Resource Summary Report

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BRENDA

RRID:SCR_002997
Type: Tool

Proper Citation

BRENDA (RRID:SCR_002997)

Resource Information

URL: http://www.brenda-enzymes.org/

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Description: Main database of functional biochemical and molecular enzyme data that provides access to seven interconnected databases. It contains 2.7 million manually annotated data on enzyme occurrence, function, kinetics and molecular properties. The majority of the data are manually extracted from the primary literature. Each entry is connected to a reference and the source organism. Enzyme ligands are stored with their structures and can be accessed via their names, synonyms or via a structure search. FRENDA (Full Reference ENzyme DAta) and AMENDA (Automatic Mining of ENzyme DAta) are based on text mining methods and represent a complete survey of PubMed abstracts with information on enzymes in different organisms, tissues or organelles. The supplemental database DRENDA provides more than 910 000 new EC number-disease relations in more than 510 000 references from automatic search and a classification of enzyme-disease-related information. KENDA (Kinetic ENzyme DAta), a new amendment extracts and displays kinetic values from PubMed abstracts. The integration of the EnzymeDetector offers an automatic comparison, evaluation and prediction of enzyme function annotations for prokaryotic genomes. The biochemical reaction database BKM-react contains non-redundant enzyme-catalyzed and spontaneous reactions and was developed to facilitate and accelerate the construction of biochemical models. The content covers information on function, structure, occurrence, preparation and application of enzymes as well as properties of mutants and engineered variants. BRENDA provides viewing options such as the display of the statistics of functional parameters and the 3D view of protein sequence and structure features. Furthermore a ligand summary shows comprehensive information on the BRENDA ligands. The enzymes are linked to their respective pathways and can be viewed in pathway maps. The disease text mining part is strongly enhanced. It is possible to submit new, not yet classified enzymes to BRENDA, which then are reviewed and classified by the International Union of Biochemistry and Molecular Biology. A new SBML output format of BRENDA kinetic

data allows the construction of organism-specific metabolic models. The enzymes are classified according to the Enzyme Commission list of enzymes. Some 5000 different enzymes are covered. Frequently enzymes with very different properties are included under the same EC number. Although they intend to give a representative overview on the characteristics and variability of each enzyme the Handbook is not a compendium. The reader will have to go to the primary literature for more detailed information. Naturally it is not possible to cover all the numerous literature references for each enzyme (for some enzymes up to 40000) if the data representation is to be concise as is intended. The data collection is being developed into a metabolic network information system with links to Enzyme expression and regulation information. BRENDA SOAP Webservice is available.

Abbreviations: BRENDA

Synonyms: Brenda: The Comprehensive Enzyme Information System, BRaunschweig ENzyme Database, Brenda: Enzyme Database, BRENDA: The Comprehensive Enzyme Information System

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

Defining Citation: PMID:23203881, PMID:21062828, PMID:14681450, PMID:12850129, PMID:11796225, PMID:11752250

Keywords: enzyme, metabolic pathway, protein sequence, protein structure, genome, structure, function, annotation, kinetics, molecular property, occurrence, preparation, application, mutant, variant, pathway, ligand, web service, sequence, substructure, FASEB list

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Availability: Free, The community can contribute to this resource

Resource Name: BRENDA

Resource ID: SCR_002997

Alternate IDs: nif-0000-30222

Alternate URLs: http://www.brenda-enzymes.info/

Old URLs: http://www.brenda.uni-koeln.de/

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250503T055547+0000

Ratings and Alerts

No rating or validation information has been found for BRENDA.

No alerts have been found for BRENDA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 379 mentions in open access literature.

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

Ranaweera KKTN, et al. (2025) In silico docking and molecular dynamics for the discovery of inhibitors of enteric methane production in ruminants - A review. Animal bioscience, 38(1), 1.

Liu W, et al. (2025) RDBSB: a database for catalytic bioparts with experimental evidence. Nucleic acids research, 53(D1), D709.

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.

Wang X, et al. (2025) BioStructNet: Structure-Based Network with Transfer Learning for Predicting Biocatalyst Functions. Journal of chemical theory and computation, 21(1), 474.

Škuta C, et al. (2025) ECBD: European chemical biology database. Nucleic acids research, 53(D1), D1383.

Guo L, et al. (2025) Mining versatile feruloyl esterases: phylogenetic classification, structural features, and deep learning model. Bioresources and bioprocessing, 12(1), 7.

Chen K, et al. (2024) Engineering and finetuning expression of SerC for balanced metabolic flux in vitamin B6 production. Synthetic and systems biotechnology, 9(2), 388.

Whiting ME, et al. (2024) A framework for quantifying individual and collective common sense. Proceedings of the National Academy of Sciences of the United States of America, 121(4), e2309535121.

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.

Alazmi M, et al. (2024) Enzyme catalytic efficiency prediction: employing convolutional neural networks and XGBoost. Frontiers in artificial intelligence, 7, 1446063.

Sauter R, et al. (2024) Accounting for NAD Concentrations in Genome-Scale Metabolic Models Captures Important Metabolic Alterations in NAD-Depleted Systems. Biomolecules, 14(5).

Vidal-Verdú À, et al. (2024) The highly differentiated gut of Pachnoda marginata hosts sequential microbiomes: microbial ecology and potential applications. NPJ biofilms and microbiomes, 10(1), 65.

Akbari A, et al. (2024) Multi-scale reactor designs extend the physical limits of CO 2 fixation. bioRxiv : the preprint server for biology.

Mejía-Manzano LA, et al. (2024) Saccharomyces cerevisiae biofactory to produce naringenin using a systems biology approach and a bicistronic vector expression strategy in flavonoid production. Microbiology spectrum, 12(1), e0337423.

de Almeida Santos G, et al. (2024) Characterization of two bacterial tyrosinases from the halophilic bacterium Hahella sp. CCB MM4 relevant for phenolic compounds oxidation in wetlands. FEBS open bio, 14(12), 2038.

Zong Z, et al. (2024) Elucidation of the noncovalent interactions driving enzyme activity guides branching enzyme engineering for ?-glucan modification. Nature communications, 15(1), 8760.

Pan Y, et al. (2024) Time and dose selective glucose metabolism for glucose homeostasis and energy conversion in the liver. NPJ systems biology and applications, 10(1), 107.

Song Y, et al. (2024) Accurately predicting enzyme functions through geometric graph learning on ESMFold-predicted structures. Nature communications, 15(1), 8180.

Li G, et al. (2024) EnzyACT: A Novel Deep Learning Method to Predict the Impacts of Single and Multiple Mutations on Enzyme Activity. Journal of chemical information and modeling, 64(15), 5912.

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.