Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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: software resource, data access protocol, 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: 20260808T190045+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 SPARC SAWG .

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. tuberculostearicum. 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.