The Awesome Power of SGD

Stacia R. Engel • Stanford University • Yeast2022

#APOYG – Awesome Power of Yeast Genetics

- - - - - SGD personnel at YGM2022 - - - - -

Mike Cherry, PhD

Stacia Engel, PhD

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Suzi Aleksander

Rob Nash, PhD

Workshop/discussion agenda

- SGD – basics, nomenclature, recent additions
- Alliance of Genome Resources
- Gene Ontology – data, tools
- YeastMine data warehouse – templates, lists

yeastgenome.org

alliancegenome.org

geneontology.org

yeastmine.yeastgenome.org

Full list of SGD staff: https://cherrylab.stanford.edu/people/sgd-staff

- SGD – basics, nomenclature, recent additions
  - Search & Explore
  - Genome version R64.3.1
  - New ncRNA systematic nomenclature
  - Updates to ‘legacy’ gene names
  - New ‘not in S288C’ systematic nomenclature
  - Updates to Reference Genome panel – *in progress*
  - Nomenclature conventions, qualifiers
  - Alleles and Allele pages
  - Updates to Interactions pages
  - New Homology pages
  - Disease pages
  - Extra bits - Supplementary data, published datasets, PubMed Central downloads
  - Submit Data
  - microPublication Biology

yeastgenome.org

Search & Explore

About Blog Download Explore Help YeastMine

SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu

quick search

1 of 20

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.

Explore SGD

Explore SGD
- returns all objects in database

Meetings

Yeast Genetics Meeting 2022
August 17 to August 21, 2022 -
University of California, Los Angeles

Fungal Pathogen Genomics
May 07 to May 12, 2023 -
Wellcome Genome Campus, Hinxton, Cambridge, UK

New & Noteworthy

A Redox Switch that Remakes a Guide Protein into an Antioxidant - **August 05, 2022**
Cells are efficient machines, honed by selection. Recent studies are showing us how cells are more efficient than we realized, with proteins discovered to have multiple functions that can be surprisingly different under changes in environment. A new paper in Molecular Cell describes Get3p as one such protein. Under non-stress conditions, Get3p acts as an [...]

Tweets by @yeastgenome

SGD Project
@yeastgenome
Check out SGD's latest blog! Guide or guard? Orchestrated interplay of nucleotide-binding and thiol oxidation controls both oxidative activation and reductive inactivation of #yeast cytosolic protein Get3pyeastgenome.org/blog/a-redox-s… @MolecularCell

Search & Explore

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SGD Saccharomyces GENOME DATABASE

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search: actin, kinase, glu

Categories

References	110,284
Downloads	85,856
Biological Processes	25,324
Alleles	19,137
Colleagues	12,476
Molecular Functions	11,756
Diseases	11,098
Genes	8,637
Cellular Components	3,854
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Complexes	617
Observables	205
Strains	56
Resources	43
Reserved Gene Names	33

291,420 results

Page 1 of 11,657 Results 25 Sort By Relevance

Reference

Kleman-Leyer K, Armbruster DW, Daniels CJ (1997) Properties of H. volcanii tRNA intron endonuclease reveal a relationship between the archaeal and eucaryal tRNA intron processing systems. Cell 89 6):839-47

To better understand the relationship between archaeal and eucaryal tRNA introns and their processing systems, we have cloned the gene encoding the tRNA intron endonucleases from the...

2 Associated Genes: Show All

Reference

Miles J, Formosa T (1992) Protein affinity chromatography with purified yeast DNA polymerase alpha detects proteins that bind to DNA polymerase. Proc Natl Acad Sci U S A 89 4):1276-80

We have overexpressed the POL1 gene of the yeast Saccharomyces cerevisiae and purified the resulting DNA polymerase alpha polypeptide in an apparently intact form. We attached the purifie...

Explore SGD
- returns all objects in database
- results updated daily

"Explore SGD" search result https://www.yeastgenome.org/search?q=&is_quick=true

Genome version R64.3.1

Chromosome	Feature	Description of change	Reference
II	YNCB0008W aka GAL10-ncRNA	New ncRNA antisense to GAL10: coordinates 276,805–280,645	Houseley et al. (2008); Pinskaya et al. (2009); Geisler et al. (2012)
II	YNCB0014W aka TBRT/XUT_2F-154	New ncRNA antisense to TAT1: coordinates 376,610–378,633	Awasthi et al. (2020)
III	RE/RE301	New recombination enhancer: coordinates 29,108–29,809	Wu and Haber (1996)
V	YELWdelta27	New Ty1 LTR: coordinates 449,274–449,626	Nene et al. (2018)
V	HPA3/YEL066W	Moved translation start to Met19: old coordinates 26,667–27,206; new coordinates 26,721–27,206	Sampath et al. (2013)
VII	OTO1/YGR227C-A	New ORF: coordinates 949052–949225 Crick	Makanae et al. (2015)
VII	ROK1/YGL171W	Two new uORFs: coordinates uORF1 182,286–182,407; coordinates uORF2 182,291–182,329	Jeon and Kim (2010)
VIII	YHR052C-B	New ORF: coordinates 212,519–212,692 Crick	He et al. (2018)
VIII	YHR054C-B	New ORF: coordinates 214,517–214,690 Crick	He et al. (2018)
VIII	SUT169/YNCH0011W	New ncRNA: coordinates 378,254–379,237	Xu et al. (2009); Geisler et al. (2012); Huber et al. (2016); Bunina et al. (2017)
X	YJR012C	Moved start to Met76: old coordinates 459,795–460,418 Crick; new coordinates 459,795–460,193 Crick	Sadhu et al. (2018)
X	YJR107C-A	New ORF: coordinates 628,457–628,693 Crick	Yagoub et al. (2015); He et al. (2018)
XI	YKL104W-A	New ORF: coordinates 245,032–245,286	He et al. (2018)
XII	YLR379W-A	New ORF: coordinates 877,444–877,716	Internal reanalysis of results from Song et al. (2015) to find and annotate missing S288C ORFs
XII	NTS1-2, NTS2-1, NTS2-2	Change feature_type/SO_term from SO:0001637 rRNA_gene to SO:0000183 non_transcribed_region	
XIII	LDO45/YMR147W	Shift stop to be same as LDO16/YMR148W, add intron: old coordinates 559,199–559,870; new coordinates 559,199–559,780, 560,156–560,812	Eisenberg-Bord et al. (2018)
XIII	YMR008C-A	New ORF: coordinates 283,081–283,548 Crick	Internal reanalysis of results from Song et al. (2015) to find and annotate missing S288C ORFs
XIII	YNCM0001W aka PHO84 lncRNA	New ncRNA: coordinates 23,564–26,578	Camblong et al. (2007)
XIV	LTO1/YNL260C	Move start to Met37: old coordinates 156,859–157,455 Crick; new coordinates 156,859–157,347 Crick	Paul et al. (2015)
XVI	YNCP0002W aka GAL4 lncRNA	New ncRNA: coordinates 79,562–82,648	Geisler et al. (2012)

