

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

IntEnz- Integrated relational Enzyme database

RRID:SCR_002992

Type: Tool

Proper Citation

IntEnz- Integrated relational Enzyme database (RRID:SCR_002992)

Resource Information

URL: <http://www.ebi.ac.uk/intenz>

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Description: IntEnz (Integrated relational Enzyme database) is a freely available resource focused on enzyme nomenclature. IntEnz is created in collaboration with the Swiss Institute of Bioinformatics (SIB). This collaboration is responsible for the production of the ENZYME resource. IntEnz contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (NC-IUBMB) on the nomenclature and classification of enzyme-catalysed reactions.

Abbreviations: IntEnz

Resource Type: data or information resource, database

Defining Citation: [PMID:14681451](#)

Keywords: enzyme categories, enzyme classification, enzyme nomenclature, enzyme reaction categories, enzyme, gold standard, bio.tools

Funding: European Union SLING 226073

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: IntEnz- Integrated relational Enzyme database

Resource ID: SCR_002992

Alternate IDs: nif-0000-03028, biotools:intenz, r3d100010803

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

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T200127+0000

Ratings and Alerts

No rating or validation information has been found for IntEnz- Integrated relational Enzyme database.

No alerts have been found for IntEnz- Integrated relational Enzyme database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Chen T, et al. (2024) Fecal microbiota transplantation from postmenopausal osteoporosis human donors accelerated bone mass loss in mice. *Frontiers in cellular and infection microbiology*, 14, 1488017.

Behzadi P, et al. (2022) Worldwide Protein Data Bank (wwPDB): A virtual treasure for research in biotechnology. *European journal of microbiology & immunology*, 11(4), 77.

Salhi A, et al. (2017) DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. *RNA biology*, 14(7), 963.

Martín-Jiménez CA, et al. (2017) Genome-Scale Reconstruction of the Human Astrocyte Metabolic Network. *Frontiers in aging neuroscience*, 9, 23.

Pundir S, et al. (2017) An update on the Enzyme Portal: an integrative approach for exploring enzyme knowledge. *Protein engineering, design & selection : PEDS*, 30(3), 245.

Attwood MM, et al. (2016) Topology based identification and comprehensive classification of four-transmembrane helix containing proteins (4TMs) in the human genome. *BMC genomics*, 17, 268.

Zhang Z, et al. (2016) UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. *Plant methods*, 12, 42.

Beckmann BM, et al. (2015) The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. *Nature communications*, 6, 10127.

Morgat A, et al. (2015) Updates in Rhea--a manually curated resource of biochemical reactions. *Nucleic acids research*, 43(Database issue), D459.

Tomar N, et al. (2013) Comparing methods for metabolic network analysis and an application to metabolic engineering. *Gene*, 521(1), 1.

Déchamps S, et al. (2010) The Kennedy phospholipid biosynthesis pathways are refractory to genetic disruption in *Plasmodium berghei* and therefore appear essential in blood stages. *Molecular and biochemical parasitology*, 173(2), 69.

Tsui IF, et al. (2007) Public databases and software for the pathway analysis of cancer genomes. *Cancer informatics*, 3, 379.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.