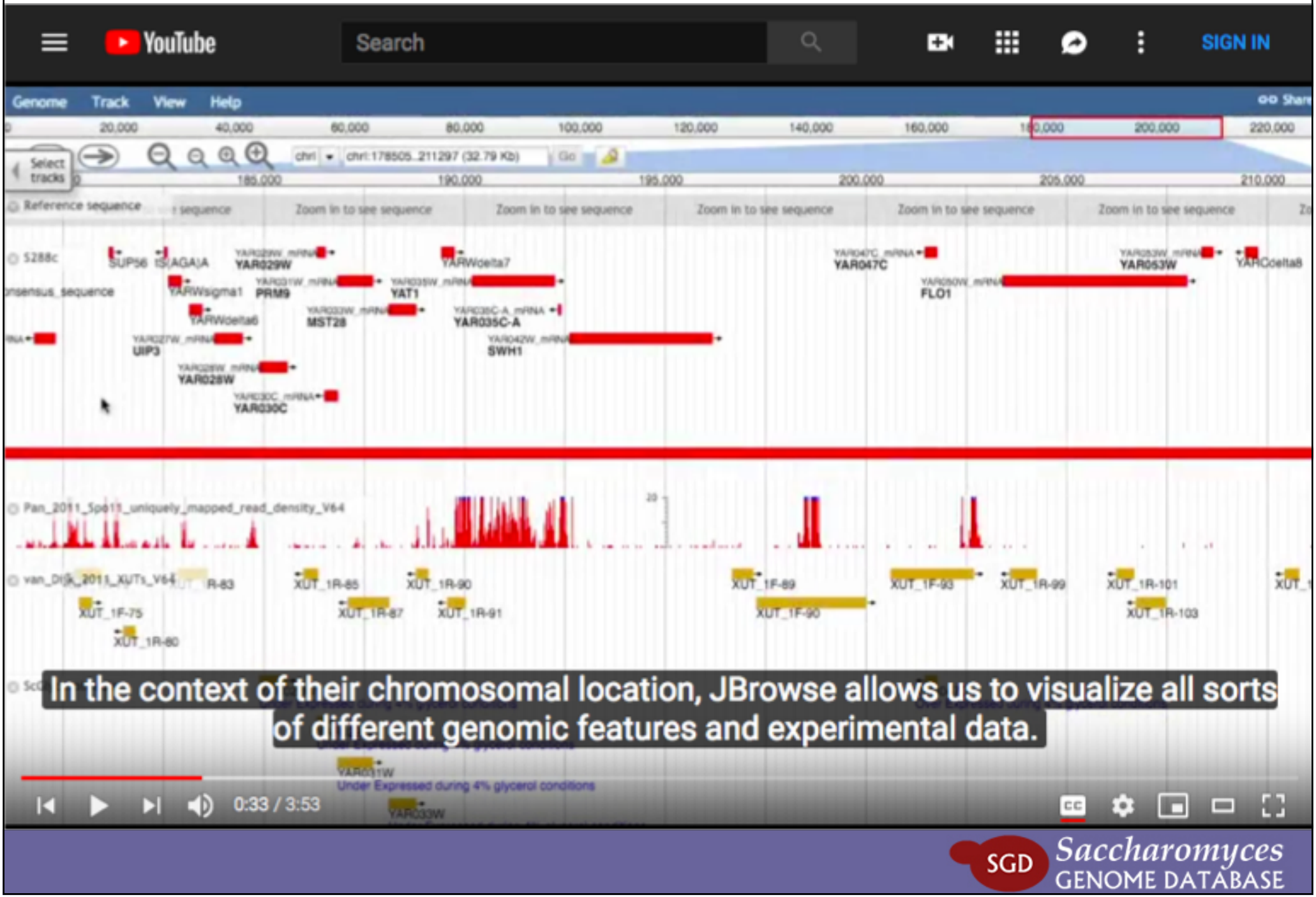
youtube.com/SaccharomycesGenomeDatabase



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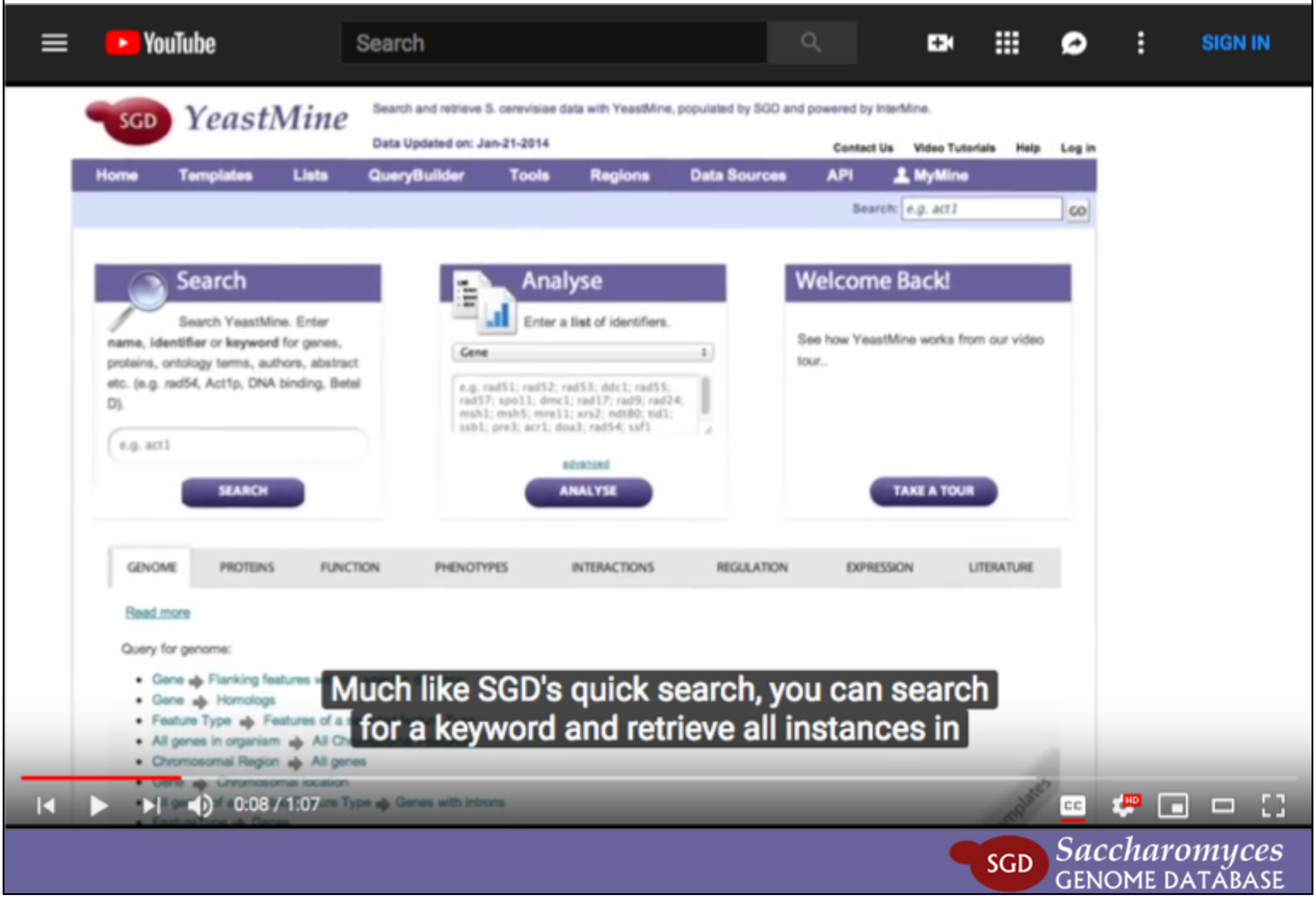

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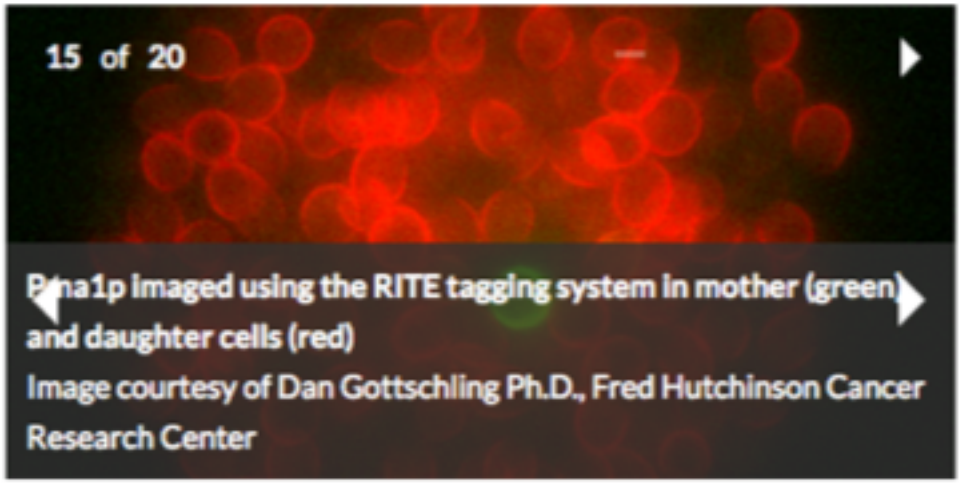
MENU

search: actin, kinase, glucose



Pma1p imaged using the RITE tagging system in mother (green) and daughter cells (red)
Image courtesy of Dan Gottschling Ph.D., Fred Hutchinson Cancer Research Center

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MENU

pma

Show all results ...

