

Resource Summary Report

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TheCellMap

RRID:SCR_018728

Type: Tool

Proper Citation

TheCellMap (RRID:SCR_018728)

Resource Information

URL: <http://thecellmap.org>

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Description: Web accessible database for visualizing and mining global yeast genetic interaction network. Allows users to easily access, visualize, explore, and functionally annotate genetic interactions, or to extract and reorganize sub networks, using data driven network layouts in intuitive and interactive manner. Used for storing and visualizing genetic interactions in *S. cerevisiae*.

Synonyms: TheCellMap.org

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

Defining Citation: [PMID:28325812](#)

Keywords: Genetic interactions, genetic network, yeast genetics, synthetic genetic array, network visualization, annotation, data, genetic interaction visualization

Funding: NHGRI R01 HG005853;
NHGRI R01 HG005084;
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NSF DBI 0953881

Availability: Free, Freely available

Resource Name: TheCellMap

Resource ID: SCR_018728

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260731T043038+0000

Ratings and Alerts

No rating or validation information has been found for TheCellMap.

No alerts have been found for TheCellMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Badrie S, et al. (2025) Dbi1 is an oxidoreductase and an assembly chaperone for mitochondrial inner membrane proteins. EMBO reports, 26(4), 911.

Leydon AR, et al. (2025) A function of TPL/TBL1-type corepressors is to nucleate the assembly of the preinitiation complex. The Journal of cell biology, 224(2).

Fischbach A, et al. (2025) mTOR signaling controls protein aggregation during heat stress and cellular aging in a translation- and Hsf1-independent manner. The Journal of biological chemistry, 301(2), 108172.

Yang SH, et al. (2025) Synthetic collinearization of a chromosome segment enables genetic dissection of incompatibility between distant genera. bioRxiv : the preprint server for biology.

Constantinou M, et al. (2024) Yeast Nat4 regulates DNA damage checkpoint signaling through its N-terminal acetyltransferase activity on histone H4. PLoS genetics, 20(10), e1011433.

Abrahámová K, et al. (2024) Truncating the spliceosomal 'rope protein' Prp45 results in Htz1 dependent phenotypes. RNA biology, 21(1), 1.

Pons C, et al. (2024) Meta-analysis of dispensable essential genes and their interactions with bypass suppressors. Life science alliance, 7(1).

Omkar S, et al. (2024) Acetylation of the yeast Hsp40 chaperone protein Ydj1 fine-tunes proteostasis and translational fidelity. bioRxiv : the preprint server for biology.

Schneider KL, et al. (2024) Elimination of virus-like particles reduces protein aggregation and extends replicative lifespan in *Saccharomyces cerevisiae*. Proceedings of the National Academy of Sciences of the United States of America, 121(14), e2313538121.

Hale JJ, et al. (2024) Genome-scale analysis of interactions between genetic perturbations and natural variation. Nature communications, 15(1), 4234.

Liao H, et al. (2024) Genome-wide identification of resistance genes and response mechanism analysis of key gene knockout strain to catechol in *Saccharomyces*

cerevisiae. *Frontiers in microbiology*, 15, 1364425.

Hale JJ, et al. (2024) Genome-scale analysis of interactions between genetic perturbations and natural variation. *bioRxiv : the preprint server for biology*.

Acar O, et al. (2022) Elastic network modeling of cellular networks unveils sensor and effector genes that control information flow. *PLoS computational biology*, 18(5), e1010181.

Toulmay A, et al. (2022) Vps13-like proteins provide phosphatidylethanolamine for GPI anchor synthesis in the ER. *The Journal of cell biology*, 221(3).

Berg MD, et al. (2022) Genetic background and mistranslation frequency determine the impact of mistranslating tRNA^{SerUGG}. *G3 (Bethesda, Md.)*, 12(7).

Wang J, et al. (2022) Computational methods, databases and tools for synthetic lethality prediction. *Briefings in bioinformatics*, 23(3).

Nitika , et al. (2022) Comprehensive characterization of the Hsp70 interactome reveals novel client proteins and interactions mediated by posttranslational modifications. *PLoS biology*, 20(10), e3001839.

Mondal S, et al. (2022) DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. *eLife*, 11.

Meldal BHM, et al. (2021) Analysing the yeast complexome-the Complex Portal rising to the challenge. *Nucleic acids research*, 49(6), 3156.

Eisele F, et al. (2021) An Hsp90 co-chaperone links protein folding and degradation and is part of a conserved protein quality control. *Cell reports*, 35(13), 109328.