



The *Saccharomyces* Genome Database (SGD; www.yeastgenome.org) is a model organism database with a goal of painting a complete picture of eukaryotic cellular processes by curating a comprehensive and diverse collection of data types for the budding yeast *Saccharomyces cerevisiae*. In addition to other data, we also have been capturing single mutant phenotypes as well as importing genetic and physical protein-protein interactions from BioGRID (thebiogrid.org) to help shed light on the role proteins play in cellular processes. While we have been collecting mutant types since we started annotating mutant phenotypes, we more recently decided to capture mutant alleles broadly and systematically. Users can now search for and find alleles associated with their genes of interest. In addition, pages dedicated to single alleles are now available and include information on allele type, molecular details of the mutation, alias names and associated references, along with all phenotype and interaction annotations where specific alleles were used. Alleles that share phenotype and/or genetic interaction annotations are graphical represented in the 'Shared Alleles' section. Users will be able explore more fully previously unlinked data types using our new allele curation model to gain additional insight into cellular processes and pathways. This work is supported by a grant from the NHGRI (U41 HG001315).

Alleles to References

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

Abstract

We generated a global genetic interaction network for *Saccharomyces cerevisiae*, constructing more than 23 million 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 profiles enabled assembly of a hierarchical model of cell function, including modules corresponding to protein complex pathways, biological processes, and cellular compartments. Negative interactions connected functionally related core bioprocesses, and identified pleiotropic genes, whereas positive interactions often mapped general regulatory core 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.

PMID: 27708008 DOI full text PMC full text PubMed

Download Citation (.nbib)

Reference Type: Journal Article | Research Support, N.I.H., Extramural

Authors: Costanzo M, VanderSluis B, Koch EN, Baryshnikova A, Pons C, Tan G, Wang W, Usaj M, Hancock SD, ...

Primary Lit For: BAP2 | CFT2 | CSF1 | DLT1 | GAP1 | IPA1 | MAY24 | MTC2 | MTC4 | MTC6 | PBR1 | ...

Additional Lit For: aac1-Δ | aac3-Δ | aad10-Δ | aad14-Δ | aad15-Δ | aad16-Δ | aad3-Δ | aad4-Δ | aad6-Δ | aah1-Δ | aap1-Δ | aar2-5001 | aat1-Δ | aat2-Δ | abd1-5 | abd1-8 | abf1-102 | abf1-102-sup1 | abf1-Δ | abf2-Δ | abm1-Δ | abp1-Δ | abp140-Δ | abz1-Δ | abz2-Δ | acx2-Δ | acb1-Δ | acc1-5007-sup1 | acc1-5009-sup1 | ace2-Δ | acf2-Δ | acf4-Δ | ach1-Δ | ack1-Δ | acf4-sup1 | acf4-Δ | acm1-Δ | acs1-Δ | acs2-5002 | acs2-5003 | act1-101 | act1-105 | act1-108 | act1-111 | act1-112 | act1-

Discover Alleles

YeastMine Query

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

Home Templates Lists QueryBuilder Tools Regions Data Sources API MyYeastMine Help Log In

Search: [e.g. act1] GO

Gene: LOOKUP: act1 for Organism: [S. cerevisiae]

Options: [Constant to be: IN] [Search Gene list: ALL_Verified_Uncharacterized_Dubious_OTFs]

Show Results

Search

278,884 results

Sort By: Relevance

Categories: References (110,171), Downloads (75,528), Molecular Functions (12,476), Molecular Biology (11,756)

Allele-centric Page

Allele: act1-111

Allele Name: act1-111

SGD ID: SGD:S000277367

Aliases: act1-D222A,E224A,E226A

Affected Gene: ACT1

Allele Type: missense variant

Description: D222A, E224A, E226A; mutant can be rescued by small molecule trimethylamine N-oxide (TMAO)

Phenotype Annotations (2 entries for 2 phenotypes)

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
ACT1	mitochondrial morphology: abnormal	classical genetics	conditional Allele: act1-111	Other		Temperature: elevated temperature, 37 °C	Reggiori F, et al. (2005) PMID:1622387
ACT1	protein/peptide modification: absent Reporter: Ape1p (API)	classical genetics	conditional Allele: act1-111	Other		Temperature: elevated temperature, 37 °C Details: pro-aminopeptidase I (API) is not processed to mature API, indicative of a CVT pathway defect	Reggiori F, et al. (2005) PMID:1622387

Showing 1 to 2 of 2 entries 10 records per page

Download (.txt)

Genetic Interaction Annotations (360 entries for 344 genes)

