

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: 20260811T043621+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 41 mentions in open access literature.

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

Billmann M, et al. (2026) Global genetic interaction network of a human cell maps conserved principles and informs functional interpretation of gene co-essentiality profiles. *Cell*, 189(12), 3736.

Horecka I, et al. (2026) Expanding TheCellMap.org to visualize a genome-scale genetic interaction network for a human cell line. *bioRxiv : the preprint server for biology*.

Coulombe-Huntington J, et al. (2026) A Chemical-Genetic Interaction Matrix Reveals Drug Mechanism and Genetic Architecture. *bioRxiv : the preprint server for biology*.

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).

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.

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.

Sabo JA, et al. (2025) Simulated Microgravity-Induced Changes in SUMOylation and Protein Expression in *Saccharomyces cerevisiae*. *International journal of molecular sciences*, 27(1).

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.

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. *Nature communications*, 15(1), 4234.

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.

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

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

Peretz I, et al. (2022) A comparative analysis of telomere length maintenance circuits in fission and budding yeast. *Frontiers in genetics*, 13, 1033113.

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.

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