New genome annotation

- release R64.3.1
- dated April 21, 2021

Updates and additions

- 7 new ORFs
- 5 new ncRNAs
- 2 new uORFs
- New recombination enhancer
- New LTR
- 3 ORFs: move start
- 1 ORF: move stop + new intron
- Changed feature_type for NTS

No change to underlying sequence

Genome version R64.3.1

New genome annotation

- release R64.3.1
- dated April 21, 2021
- No change to genomic sequence

Updates additions

- 7 new ORFs: OTO1/YGR227C-A, YHR052C-B, YHR054C-B, YJR107C-A, YKL104W-A, YLR379W-A, YMR008C-A
- 5 new ncRNAs: GAL10-ncRNA, TBRT/XUT_2F-154, SUT169, PHO84 lncRNA, GAL4 lncRNA
- 2 new uORFs for ROK1/YGL171W
- New recombination enhancer: RE
- New LTR: YELWdelta27
- 3 ORFs with shifted translation starts: HPA3/YEL066W, YJR012C, LTO1/YNL260C
- 1 ORF with shifted translation stop plus new intron: LDO45/YMR147W
- Changed feature_type (and SO_term) for non-transcribed spacers: NTS1-2, NTS2-1, NTS2-2

Genome version R64.3.1

GCF_000146045.2	RefSeq Assembly
NC_001133.9	Chromosome I
NC_001134.8	Chromosome II
NC_001135.5	Chromosome III
NC_001136.10	Chromosome IV
NC_001137.3	Chromosome V
NC_001138.5	Chromosome VI
NC_001139.9	Chromosome VII
NC_001140.6	Chromosome VIII
NC_001141.2	Chromosome IX
NC_001142.9	Chromosome X
NC_001143.9	Chromosome XI
NC_001144.5	Chromosome XII
NC_001145.3	Chromosome XIII
NC_001146.8	Chromosome XIV
NC_001147.6	Chromosome XV
NC_001148.4	Chromosome XVI
NC_001224.1	Mitochondrion

NCBI RefSeq accession numbers for *Saccharomyces cerevisiae* S288C reference genome version R64.3.1

To find these records:

- Search SGD for 'S288C' to find strain page

https://www.yeastgenome.org/strain/S288C

- Search NCBI for 'S288C'

https://www.ncbi.nlm.nih.gov/genome/?term=S288C

Genome version R64.3.1 - New ncRNA systematic nomenclature

New systematic nomenclature for yeast ncRNAs – 430 genes

- tRNA, snoRNA, rRNA, ncRNA, snRNA, telomerase RNA

Similar to, but distinct from, that used for ORFs

Four uppercase letters, a four-digit number, and another letter:

- Y for “Yeast”
- NC for “noncoding”
- A-Q for the chromosome on which the ncRNA gene resides
  - “A” is chromosome I, “B” is chromosome II, up to “P” for chromosome XVI
  - “Q” for the mitochondrial chromosome
- Four-digit number corresponding to sequential order of ncRNA gene on the chromosome starting from the left telomere and counting toward the right telomere
- W or C indicating whether ncRNA gene is encoded on “Watson” or “Crick” strand
  - “Watson” runs 5’ to 3’ from left telomere to right telomere
  - “Crick” runs 3’ to 5’
- *Example: YNCP0002W is 2nd ncRNA gene from left end of chromosome XVI, encoded on Watson strand.*

Genome version R64.3.1 – "legacy" gene name updates

Accepted format for standard gene names in *S. cerevisiae* = 3 uppercase letters + number

- Letters typically signify a phrase that provides information about function, mutant phenotype, or process, etc.
  - referred to as "Name Description" in SGD
- "ADE" for "ADEnine biosynthesis"
- "CDC" for "Cell Division Cycle"
- Many types of chromosomal features follow this basic format: ORF, RNA, ARS, CEN, or genetic locus, etc.

Some non-compliant *S. cerevisiae* gene names pre-date current nomenclature standards

- *MRLP38, RPL1A, OM45*

Other historical names predate nomenclature standards and the database, are less computer-friendly due to punctuation; these names have been updated

- *ADE5,7 → ADE57*
- *ARG5,6 → ARG56*
- *DUR1,2 → DUR12*
- *IMP2' → IMP21*

New "not in S288C" systematic nomenclature

New systematic nomenclature for yeast genes not found in S288C reference genome

Similar to, but distinct from, that used for ORFs and RNAs

Three uppercase letters + four-digit number:

- Y for "Yeast"
- SC for "*Saccharomyces cerevisiae*"
- Four-digit number corresponding to sequential order in which the gene was added to SGD

Three uppercase letters + four-digit number:

- Y for "Yeast"
- SC for "*Saccharomyces cerevisiae*"
- Four-digit number corresponding to sequential order in which the gene was added to SGD

Currently 55 "not in S288C" genes in SGD: MAL21/YSC0004, MATA/YSC0046, etc.

