

Resource Summary Report

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Many Microbe Microarrays Database

RRID:SCR_007767

Type: Tool

Proper Citation

Many Microbe Microarrays Database (RRID:SCR_007767)

Resource Information

URL: <http://m3d.mssm.edu>

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Description: M3D is a resource for analyzing and retrieving gene expression data for microbes. The database currently contains Affymetrix expression compendia for *Escherichia coli*, *Saccharomyces cerevisiae*, and *Shewanella oneidensis*. M3D (Many Microbe Microarrays) was developed by the Gardner Lab at Boston University to facilitate the exchange and analysis of high quality, curated, microbial gene expression data. Currently, the database only includes data obtained using Affymetrix GeneChip technology, because the high quality of the platform facilitates cross-laboratory integration of data sets. The database allows downloading of raw data (CEL files) or preprocessed data that has been uniformly normalized with RMA. M3D also enables convenient web-based expression data exploration and visualization - accessible via the Analysis page.

Synonyms: M3D

Resource Type: data or information resource, database

Resource Name: Many Microbe Microarrays Database

Resource ID: SCR_007767

Alternate IDs: nif-0000-03091

Alternate URLs: http://cgs.wustl.edu/~faithj/m3d_mirror/

Old URLs: <http://m3d.bu.edu/>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260804T043331+0000

Ratings and Alerts

No rating or validation information has been found for Many Microbe Microarrays Database.

No alerts have been found for Many Microbe Microarrays Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Alonso AM, et al. (2023) Dicodon-based measures for modeling gene expression. *Bioinformatics* (Oxford, England), 39(6).

Cassan O, et al. (2021) Inferring and analyzing gene regulatory networks from multi-factorial expression data: a complete and interactive suite. *BMC genomics*, 22(1), 387.

Kumar CMS, et al. (2021) Chaperonin Abundance Enhances Bacterial Fitness. *Frontiers in molecular biosciences*, 8, 669996.

Yang B, et al. (2021) Reverse engineering gene regulatory network based on complex-valued ordinary differential equation model. *BMC bioinformatics*, 22(Suppl 3), 448.

Campos AI, et al. (2019) Metabolomics-Driven Exploration of the Chemical Drug Space to Predict Combination Antimicrobial Therapies. *Molecular cell*, 74(6), 1291.

Santos-Zavaleta A, et al. (2018) A unified resource for transcriptional regulation in *Escherichia coli* K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. *BMC biology*, 16(1), 91.

Yu D, et al. (2017) Enhanced construction of gene regulatory networks using hub gene information. *BMC bioinformatics*, 18(1), 186.

Salleh FH, et al. (2017) Multiple Linear Regression for Reconstruction of Gene Regulatory Networks in Solving Cascade Error Problems. *Advances in bioinformatics*, 2017, 4827171.

Noh H, et al. (2016) Inferring gene targets of drugs and chemical compounds from gene expression profiles. *Bioinformatics* (Oxford, England), 32(14), 2120.

Disselkoe C, et al. (2016) A Bayesian Framework for the Classification of Microbial Gene Activity States. *Frontiers in microbiology*, 7, 1191.

Khedkar S, et al. (2016) Comparative Genomics of Interreplicore Translocations in Bacteria: A Measure of Chromosome Topology? *G3* (Bethesda, Md.), 6(6), 1597.

Imam S, et al. (2015) An integrated approach to reconstructing genome-scale transcriptional regulatory networks. *PLoS computational biology*, 11(2), e1004103.

Powers S, et al. (2015) Cautions about the reliability of pairwise gene correlations based on expression data. *Frontiers in microbiology*, 6, 650.

Srinivasan R, et al. (2015) The genome-scale interplay amongst xenogene silencing, stress response and chromosome architecture in *Escherichia coli*. *Nucleic acids research*, 43(1), 295.

Ma S, et al. (2014) De-novo learning of genome-scale regulatory networks in *S. cerevisiae*. *PloS one*, 9(9), e106479.

Hegde SR, et al. (2014) Differential enrichment of regulatory motifs in the composite network of protein-protein and gene regulatory interactions. *BMC systems biology*, 8, 26.

Pandey SP, et al. (2014) Central role for RNase YbeY in Hfq-dependent and Hfq-independent small-RNA regulation in bacteria. *BMC genomics*, 15, 121.

Bevilacqua V, et al. (2013) Scalable high-throughput identification of genetic targets by network filtering. *BMC bioinformatics*, 14 Suppl 8(Suppl 8), S5.

Zhang Q, et al. (2012) A model-based method for gene dependency measurement. *PloS one*, 7(7), e40918.

Wessely F, et al. (2011) Optimal regulatory strategies for metabolic pathways in *Escherichia coli* depending on protein costs. *Molecular systems biology*, 7, 515.