Resource Summary Report

Generated by NIF on May 22, 2025

ExplorEnz

RRID:SCR_002665
Type: Tool

Proper Citation

ExplorEnz (RRID:SCR_002665)

Resource Information

URL: http://www.enzyme-database.org

Proper Citation: ExplorEnz (RRID:SCR_002665)

Description: Enzyme database developed as a way to access the data of the IUBMB Enzyme Nomenclature List. The data, which are stored in a MySQL database, preserve the formatting of chemical names according to IUPAC standards. A simple, easy to use, web-based query interface is provided (Search), along with an advanced search engine for more complex queries (Advanced Search). Forms are provided to submit suggestions for new enzyme entries or to report errors in existing entries. Downloads of the database are available via FTP as SQL or XML.

Abbreviations: ExplorEnz

Synonyms: ExplorEnz - The Enzyme Database, ExplorEnz Database, ExplorEnz- The Enzyme Database

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

Defining Citation: PMID:18776214, PMID:17662133

Keywords: enzyme, enzyme nomenclature, nomenclature

Funding: Science Foundation Ireland SFI 02/IN.1/B043-Tipton

Resource Name: ExplorEnz

Resource ID: SCR_002665

Alternate IDs: nif-0000-02827

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250522T060040+0000

Ratings and Alerts

No rating or validation information has been found for ExplorEnz.

No alerts have been found for ExplorEnz.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

McDonald AG, et al. (2024) Simulated digestions of free oligosaccharides and mucin-type O-glycans reveal a potential role for Clostridium perfringens. Scientific reports, 14(1), 1649.

Wu S, et al. (2024) Multi-omic analysis tools for microbial metabolites prediction. Briefings in bioinformatics, 25(4).

Deel HL, et al. (2024) Rethreading the needle: A novel molecular index of soil health (MISH) using microbial functional genes to predict soil health management. PloS one, 19(12), e0314072.

Akkurt Arslan M, et al. (2023) Profiling tear film enzymes reveals major metabolic pathways involved in the homeostasis of the ocular surface. Scientific reports, 13(1), 15231.

Vázquez R, et al. (2023) What's in a Name? An Overview of the Proliferating Nomenclature in the Field of Phage Lysins. Cells, 12(15).

Mamani-Huarcaya BM, et al. (2023) Leaf Proteomic Analysis in Seedlings of Two Maize Landraces with Different Tolerance to Boron Toxicity. Plants (Basel, Switzerland), 12(12).

McDonald AG, et al. (2022) Parameter Reliability and Understanding Enzyme Function. Molecules (Basel, Switzerland), 27(1).

Drula E, et al. (2022) The carbohydrate-active enzyme database: functions and literature. Nucleic acids research, 50(D1), D571.

Hill R, et al. (2022) Lifestyle Transitions in Fusarioid Fungi are Frequent and Lack Clear Genomic Signatures. Molecular biology and evolution, 39(4).

Oommen A, et al. (2021) Transcriptomic Analysis of Respiratory Tissue and Cell Line Models to Examine Glycosylation Machinery during SARS-CoV-2 Infection. Viruses, 13(1).

Autry JM, et al. (2020) Sarcolipin Exhibits Abundant RNA Transcription and Minimal Protein Expression in Horse Gluteal Muscle. Veterinary sciences, 7(4).

Gómez-Cerón S, et al. (2019) Data set of in silico simulation for the production of clavulanic acid and cephamycin C by Streptomyces clavuligerus using a genome scale metabolic model. Data in brief, 24, 103992.

Zhou X, et al. (2019) Marek's Disease Virus Regulates the Ubiquitylome of Chicken CD4+ T Cells to Promote Tumorigenesis. International journal of molecular sciences, 20(9).

Pelicaen R, et al. (2019) Genome-Scale Metabolic Reconstruction of Acetobacter pasteurianus 386B, a Candidate Functional Starter Culture for Cocoa Bean Fermentation. Frontiers in microbiology, 10, 2801.

Mathieu S, et al. (2018) Ancient acquisition of "alginate utilization loci" by human gut microbiota. Scientific reports, 8(1), 8075.

Wackett LP, et al. (2018) Microbial biocatalysis databases: An annotated selection of World Wide Web sites relevant to the topics in microbial biotechnology. Microbial biotechnology, 11(2), 429.

Percudani R, et al. (2013) Ureidoglycolate hydrolase, amidohydrolase, lyase: how errors in biological databases are incorporated in scientific papers and vice versa. Database : the journal of biological databases and curation, 2013, bat071.

Nakae S, et al. (2013) Structure of novel enzyme in mannan biodegradation process 4-O-?-D-mannosyl-D-glucose phosphorylase MGP. Journal of molecular biology, 425(22), 4468.

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

Sammond DW, et al. (2012) Cellulase linkers are optimized based on domain type and function: insights from sequence analysis, biophysical measurements, and molecular simulation. PloS one, 7(11), e48615.