- 15 more YSC0000 names reserved by researchers and awaiting publication

Updates to Reference Genome Panel – in progress

Updated genome annotation for ‘alternative reference genomes’

- CEN.PK2-1Ca
- D273-10B
- FL100
- JK9-3d
- RM11-1A
- SEY6210
- Σ1278b

No changes to any genomic sequences

Updates are really all additions

- RNAs – tRNA, snRNAs, ncRNAs
- Autonomously Replicating Sequences (ARS elements)
- Centromeres

Files updated on SGD Download site; GenBank update in progress…

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yeastgenome.org

SGDID

- local database identifier
- in combo with source is 'curie'

Systematic Name

- generated by systematic sequencing project in 1990s

Standard Name

- 1st name published in peer-reviewed paper describing characterization
- or, amalgam of
  - consensus of community
  - literature usage
  - clarity relative to function
  - priority in literature

Alias names

- alternate names used in literature

Most stable identifier

Least stable identifier

Nomenclature

SGDID

- local database identifier
- in combo with source is 'curie'

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  - consensus of community
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  - clarity relative to function
  - priority in literature

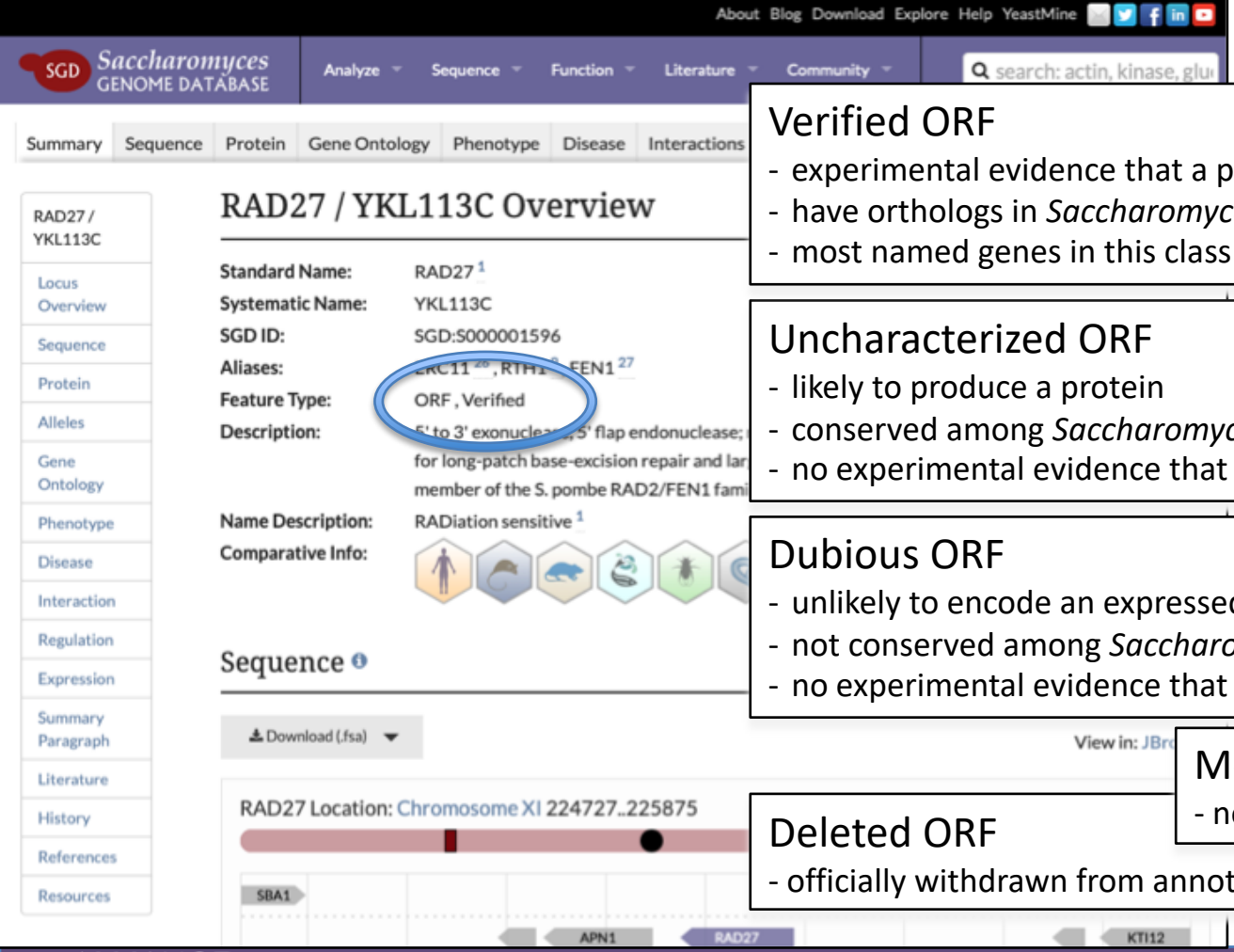
Alias names

- alternate names used in literature

Where to access data

- YeastMine: 'Retrieve SGD chromosomal Features'
- Downloads: GFF

Nomenclature



Verified ORF

- experimental evidence that a protein is produced
- have orthologs in *Saccharomyces* species
- most named genes in this class

Uncharacterized ORF

- likely to produce a protein
- conserved among *Saccharomyces* species
- no experimental evidence that product is made

Dubious ORF

- unlikely to encode an expressed protein
- not conserved among *Saccharomyces* species
- no experimental evidence that product is made

Merged ORF

- no longer considered distinct entity

Deleted ORF

- officially withdrawn from annotation

Fisk et al. (2006) Saccharomyces cerevisiae S288C genome annotation: a working hypothesis. Yeast 23(12):857-65.

Nomenclature

Verified ORF

- experimental evidence that a protein is produced
- have orthologs in *Saccharomyces* species
- most named genes in this class

Uncharacterized ORF

- likely to produce a protein
- conserved among *Saccharomyces* species
- no experimental evidence that product is made

count	qualifier
682	Dubious
688	Uncharacterized
5241	Verified

DOI: 10.1534/genetics.107.074468

Review

Why Are There Still Over 1000 Uncharacterized Yeast Genes?

Lourdes Peña-Castillo and Timothy R. Hughes[1]

Banting and Best Department of Medical Research, University of Toronto, Toronto, Ontario M5S 3E1, Canada

ABSTRACT

The yeast genetics community has embraced genomic biology, and there is a general understanding that

