

Resource Summary Report

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Yeast consensus metabolic network - A consensus reconstruction of yeast metabolism

RRID:SCR_002135

Type: Tool

Proper Citation

Yeast consensus metabolic network - A consensus reconstruction of yeast metabolism (RRID:SCR_002135)

Resource Information

URL: <http://www.comp-sys-bio.org/yeastnet/>

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Description: This is a portal to the consensus yeast metabolic network as reconstructed from the genome sequence and literature. It is a highly annotated metabolic map that is periodically updated by a team of collaborators from various research groups. The first version of this reconstruction was published in Herrgrd, Swainston et al. (2008) A consensus yeast metabolic reconstruction obtained from a community approach to systems biology Nature Biotechnol. 26, 1155-1160 (you can access that network here). A second version has now been released and is awaiting publication. We plan on continuing to update this resource towards a complete metabolic network of yeast. All versions will remain accessible for historical purposes, however it is highly recommended that you always use the latest one since that is the most up to date. This effort started on the shoulders of a number of reconstructions of the metabolic network of yeast based on genomic and literature data that were published separately. (iMM904 and iLL672) However, due to the different approaches utilized in them, those earlier reconstructions had a significant number of differences. In addition they suffered from the use of non-standard names and overall they were not annotated with methods that are machine-readable. A community effort in 2007, led by the Manchester Centre for Integrative Systems Biology and the YSBN resulted in a consensus network representation of yeast metabolism, reconciling the earlier results. That effort is now ongoing under the leadership of the MCISB and with collaboration with colleagues under the UNICELLSYS FP7 project. Availability The network reconstruction is primarily assembled and provided as an SBML file enriched with MIRIAM-compliant annotations (which are embedded in the SBML through RDF). All small and macro- molecules are referenced to an authoritative database (e.g. Uniprot, ChEBI, etc.). All molecules and reactions are also annotated with appropriate publications that contain supporting evidence. Thus this network is entirely

traceable and is presented in a computational framework. SBML is a format that is understood by a large number of software applications (see sbml.org). While the SBML file is the most efficient computational resource for these data, casual users also need access to the network. That is provided by a searchable relational database accessed directly from this website. The database pages also allow readers to add comments to any chemical species or reaction. Such comments are taken into consideration by the team collating new versions of the network and can lead to corrections and additions to the network. This reconstruction is provided in the following formats: :* an SBML file containing the reaction network and annotations, located to specific sub-cellular compartments :* an SBML file containing the reaction network and annotations without subcellular compartmentation (all reactions happening in a single compartment). :* a searchable relational database, which uses the B-Net software from Pedro Mendes' group. The database version of this data set is managed with the B-Net software created in Pedro Mendes' group at the Virginia Bioinformatics Institute. B-Net's schema is a detailed representation of the underlying biochemistry and regulation. A number of reconstructions of the metabolic network of yeast based on genomic and literature data have been published. However, due to different approaches utilized in the reconstruction as well as different interpretations of the literature, the earlier reconstructions have significant number of differences. A community effort resulted in a consensus network model of yeast metabolism, combining results from previous models.

Synonyms: Yeast consensus metabolic network

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

Keywords: genomic, literature, metabolic network, yeast

Availability: Free, Freely available

Resource Name: Yeast consensus metabolic network - A consensus reconstruction of yeast metabolism

Resource ID: SCR_002135

Alternate IDs: nif-0000-20926

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260817T040318+0000

Ratings and Alerts

No rating or validation information has been found for Yeast consensus metabolic network - A consensus reconstruction of yeast metabolism.

No alerts have been found for Yeast consensus metabolic network - A consensus reconstruction of yeast metabolism.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Contador CA, et al. (2015) Analyzing redox balance in a synthetic yeast platform to improve utilization of brown macroalgae as feedstock. *Metabolic engineering communications*, 2, 76.

Salehzadeh-Yazdi A, et al. (2014) Computational analysis of reciprocal association of metabolism and epigenetics in the budding yeast: a genome-scale metabolic model (GSMM) approach. *PLoS one*, 9(11), e111686.

Xu YF, et al. (2013) Nucleotide degradation and ribose salvage in yeast. *Molecular systems biology*, 9, 665.

Chindelevitch L, et al. (2012) MetaMerge: scaling up genome-scale metabolic reconstructions with application to *Mycobacterium tuberculosis*. *Genome biology*, 13(1), r6.

Zhu Q, et al. (2011) Chemical basis of metabolic network organization. *PLoS computational biology*, 7(10), e1002214.

Dobson PD, et al. (2010) Further developments towards a genome-scale metabolic model of yeast. *BMC systems biology*, 4, 145.

Kell DB, et al. (2010) Towards a unifying, systems biology understanding of large-scale cellular death and destruction caused by poorly liganded iron: Parkinson's, Huntington's, Alzheimer's, prions, bactericides, chemical toxicology and others as examples. *Archives of toxicology*, 84(11), 825.

Smallbone K, et al. (2010) Towards a genome-scale kinetic model of cellular metabolism. *BMC systems biology*, 4, 6.