# Resource Summary Report

Generated by kravitz2 on Aug 8, 2026

## YDPM - Yeast Deletion Project

RRID:SCR_007977
Type: Tool

### Proper Citation

YDPM - Yeast Deletion Project (RRID:SCR_007977)

### Resource Information

**URL:** http://www-deletion.stanford.edu/YDPM/YDPM_index.html

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**Description:** This database contains different yeast strains searchable by ORF and gene name, and serves to support the Yeast Deletion and the Mitochondrial Proteomics Project. The database is hyperlinked with other public databases. The project aims to increase the understanding of mitochondrial function and biogenesis in the context of the cell. In the Deletion Project, strains from the deletion collection were monitored under 9 different media conditions selected for the study of mitochondrial function. 5791 heterozygous diploid and 4706 homozygous diploid deletion strains were monitored in parallel using molecular barcodes on fermentable (YPD, YPDGE) and non-fermentable substrates (YPG, YPE, YPL). The YDPM database contains both the raw data and growth rates calculated for each strain in each media condition. Strains can be searched by ORF or Gene name to access growth measurements and data plots for each strain. Category: Genomics Databases (non-vertebrate) Subcategory: Fungal genome databases Category: Organelle databases Subcategory: Mitochondrial genes and proteins

**Synonyms:** YDMP

**Resource Type:** database, data or information resource

**Resource Name:** YDPM - Yeast Deletion Project

**Resource ID:** SCR_007977

**Alternate IDs:** nif-0000-03648

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260808T190419+0000

### Ratings and Alerts

No rating or validation information has been found for YDPM - Yeast Deletion Project.

No alerts have been found for YDPM - Yeast Deletion Project.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 13 mentions in open access literature.

**Listed below are recent publications.** The full list is available at kravitz2 .


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

Nadal-Ribelles M, et al. (2025) A single-cell resolved genotype-phenotype map using genome-wide genetic and environmental perturbations. Nature communications, 16(1), 2645.

Xie J, et al. (2022) Large-scale genomic and transcriptomic profiles of rice hybrids reveal a core mechanism underlying heterosis. Genome biology, 23(1), 264.

Mannakee BK, et al. (2016) Selection on Network Dynamics Drives Differential Rates of Protein Domain Evolution. PLoS genetics, 12(7), e1006132.

He X, et al. (2009) On the growth of scientific knowledge: yeast biology as a case study. PLoS computational biology, 5(3), e1000320.

Wang Z, et al. (2009) Abundant indispensable redundancies in cellular metabolic networks. Genome biology and evolution, 1, 23.

Wang Z, et al. (2009) Why is the correlation between gene importance and gene evolutionary rate so weak? PLoS genetics, 5(1), e1000329.

Ihmels J, et al. (2007) Backup without redundancy: genetic interactions reveal the cost of duplicate gene loss. Molecular systems biology, 3, 86.

Perocchi F, et al. (2006) Assessing systems properties of yeast mitochondria through an interaction map of the organelle. PLoS genetics, 2(10), e170.

Bilu Y, et al. (2005) The design of transcription-factor binding sites is affected by combinatorial regulation. Genome biology, 6(12), R103.

He X, et al. (2005) Gene complexity and gene duplicability. Current biology : CB, 15(11), 1016.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Ishikawa D, et al. (2004) Two novel proteins in the mitochondrial outer membrane mediate beta-barrel protein assembly. The Journal of cell biology, 166(5), 621.