

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: 20260815T182518+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 94 mentions in open access literature.

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

Lazzari G, et al. (2026) Gempipe: a tool for drafting, curating, and analyzing pan and multi-strain genome-scale metabolic models. *mSystems*, 11(1), e0100725.

Hajjar G, et al. (2026) Metabolite names and identifiers: how far are we from interoperability? *Metabolomics : Official journal of the Metabolomic Society*, 22(2).

Vayena E, et al. (2026) In silico analysis and comparison of the metabolic capabilities of different organisms by reducing metabolic complexity. *Microbiome*, 14(1).

Alwer S, et al. (2026) KinForm: kinetics-informed feature optimised representation models for enzyme kcat and KM prediction. *NPJ systems biology and applications*, 12(1).

Moretti S, et al. (2026) MetaNetX: a bridge between metabolic resources for enhanced curation and multi-omics data harmonization. *Nucleic acids research*, 54(D1), D617.

Goryanin I, et al. (2026) EHMN 2026: A Thermodynamically Refined, SBML-Standardised Human Metabolic Network for Genome-Scale Analysis and QSP Integration. *Metabolites*, 16(4).

Wang K, et al. (2026) Hypergraph learning with multi-dimensional metabolite feature extractions and static-dynamic attention mechanisms to fill missing reactions in metabolic networks. *Briefings in bioinformatics*, 27(3).

Mostolizadeh R, et al. (2026) MCC: automated mass and charge curation at the genome scale applied to *C. tuberculo*stearicum. *Microbiology spectrum*, 14(2), e0320024.

Brydon-Brown L, et al. (2026) Predicting enzyme-compound associations for enzyme-catalysed reactions. *Journal of cheminformatics*, 18(1).

Corbín-Agustí P, et al. (2026) Incorporation of Cryptic Plasmid Energetics Improves Genome-Scale Metabolic Predictions in Probiotic *E. coli* Nissle 1917. *Microbial biotechnology*, 19(5), e70361.

Hartley AD, et al. (2026) MechFind: a computational framework for de novo prediction of enzyme mechanisms. *Nature communications*, 17(1).

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.

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

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

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).

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.

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

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.

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