PMA1 / YGL008C Gene

PMA2 / YPL036W Gene

PMC1 / YGL006W Gene

PMD1 / YER132C Gene

PMP1 / YCR024C-A Gene

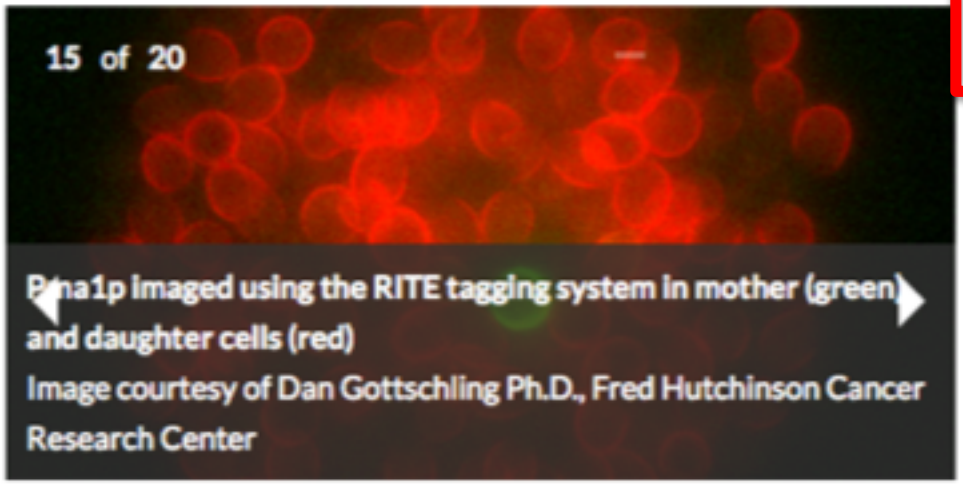
PMR1 / YGL167C Gene

PMT6 / YGR199W Gene

PMU1 / YKL128C Gene

PML1 / YLR016C Gene

PMP3 / YDR276C Gene



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PMA1 / YGL008C
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Regulation
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Summary Paragraph
Literature
History

PMA1 / YGL008C Overview

Standard Name: PMA1 [1]

Systematic Name: YGL008C

SGD ID: SGD:S000002976

Aliases: KTI10 [27]

Feature Type: ORF , Verified

Description: Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p; Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+] [2 3 4 5 6 7 8]

Name Description: Plasma Membrane ATPase

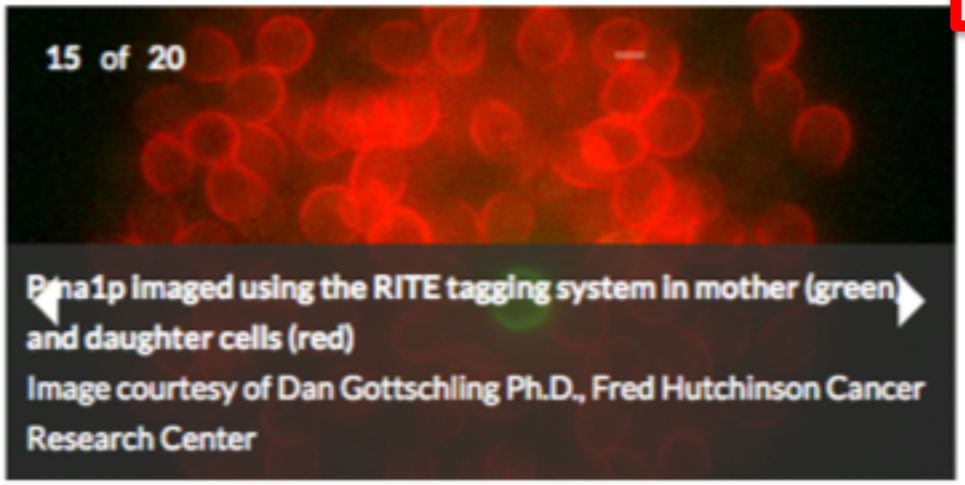
Comparative Info: Integrated model organism details available at the Alliance of Genome Resources website

SGD Saccharomyces GENOME DATABASE

MENU

pma

Show all results ...



PMA1 / YGL008C	Gene
PMA2 / YPL036W	Gene
PMC1 / YGL006W	Gene
PMD1 / YER132C	Gene
PMP1 / YCR024C-A	Gene
PMR1 / YGL167C	Gene
PMT6 / YGR199W	Gene
PMU1 / YKL128C	Gene
PML1 / YLR016C	Gene
PMP3 / YDR276C	Gene

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Categories

- References 294
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- Genes 15
- Biological Processes 10
- Cellular Components 8
- Colleagues 6
- Molecular Functions 5

365 results for × "pma"

Page 1 of 15 | Results: 25 | Sort By: Relevance

response to phorbol 13-acetate 12-myristate

Biological Process

Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene

synonyms: response to *PMA*

cellular response to phorbol 13-acetate 12-myristate

Biological Process

Any process that results in a change in state or activity of a cell (in terms of movement, secretion, enzyme production, gene expression,

synonyms: cellular response to response to *PMA*

Show all categories

15 results for × "pma" × Gene

Genes / Genomic Features

Page 1 of 1 | Results: 25 | Sort By: Relevance

List | Wrapped

Feature Type

ORF 15

Molecular Function

nucleotide binding (direct) 4

ATP binding (direct) 4

hydrolase activity (direct) 3

transmembrane transporter activity 2

transferase activity (direct) 2

Show more

Cellular Component

cytoplasm 10

EPS1 / YIL005W

Gene

ER protein with chaperone and co-chaperone activity; involved in retention of resident ER proteins; has a role in recognizing proteins

name description: ER-retained *Pma1* Suppressing

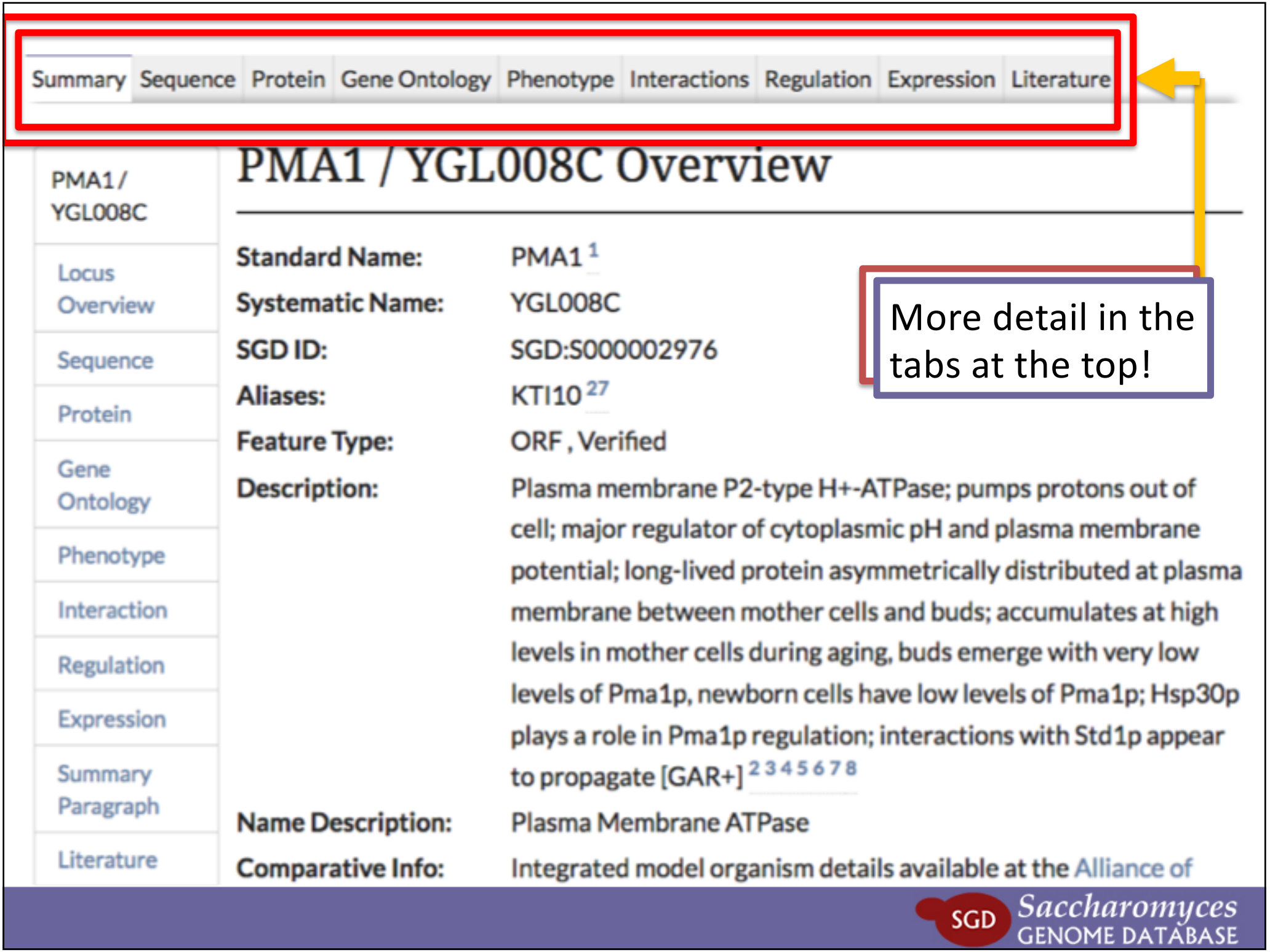
PMA1 / YGL008C

Gene

Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential;

protein: H(+)-exporting P2-type ATPase *PMA1*

name: *PMA1* / YGL008C


Summary
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More detail in the tabs at the top!
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PMA1 / YGL008C Overview

Scroll/click for more summaries!

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GD:S000002976

TI10 [27]

RF , Verified

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PMA1 / YGL008C

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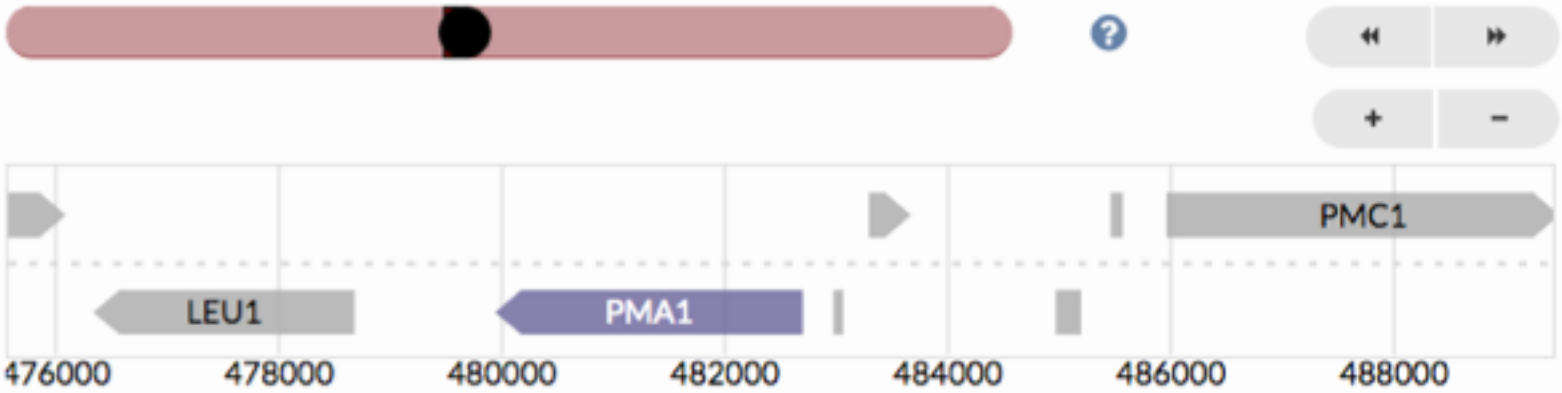
Sequence

Sequence Details

Download (.fsa)

