

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: database, data or information resource

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;
European Union FELICS 021902 (RII3)

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: 20260803T040351+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 402 mentions in open access literature.

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

Godinez-Macias KP, et al. (2025) Revisiting the Plasmodium falciparum druggable genome using predicted structures and data mining. NPJ drug discovery, 2(1), 3.

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.

Halfon CG, et al. (2025) Do People Judge Sexual Harassment Differently Based on the Type of Job a Victim Has? Behavioral sciences (Basel, Switzerland), 15(6).

M??kinen ME, et al. (2025) Novel Data-Driven Mechanistic Modeling of Untargeted Metabolome Data Reveals Feed Component Effects in CHO Cell Bioprocess Using Column Generation-Based EFMs. Biotechnology journal, 20(7), e70008.

Zhao J, et al. (2025) MODA: a graph convolutional network-based multi-omics integration framework for unraveling hub molecules and disease mechanisms. Briefings in bioinformatics, 26(5).

Joshi D, et al. (2025) An augmented transformer model trained on protein family specific variant data leads to improved prediction of variants of uncertain significance. Human

genetics, 144(2-3), 143.

Qiu S, et al. (2025) Seq2Topt: a sequence-based deep learning predictor of enzyme optimal temperature. *Briefings in bioinformatics*, 26(2).

Boada Y, et al. (2025) Synthetic biology design principles enable efficient bioproduction of Heparosan with low molecular weight and low polydispersion index for the biomedical industry. *Synthetic biology (Oxford, England)*, 10(1), ysaf006.

Roy UK, et al. (2025) Impact of redox control on transcriptional reprogramming for salt tolerance in coastal rice landraces. *Scientific reports*, 15(1), 42994.

Bonner ER, et al. (2025) Review Article: Novel Enzyme Therapy Design for Gluten Peptide Digestion Through Exopeptidase Supplementation. *Alimentary pharmacology & therapeutics*, 61(7), 1123.

Boorla VS, et al. (2025) CatPred: a comprehensive framework for deep learning in vitro enzyme kinetic parameters. *Nature communications*, 16(1), 2072.

Zhou L, et al. (2025) Dual functional POGases from bacteria encompassing broader O-glycanase and adhesin activities. *Nature communications*, 16(1), 1960.

Hernández-Esquivel L, et al. (2025) Modeling Krebs cycle from liver, heart and hepatoma mitochondria, supported Complex I as target for specific inhibition of cancer cell proliferation. *Frontiers in oncology*, 15, 1557638.

Otani S, et al. (2025) Genomic and functional co-diversification imprint African Hominidae microbiomes to signal dietary and lifestyle adaptations. *Gut microbes*, 17(1), 2484385.

Chen Z, et al. (2025) Structural mimicry of UM171 and neomorphic cancer mutants co-opts E3 ligase KBTBD4 for HDAC1/2 recruitment. *Nature communications*, 16(1), 3144.

Al Zubaidi SM, et al. (2025) An enzyme activation network reveals extensive regulatory crosstalk between metabolic pathways. *Molecular systems biology*, 21(7), 870.

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.

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

Cofer TM, et al. (2025) The carboxylesterase AtCXE12 converts volatile (Z)-3-hexenyl acetate to (Z)-3-hexenol in *Arabidopsis* leaves. *Plant physiology*, 197(4).

Liu Y, et al. (2025) Systematic design and evaluation of artificial CO₂ assimilation pathways. *Synthetic and systems biotechnology*, 10(4), 1107.