Resource Summary Report

Generated by dkNET on Aug 19, 2026

Saccharomyces Genome Deletion Project

RRID:SCR_014961
Type: Tool

Proper Citation

Saccharomyces Genome Deletion Project (RRID:SCR_014961)

Resource Information

URL: http://www-sequence.stanford.edu/group/yeast_deletion_project/

Proper Citation: Saccharomyces Genome Deletion Project (RRID:SCR_014961)

Description: Database and project to reveal open reading frames (ORFs) in the yeast genome in order to discover their functions. A PCR-based gene deletion strategy is used to assign functions through phenotypic analysis of mutants.

Resource Type: project portal, data or information resource, portal, database

Keywords: yeast, open reading frames, ORF, genome, deletion, Saccharomyces cerevisiae

Availability: Free

Resource Name: Saccharomyces Genome Deletion Project

Resource ID: SCR_014961

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260819T044414+0000

Ratings and Alerts

No rating or validation information has been found for Saccharomyces Genome Deletion Project.

No alerts have been found for Saccharomyces Genome Deletion Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Choi YJ, et al. (2022) Nst1, Densely Associated to P-Body in the Post-Exponential Phases of Saccharomyces cerevisiae, Shows an Intrinsic Potential of Producing Liquid-Like Condensates of P-Body Components in Cells. International journal of molecular sciences, 23(5).

Lam FH, et al. (2021) Engineered yeast tolerance enables efficient production from toxified lignocellulosic feedstocks. Science advances, 7(26).

Hu SH, et al. (2021) Significance of AtMTM1 and AtMTM2 for Mitochondrial MnSOD Activation in Arabidopsis. Frontiers in plant science, 12, 690064.

Després PC, et al. (2020) Perturbing proteomes at single residue resolution using base editing. Nature communications, 11(1), 1871.

Fernández-Del-Río L, et al. (2020) Genes and lipids that impact uptake and assimilation of exogenous coenzyme Q in Saccharomyces cerevisiae. Free radical biology & medicine, 154, 105.

Soncini SR, et al. (2020) Spontaneous mutations that confer resistance to 2-deoxyglucose act through Hxk2 and Snf1 pathways to regulate gene expression and HXT endocytosis. PLoS genetics, 16(7), e1008484.

Peláez-Soto A, et al. (2020) Proteomic Analysis of Saccharomyces cerevisiae Response to Oxidative Stress Mediated by Cocoa Polyphenols Extract. Molecules (Basel, Switzerland), 25(3).

Vera Rodriguez A, et al. (2019) Engineered SUMO/protease system identifies Pdr6 as a bidirectional nuclear transport receptor. The Journal of cell biology, 218(6), 2006.

Zhao Y, et al. (2018) Comparative Analysis of Mutant Huntingtin Binding Partners in Yeast Species. Scientific reports, 8(1), 9554.

Perez-Samper G, et al. (2018) The Crabtree Effect Shapes the Saccharomyces cerevisiae Lag Phase during the Switch between Different Carbon Sources. mBio, 9(5).

Krol K, et al. (2017) Ribosomal DNA status inferred from DNA cloud assays and mass spectrometry identification of agarose-squeezed proteins interacting with chromatin (ASPIC-MS). Oncotarget, 8(15), 24988.

Lepore D, et al. (2016) Cell cycle-dependent phosphorylation of Sec4p controls membrane deposition during cytokinesis. The Journal of cell biology, 214(6), 691.

Chang DT, et al. (2013) YGA: identifying distinct biological features between yeast gene sets. Gene, 518(1), 26.

Teng X, et al. (2013) Genome-wide consequences of deleting any single gene. Molecular cell, 52(4), 485.

Devireddy LR, et al. (2010) A mammalian siderophore synthesized by an enzyme with a bacterial homolog involved in enterobactin production. Cell, 141(6), 1006.

Ruotolo R, et al. (2010) Chemogenomic profiling of the cellular effects associated with histone H3 acetylation impairment by a quinoline-derived compound. Genomics, 96(5), 272.

Kaniak A, et al. (2009) Msh1p counteracts oxidative lesion-induced instability of mtDNA and stimulates mitochondrial recombination in Saccharomyces cerevisiae. DNA repair, 8(3), 318.

Chang M, et al. (2006) Genomic approaches for identifying DNA damage response pathways in S. cerevisiae. Methods in enzymology, 409, 213.

Huang ME, et al. (2005) A biological network in Saccharomyces cerevisiae prevents the deleterious effects of endogenous oxidative DNA damage. Molecular cell, 17(5), 709.