- SGD – basics, nomenclature, recent additions
  - Search & Explore
  - Genome version R64.3.1
  - New ncRNA systematic nomenclature
  - Updates to ‘legacy’ gene names
  - New ‘not in S288C’ systematic nomenclature
  - Updates to Reference Genome panel – *in progress*
  - Nomenclature conventions
  - **Alleles and Allele pages**
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  - Extra bits - Supplementary data, published datasets, PubMed Central downloads
  - Submit Data
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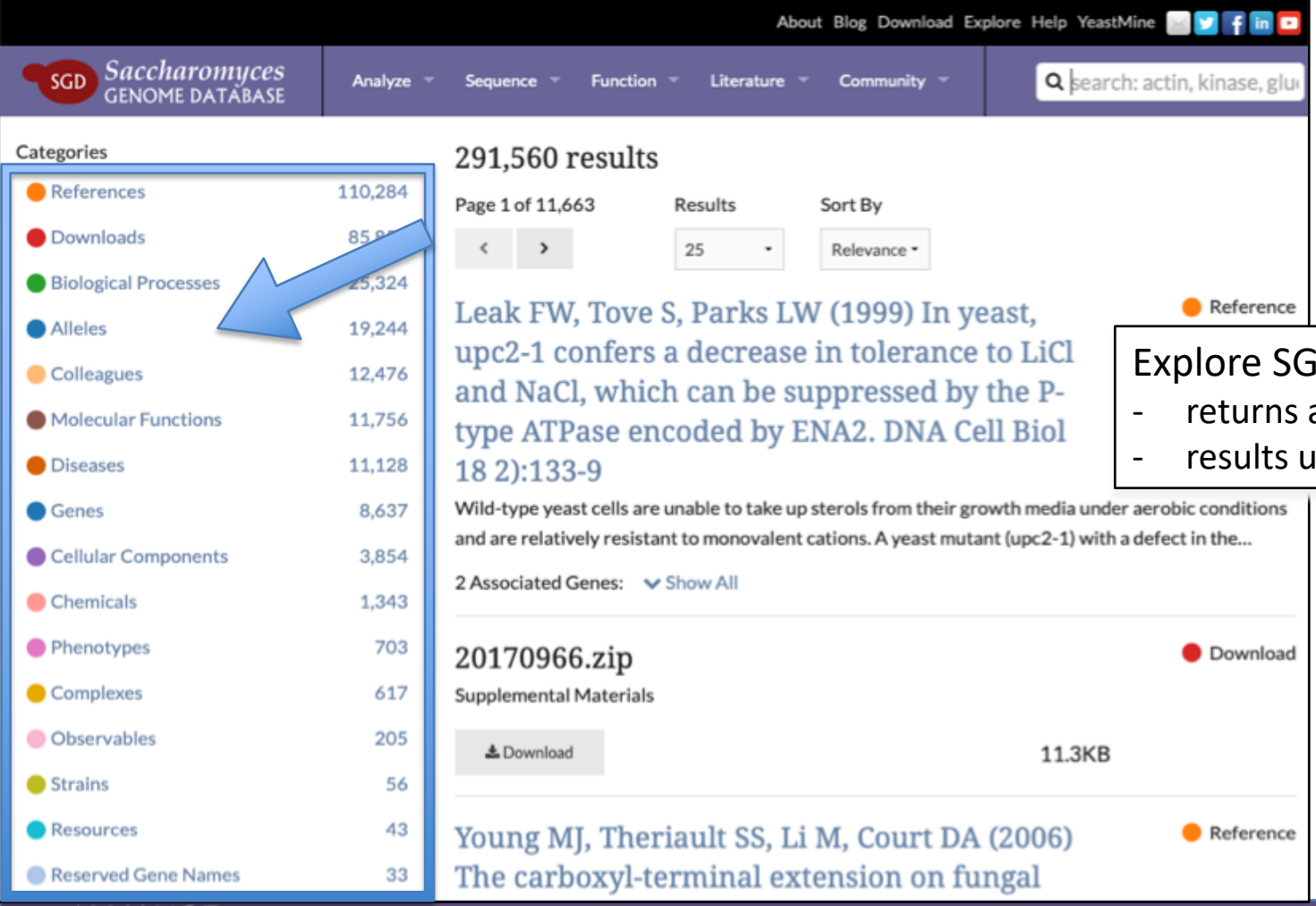
Alleles



Explore SGD
- returns all objects in database
- results updated daily

"Explore SGD" search result https://www.yeastgenome.org/search?q=&is_quick=true

Alleles

About Blog Download Explore Help YeastMine

SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

rad27

Show all categories

Alleles

References

Costanzo M, et al. (2016)	5,797
Neumüller RA, et al. (2013)	293
Hendry JA, et al. (2015)	287
van Pel DM, et al. (2013)	270
Ben-Aroya S, et al. (2008)	249

Show more

Allele Types

missense variant	7,380
feature ablation	6,744
gene variant	3,586
feature truncation	755
stop gained	272

Show more

19,244 results × Allele

Page 1 of 770 Results 25 Sort By Relevance

hut1-Δ

ctf4-Δ

mms1-Δ

rvs161-Δ

slx5-Δ

mrm2-Δ

apl6-Δ

Categories in Allele Search

- Publication
- Allele type – terms from Sequence Ontology
- Gene
- Phenotype

SGD YeastMine

Search and retrieve *S. cerevisiae* data with YeastMine, populated by SGD and pc

Data Updated on: Aug-9-2022

Contact Us Video

Home Templates Lists QueryBuilder Tools Regions Data Sources

Templates

Templates are predefined queries, each has a simple form and a description. Click on a template to run it, you can se by category.

Filter: allele Filter: -- all categories -- Reset

Actions: Export selected Options: Show descriptions Show Tags

Genes --> Alleles

Retrieve alleles of a given gene.

Alleles

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search: actin, kinase, glu

Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Reg

RAD27 / YKL113C

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

RAD27 / YKL113C Overview

Standard Name: RAD27 [1]

Systematic Name: YKL113C

SGD ID: SGD:S000001596

Aliases: ERC11 [26], RTH1 [9], FEN1 [27]

Feature Type: ORF, Verified

Description: 5' to 3' exonuclease, 5' flap endonuclease; requir
for long-patch base-excision repair and large loo
of the S. pombe RAD2/FEN1 family; relocalizes t

Name Description: RADiation sensitive [1]

Comparative Info:

Alleles

rad27-A358* | rad27-D179A | rad27-G67S | rad27-K325 | rad27-Δ

View all RAD27 alleles in SGD search | YeastMine

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search: actin, kinase, glu

Summary Literature

Allele: rad27-G67S

- Overview
- Phenotype Annotations
- References
- Resources

Allele: rad27-G67S

Allele Name: rad27-G67S [1]

SGD ID: SGD:S000286623

Affected Gene: RAD27

Allele Type: missense variant [1]

Description: rad27-G67S cells exhibit relatively high level of DNA slippage events; G67S protein carries in vitro weak exonuclease activity on bubble intermediates; rad27-G67S mutants display same Cd2+-hypersensitivity as rad27-Δ cells suggesting that cadmium can induce formation or stabilization of bubble intermediates that cannot be degraded by rad27-G67S protein during processing of Okazaki fragments [1]

