



Data Integration Through Allele Curation at SGD



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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 graphically 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: a wiring diagram of cellular function. *Science* 353(6306)

Abstract

Related References

Gene Ontology Annotations

Phenotype Annotations

Interaction Annotations

Published Datasets

Downloadable Files

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 interaction 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 genes and core bioprocesses, and identified pleiotropic genes, whereas positive interactions often mapped general regulatory components 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: 2770808 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, Hanchal SD, ... [Show all](#)

Primary Lit For: BAP2 | CFT2 | CSF1 | DLT1 | GAP1 | IP1 | MAY1 | MEC2 | MTC4 | MTC6 | PBR1 | ... [Show all](#)

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 | abd1-102 | abf1-102-sup1 | abf1-102-sup2 | abf2-Δ | abm1-Δ | abp1-Δ | abp140-Δ | abz1-Δ | abz2-Δ | act1-Δ | act1-Δ | acc1-5007-sup1 | acc1-5009-sup1 | ace2-Δ | acf2-Δ | acf4-Δ | ach1-Δ | ack1-Δ | ack4-Δ | acl4-Δ | acm1-Δ | acs1-Δ | acs2-5002 | lacs2-5003 | act1-101 | act1-105 | act1-108 | act1-111 | act1-112 | act1-1

Discover Alleles

YeastMine Query

The screenshot shows the YeastMine Query interface. At the top, there's a search bar with 'act1' entered. Below it, a table displays search results with columns for Gene, Phenotype, Experiment Type, Mutant Information, Strain Background, Chemical, and Details. One row is highlighted for ACT1, mitochondrial morphology: abnormal, classical genetics, conditional allele: act1-111, Other strain background, and temperature: elevated temperature, 37°C. Another row for ACT1, protein/modification: absent, classical genetics, conditional allele: act1-111, Other strain background, and temperature: elevated temperature, 37°C is also shown. A red arrow points from the 'Alleles' section of the 'Alleles to References' page to this table.

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 1

Description: D222A, E224A, E226A; mutant can be rescued by small molecule trimethylamine N-oxide (TMAO)¹

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:16221887
ACT1	protein/modification: absent	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:16221887

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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	high-throughput	Hit-Bait		-0.1994	0.0002859	Costanzo M, et al. (2016) PMID:2770808
ACT1	ACK1	ack1-Δ, act1-111	Negative	high-throughput	Hit-Bait		-0.1474	0.04338	Costanzo M, et al. (2016) PMID:2770808
TFC3	ACT1	tfc3-g34y, act1-111	Negative	high-throughput	Bait-Hit		-0.1485	0.03476	Costanzo M, et al. (2016) PMID:2770808
STU1	ACT1	stu1-5, act1-111	Negative	high-throughput	Bait-Hit		-0.2487	0.00004577	Costanzo M, et al. (2016) PMID:2770808
PKC1	ACT1	pkc1-Δ, act1-111	Negative	high-throughput	Bait-Hit		-0.174	0.02246	Costanzo M, et al. (2016) PMID:2770808
RER2	ACT1	rer2-5009	Negative	high-	Bait-		-0.1784	0.003515	Costanzo M, et al. (2016) PMID:2770808

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Alleles to Locus Data

Locus Page

The screenshot shows the ACT1 YFL039C Overview page. It includes sections for Standard Name, Systematic Name, SGD ID, Aliases, Feature Type, Locus Overview, Sequence, Protein, and Alleles. The Alleles section is circled in red. Below it, the Gene Ontology and Phenotype pages are also shown.

Retrieving Allele Data

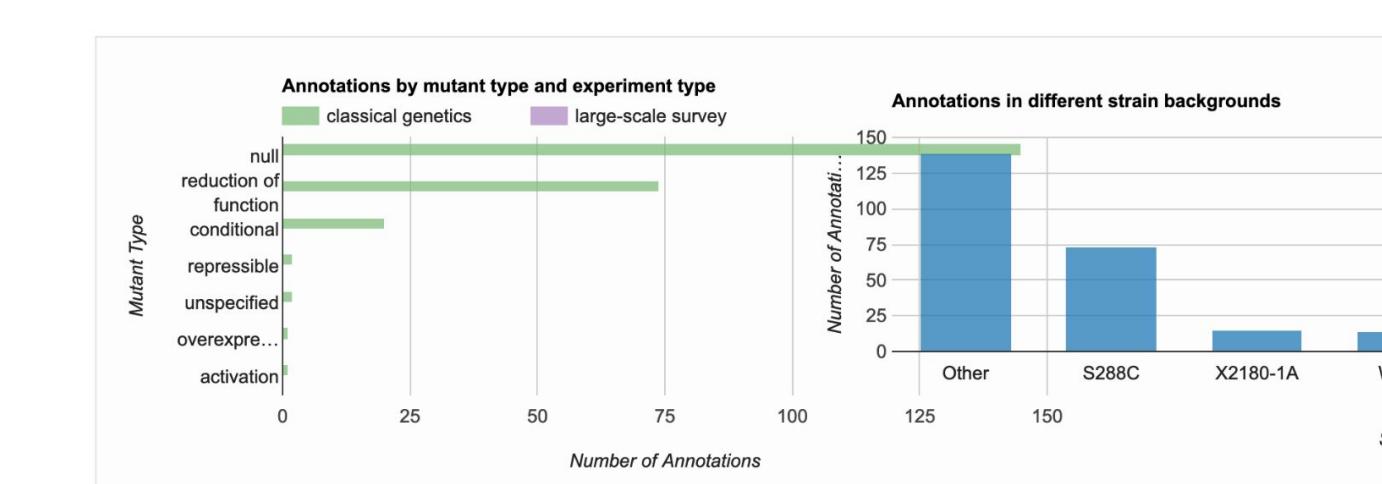
The screenshot shows a search results page for 'act1'. It lists 64 results for 'act1-' and 'act1-111'. The 'act1-111' result is highlighted with a red circle. Below it, the 'Allele Types' and 'Allele Loci' sections are also circled in red. The page includes a table with columns for Allele, Allele Type, and Allele Loci.

Associated Phenotypes

Phenotype: protein/peptide modification: absent

Observable: protein/peptide modification

Qualifier: absent



Annotations

245 entries for 104 genes

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
ACT1	protein/peptide modification: absent	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:16221887
ACT1	protein/peptide modification: absent	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:16221887

Shared Alleles

FOCUS ALLELE POSITIVE INTERACTION NEGATIVE INTERACTION PHENOTYPE

