Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

RHEA

RRID:SCR_004713
Type: Tool

Proper Citation

RHEA (RRID:SCR_004713)

Resource Information

URL: http://www.rhea-db.org/

Proper Citation: RHEA (RRID:SCR_004713)

Description: Manually annotated reaction database where all reaction participants (reactants and products) are linked to the ChEBI database (Chemical Entities of Biological Interest) which provides detailed information about structure, formula and charge. Rhea provides built-in validations that ensure both elemental and charge balance of the reactions. The database has been populated with the reactions found in the Enzyme Commission (EC) list (and in the IntEnz and ENZYME databases), extending it with additional known reactions of biological interest. While the main focus of Rhea is enzyme-catalyzed reactions, other biochemical reactions are also included. Rhea is a manually annotated resource and it provides: stable reaction identifiers for each of its reactions; directionality information if the physiological direction of the reaction is known; the possibility to link several reactions together to form overall reactions; extensive cross-references to other resources including enzyme-catalyzed and other metabolic reactions, such as the EC list (in IntEnz), KEGG, MetaCyc and UniPathway; and chemical substructure and similarity searches on compounds in Rhea.

Abbreviations: RHEA

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:27789701

Keywords: biochemical reaction, reaction, enzyme-catalyzed reaction, spontaneous reaction, enzyme, chemical reaction, gold standard, FASEB list

Funding: Swiss Federal Government SERI ;
SystemsX.ch ;
Swiss Initiative in Systems Biology ;
EMBL ;

European Union

Availability: Public, Free, Acknowledgement requested, Available for download, The community can contribute to this resource

Resource Name: RHEA

Resource ID: SCR_004713

Alternate IDs: r3d100010891, nlx_70986

Alternate URLs: https://doi.org/10.17616/R3332H

License: Creative Commons Attribution License

License URLs: http://www.rhea-db.org/licensedisclaimer

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260912T195616+0000

Ratings and Alerts

No rating or validation information has been found for RHEA.

No alerts have been found for RHEA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 185 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

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

Paul LS, et al. (2026) A culturomics approach reveals cross-feeding capacity of intestinal pig bacteria upon release of inositol from phytate. Microbiome, 14(1), 44.

Das S, et al. (2026) Dietary fiber content influences small intestinal histomorphology and cecal microbial composition of laying hens. Poultry science, 105(10), 107292.

Tian Y, et al. (2026) Computational glycosyltransferases masked deoxynivalenol toxicity and halted FHB spread in wheat grains. Journal of advanced research, 83, 129.

Rocks JW, et al. (2026) Dual-encoder contrastive learning accelerates enzyme discovery. Proceedings of the National Academy of Sciences of the United States of America,

123(12), e2520070123.

Yi X, et al. (2026) CACLENS: A Multitask Deep Learning System for Enzyme Discovery. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(9), e18063.

Chen X, et al. (2026) The tomato seed microbiome is mainly shaped by host genotype and production site. mSystems, 11(1), e0144125.

Laakso H, et al. (2026) Impact of chronic low-dose external gamma- and internal tritium beta-irradiation on the gut microbiome in the context of intestinal tumorigenesis in ApcMin/+ mice. mSystems, 11(4), e0115625.

Lindsay EC, et al. (2026) Gut microbial composition varies with host metabolic phenotype in juvenile Atlantic salmon. The Journal of experimental biology, 229(9).

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

Kim GB, et al. (2025) Comprehensive evaluation of the capacities of microbial cell factories. Nature communications, 16(1), 2869.

Marzouk NH, et al. (2025) Proinflammatory and GABA eating bacteria in Parkinson's disease gut microbiome from a meta-analysis prospective. NPJ Parkinson's disease, 11(1), 145.

Takács-Lovász K, et al. (2025) Altered aminoacid and lipid metabolism in a rat orofacial inflammation model determined by omics approach: potential role in trigeminal sensitisation. The journal of headache and pain, 26(1), 108.

Luo Z, et al. (2025) Determinants of vacancy formation and migration in high-entropy alloys. Science advances, 11(1), eadr4697.

Göttert S, et al. (2025) The microbial metabolite desaminotyrosine protects against graft-versus-host disease via mTORC1 and STING-dependent intestinal regeneration. Nature communications, 16(1), 9282.

Baumeister T, et al. (2025) Loss of FXR or Bile Acid-dependent Inhibition Accelerate Carcinogenesis of Gastroesophageal Adenocarcinoma. Cellular and molecular gastroenterology and hepatology, 19(8), 101505.

Hutchison MG, et al. (2025) Evaluating User Experience and Satisfaction in a Concussion Rehabilitation App: Usability Study. JMIR formative research, 9, e67275.

Coleman OI, et al. (2025) ATF6 activation alters colonic lipid metabolism causing tumour-associated microbial adaptation. Nature metabolism, 7(9), 1830.

Deng X, et al. (2025) Long-chain acyl-CoA synthetases: biological functions, diseases and therapeutic targets. Molecular biomedicine, 6(1), 117.

Mou Y, et al. (2025) Outdoor air pollution, road traffic noise, and allostatic load in children aged 6-11 years: evidence from six European cohorts. European journal of epidemiology, 40(5), 537.