## **Resource Summary Report**

Generated by <u>dkNET</u> on May 19, 2025

# **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:** service resource, database, data or information resource, storage service resource, data repository

#### 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: nlx\_70986

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

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250517T055652+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: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 150 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Lv L, et al. (2025) A tunable and reversible thermo-inducible bio-switch for streptomycetes. Nucleic acids research, 53(2).

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

Zeng Z, et al. (2025) CLAIRE: a contrastive learning-based predictor for EC number of

chemical reactions. Journal of cheminformatics, 17(1), 2.

Stroeva AR, et al. (2024) Structure of Benthic Microbial Communities in the Northeastern Part of the Barents Sea. Microorganisms, 12(2).

Goodrich JA, et al. (2024) Integrating Multi-Omics with environmental data for precision health: A novel analytic framework and case study on prenatal mercury induced childhood fatty liver disease. Environment international, 190, 108930.

Guimbaud JB, et al. (2024) Machine learning-based health environmental-clinical risk scores in European children. Communications medicine, 4(1), 98.

Witting M, et al. (2024) Challenges and perspectives for naming lipids in the context of lipidomics. Metabolomics : Official journal of the Metabolomic Society, 20(1), 15.

Curry KD, et al. (2024) Reference-free structural variant detection in microbiomes via longread co-assembly graphs. Bioinformatics (Oxford, England), 40(Suppl 1), i58.

Orgler E, et al. (2024) Archaea influence composition of endoscopically visible ileocolonic biofilms. Gut microbes, 16(1), 2359500.

Böswald LF, et al. (2024) Characterization of the gastrointestinal microbiome of the Syrian hamster (Mesocricetus auratus) and comparison to data from mice. FEBS open bio, 14(10), 1701.

Shi Y, et al. (2024) PhenoMultiOmics: an enzymatic reaction inferred multi-omics network visualization web server. Bioinformatics (Oxford, England), 40(11).

Mahar JE, et al. (2024) The diverse liver viromes of Australian geckos and skinks are dominated by hepaciviruses and picornaviruses and reflect host taxonomy and habitat. Virus evolution, 10(1), veae044.

Santhanam B, et al. (2024) Exploring GPCR signaling pathway networks as cancer therapeutic targets. Cell genomics, 4(5), 100560.

Robinson CRP, et al. (2024) Host species and geography impact bee-associated RNA virus communities with evidence for isolation by distance in viral populations. ISME communications, 4(1), ycad003.

Lai PT, et al. (2024) EnzChemRED, a rich enzyme chemistry relation extraction dataset. Scientific data, 11(1), 982.

Rhimi S, et al. (2024) Industrial diet intervention modulates the interplay between gut microbiota and host in semi-stray dogs. Animal microbiome, 6(1), 69.

Curry KD, et al. (2024) Reference-free Structural Variant Detection in Microbiomes via Longread Coassembly Graphs. bioRxiv : the preprint server for biology.

Martin LC, et al. (2024) Short-read full-length 16S rRNA amplicon sequencing for

characterisation of the respiratory bacteriome of captive and free-ranging African elephants (Loxodonta africana). Scientific reports, 14(1), 14768.

Arora C, et al. (2024) The landscape of cancer-rewired GPCR signaling axes. Cell genomics, 4(5), 100557.

Ramaboli MC, et al. (2024) Diet changes due to urbanization in South Africa are linked to microbiome and metabolome signatures of Westernization and colorectal cancer. Nature communications, 15(1), 3379.