

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: Database for functional enzyme and ligand-related information maintained as part of the German ELIXIR Node. Provides advanced query systems, evaluation tools, and various visualization options for the detailed assessment of enzyme properties. Enzyme data in BRENDA are classified according to the Enzyme Commission (EC) nomenclature of IUBMB.

Abbreviations: BRENDA

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

Resource Type: data or information resource, database

Defining Citation: [PMID:33211880](#), [PMID:30395242](#), [PMID:28438579](#), [PMID:27924025](#), [PMID:25378310](#), [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

Funding: European Union SLING 226073;
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Availability: Free, Freely available,

Resource Name: BRENDA

Resource ID: SCR_002997

Alternate IDs: r3d100010616, nif-0000-30222

Alternate URLs: <http://www.brenda-enzymes.info/>, <https://doi.org/10.17616/R39W42>

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

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Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T195549+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 446 mentions in open access literature.

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

Kasem GS, et al. (2026) Whole-cell modeling predicts alternative proteome allocation strategies in the archaeon *Methanococcus maripaludis*. *Scientific reports*, 16(1).

Liu B, et al. (2026) Ultra-rapid and high-titer biomanufacturing of trehalose 6-phosphate by an in vitro synthetic biology platform. *Bioresources and bioprocessing*, 13(1).

Perrone GCM, et al. (2026) Structural basis of ligand selectivity in FAD/NAD(P)H-dependent dehydrogenases: insights from trypanothione reductase and type II NADH dehydrogenase. *Protein science : a publication of the Protein Society*, 35(7), e70664.

Lopez-Pascual A, et al. (2026) Transcriptomic profiling of epigenetic regulators and metabolic reprogramming in human cholangiocarcinoma. *Frontiers in cell and developmental biology*, 14, 1765945.

Willers VP, et al. (2026) Plug-and-play - enzymatic amino acid production from methanol and carbon dioxide. *Nature communications*, 17(1).

Pan T, et al. (2026) A geometric deep learning framework for genome-wide prediction of enzyme turnover number. *Genome biology*, 27(1).

Rychl?? N, et al. (2026) Cloning, expression and characterisation of short-chain dehydrogenase/reductase SDR12 (A0A7I5E7J1) from a parasitic nematode *Haemonchus contortus*. *Scientific reports*, 16(1).

Kim M, et al. (2026) Ontology-aware DNA methylation classification with a curated atlas of human tissues and cell types. *Cell reports methods*, 6(3), 101328.

Cardinali-Rezende J, et al. (2026) Motility and growth *Burkholderia* two-component: a new regulatory system of *Burkholderia seminalis*. *Applied microbiology and biotechnology*, 110(1).

James K, et al. (2026) Comparative Responses of Self-Regulated Exercise, Thermoregulation, and Neuromuscular Function to Monophasic Oral Contraceptives Across One Menstrual Cycle. *European journal of sport science*, 26(1), e70083.

Lyu B, et al. (2026) GotEnzymes2: expanding coverage of enzyme kinetics and thermal properties. *Nucleic acids research*, 54(D1), D583.

Eisentraut L, et al. (2026) Establishing *Saccharomyces cerevisiae* as a host for renewable acrylic acid production. *Microbial cell factories*, 25(1).

Azamar KMM, et al. (2026) Comparative Genomic and Functional Profiling of ECM-Targeting Enzymes in *Bacteroides*, a Key Genus of the Human Gut Microbiome. *bioRxiv* : the preprint server for biology.

Appleby MV, et al. (2026) Modelling of radiation damage and beam-induced heating of room-temperature samples at extremely high flux MX beamlines. *IUCrJ*, 13(Pt 2), 184.

Li S, et al. (2026) Unveiling a catalytically promiscuous feruloyl esterase from *Clostridium acetobutylicum*. *Applied microbiology and biotechnology*, 110(1).

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.

Alwer S, et al. (2026) KinForm: kinetics-informed feature optimised representation models for enzyme kcat and KM prediction. *NPJ systems biology and applications*, 12(1).

Kuijpers RI, et al. (2026) Gap Analysis of Metabolic Conversions of Off-Flavors and Antinutrients in Plant-Based Substrates. *Comprehensive reviews in food science and food safety*, 25(3), e70449.

Steuer A, et al. (2026) De novo design and experimental characterization of bitter peptides. *NPJ science of food*, 10(1).

Cai Y, et al. (2026) Enhancing kcat prediction through residue-aware attention mechanism and pre-trained representations. *Communications biology*, 9(1), 273.