Resource Summary Report

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YMDB - Yeast Metabolome Database

RRID:SCR_005890
Type: Tool

Proper Citation

YMDB - Yeast Metabolome Database (RRID:SCR_005890)

Resource Information

URL: http://www.ymdb.ca/

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Description: A manually curated database of small molecule metabolites found in or produced by Saccharomyces cerevisiae (also known as Baker's yeast and Brewer's yeast). This database covers metabolites described in textbooks, scientific journals, metabolic reconstructions and other electronic databases. YMDB contains metabolites arising from normal S. cerevisiae metabolism under defined laboratory conditions as well as metabolites generated by S. cerevisiae when used in baking and in the production of wines, beers and spirits. YMDB currently contains 2027 small molecules with 857 associated enzymes and 138 associated transporters. Each small molecule has 48 data fields describing the metabolite, its chemical properties and links to spectral and chemical databases. Each enzyme/transporter is linked to its associated metabolites and has 30 data fields describing both the gene and corresponding protein. Users may search through the YMDB using a variety of database-specific tools. The simple text query supports general text queries of the textual component of the database. By selecting either metabolites or proteins in the search for field it is possible to restrict the search and the returned results to only those data associated with metabolites or with proteins. Clicking on the Browse button generates a tabular synopsis of YMDB's content. This browser view allows users to casually scroll through the database or re-sort its contents. Clicking on a given MetaboCard button brings up the full data content for the corresponding metabolite. A complete explanation of all the YMDB fields and sources is available. Under the Search link users will find a number of search options listed in a pull-down menu. The Chem Query option allows users to draw (using MarvinSketch applet or a ChemSketch applet) or to type (SMILES string) a chemical compound and to search the YMDB for chemicals similar or identical to the query compound. The Advanced Search option supports a more sophisticated text search of the text portion of YMDB. The Sequence Search button allows users to conduct BLASTP (protein) sequence searches of all sequences contained in YMDB. Both single and multiple sequence (i.e. whole proteome) BLAST queries are supported. YMDB also supports a Data Extractor option that allows specific data fields or combinations of data fields to be searched and/or extracted. Spectral searches of YMDB's

reference compound NMR and MS spectral data are also supported through its MS, MS/MS, GC/MS and NMR Spectra Search links. Users may download YMDB's complete textual data, chemical structures and sequence data by clicking on the Download button.

Abbreviations: YMDB

Synonyms: Yeast Metabolome Database (YMDB), Yeast Metabolome Database

Resource Type: database, data or information resource

Defining Citation: PMID:22064855

Keywords: small molecule, metabolite, enzyme, transporter, gene, protein, chemical property, reaction, pathway, class, protein, proteome, blastp, nmr, ms spectra, chemical structure

Funding: Canadian Institutes of Health Research

Availability: Freely available - Explicit permission / acknowledgment of the source material and original publication is required for commercial purposes. We ask users who download significant portions of the database cite the YMDB paper in any resulting publications.

Resource Name: YMDB - Yeast Metabolome Database

Resource ID: SCR_005890

Alternate IDs: nlx_151612, r3d100012733

Alternate URLs: https://doi.org/10.17616/R3Z51K

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260725T191141+0000

Ratings and Alerts

No rating or validation information has been found for YMDB - Yeast Metabolome Database.

No alerts have been found for YMDB - Yeast Metabolome 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 .

Butcher J, et al. (2025) Microbial bioremediation of persistent organic pollutants in plant tissues provides crop growth promoting liquid fertilizer. Nature communications, 16(1), 5768.

Pérez-Gómez O, et al. (2025) Metabolite-Driven Modulation of Biofilm Formation in Shewanella: Insights from Shewanella sp. Pdp11 Extracellular Products. Microbial ecology, 88(1), 55.

Matsuda F, et al. (2024) Data Processing of Product Ion Spectra: Methods to Control False Discovery Rate in Compound Search Results for Untargeted Metabolomics. Mass spectrometry (Tokyo, Japan), 13(1), A0155.

Villette C, et al. (2023) Mass spectrometry imaging for biosolids characterization to assess ecological or health risks before reuse. Nature communications, 14(1), 4244.

Semitsoglou-Tsiapou S, et al. (2022) Photochemical (UV-vis/H2O2) degradation of carotenoids: Kinetics and molecular end products. Chemosphere, 286(Pt 3), 131697.

Wang X, et al. (2020) JUMPm: A Tool for Large-Scale Identification of Metabolites in Untargeted Metabolomics. Metabolites, 10(5).

González-Jiménez MDC, et al. (2020) Comparative Study of the Proteins Involved in the Fermentation-Derived Compounds in Two Strains of Saccharomyces cerevisiae during Sparkling Wine Second Fermentation. Microorganisms, 8(8).

Brandt P, et al. (2020) Catch the wave: Metabolomic analyses in human pathogenic fungi. PLoS pathogens, 16(8), e1008757.

Li L, et al. (2018) Metabolomic profiling for the identification of potential biomarkers involved in a laboratory azole resistance in Candida albicans. PloS one, 13(2), e0192328.

Aru V, et al. (2018) Cool-Climate Red Wines-Chemical Composition and Comparison of Two Protocols for ^{1}H-NMR Analysis. Molecules (Basel, Switzerland), 23(1).

Ramirez-Gaona M, et al. (2017) YMDB 2.0: a significantly expanded version of the yeast metabolome database. Nucleic acids research, 45(D1), D440.

van Rijswijk M, et al. (2017) The future of metabolomics in ELIXIR. F1000Research, 6.

Zhao Y, et al. (2016) Reconstruction and applications of consensus yeast metabolic network based on RNA sequencing. FEBS open bio, 6(4), 264.

Fukushima A, et al. (2013) Recent progress in the development of metabolome databases for plant systems biology. Frontiers in plant science, 4, 73.