

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

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: service resource, database, storage service resource, data repository, 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

Availability: Free, Available for download, Freely available

Resource Name: ExplorEnz

Resource ID: SCR_002665

Alternate IDs: nif-0000-02827

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260728T043132+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 23 mentions in open access literature.

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

Hill R, et al. (2025) Evolutionary genomics reveals variation in structure and genetic content implicated in virulence and lifestyle in the genus *Gaeumannomyces*. *BMC genomics*, 26(1), 239.

Delgado-Nungaray JA, et al. (2025) Influence of Amino Acids on Quorum Sensing-Related Pathways in *Pseudomonas aeruginosa* PAO1: Insights from the GEM iJD1249. *Metabolites*, 15(4).

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.

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.

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

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.

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).

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).

- 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).
- 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).
- 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.
- 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.