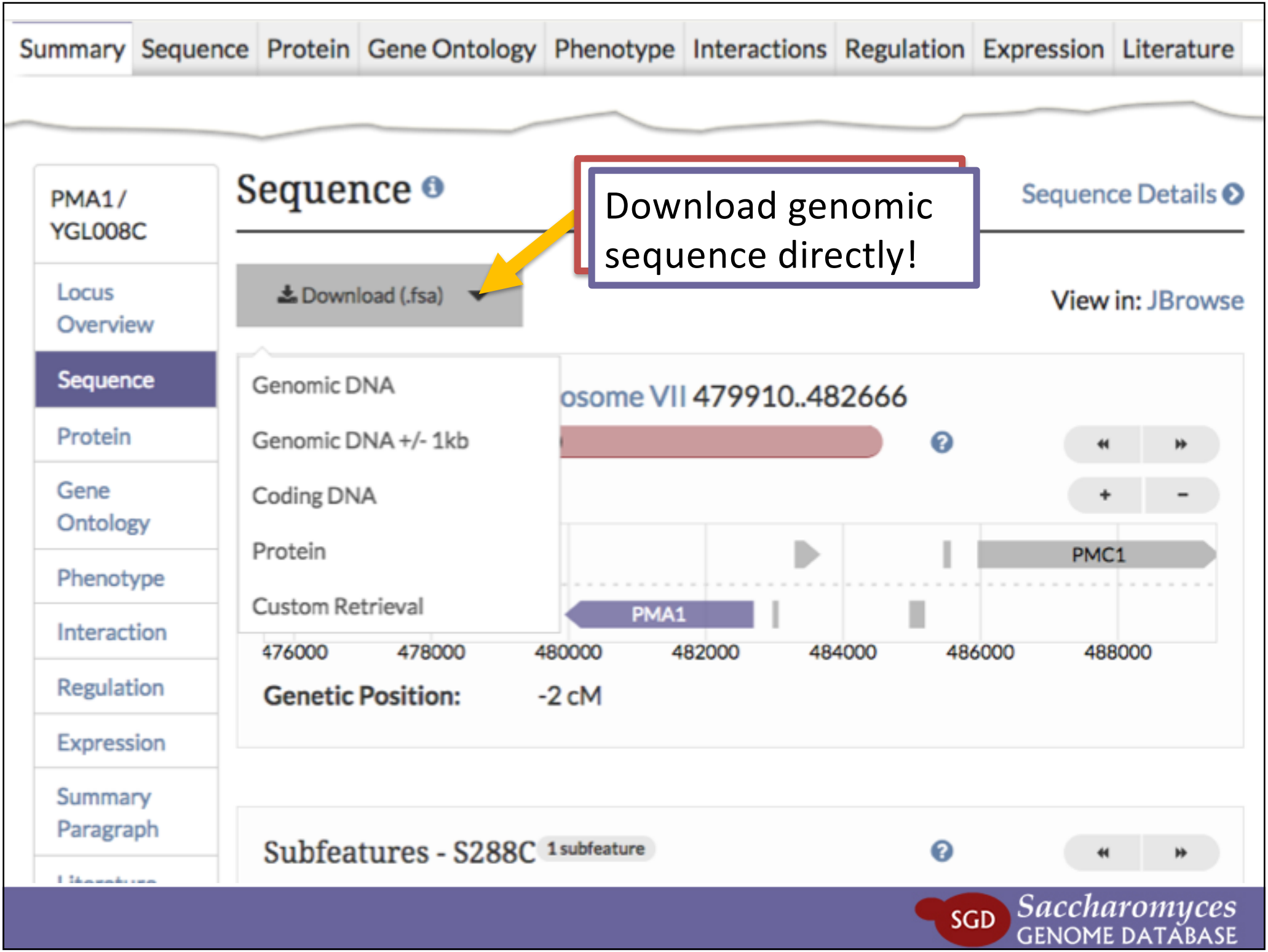
View in: JBrowse

PMA1 Location: Chromosome VII 479910..482666



Genetic Position: -2 cM

Subfeatures - S288C 1 subfeature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Genomic DNA +/- 1kb
Coding DNA
Protein
Custom Retrieval
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PMC1
PMA1
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478000
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482000
484000
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Genetic Position: -2 cM
Subfeatures - S288C
1 subfeature
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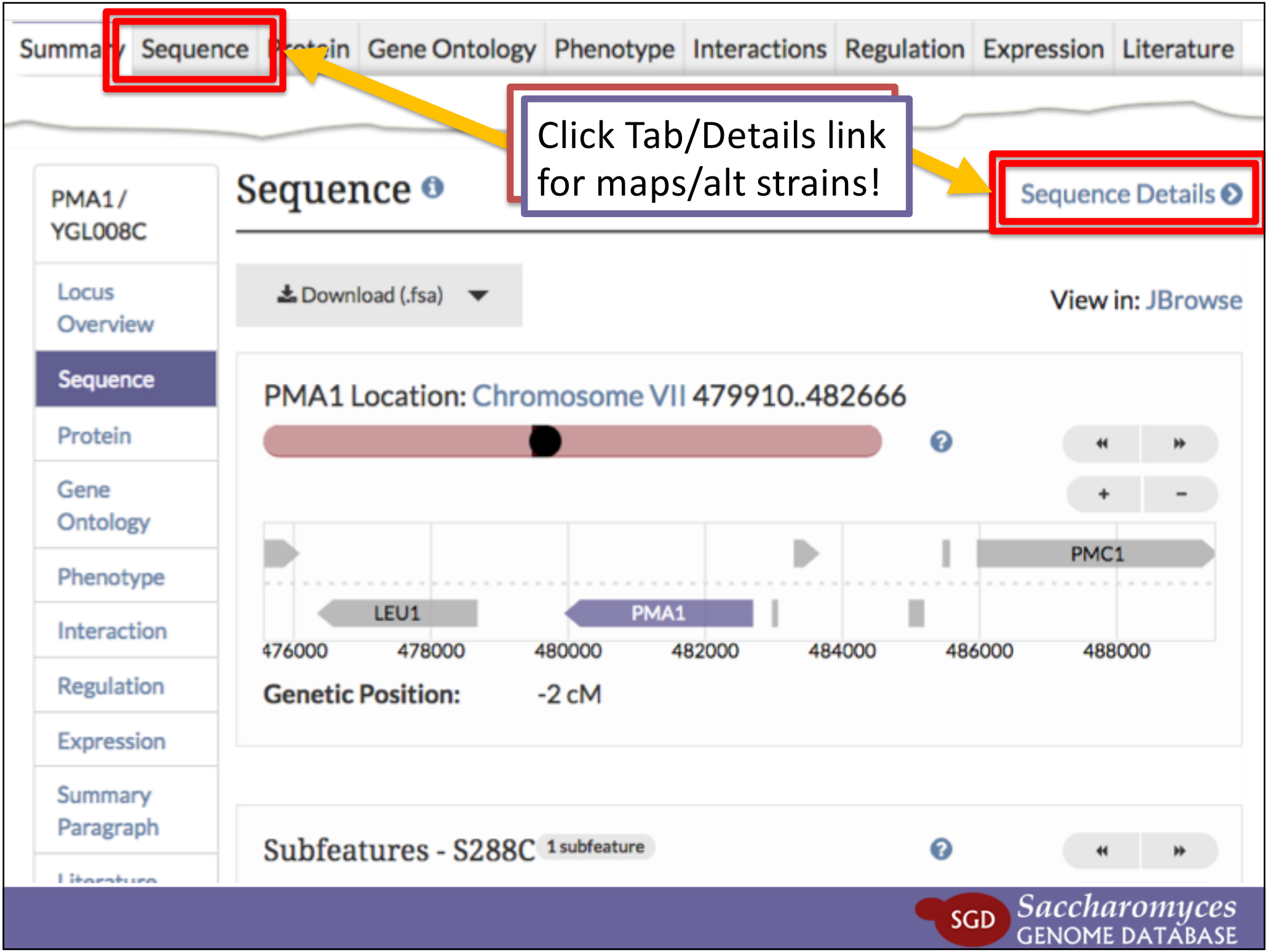
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Protein
Gene Ontology
Phenotype
Interaction
Regulation
Expression
Summary Paragraph
Sequence
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PMA1 Location: Chromosome VII 479910..482666
PMC1
LEU1
PMA1
476000
478000
480000
482000
484000
486000
488000
Genetic Position: -2 cM
Subfeatures - S288C
1 subfeature
SGD
Saccharomyces
GENOME DATABASE