Phenotype Annotations

1 entry for 1 phenotype

Filter table

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
RAD27	resistance to chemicals: decreased	classical genetics	reduction of function Allele: rad27-G67S	S288C	50 uM cadmium dichloride		Serero A, et al. (2008) PMID:18504590

Alleles

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search: actin, kinase, glu

Show all categories

Alleles

References

- Karanja KK and Livingston DM (2009) 2
- Costanzo M, et al. (2016) 1
- Hamza A, et al. (2021) 1
- Hendry JA, et al. (2015) 1
- Serero A, et al. (2008) 1

Allele Types

- missense variant 2
- stop gained 2
- feature ablation 1

Allele Loci

- RAD27 5

Phenotypes

- resistance to chemicals: decreased 2
- UV resistance: decreased 1
- bud morphology: abnormal 1
- budding index: increased 1
- cell size: increased 1

5 results × RAD27 × Allele

Page 1 of 1 | Results 25 | Sort By Relevance

rad27-Δ
allele loci: *RAD27*

rad27-K325*
allele loci: *RAD27*

rad27-A358*
allele loci: *RAD27*

rad27-D179A
allele loci: *RAD27*

RAD27-G67S
allele loci: *RAD27*

SGD YeastMine

Search and retrieve *S. cerevisiae* data with YeastMine, populated by SGD and powered by InterMine.

Data Updated on: Aug-9-2022

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Search: e.g. act1 GO

Genes → Alleles

Retrieve alleles of a given gene.

Manage Columns | Manage Filters | Manage Relationships | Save as List | Generate Python code | Export

Showing rows 1 to 5 of 5

Gene Primary DBID	Gene Systematic Name	Gene Standard Name	Gene Name	Alleles Name	Alleles Allele Class	Alleles Description	Alleles Alias Name
S000001596	YKL113C	RAD27	RADiation sensitive	rad27-A358*	stop gained	NO VALUE	NO VALUE
S000001596	YKL113C	RAD27	RADiation sensitive	rad27-D179A	missense variant	NO VALUE	NO VALUE
S000001596	YKL113C	RAD27	RADiation sensitive	RAD27-G67S	missense variant	NO VALUE	NO VALUE
S000001596	YKL113C	RAD27	RADiation sensitive	rad27-K325*	stop gained	NO VALUE	NO VALUE
S000001596	YKL113C	RAD27	RADiation sensitive	rad27-Δ	feature ablation	NO VALUE	S000286296

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Interactions, Alleles

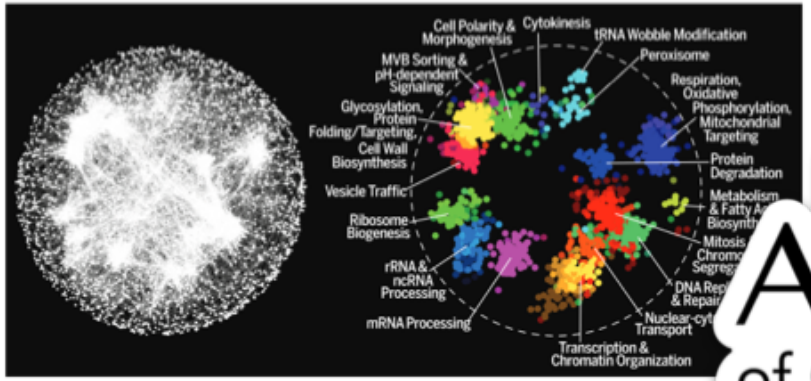
RESEARCH ARTICLE

SCIENCE sciencemag.org

YEAST GENETICS

A global genetic interaction network maps a wiring diagram of cellular function

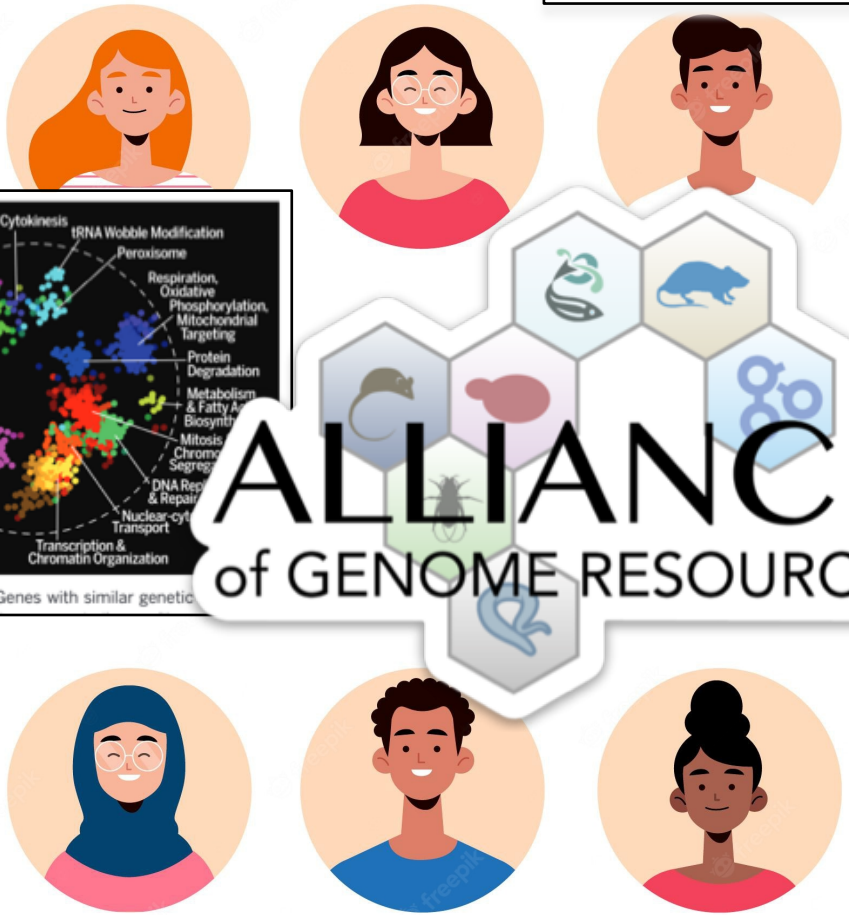
Michael Costanzo,[1*] Benjamin VanderSluis,[2,3
Anastasia Baryshnikova,[4*] Carles Pons,[2*†] Gu
Julia Hanchard,[1,5] Susan D. Lee,[6] Vicent Pele
Maximilian Billmann,[8] Jolanda van Leeuwen,
Elena Kuzmin,[1,5] Justin Nelson,[2,10] Jeff S. Pio
Sondra Bahr,[1] Yiqun Chen,[1] Raamesh Deshpa
Sheena C. Li,[1,11] Zhijian Li,[1] Mojca Mattiazzi
Bryan-Joseph San Luis,[1] Sara Sharifpoor,[1] Em
Jamie Snider,[1] Harsha Garadi Suresh,[1] Yizha
Noel Malod-Dognin,[14] Vuk Janjic,[15] Natasa Pr
Igor Stagljar,[1,5,17] Tian Xia,[2,18] Yoshikazu Oh
Brian Raught,[12] Michael Boutros,[8] Lars M. St
Adam P. Rosebrock,[1,5] Amy A. Caudy,[1,5] Chad
Brenda Andrews,[1,5#] Charles Boone[1,5,11#]