Interactor	Interactor Allele	Assay	Annotation	Action	Phenotype	SGA score	P-value	Reference
ACT1	ABM1	abm1-Δ, act1-111	Negative Genetic	high-throughput	Hit-Bait	-0.1994	0.0002859	Costanzo M, et al. (2016) PMID:27708008
ACT1	ACK1	ack1-Δ, act1-111	Negative Genetic	high-throughput	Hit-Bait	-0.1474	0.04338	Costanzo M, et al. (2016) PMID:27708008
TFC3	ACT1	tfc3-g349e, act1-111	Negative Genetic	high-throughput	Bait-Hit	-0.1485	0.03476	Costanzo M, et al. (2016) PMID:27708008
STU1	ACT1	stu1-5, act1-111	Negative Genetic	high-throughput	Bait-Hit	-0.2487	0.000004577	Costanzo M, et al. (2016) PMID:27708008
PKC1	ACT1	pkc1-4, act1-111	Negative Genetic	high-throughput	Bait-Hit	-0.174	0.02246	Costanzo M, et al. (2016) PMID:27708008
PER2	ACT1	rer2-500e	Negative	high-throughput	Bait-	-0.1784	0.002616	Costanzo M, et al. (2016)

Alleles to Locus Data

Locus Page

ACT1 / YFL039C Overview

Standard Name: ACT1

Systematic Name: YFL039C

SGD ID: SGD:S000001855

Aliases: ABY1_END7

Feature Type: ORF, Verified

Alleles (9)

act1-1 | act1-101 | act1-102 | act1-103 | act1-104 | act1-105 | act1-106 | ...

Gene Ontology (9)

Phenotype Page

ACT1 / YFL039C Phenotype

Summary: Essential gene; conditional mutants show pleiotropic defects including abnormal actin cytoskeleton, chromosome instability, altered subcellular morphology, increased sensitivity to heat, multiple chemicals and osmotic stress; overexpression leads to growth arrest

Annotations (94 entries for 38 phenotypes)

Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
actin cytoskeleton morphology: abnormal	classical genetics	conditional Allele: act1-111	Other		Temperature: elevated temperature, 37 °C Details: actin cables disappear and cortical actin patches become delocalized	Chen X and Rubenstein PA (1995) PMID:8740777
actin cytoskeleton morphology: abnormal	classical genetics	reduction of function Allele: act1-K138M	Other		Details: K138M cables are fragmented and lack any dominant orientation, resulting in a meshwork	Krich KA and Rubenstein PA (2012) PMID:22639494

Interactions Page

ACT1 / YFL039C Interactions

Source: All physical and genetic interaction annotations listed in SGD are curated by BioGRID.

Genetic Interactions (903 entries for 2247 genes)

Interactor	Allele	Assay	Annotation	Action	Phenotype	SGA score	P-value	Reference
AAC3	aac3-Δ, act1-111	Negative Genetic	high-throughput	HR		-0.1484	0.01119	Costanzo M, et al. (2016) PMID:27708008
AAD10	aad10-Δ, act1-124	Negative Genetic	high-throughput	HR		-0.1214	0.01925	Costanzo M, et al. (2016) PMID:27708008
AAD14	aad14-Δ, act1-3	Negative Genetic	high-throughput	HR		-0.1312	0.03328	Costanzo M, et al. (2016) PMID:27708008

Retrieving Allele Data

64 results for act1-111

Page 1 of 3 Results Sort By: Relevance

References

Costanzo M, et al. (2016)