GLC7 / YER133W

Sequence Overview

Reference Strain: S288C

Alternative Reference Strains

Other Strains

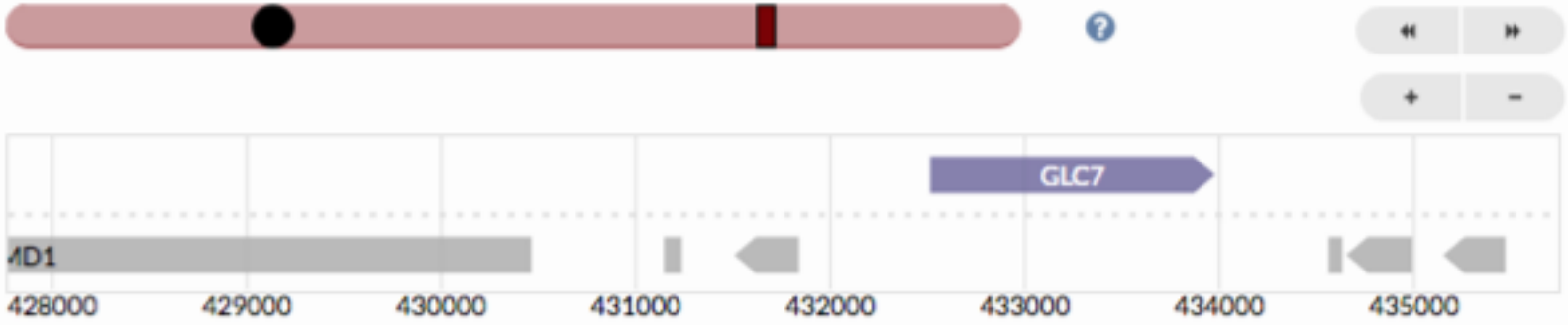
History

Resources

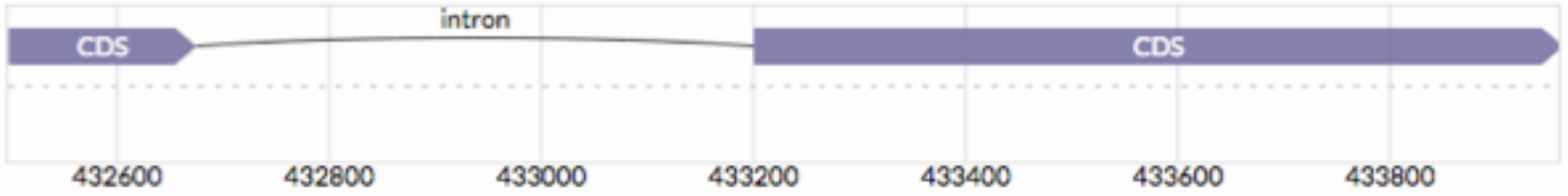
Reference Strain: S288C

View in: JBrowse

GLC7 Location: Chromosome V 432495..433958



Subfeatures - S288C 3 subfeatures



Filter table

GLC7 / YER133W

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- History
- Resources

Sequence - S288C

Genomic DNA

CDS INTRON

- ✓ genomic
- ✓ coding
- ✓ protein
- ✓ genomic +/- 1kb

```
   1 ATGGACTCAC AACCAGTTGA CGTTGATAAT ATCATCGA
  61 TCTAAACCTG GTCAACAAGT TGATCTAGAA GAAAATGAAA
 121 GCCAGATCTA TATTCATAAA GCAACCCATT TTACTAGAGT
 181 TGTTAATGTT GAACTTCGCA GTCAAGAGAT AGAATGCCTA
 241 GTTCTACTCC TGTTGCGGCA GTAAGATAGT TACAGCAGTT A
 301 ATTTACCAAG CATCTGATGT TAGCCTACTC ATATGTCGAG ATAGCCGAGA TAATGTGTGT
 361 GTTTAGCTCT TCATTTTTCT ATCTTATTAG GCATTTTTTT ACCAAGATTT CCTTATGTTT
 421 TGTATCATCA TCCGGCCGGC GCCTCCCATA TTCAGAAAAA TCCCCCTTGC TCACACTAAA
 481 AAAAGAAGGC ATTTTTTCGT TATGAAGAAA ACGAATCTTT TTTTTTTTTG AGCCCGAGAG
 541 AAAGGTCGGA CGAAAACCAA GAAATGTGGA TTTGCAGAAG GCATTGGGAG AAATGAAGCG
 601 TTTTTGACAG CAGTAATTGT TCTCTTAAAG TCAACGGAAT GAGCTAGATT TAGTGACAAA
 661 TTCATTTACT AACTTATTTT TTTCTATTTT TTTTTTTTTT AGATATGTGG TGACATTCAT
 721 GGGCAATACT ATGATTTACT ACGTCTATTT GAGTACGGTG GATTCCCGCC AGAATCTAAT
 781 TATCTATTTT TGGGTGATTA TGTCGACCGT GGTAAACAAT CCTTAGAGAC TATTTGTCTA
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1081 AGAAGGGTGA TGAGGCCAAC AGATATTCCC GACGTTGGCT TATTATGTGA CTTATTGTGG
1141 TCAGATCCAG ATAAAGATAT CGTAGGTTGG AGTGAAAATG ATAGAGGTGT TTCTTTCACT
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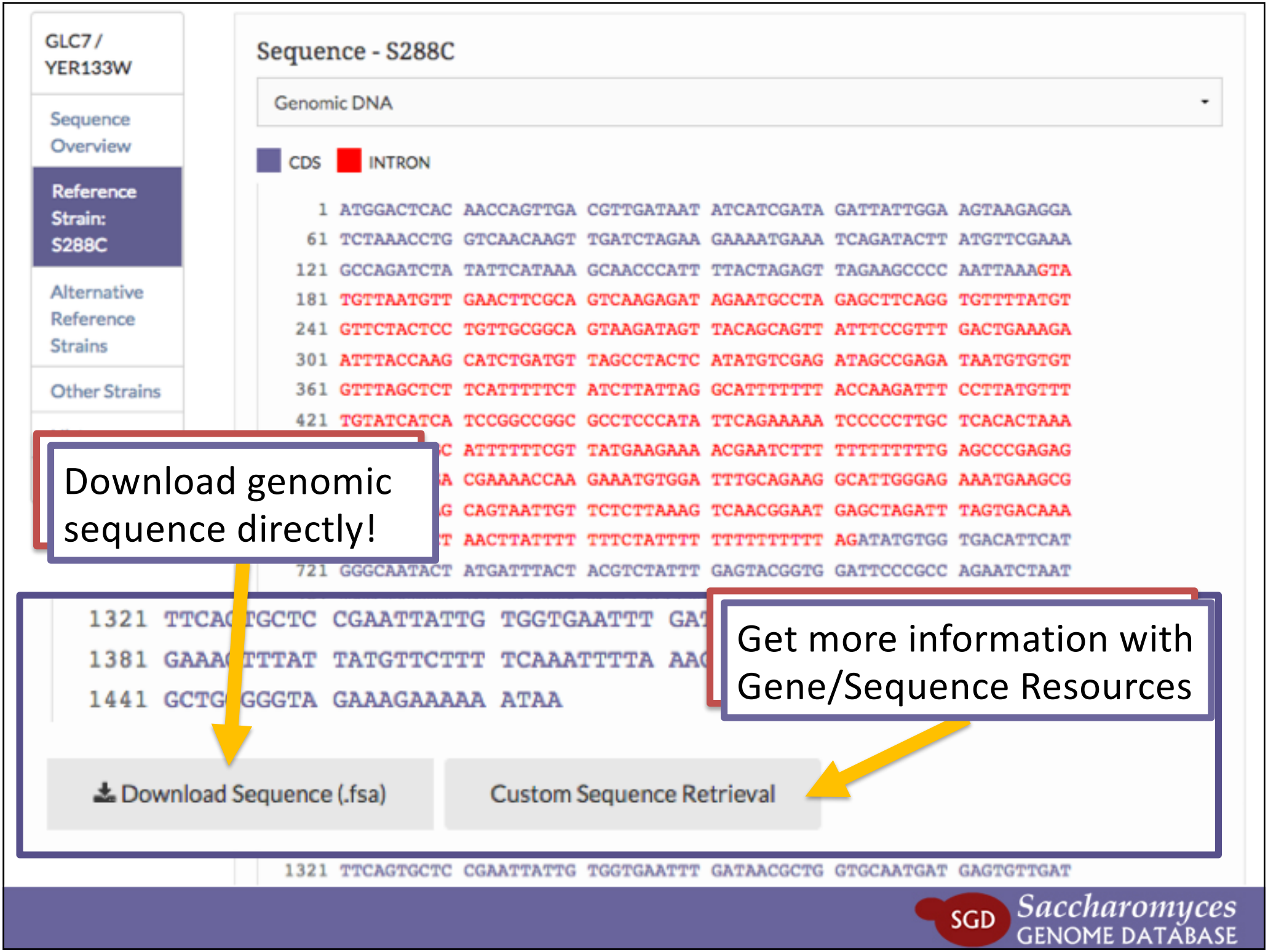
GLC7 / YER133W
Sequence Overview
Reference Strain: S288C
Alternative Reference Strains
Other Strains
Sequence - S288C
Genomic DNA
CDS
INTRON
1 ATGGACTCAC AACCAGTTGA CGTTGATAAT ATCATCGATA GATTATTGGA AGTAAGAGGA
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241 GTTCTACTCC TGTTGCGGCA GTAAGATAGT TACAGCAGTT ATTTCCGTTT GACTGAAAGA
301 ATTTACCAAG CATCTGATGT TAGCCTACTC ATATGTCGAG ATAGCCGAGA TAATGTGTGT
361 GTTTAGCTCT TCATTTTTCT ATCTTATTAG GCATTTTTTT ACCAAGATTT CCTTATGTTT
421 TGTATCATCA TCCGGCCGGC GCCTCCCATA TTCAGAAAAA TCCCCCTTGC TCACACTAAA
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CGAAAACCAA GAAATGTGGA TTTGCAGAAG GCATTGGGAG AAATGAAGCG
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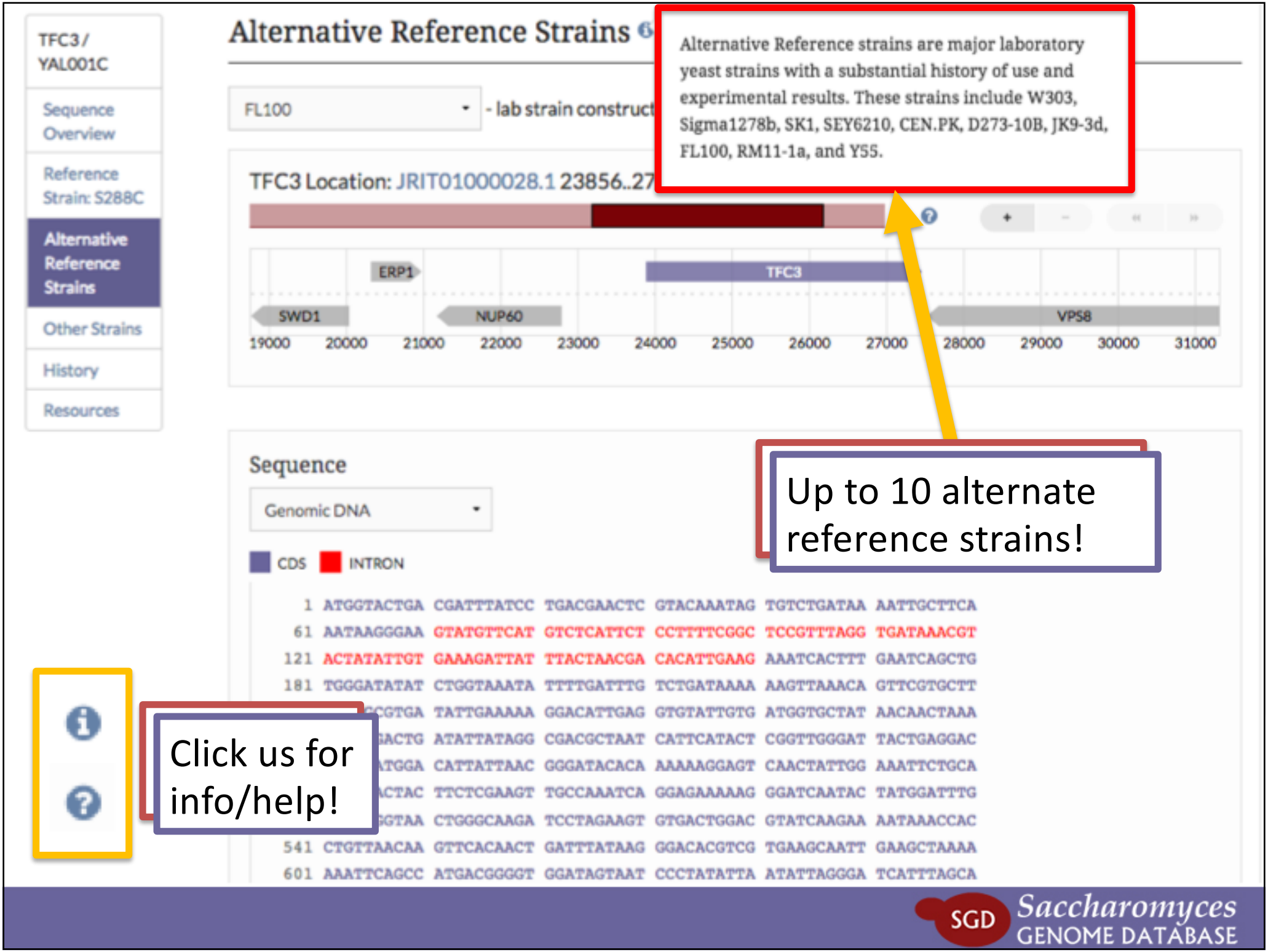
AACTTATTTT TTTCTATTTT TTTTTTTTTT AGATATGTGG TGACATTCAT
721 GGGCAATACT ATGATTTACT ACGTCTATTT GAGTACGGTG GATTCCCGCC AGAATCTAAT
1321 TTCAGTGCTC CGAATTATTG TGGTGAATTT GATAACGCTG GTGCAATGAT GAGTGTTGAT
Download genomic sequence directly!