A global network of genetic interaction profile similarities. (Left) Genes with similar genetic

We generated a global genetic interaction network for *Saccharomyces cerevisiae*, constructing more than 23 million double mutants, identifying about 550,000 negative and about 350,000 positive genetic interactions. This comprehensive network maps genetic interactions for essential gene pairs, highlighting essential genes as densely connected hubs. Genetic interaction profiles enabled assembly of a hierarchical model of cell function, including modules corresponding to protein complexes and pathways, biological processes, and cellular compartments. Negative interactions connected functionally related genes, mapped core bioprocesses, and identified pleiotropic genes, whereas positive interactions often mapped general regulatory connections among gene pairs, rather than shared functionality. The global network illustrates how coherent sets of genetic interactions connect protein complex and pathway modules to map a functional wiring diagram of the cell.

23 SEPTEMBER 2016 • VOL 353 ISSUE 6306



ALLIANCE of GENOME RESOURCES

Interactions, Alleles

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Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Regulation Expression Literature Homology

RAD27 / YKL113C

Interactions Overview

Genetic Interactions

Physical Interactions

Interaction Network

Resources

Genetic Interactions

Help

Genetic Interactions

1410 entries for 613 genes

PMID:27708008

	Interactor	Allele	Assay	Annotation	Action	Phenotype	SGA score	P-value
	POL1	pol1-13, rad27-Δ	Positive Genetic	high-throughput	Hit		0.2429	0.00007366
	SIN4	sin4-Δ, rad27-Δ	Positive Genetic	high-throu				
	GCD11	gcd11-5001-supp1, rad27-Δ	Positive Genetic	high-throu				

Physical Genetic Interse

Physical Interactions

Physical Interactions

31 entries for 22 genes

	Interactor	Assay	Annotation
	APJ1	Affinity Capture-MS	high-throughput
	CDC9	Reconstituted Complex	manually curated

Templates

Templates are predefined queries, each has a simple form and a des by category.

Filter: Filter: Interactions Reset

Actions: Export selected Options: Show descriptions Show Tags

You are not logged in. L

- Gene --> Complex + Details
  Retrieve the complex details including other members that are part of the co
- Gene --> Genetic Interactions
  Retrieve all genetic interactions for a specified gene.
- Gene --> Physical Interactions
  Retrieve all physical interactions for a specified gene.
- Literature --> Interaction
  Retrieve all the interactions curated from the specified PubMed ID (PMID).
- Complex --> Details + Participants
  For a given macromolecular complex, retrieve Gene Ontology annotations a stoichiometry, and their biological roles in the complex.

- SGD – basics, nomenclature, recent additions
  - Search & Explore
  - Genome version R64.3.1
  - New ncRNA systematic nomenclature
  - Updates to ‘legacy’ gene names
  - New ‘not in S288C’ systematic nomenclature
  - Updates to Reference Genome panel – *in progress*
  - Nomenclature conventions
  - Alleles and Allele pages
  - Updates to Interactions pages
  - **New Homology pages**
  - Disease pages
  - Extra bits - Supplementary data, published datasets, PubMed Central downloads
  - Submit Data
  - microPublication Biology

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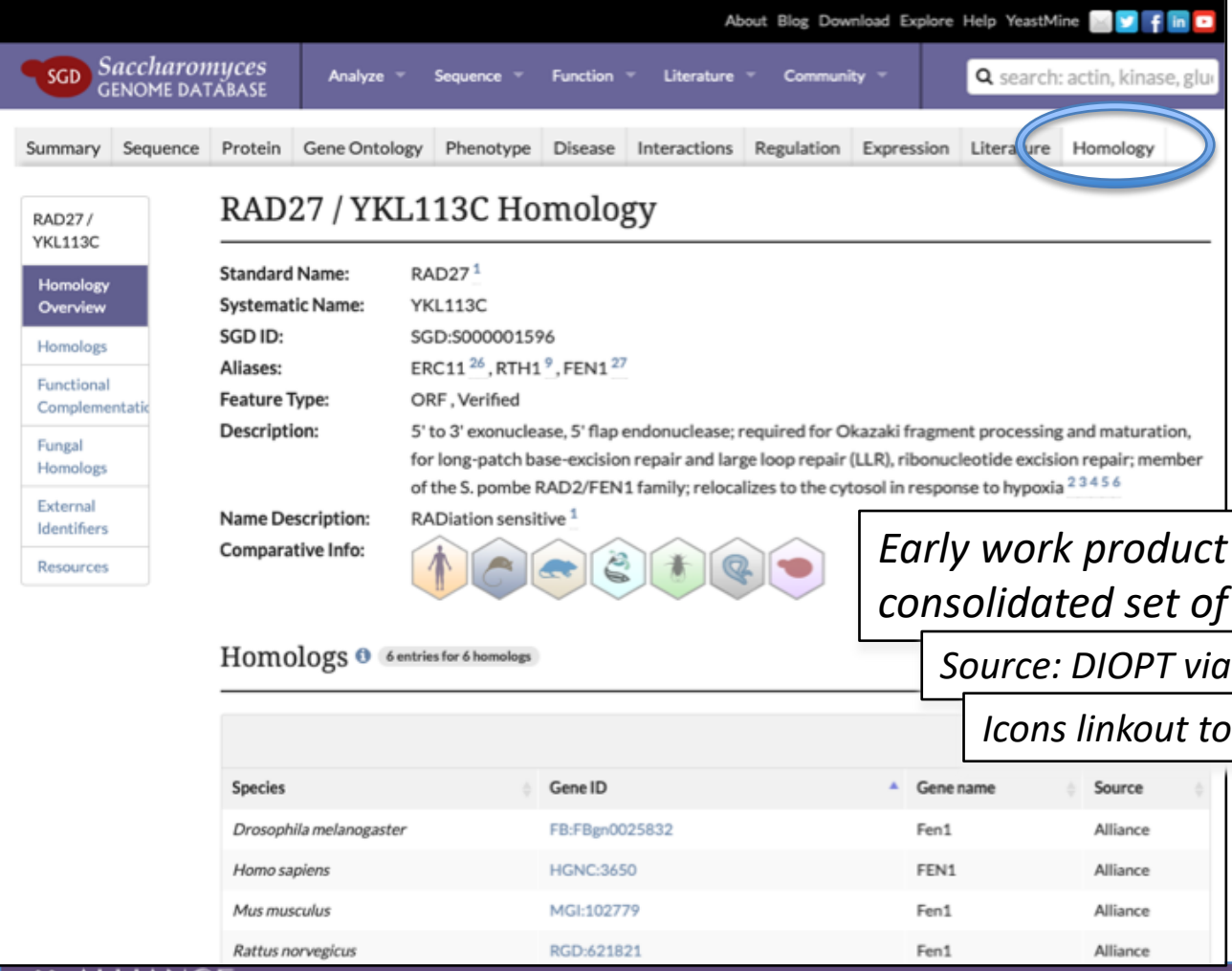
Homology



