

Resource Summary Report

Generated by T1D on Aug 2, 2026

eQuilibrator

RRID:SCR_006011

Type: Tool

Proper Citation

eQuilibrator (RRID:SCR_006011)

Resource Information

URL: <http://equilibrator.weizmann.ac.il/>

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Description: Web interface designed for thermodynamic analysis of biochemical systems. eQuilibrator enables free-text search for biochemical compounds and reactions and provides thermodynamic estimates for both in a variety of conditions. It can provide estimates for compounds in the KEGG database, and individual compounds and enzymes can be searched for by their common names (water, glucosamine, hexokinase). Reactions can be entered in a free-text format that eQuilibrator parses automatically. eQuilibrator also allows manipulation of the conditions of a reaction - pH, ionic strength, and reactant and product concentrations.

Synonyms: eQuilibrator - biochemical thermodynamics calculator

Resource Type: software resource, data or information resource, web application, database

Defining Citation: [PMID:22064852](https://pubmed.ncbi.nlm.nih.gov/22064852/)

Keywords: web interface, thermodynamics, biochemical system, bio.tools, FASEB list

Funding: Azrieli Foundation ;
Israel Academy of Sciences and Humanities ;
European Research Council 260392 - SYMPAC

Availability: Open source

Resource Name: eQuilibrator

Resource ID: SCR_006011

Alternate IDs: nlx_151400, biotools:equilibrator

Alternate URLs: <https://bio.tools/equilibrator>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260801T190302+0000

Ratings and Alerts

No rating or validation information has been found for eEquilibrator.

No alerts have been found for eEquilibrator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 101 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Chainani Y, et al. (2025) Merging the computational design of chimeric type I polyketide synthases with enzymatic pathways for chemical biosynthesis. *Nature communications*, 16(1), 5787.

Keller P, et al. (2025) Identification of overoxidizing and non-overoxidizing NAD-dependent methanol dehydrogenases and implications for synthetic methylotrophy. *Nature communications*, 16(1), 10967.

Cannon WR, et al. (2025) Redox poise in *R. rubrum* phototrophic growth drives large-scale changes in macromolecular pathways. *PLoS computational biology*, 21(6), e1013015.

Elizondo BR, et al. (2025) Complex Kinetic Models Predict ??-Carotene Production and Reveal Flux Limitations in Recombinant *Saccharomyces cerevisiae* Strains. *ACS synthetic biology*, 14(9), 3457.

Liu Y, et al. (2025) Systematic design and evaluation of artificial CO₂ assimilation pathways. *Synthetic and systems biotechnology*, 10(4), 1107.

Strachan CR, et al. (2025) Distinct lactate utilization strategies drive niche differentiation between two co-existing *Megasphaera* species in the rumen microbiome. *The ISME journal*, 19(1).

O'Keeffe S, et al. (2025) Ensemble quantitation of absolute metabolite concentrations in T cells reveals conserved features of immunometabolism. *bioRxiv : the preprint server for biology*.

Corrao M, et al. (2025) A compact model of Escherichia coli core and biosynthetic metabolism. PLoS computational biology, 21(10), e1013564.

Timouma S, et al. (2024) Development of a genome-scale metabolic model for the lager hybrid yeast S. pastorianus to understand the evolution of metabolic pathways in industrial settings. mSystems, 9(6), e0042924.

Voorsluijs V, et al. (2024) Calcium oscillations optimize the energetic efficiency of mitochondrial metabolism. iScience, 27(3), 109078.

Versluis DM, et al. (2024) 2'-Fucosyllactose helps butyrate producers outgrow competitors in infant gut microbiota simulations. iScience, 27(3), 109085.

Mrnjavac N, et al. (2024) The radical impact of oxygen on prokaryotic evolution-enzyme inhibition first, uninhibited essential biosyntheses second, aerobic respiration third. FEBS letters, 598(14), 1692.

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

Wei X, et al. (2024) ATP-free in vitro biotransformation of starch-derived maltodextrin into poly-3-hydroxybutyrate via acetyl-CoA. Nature communications, 15(1), 3267.

Brown GC, et al. (2024) Bioenergetic myths of energy transduction in eukaryotic cells. Frontiers in molecular biosciences, 11, 1402910.

Guo F, et al. (2024) Evolutionary engineering of Saccharomyces cerevisiae: Crafting a synthetic methylotroph via self-reprogramming. Science advances, 10(51), eadq3484.

Ji J, et al. (2024) PredCMB: predicting changes in microbial metabolites based on the gene-metabolite network analysis of shotgun metagenome data. Bioinformatics (Oxford, England), 41(1).

Wei F, et al. (2024) Unveiling Metabolic Engineering Strategies by Quantitative Heterologous Pathway Design. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(45), e2404632.

Dahal S, et al. (2023) Genome-scale model of Pseudomonas aeruginosa metabolism unveils virulence and drug potentiation. Communications biology, 6(1), 165.

Chen L, et al. (2023) Biosynthesis of Lacto-N-biose I from starch and N-acetylglucosamine via an in vitro synthetic enzymatic biosystem. Synthetic and systems biotechnology, 8(3), 555.