Get more information with Gene/Sequence Resources
Download Sequence (.fsa)
Custom Sequence Retrieval
SGD
Saccharomyces
GENOME DATABASE


TFC3 / YAL001C
Sequence Overview
Reference Strain: S288C
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History
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Alternative Reference Strains
Alternative Reference strains are major laboratory yeast strains with a substantial history of use and experimental results. These strains include W303, Sigma1278b, SK1, SEY6210, CEN.PK, D273-10B, JK9-3d, FL100, RM11-1a, and Y55.
FL100
- lab strain construct
TFC3 Location: JRIT01000028.1 23856..27
ERP1
TFC3
SWD1
NUP60
VPS8
19000 20000 21000 22000 23000 24000 25000 26000 27000 28000 29000 30000 31000
Sequence
Genomic DNA
CDS
INTRON
1 ATGGTACTGA CGATTTATCC TGACGAACTC GTACAAATAG TGTCTGATAA AATTGCTTCA
61 AATAAGGGAA GTATGTTCAT GTCTCATTCT CCTTTTCGGC TCCGTTTAGG TGATAAACGT
121 ACTATATTGT GAAAGATTAT TTACTAACGA CACATTGAAG AAATCACTTT GAATCAGCTG
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541 CTGTTAACAA GTTCACAACT GATTTATAAG GGACACGTCG TGAAGCAATT GAAGCTAAAA
601 AAATTCAGCC ATGACGGGGT GGATAGTAAT CCCTATATTA ATATTAGGGA TCATTTAGCA
Up to 10 alternate reference strains!
Click us for info/help!
SGD Saccharomyces GENOME DATABASE

PMA1 / YGL008C
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PMA1 / YGL008C Overview

Standard Name: PMA1 [1]

Systematic Name: YGL008C

SGD ID: SGD:S000002976

Aliases: KTI10 [27]

Feature Type: ORF , Verified

Description: Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p; Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+] [2 3 4 5 6 7 8]

Name Description: Plasma Membrane ATPase

Comparative Info: Integrated model organism details available at the Alliance of

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

SOD1 / YJR104C

- Protein Overview
- Experimental Data
- Domains and Classification
- Sequence
- External Identifiers
- Resources

Experimental Data

More coming soon from the Brown Lab (U. Toronto)!

Filter table

Experiment	Result	Reference
abundance	519000 molecules/cell	Ghaemmaghami S, et al. (2003)
abundance	4445 arbitrary fluorescence units	Newman JR, et al. (2006)
abundance	120616 molecules/cell	Kulak NA, et al. (2014)
abundance	3893 arbitrary fluorescence units	Chong YT, et al. (2015)
half-life	6.2 hr	Christiano R, et al. (2014)

Download (.txt)

Domains and Classification

11 entries for 8 domains

Domains and Classification

11 entries for 8 domains

Shout-out to the other databases!

Protein Coordinates	Accession ID	Description	Source	No. of Genes with Domain
1-154	G3DSA:2.60.40.200	Superoxide dismutase, copper/zinc binding domain	Gene3D	2
