Resource Summary Report

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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: database, data or information resource

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 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: 20260803T040401+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 1920 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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

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.

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

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

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.

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

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.

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.

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

Yorimitsu T, et al. (2025) Potential ER tubular lumen sensing by intrinsically disordered regions. Journal of cell science, 138(5).

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.

Nadal-Ribelles M, et al. (2025) Transcriptional heterogeneity shapes stress-adaptive responses in yeast. Nature communications, 16(1), 2631.

Lumbroso G, et al. (2025) The B-type cyclin Clb4 prevents meiosis I sister centromere separation in budding yeast. G3 (Bethesda, Md.), 15(9).

Calegari-Alves YP, et al. (2025) CRYPTOMICSDB: Revealing the Molecular Landscape of Cryptococcosis. Journal of fungi (Basel, Switzerland), 11(6).

Nickens DG, et al. (2025) Dimerization of Cdc13 is essential for dynamic DNA exchange on telomeric DNA. The Journal of biological chemistry, 301(8), 110496.

Chen RR, et al. (2025) Identification of key transcription factors, including DAL80 and CRZ1, involved in heat and ethanol tolerance in Saccharomyces cerevisiae. Biotechnology for biofuels and bioproducts, 18(1), 50.

Pareek A, et al. (2025) Core histones govern echinocandin susceptibility in Candida glabrata. Microbiology spectrum, 13(6), e0239924.

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).