Early work product from Alliance: consolidated set of orthologs

Source: DIOPT via Alliance API

Icons linkout to Alliance gene pages

https://www.flyrnai.org/cgi-bin/DRSC_orthologs.pl

Homology

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Analyze Sequence Function Literature Community

search: actin, kinase, glu

Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Regulation Expression Literature Homology

RAD27 / YKL113C

- Homology Overview
- Homologs
- Functional Complementatic
- Fungal Homologs
- External Identifiers
- Resources

RAD27 / YKL113C Homology

Standard Name: RAD27 [1]
Systematic Name: YKL113C
SGD ID:
Aliases:
Feature Type:
Description:

Name Descriptic
Comparative Inf

Homologs

Species
Drosophila melan
Homo sapiens
Mus musculus
Rattus norvegicu

Functional Complementation

6 entries for 6 complements

Species	Gene ID	Strain backgrou
Homo sapiens	HGNC:3511	S288C
Homo sapiens	HGNC:3650	S288C
Homo sapiens	HGNC:3650	S288C
Homo sapiens	HGNC:3650	S288C

Fungal Homologs

19 entries for 19

Species	Gene ID
A. flavus NRRL3357	AFLA_103310
A. fumigatus Af293	Afu3g06060
A. nidulans FGSC A4	AN2764
A. niger ATCC 1015	ASPNIDRAFT_481

Templates

Templates are predefined queries, each has a simple form and a description. Click on a template to by category.

Filter: Filter: Homology Reset

Actions: Export selected Options: Show descriptions Show Tags

You are not logged in. Log in to mark items as favourite

- Yeast gene --> OMIM human homolog(s) --> OMIM Disease Phenotype(s)
  Retrieve human homolog(s) of yeast gene(s) and and any of their associated OMIM disease phenotypes.
- Human Gene -> Yeast Homolog(s) -> OMIM Disease Phenotype
  For a given human gene(s) retrieve associated OMIM disease phenotype(s) and yeast homolog(s).
- Gene --> Non-Fungal and S. cerevisiae Homologs
  Retrieve all DIOPT homologs for a specified S. cerevisiae gene.
- Gene --> Functional Complementation
  For a given yeast gene(s), retrieve information about cross-species functional complementation between y
- OMIM Disease Phenotype --> human gene(s) --> yeast homolog(s)
  Specify OMIM phenotype(s) (by keyword or name) and retrieve all associated human gene(s) and the yeas
- Gene --> Fungal Homologs
  Retrieve fungal homologs for a specified S. cerevisiae gene.

Disease

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Summary Sequence Protein Gene Ontology Phenotype Disease Interactions Regulation Expression Literature Homology

DYN1 / YKR054C

Disease Overview

Manually Curated

High-throughput

Computational

Shared Annotations

DYN1 / YKR054C Disease

Disease Help

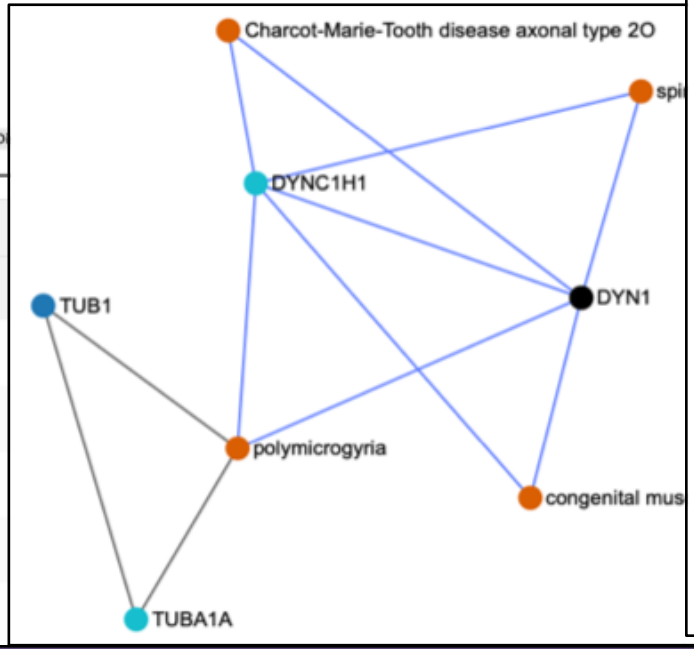
Summary: Yeast DYN1 is homologous to human DYNC1H1, and has been used to study malformations of cortical development (MCD), polymicrogyria, spinal muscular atrophy with lower extremity dominance (SMA-LED), congenital muscular dystrophy (CMD), and Charcot-Marie-Tooth disease (CMT)

Download All Annotations (.txt)

Manually Curated

7 entries for 4 D

Disease Ontology Term
congenital muscular dystrophy
congenital muscular dystrophy
spinal muscular atrophy with lower extremity predominant 1
spinal muscular atrophy with lower extremity predominant 1
polymicrogyria



DISEASE ONTOLOGY

ALLIANCE of GENOME RESOURCES

Templates

Templates are predefined queries, each has a simple form and a descriptio by category.

