

Resource Summary Report

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[MetaNetX](#)

RRID:SCR_015882

Type: Tool

Proper Citation

MetaNetX (RRID:SCR_015882)

Resource Information

URL: <https://www.metanetx.org/>

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Description: Web application to perform automated model construction and genome annotation for large-scale metabolic networks. Platform for accessing, analyzing and manipulating genome-scale metabolic networks (GSM) as well as biochemical pathways.

Synonyms: MNXref, MetaNetX: Automated Model Construction and Genome Annotation for Large-Scale Metabolic Networks

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:26527720](#), [PMID:23357920](#), [PMID:23172809](#)

Keywords: automated model construction, genome annotation, model, construction, genome, annotation, metabolic network, repository, gsm, biochemical, pathway

Funding: Swiss National Science Foundation ;
Swiss Federal Government ;
SIB Swiss Institute of Bioinformatics

Availability: Free, Freely available

Resource Name: MetaNetX

Resource ID: SCR_015882

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260805T044344+0000

Ratings and Alerts

No rating or validation information has been found for MetaNetX.

No alerts have been found for MetaNetX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Anand M, et al. (2025) minChemBio: Expanding Chemical Synthesis with Chemo-Enzymatic Pathways Using Minimal Transitions. *ACS synthetic biology*, 14(3), 756.

Otte A, et al. (2025) High-resolution multiomics links nutrients and mixotrophy to toxicity in a harmful bloom of the haptophyte *Chrysochromulina leadbeateri*. *Science advances*, 11(26), eadv3390.

Delgado-Nungaray JA, et al. (2025) Influence of Amino Acids on Quorum Sensing-Related Pathways in *Pseudomonas aeruginosa* PAO1: Insights from the GEM iJD1249. *Metabolites*, 15(4).

Yar?c? M, et al. (2025) RSEA: A Web Server for Pathway Enrichment Analysis of Metabolic Reaction Sets. *Biotechnology and bioengineering*, 122(8), 2251.

Zeng Z, et al. (2025) CLAIRE: a contrastive learning-based predictor for EC number of chemical reactions. *Journal of cheminformatics*, 17(1), 2.

Tec-Campos D, et al. (2025) A genome-scale metabolic model for the denitrifying bacterium *Thauera* sp. MZ1T accurately predicts degradation of pollutants and production of polymers. *PLoS computational biology*, 21(1), e1012736.

Hu T, et al. (2025) Genome-scale metabolic modeling reveals specific vaginal *Lactobacillus* strains and their metabolites as key inhibitors of *Candida albicans*. *Microbiology spectrum*, 13(6), e0298424.

Matveishina EK, et al. (2025) GEMsembler: consensus model assembly and structural comparison of genome-scale metabolic models across tools improve functional performance. *mSystems*, 10(10), e0057425.

Gricourt G, et al. (2025) BioRGroup dataset: R-group expansion of ChEBI molecules referenced in the Rhea database. *Scientific data*, 12(1), 1692.

Burgos I, et al. (2025) Genome-scale metabolic modeling of *Ruminiclostridium cellulolyticum*: a microbial cell factory for valorization of lignocellulosic biomass. *mSystems*, 10(10), e0096025.

Ding S, et al. (2025) From reactants to products: computational methods for biosynthetic pathway design. *Synthetic and systems biotechnology*, 10(3), 1038.

Leonidou N, et al. (2025) Genome-scale metabolic model of *Staphylococcus epidermidis* ATCC 12228 matches in vitro conditions. *mSystems*, 10(6), e0041825.

Gao Y, et al. (2024) Development and applications of metabolic models in plant multi-omics research. *Frontiers in plant science*, 15, 1361183.

Carter EL, et al. (2024) A temperature-induced metabolic shift in the emerging human pathogen *Photobacterium aerophilum*. *mSystems*, 9(11), e0097023.

Liu CH, et al. (2024) LipidSig 2.0: integrating lipid characteristic insights into advanced lipidomics data analysis. *Nucleic acids research*, 52(W1), W390.

Kumar M, et al. (2024) Mixotrophic growth of a ubiquitous marine diatom. *Science advances*, 10(29), eado2623.

Qian W, et al. (2024) A general model for predicting enzyme functions based on enzymatic reactions. *Journal of cheminformatics*, 16(1), 38.

Giordano N, et al. (2024) Genome-scale community modelling reveals conserved metabolic cross-feedings in epipelagic bacterioplankton communities. *Nature communications*, 15(1), 2721.

Balzerani F, et al. (2024) Extending PROXIMAL to predict degradation pathways of phenolic compounds in the human gut microbiota. *NPJ systems biology and applications*, 10(1), 56.

Gollub MG, et al. (2024) ENKIE: a package for predicting enzyme kinetic parameter values and their uncertainties. *Bioinformatics (Oxford, England)*, 40(11).