3-153	PTHR10003		PANTHER	2
3-153	PTHR10003:SF48		PANTHER	1
4-152	SSF49329	Superoxide dismutase, copper/zinc binding domain	SUPERFAMILY	2
12-150	PF00080	Sod_Cu; Superoxide dismutase, copper/zinc binding domain	Pfam	2
45-67	PR00068	CUZNDISMTASE; Superoxide dismutase, copper/zinc binding domain	PRINTS	1
45-55	PS00087	SOD_CU_ZN_1; Superoxide dismutase, copper/zinc, binding site	PROSITE	1
81-90	PR00068	CUZNDISMTASE; Superoxide dismutase, copper/zinc binding domain	PRINTS	1
100-122	PR00068	CUZNDISMTASE; Superoxide dismutase, copper/zinc binding	PRINTS	1

SOD1 / YJR104C

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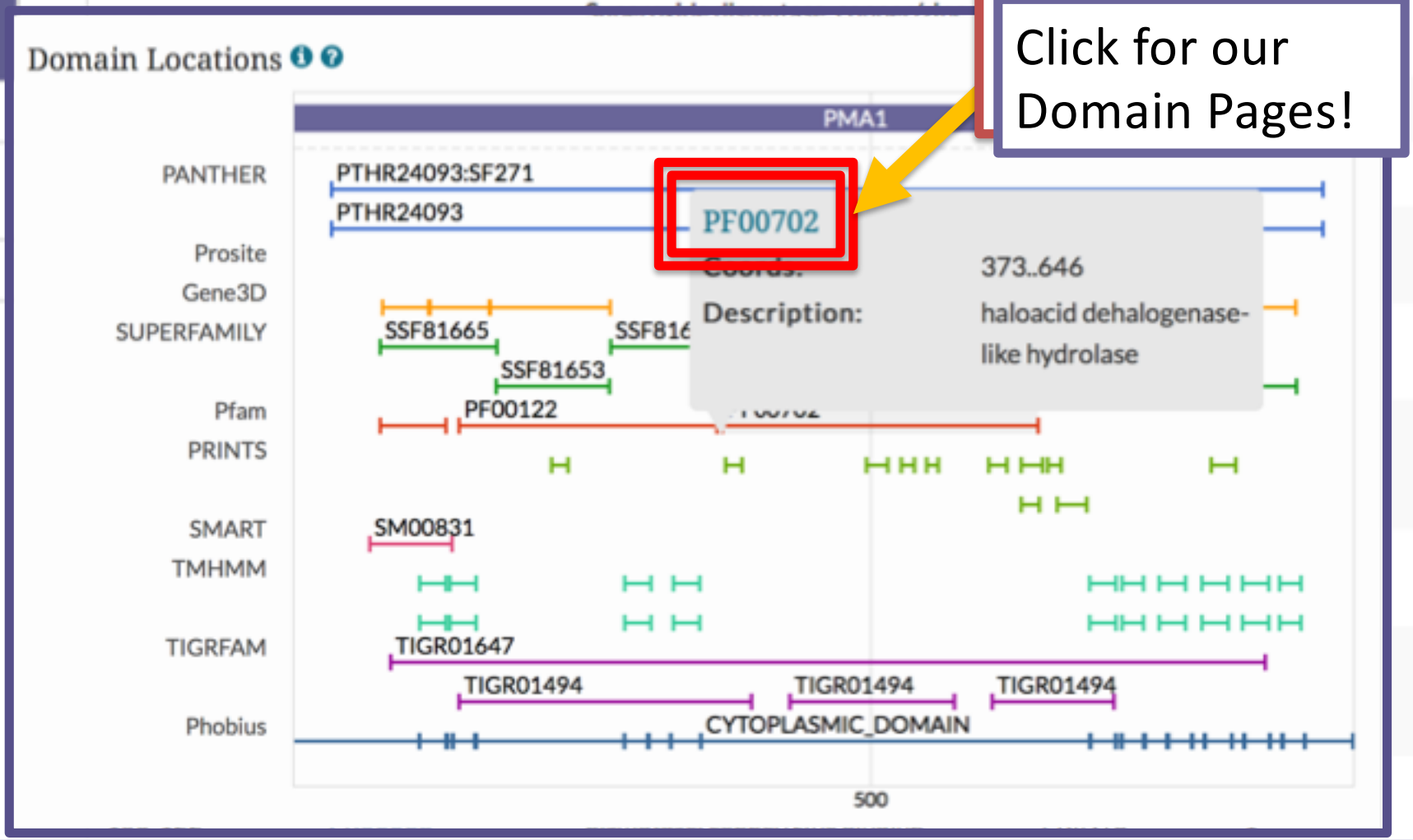
Domains and Classification

11 entries for 8 domains

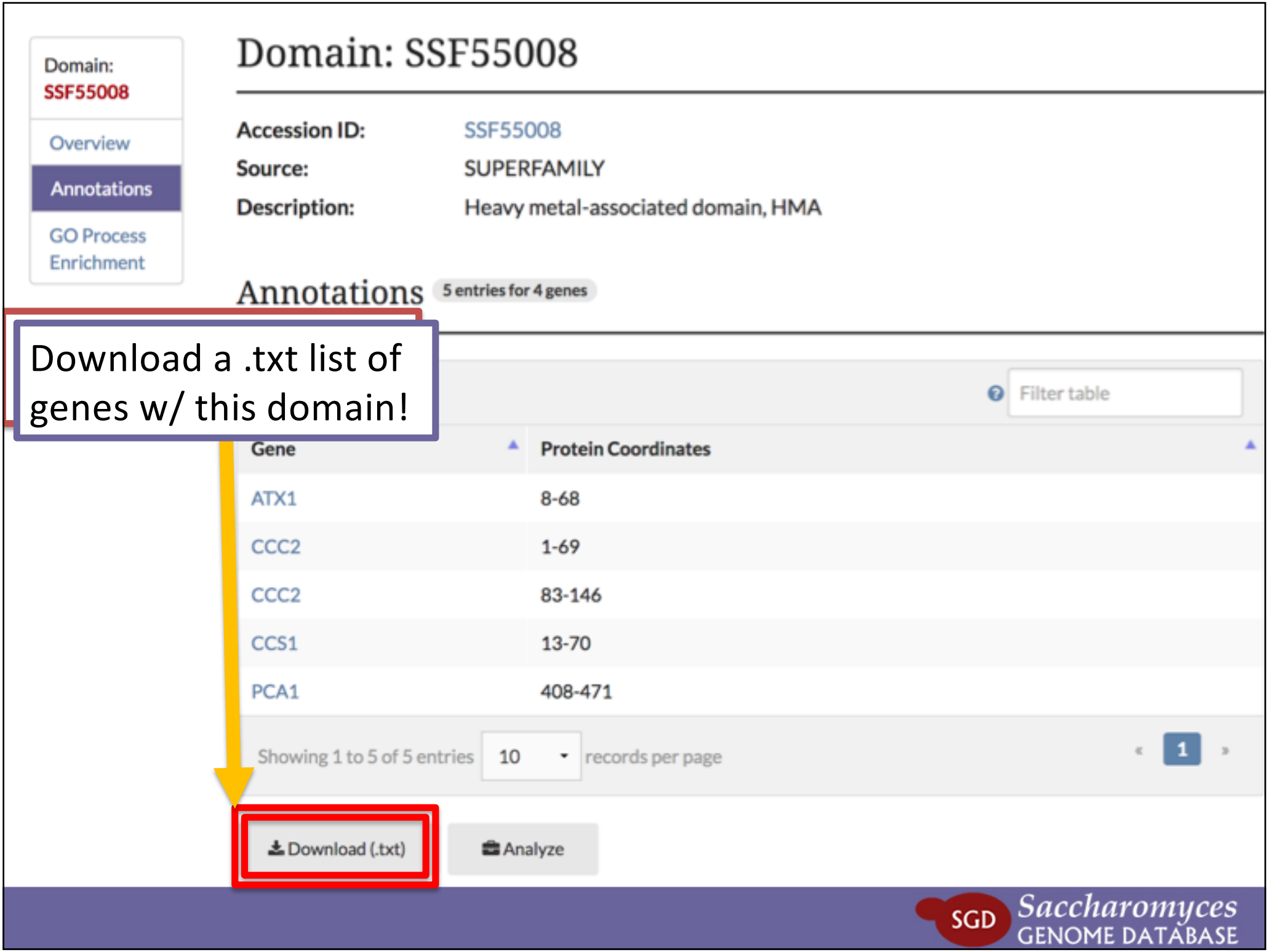
Filter table

Protein Coordinates	Accession ID	Description	Source	No. of Genes with Domain

Domain Locations



Click for our Domain Pages!


Domain:
SSF55008
Overview
Annotations
GO Process Enrichment
Domain: SSF55008
Accession ID: SSF55008
Source: SUPERFAMILY
Description: Heavy metal-associated domain, HMA
Annotations
5 entries for 4 genes
Download a .txt list of genes w/ this domain!
Filter table
Gene
Protein Coordinates
ATX1 8-68
CCC2 1-69
CCC2 83-146
CCS1 13-70
PCA1 408-471
Showing 1 to 5 of 5 entries
10
records per page
1
Download (.txt)
Analyze
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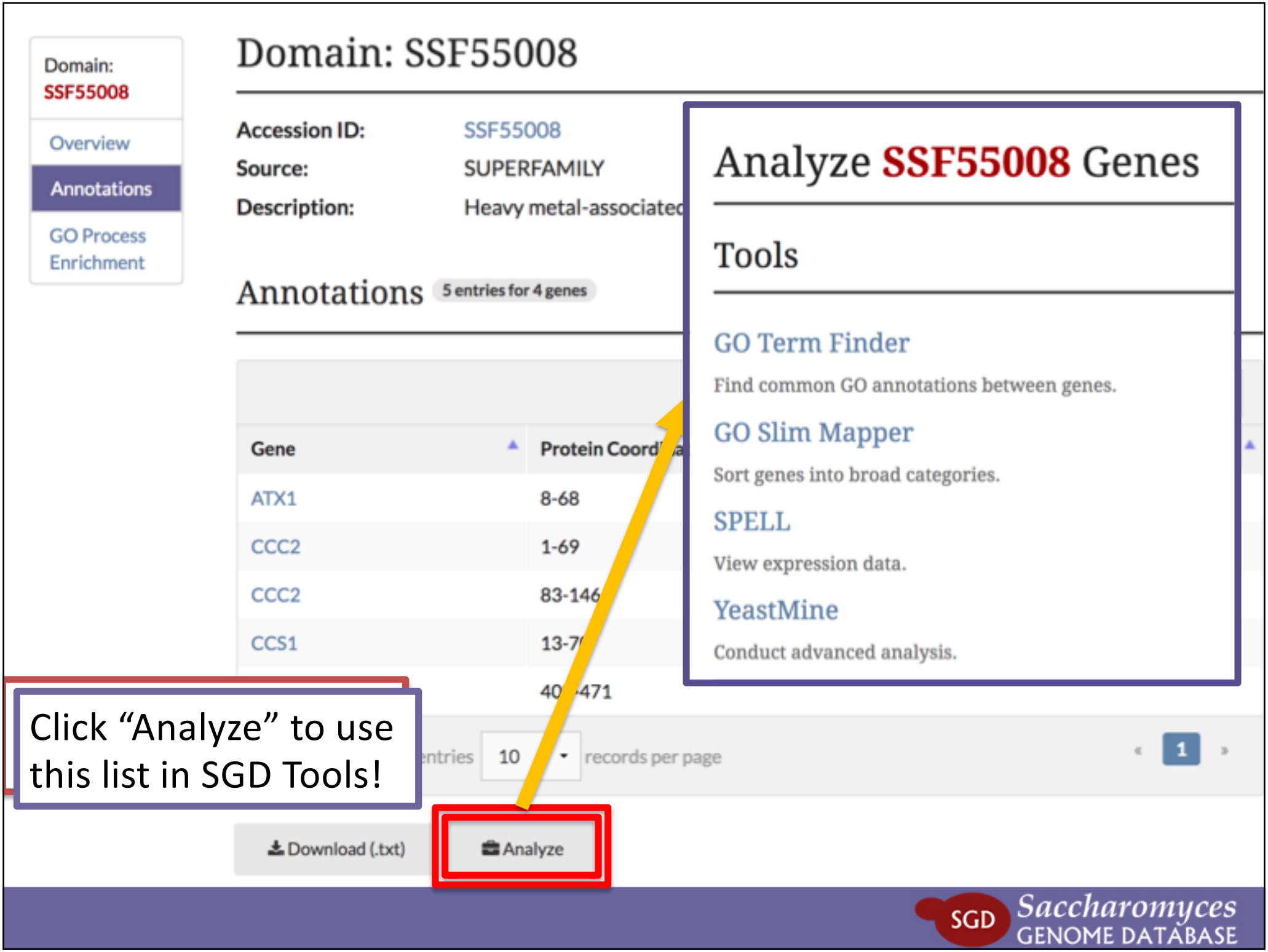
Domain: SSF55008
Overview
Annotations
GO Process Enrichment
Domain: SSF55008
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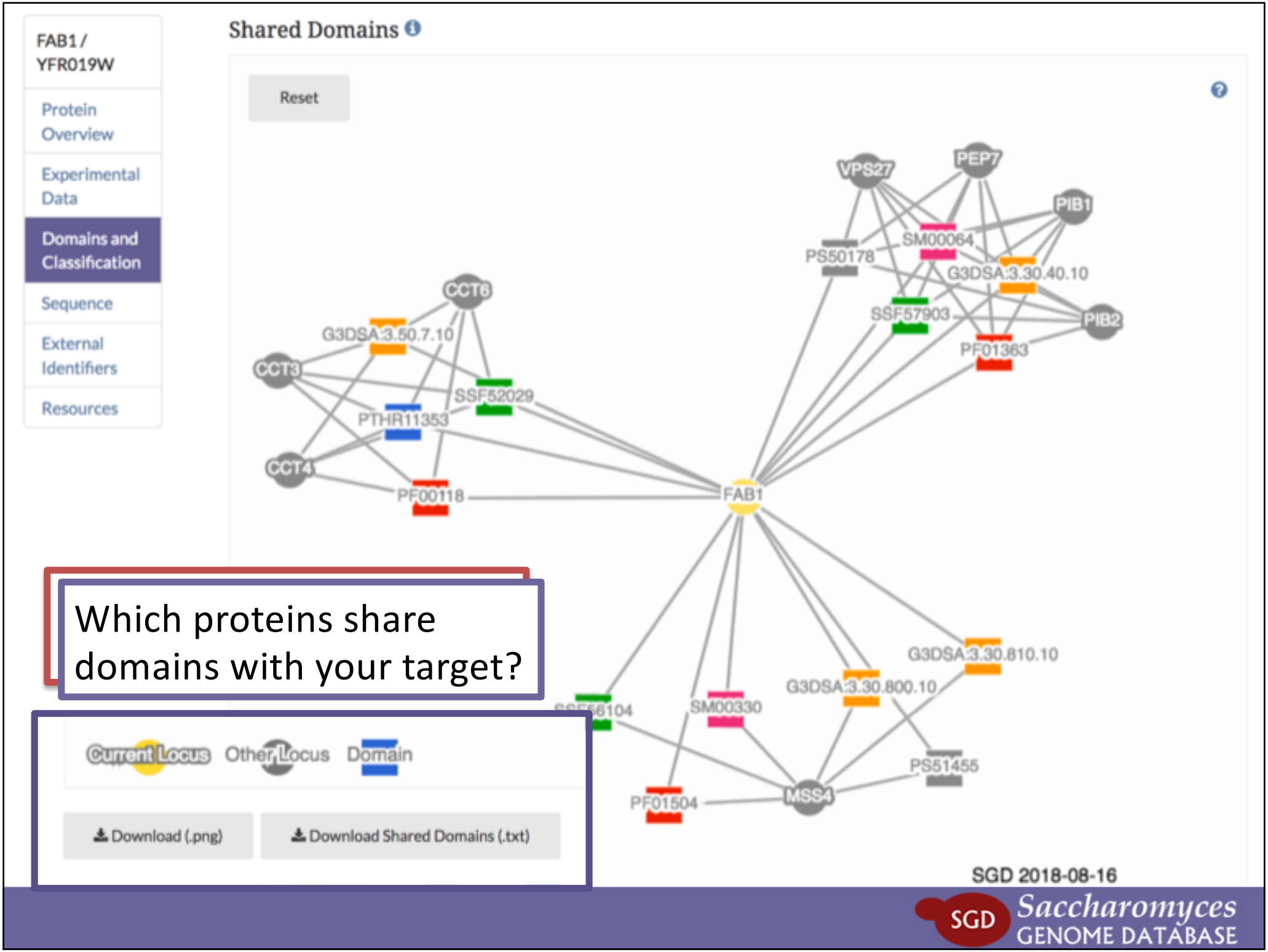
Source: SUPERFAMILY
Description: Heavy metal-associated
Annotations
5 entries for 4 genes
Gene
Protein Coord
ATX1 8-68
CCC2 1-69
CCC2 83-146
CCS1 13-7
40 -471
entries 10 records per page
1
Download (.txt)
Analyze
Analyze SSF55008 Genes
Tools
GO Term Finder
Find common GO annotations between genes.
GO Slim Mapper
Sort genes into broad categories.
SPELL
View expression data.
YeastMine
Conduct advanced analysis.
Click “Analyze” to use this list in SGD Tools!
SGD Saccharomyces GENOME DATABASE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VPS27
PEP7
PIB1
PS50178
SM00064
G3DSA:3.30.40.10
SSF57903
PIB2
PF01363
CCT6
G3DSA:3.50.7.10
CCT3
SSF52029
PTHR11353
CCT4
PF00118
FAB1
G3DSA:3.30.810.10
G3DSA:3.30.800.10
SM00330
PS51455
PF01504
MSS4
Which proteins share domains with your target?
Current Locus
Other Locus
Domain
Download (.png)
Download Shared Domains (.txt)
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SGD
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GENOME DATABASE

HHT1 / YBR010W

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Sequence

Strain

S288C - Reference Genome

