## **Resource Summary Report**

Generated by <u>NIF</u> on May 3, 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, webbased 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, storage service resource, data repository, service resource, data or information resource

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: 20250503T055525+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: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

McDonald AG, et al. (2024) Simulated digestions of free oligosaccharides and mucin-type Oglycans 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.