

Resource Summary Report

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

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 [nidm-terms](#) .

Ogishima S, et al. (2015) Modularity in the evolution of yeast protein interaction network. *Bioinformatics*, 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.