Resource Summary Report

Generated by RRID on May 17, 2025

CYGD - Comprehensive Yeast Genome Database

RRID:SCR_002289
Type: Tool

Proper Citation

CYGD - Comprehensive Yeast Genome Database (RRID:SCR_002289)

Resource Information

URL: http://mips.gsf.de/genre/proj/yeast/index.jsp

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Description: The MIPS Comprehensive Yeast Genome Database (CYGD) aims to present information on the molecular structure and functional network of the entirely sequenced, well-studied model eukaryote, the budding yeast Saccharomyces cerevisiae. In addition, the data of various projects on related yeasts are used for comparative analysis.

Abbreviations: CYGD

Synonyms: MIPS Saccharomyces cerevisiae genome database, MIPS Comprehensive Yeast Genome Database, Comprehensive Yeast Genome Database

Resource Type: service resource, production service resource, data analysis service, database, analysis service resource, data or information resource

Defining Citation: PMID:15608217

Keywords: saccharomyces cerevisiae, yeast, yeast genome, genome

Funding: Federal Ministry of Education Science Research and Technology ;
European Union ;
Government of the Brussels Region - Belgium ;
DFG

Resource Name: CYGD - Comprehensive Yeast Genome Database

Resource ID: SCR_002289

Alternate IDs: nif-0000-02713

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250517T055526+0000

Ratings and Alerts

No rating or validation information has been found for CYGD - Comprehensive Yeast Genome Database.

No alerts have been found for CYGD - Comprehensive Yeast Genome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Ogishima S, et al. (2015) Modularity in the evolution of yeast protein interaction network. Bioinformation, 11(3), 127.

Jin L, et al. (2014) Pathway-based analysis tools for complex diseases: a review. Genomics, proteomics & bioinformatics, 12(5), 210.

Cimini D, et al. (2009) Global transcriptional response of Saccharomyces cerevisiae to the deletion of SDH3. BMC systems biology, 3, 17.

Cui G, et al. (2008) An algorithm for finding functional modules and protein complexes in protein-protein interaction networks. Journal of biomedicine & biotechnology, 2008, 860270.

Berthon J, et al. (2008) Genomic context analysis in Archaea suggests previously unrecognized links between DNA replication and translation. Genome biology, 9(4), R71.

Dror O, et al. (2008) Structural similarity of genetically interacting proteins. BMC systems biology, 2, 69.

Ingalls BP, et al. (2007) Systems level modeling of the cell cycle using budding yeast. Cancer informatics, 3, 357.

Fischer G, et al. (2006) Highly variable rates of genome rearrangements between hemiascomycetous yeast lineages. PLoS genetics, 2(3), e32.

Kimura S, et al. (2006) DNA microarray analyses reveal a post-irradiation differential time-dependent gene expression profile in yeast cells exposed to X-rays and gamma-rays. Biochemical and biophysical research communications, 346(1), 51.

Johnson O, et al. (2006) A traveling salesman approach for predicting protein functions. Source code for biology and medicine, 1, 3.

Eide DJ, et al. (2005) Characterization of the yeast ionome: a genome-wide analysis of nutrient mineral and trace element homeostasis in Saccharomyces cerevisiae. Genome biology, 6(9), R77.

Budd ME, et al. (2005) A network of multi-tasking proteins at the DNA replication fork preserves genome stability. PLoS genetics, 1(6), e61.

Boyer J, et al. (2004) Large-scale exploration of growth inhibition caused by overexpression of genomic fragments in Saccharomyces cerevisiae. Genome biology, 5(9), R72.

Banerjee D, et al. (2004) Genome-wide expression profile of steroid response in Saccharomyces cerevisiae. Biochemical and biophysical research communications, 317(2), 406.