```
  1 MARTKQTARK STGGKAPRKQ LASKAARKSA PSTGGVKKPH RYKPGTVALR EIRRFQKSTE
 61 LLIRKLPFQR LVREIAQDFK TDLRFQSSAI GALQESVEAY LVSLFEDTNL AAIHAKRVTI
121 QKKDIKLARR LRGERS*
```

* Blue amino acids indicate modification sites. More information below.

Download Sequence (.fsa)

Post-translational modifications mapped and listed!

Post-translational Modifications - S288C

99 ... for 20 sites

Filter table

Site	Modification	Modifier	Reference
R3	dimethylated residue		Kirmizis A, et al. (2009) PMID: 19270702
R3	methylated residue		Kirmizis A, et al. (2009) PMID: 19270702
K5	methylated residue	SET1	Guillemette B, et al. (2011) PMID: 21483810
K5	acetylated residue	GCN5	Guillemette B, et al. (2011) PMID: 21483810
K5	methylated residue	SET1	De Vos D, et al. (2011) PMID: 21760613

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

PMA1 / YGL008C

- Locus Overview
- Sequence
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- Phenotype
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- Expression
- Summary Paragraph
- Literature

PMA1 / YGL008C Overview

Standard Name: PMA1 [1]

Systematic Name: YGL008C

SGD ID: SGD:S000002976

Aliases: KTI10 [27]

Feature Type: ORF , Verified

Description: Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p; Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+] [2 3 4 5 6 7 8]

Name Description: Plasma Membrane ATPase

Comparative Info: Integrated model organism details available at the Alliance of

PMA1 / YGL008C
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Gene Ontology

Gene Ontology Details

Summary: Proton pump localized to membrane rafts in the plasma membrane; regulates intracellular pH by pumping protons out of the cell

View computational annotations

Quick list of manually curated GO annotations!

Molecular Function

Manually Curated:
- proton-exporting ATPase activity, phosphorylative mechanism (IDA)

Biological Process

Manually Curated:
- proteasome storage granule assembly (IMP)
- proton transmembrane transport (IDA)
- regulation of pH (IEP)

PMA1 / YGL008C

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Phenotype

Phenotype Details

Summary: Essential gene; mutations cause heat sensitivity, reduced innate thermotolerance, killer toxin resistance, longer replicative lifespan, and increased formation of the [GAR+] prion; in large-scale studies, heterozygous null mutant has decreased competitive fitness and shows altered resistance to various chemicals; overexpression also confers a growth disadvantage

Quick list of cellular phenotypes!

Classical Genetics

conditional:
- heat sensitivity: increased
- innate thermotolerance: decreased
- resistance to chemicals: decreased
- resistance to chemicals: increased

repressible:
- chemical compound accumulation: increased
- resistance to chemicals: decreased

unspecified:
- killer toxin resistance: increased

PMA1 / YGL008C
Locus Overview
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Literature

PMA1 / YGL008C Overview

Standard Name: PMA1 [1]

Systematic Name: YGL008C

SGD ID: SGD:S000002976

Aliases: KTI10 [27]

Feature Type: ORF , Verified

Description: Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p; Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+] [2 3 4 5 6 7 8]

Name Description: Plasma Membrane ATPase

Comparative Info: Integrated model organism details available at the Alliance of

MSS4 / YDR208W
Phenotype Overview
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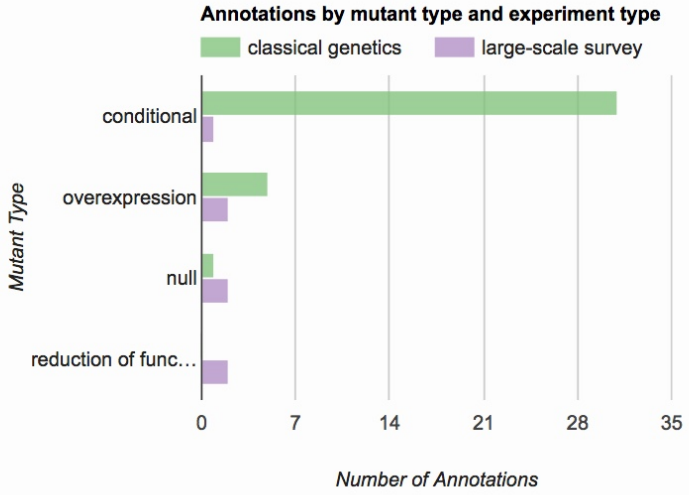
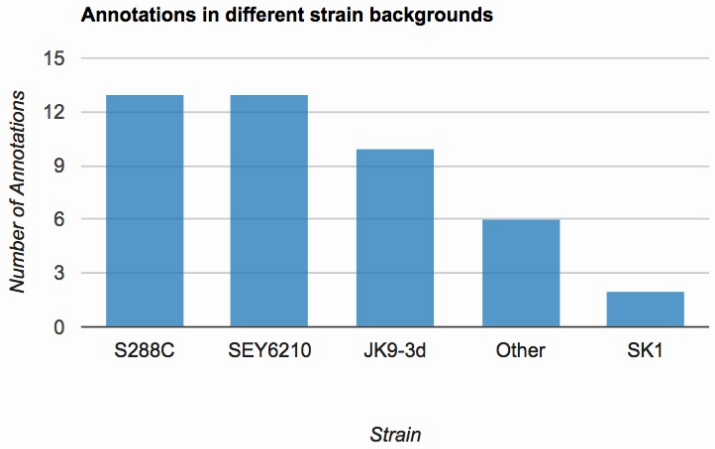
MSS4 / YDR208W Phenotype

Phenotype Help





Annotations note the allele, strain, chemicals, and other details!

resistance to chemicals: normal	classical genetics	overexpression **Allele:** Mss4-D598A	Other	500 ng/ml myriocin		
resistance to chemicals: normal	classical genetics	overexp **Allele:** D636A		myriocin		Kobayashi T, et al. (2005) PMID:15741172
