

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

SGD

RRID:SCR_004694

Type: Tool

Proper Citation

SGD (RRID:SCR_004694)

Resource Information

URL: <http://www.yeastgenome.org/>

Proper Citation: SGD (RRID:SCR_004694)

Description: A curated database that provides comprehensive integrated biological information for *Saccharomyces cerevisiae* along with search and analysis tools to explore these data. SGD allows researchers to discover functional relationships between sequence and gene products in fungi and higher organisms. The SGD also maintains the *S. cerevisiae* Gene Name Registry, a complete list of all gene names used in *S. cerevisiae* which includes a set of general guidelines to gene naming. Protein Page provides basic protein information calculated from the predicted sequence and contains links to a variety of secondary structure and tertiary structure resources. Yeast Biochemical Pathways allows users to view and search for biochemical reactions and pathways that occur in *S. cerevisiae* as well as map expression data onto the biochemical pathways. Literature citations are provided where available.

Abbreviations: SGD, SGD LOCUS, SGD REF

Synonyms: SGD LOCUS, *Saccharomyces* Genome Database, SGD REF

Resource Type: data or information resource, database

Defining Citation: [PMID:24265222](#), [PMID:12519985](#), [PMID:9399804](#)

Keywords: database, yeast, pathway, analysis, gene, nomenclature, predicted sequence, fungi, functional relationship, protein structure, bio.tools, FASEB list

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NHGRI 2U41HG002273-13;
NHGRI 5R01HG004834-04

Availability: Free for academic use, The community can contribute to this resource, Non-commercial

Resource Name: SGD

Resource ID: SCR_004694

Alternate IDs: nif-0000-03456, biotools:sgd, r3d100010419, OMICS_01661

Alternate URLs: <https://bio.tools/sgd>, <https://doi.org/10.17616/R3N313>

Old URLs: <http://genome-www.stanford.edu/Saccharomyces/>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T133125+0000

Ratings and Alerts

No rating or validation information has been found for SGD.

No alerts have been found for SGD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1950 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. PLoS biology, 24(6), e3003855.

Schrott S, et al. (2026) Mrx6 binds the Lon protease Pim1 N-terminal domain to confer selective substrate specificity and regulate mtDNA copy number. Nucleic acids research, 54(2).

Schöppner P, et al. (2026) Structural evolution of a fungal cell wall protein family for β -glucan-binding and cell separation. mBio, 17(6), e0353525.

Scharff-Poulsen P, et al. (2026) Structural bases of signal generation and transduction by the SPS amino acid sensor of *Saccharomyces cerevisiae*. G3 (Bethesda, Md.), 16(3).

Qu X, et al. (2026) Investigation of epilepsy-related genes in a *Drosophila* model. Neural regeneration research, 21(1), 195.

Martínez AA, et al. (2026) Weak pervasive incompatibilities and compensatory adaptation drive hybrid genome evolution in yeast. *bioRxiv : the preprint server for biology*.

Becerra-Rodríguez C, et al. (2026) Domestication drives repeated evolution of sexual-aseexual life cycle trade-offs in yeast. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2526682123.

Nielsen J, et al. (2025) The Power of Yeast. *Yeast (Chichester, England)*, 42(12), 303.

Jiang B, et al. (2025) Protocol for adaptive laboratory evolution of *S. cerevisiae* by PEG/LiAc transformation and sequencing. *STAR protocols*, 6(2), 103857.

Kanai M, et al. (2025) Efficient genes identification via quantitative trait loci analysis by crossbreeding of sake and laboratory yeast. *Applied microbiology and biotechnology*, 109(1), 84.

Hancock LP, et al. (2025) Competitive binding of actin and SH3 domains at proline-rich regions of Las17/WASP regulates actin polymerisation. *Communications biology*, 8(1), 759.

Theulot B, et al. (2025) Telomere-to-telomere DNA replication timing profiling using single-molecule sequencing with Nanotiming. *Nature communications*, 16(1), 242.

Tangpranomkorn S, et al. (2025) A land plant-specific VPS13 mediates polarized vesicle trafficking in germinating pollen. *The New phytologist*, 245(3), 1072.

Liu Z, et al. (2025) F-box protein Fbx23 acts as a transcriptional coactivator to recognize and activate transcription factor Ace1. *PLoS genetics*, 21(1), e1011539.

Tripathy MK, et al. (2025) Modified pea apyrase has altered nuclear functions and enhances the growth of yeast and Arabidopsis. *Frontiers in plant science*, 16, 1584871.

Mohajan S, et al. (2025) Nuclear basket proteins Nup2 and Mlp1 drive heat shock-induced 3D genome restructuring downstream of transcriptional activation. *The Journal of biological chemistry*, 301(9), 110568.

Fabbre A, et al. (2025) Ist2 promotes lipid transfer by Osh6 via its membrane tethering and lipid scramblase activities. *Science advances*, 11(46), eadz2217.

Brewis HT, et al. (2025) Characterizing the regulatory effects of H2A.Z and SWR1-C on gene expression during hydroxyurea exposure in *Saccharomyces cerevisiae*. *PLoS genetics*, 21(1), e1011566.

Pasionek I, et al. (2025) The extra-terminal domain drives the role of BET proteins in transcription. *bioRxiv : the preprint server for biology*.

Clark-Flores D, et al. (2025) Vacuolar Proteases of *Candida auris* from Clades III and IV and Their Relationship with Autophagy. *Journal of fungi (Basel, Switzerland)*, 11(5).