Filter: Filter: Disease Reset

Actions: Export selected Options: Show descriptions Show Tags

Gene --> DO Terms
Retrieve all Disease Ontology (DO) annotations for a specified gene. Wild card q

DO Term Identifier --> DO Term name
*Retrieve the Disease Ontology (DO) term names and descriptions for a specified (such as DOID:162) or the numerical value preceded by a wild card (such as *00*

DO Term Identifier --> Genes
Retrieve all genes annotated to a particular Disease Ontology (DO) ID with a part

DO Term name --> All genes
Retrieve all genes annotated to a specified Disease Ontology (DO) Term.

DO Term name --> DO Term Identifier
Retrieve the DO term identifier (DOID) and description for a specified DO term na

DO Term name [and children of this term] --> All genes
Retrieve all genes that are annotated to the specified DO term and children of tha

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  - New ‘not in S288C’ systematic nomenclature
  - Updates to Reference Genome panel – *in progress*
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Extra bits

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Reference: Costanzo M, et al. (2016)

Abstract

Related References

Gene Ontology Annotations

Phenotype Annotations

Interaction Annotations

Published Datasets

Downloadable Files

Reference: **Costanzo M, et al. (2016)** A global genetic interaction network maps a wiring diagram of cellular function. *Science* 353(6306)

Abstract

Reference Help

We generated a global genetic interaction network for Saccharomyces cerevisiae, constructing more than 23 million double mutants, identifying about 550,000 negative and about 350,000 positive genetic interactions. This comprehensive network maps genetic interactions for essential gene pairs, highlighting essential genes as densely connected hubs. Genetic interaction profiles enabled assembly of a hierarchical model of cell function, including modules corresponding to protein complexes and pathways, biological processes, and cellular compartments. Negative interactions connected

Published Datasets

1 dataset for 1 reference

Dataset
Genomewide poly(A) si and related mutants

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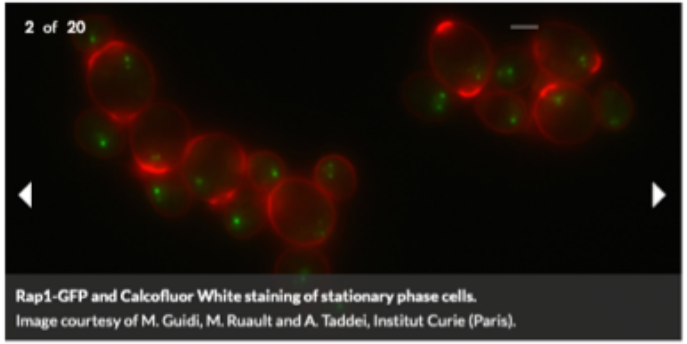

Rap1-GFP and Calcofluor White staining of stationary phase cells.
Image courtesy of M. Guidi, M. Ruault and A. Taddei, Institut Curie (Paris).

Information About Your Recently Published Paper

Your email (required)

Pubmed ID of your paper (required)

Citation

Does this paper contain novel characterizations of the function, role, or localization of a gene product(s)? Yes

If yes, please summarize briefly the novel results.

If this paper focuses on specific genes/proteins, please identify them here (enter a list of gene names/systematic names).

Does this study include large-scale datasets that you would like to see incorporated into SGD? Yes

If yes, please describe briefly the type(s) of data.

Is there anything else that you would like us to know about this paper?

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Meetings

Yeast Genetics Meeting 2022
August 17 to August 21, 2022 -
University of California, Los Angeles

Fungal Pathogen Genomics
May 07 to May 12, 2023 -
Wellcome Genome Campus, Hinxton, Cambridge, UK

New & Note

Sen1p Is the Traffic Cop III - **August 12, 2022**
One way to imagine DN
a lot of competing traffi
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cells is Sen1p. Two recer
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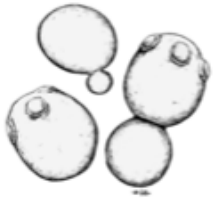
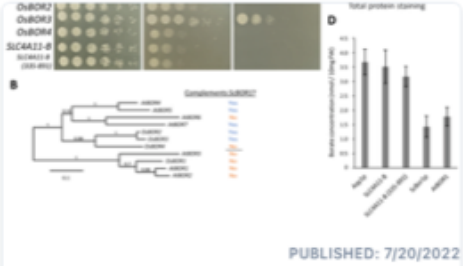


Species: S. cerevisiae

Phenotype Data 19 | Expression Data 3 | Genotype Data 0
Methods 1 | Software 0 | Database Updates 0
Genetic Screens 0 | Integrations 0 | Interaction Data 0
Models of Human Disease 3 | Phylogenetic Data 1
Science and Society 0 | Electrophysiology Data 0 | Biochemistry 3
Structural Biology Data 0

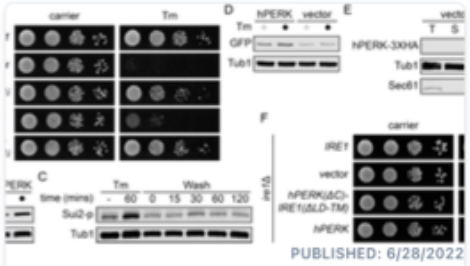


PUBLISHED: 7/20/2022

NEW FINDING NEGATIVE RESULT

Human *SLC4A11* does not complement *BOR1* or support borate transport in *Saccharomyces cerevisiae*

Jean L. Beltran, Richara K. Bain, Marie J. Stiefel, Alexis S. McDonnell, Natalie N. Carr and Bryan H. Thurtle-Schmidt



PUBLISHED: 6/28/2022

NEW FINDING

Human PERK rescues unfolded protein response-deficient yeast cells

Wei Sheng Yap and Guillaume Thibault

microPublication Biology

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3 Associated Genes: Show All

Doss EM, Tragesser-Tiña ME, Huang Y, Smaldino PJ, True JD, Kalinski AL, Rubenstein EM (2022) APC/C Cdh1p) and Slx5p/Slx8p ubiquitin ligases confer — Reference

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