act1-129

synonyms: act1-R177A,D179A

allele loci: ACT1

name: act1-129

act1-111

synonyms: act1-D222A,E224A,E226A

allele loci: ACT1

name: act1-111

act1-105

synonyms: act1-E311A,R312A

allele loci: ACT1

name: act1-105

act1-136

name: act1-136

allele loci: ACT1

act1-125

name: act1-125

allele loci: ACT1

Phenotypes

resistance to chemicals: decreased 8

invasive 6

protein/peptide modification: absent 5

heat sensitivity: increased 5

vegetative growth: decreased rate 4

Associated Phenotypes

Phenotype: protein/peptide modification: absent

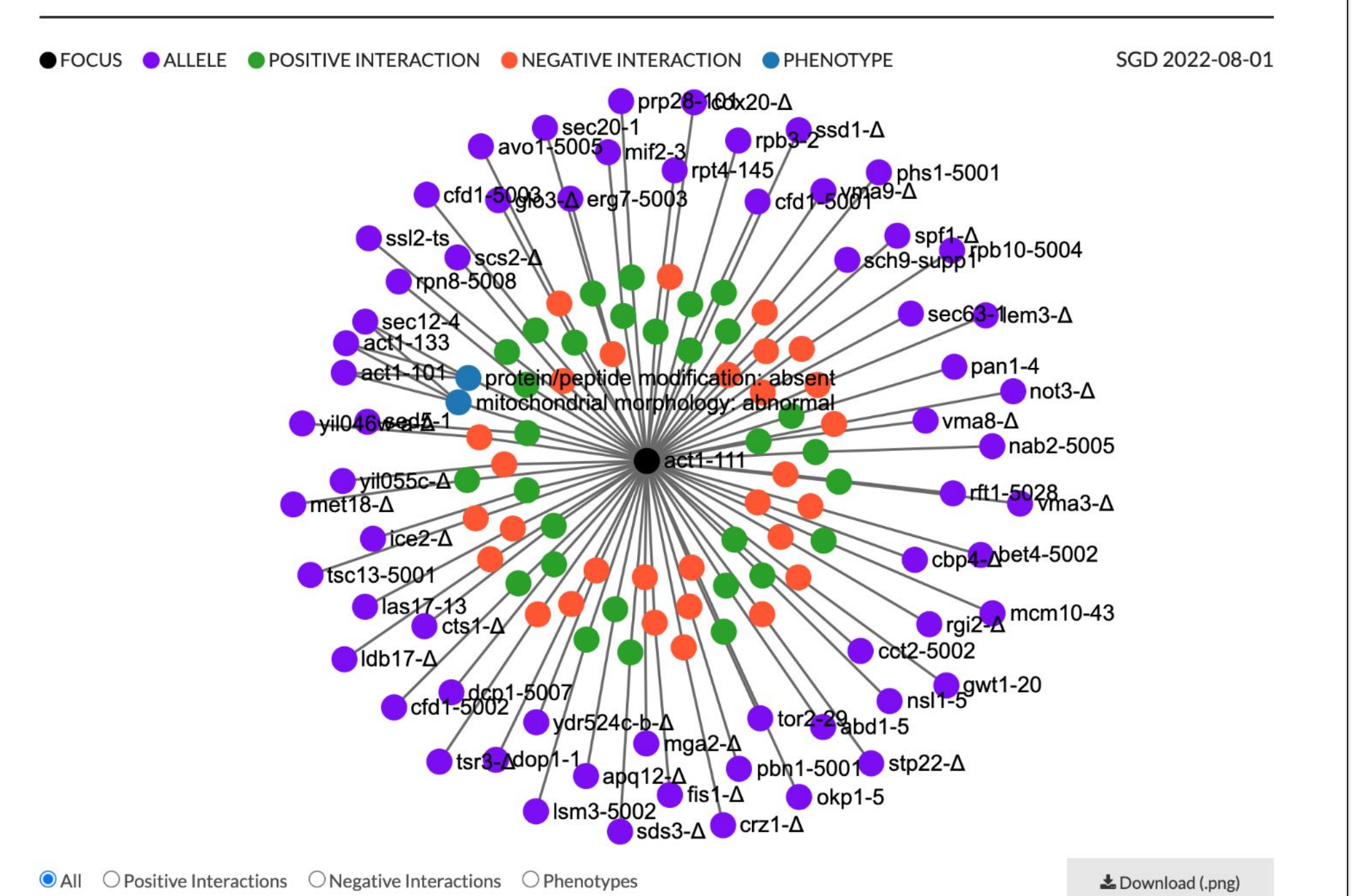
Observable: protein/peptide modification

Qualifier: absent

Annotations (245 entries for 194 genes)

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
ACT1	protein/peptide modification: absent Reporter: Ape1p (API)	classical genetics	conditional Allele: act1-111	Other		Temperature: elevated temperature, 37 °C Details: pro-aminopeptidase I (API) is not processed to mature API, indicative of a CVT pathway defect	Reggiori F, et al. (2005) PMID:1622387
ACT1	protein/peptide modification: absent Reporter: Ape1p (API)	classical genetics	conditional Allele: act1-101	Other		Temperature: elevated temperature, 37 °C Details: pro-aminopeptidase I (API) is not processed to mature API, indicative of a CVT pathway defect	Reggiori F, et al. (2005) PMID:1622387

Shared Alleles



References

1. Hassell DS, et al. (2021) Chemical rescue of mutant proteins in living *Saccharomyces cerevisiae* cells by naturally occurring small molecules. *G3 (Bethesda)* 11(9) PMID:34844143

SGD Paper DOI full text PMC full text PubMed

Resources

Mutant Strains
Addgene Plasmids | DNASU Plasmids | PlasmID | Thermo Scientific | YGRC

Phenotype Resources
dHITS | FIDB | HIPHOP Chemogenomics | HIP HOP Profiles | PhenoM | PROPHECY | SCMD | ScreenTroll | TheCellVision

Ontology
Yeast Phenotype Ontology

Interactions Resources
BioGRID | CYC2008 | DIP | GeneMANIA | IMP | InterlogFinder | ModelArchive | TheCellMap | YeastRC Mass Spec | YeastRC Two-Hybrid