sporulation: decreased	homozygous diploid	conditional **Allele:** mss4-2	SK1	**Temperature:** elevated temperature, 34.5 deg C		Rudge SA, et al. (2004) PMID:14528019

kinase-dead mutant

MSS4 / YDR208W

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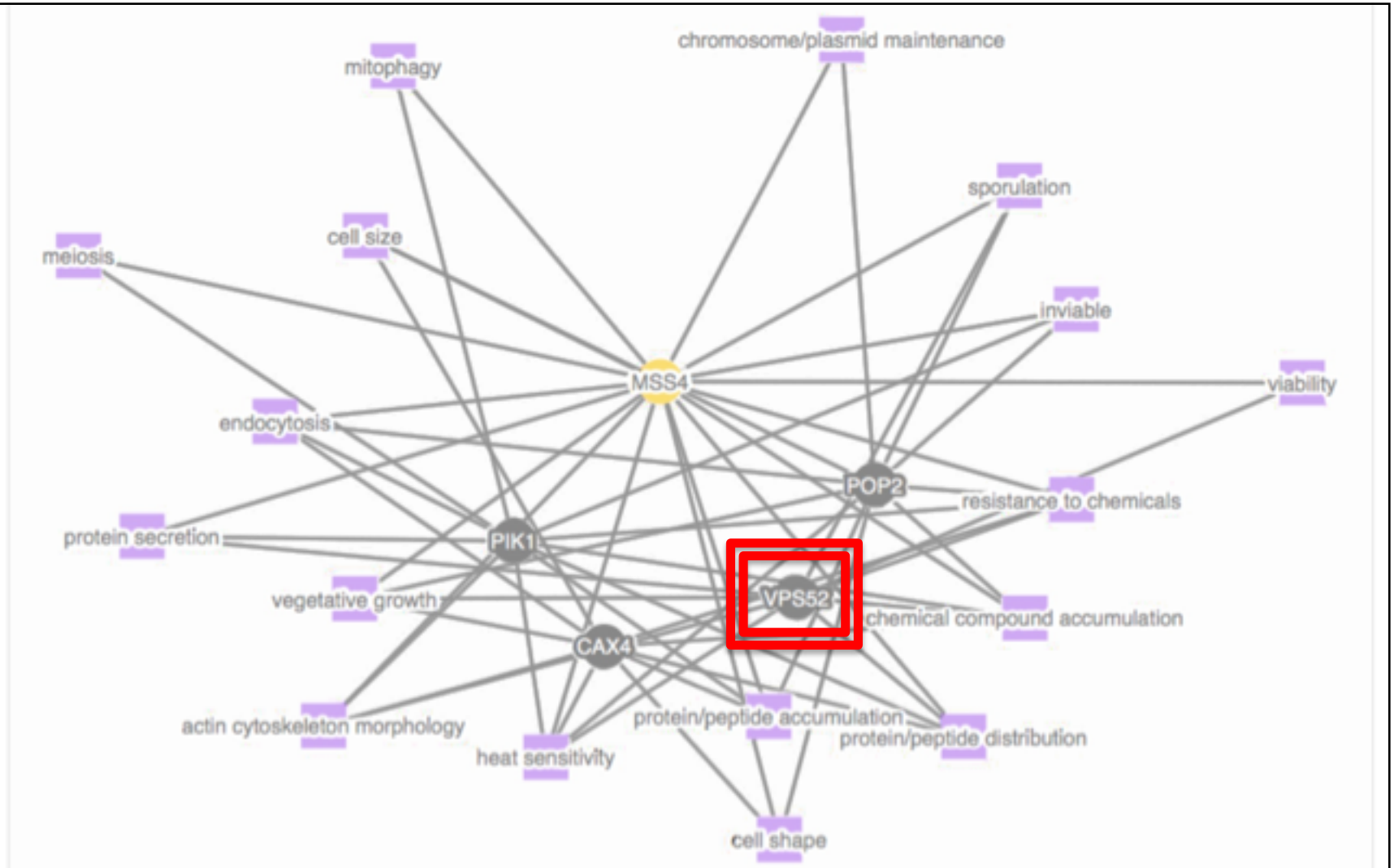

Filter out genes that share less phenotypes!

Download (.png)

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MSS4 / YDR208W

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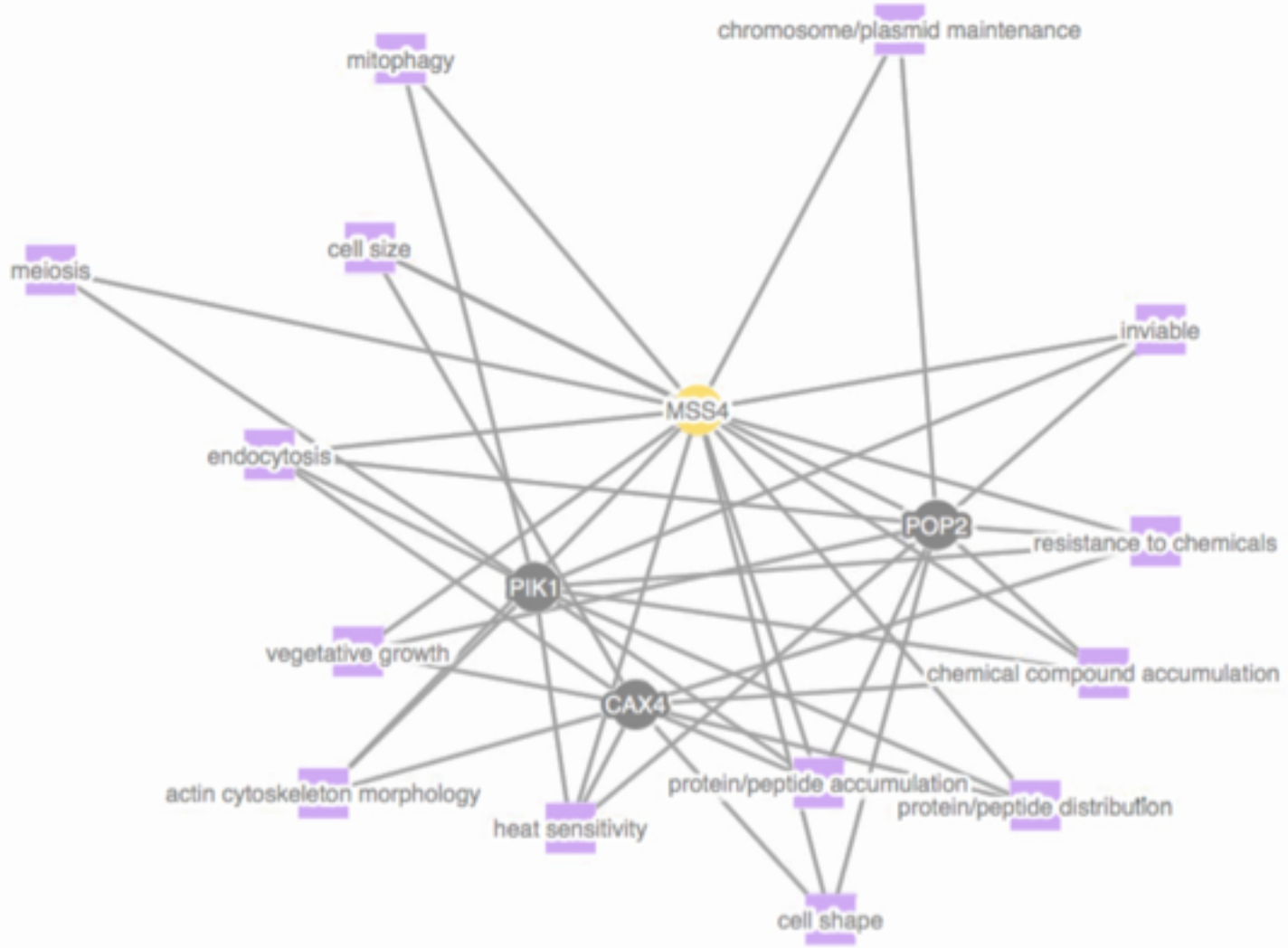
Shared Phenotypes

Resources



Current Locus Other Locus Phenotype

SGD 2017-08-31

Filter Genes by # of Phenotypes Shared With MSS4:

9 10 11

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PMA1 / YGL008C Overview

Standard Name: PMA1 [1]

Systematic Name: YGL008C

SGD ID: SGD:S000002976

Aliases: KTI10 [27]

Feature Type: ORF , Verified

Description: Plasma membrane P2-type H+-ATPase; pumps protons out of cell; major regulator of cytoplasmic pH and plasma membrane potential; long-lived protein asymmetrically distributed at plasma membrane between mother cells and buds; accumulates at high levels in mother cells during aging, buds emerge with very low levels of Pma1p, newborn cells have low levels of Pma1p; Hsp30p plays a role in Pma1p regulation; interactions with Std1p appear to propagate [GAR+] [2 3 4 5 6 7 8]

Name Description: Plasma Membrane ATPase

Comparative Info: Integrated model organism details available at the Alliance of

YOX1 / YML027W Regulation

Regulation Help

YOX1 encodes a helix-turn-helix transcriptional repressor of the homeodomain family. Yox1p restricts transcription of genes containing early cell cycle boxes (ECBs) to M-G1 phase. Yox1p is an ancillary transcription factor that binds alongside Mcm1p on promoters. Examples include important cell cycle genes such as SWI4 and CLN3, themselves rate-limiting for cell cycle progression, and essential for the control of subsequent waves of gene expression at G1-S. Yox1p binds upstream of genes involved in spindle function, DNA synthesis and repair, and also associates with a small portion of intergenic regions adjacent to tRNA genes. Removal of Yox1p from promoters allows gene expression at M-G1. YOX1 is under transcriptional regulation by SBF, and Mcm1p controls the expression of SWI4 which encodes a component of SBF, thereby setting up a negative feedback loop. The transcription of the CDC20 APC (anaphase promoting complex) activator is repressed by Yox1p and kept very low during S phase. Upon mitotic onset, Yox1p abundance declines and the CDC20 gene is actively transcribed. Cdc28p negatively regulates YOX1 transcription, thereby keeping intracellular levels of Yox1p low, and promoting the transcription of CDC20. Yox1p is an unstable protein, so that suppression of its transcription results in rapid reduction of intracellular protein levels.

Acker J, et al. (2013) Yeast RNA polymerase III transcription factors and effectors. Biochim Biophys Acta 1829(3-4):283-95 PMID:23063749

YVC1 / YOR087W

- Regulation Overview
- Regulators
- Regulation Network

Regulators

Manually Curated

2 entries for 2 genes

Filter table

Regulator	Regulator Type	Direction	Regulation Of	Happens During	Evidence	Strain Background
GTT1	protein modifier	positive	protein activity	cellular response to stress	western blot evidence	S288C
TRX2	protein modifier	negative	protein activity		western blot evidence	S288C

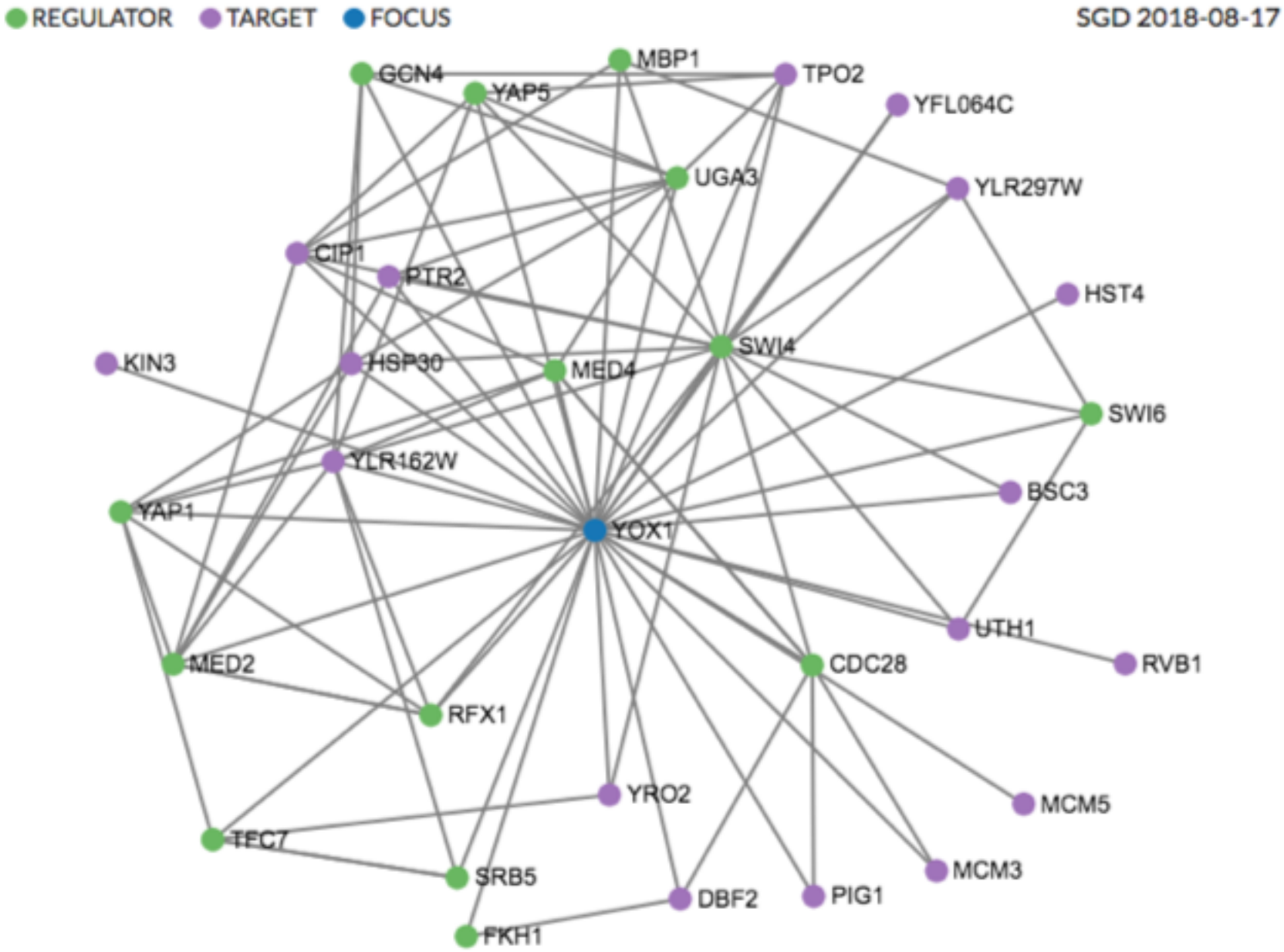
of 2 entries 10 record 1 »

xt) Analyze

Regulation by:
Transcription factors
Chromatin modifiers
Protein modifiers

Regulation of:
Transcription
Protein activity

Regulation Network



Come say hello!

SGD

SGD

Thank you!

SGD Website

yeastgenome.org

Questions/Comments

sgd-helpdesk@lists.stanford.edu

YouTube Channel

youtube.com/SaccharomycesGenomeDatabase