Resource Summary Report

Generated by NIF on Apr 20, 2025

ENZYME

RRID:SCR_002487
Type: Tool

Proper Citation

ENZYME (RRID:SCR_002487)

Resource Information

URL: http://www.expasy.org/enzyme/

Proper Citation: ENZYME (RRID:SCR_002487)

Description: A repository of information relative to the nomenclature of enzymes. It is primarily based on the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided. These include * EC number * Recommended name * Alternative names (if any) * Catalytic activity * Cofactors (if any) * Pointers to the Swiss-Prot protein sequence entry(ies) that correspond to the enzyme (if any) * Pointers to human disease(s) associated with a deficiency of the enzyme (if any) We believe that the ENZYME database can be useful to anybody working with enzymes and that it can be of help in the development of computer programs involved with the manipulation of metabolic pathways. Available services include downloading ENZYME by FTP as well as report forms for a new ENZYME entry or for an error/update in an existing entry.

Abbreviations: ENZYME

Synonyms: Enzyme nomenclature database

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

Defining Citation: PMID:10592255

Keywords: enzyme commission, enzyme name, nomenclature, enzyme categories, enzyme classification, enzyme nomenclature, enzyme reaction categories, gold standard

Funding:

Resource Name: ENZYME

Resource ID: SCR_002487

Alternate IDs: nif-0000-02803

Alternate URLs: http://www.expasy.ch/enzyme/

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250420T014106+0000

Ratings and Alerts

No rating or validation information has been found for ENZYME.

No alerts have been found for ENZYME.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Baltsavia I, et al. (2025) MjCyc: Rediscovering the pathway-genome landscape of the first sequenced archaeon, Methanocaldococcus (Methanococcus) jannaschii. iScience, 28(1), 111546.

Passin V, et al. (2025) Depletion of macrophages and osteoclast precursors mitigates iron overload-mediated bone loss. IUBMB life, 77(1), e2928.

Guerrero-Egido G, et al. (2024) bacLIFE: a user-friendly computational workflow for genome analysis and prediction of lifestyle-associated genes in bacteria. Nature communications, 15(1), 2072.

Cattin-Ortolá J, et al. (2024) Cargo selective vesicle tethering: The structural basis for binding of specific cargo proteins by the Golgi tether component TBC1D23. Science advances, 10(13), eadl0608.

Ashour DJ, et al. (2023) Zasp52 strengthens whole embryo tissue integrity through

supracellular actomyosin networks. Development (Cambridge, England), 150(7).

Alp M, et al. (2023) Drug screening of ?-amylase inhibitors as candidates for treating diabetes. Journal of cellular and molecular medicine, 27(15), 2249.

Pavic K, et al. (2023) Structural mechanism for inhibition of PP2A-B56? and oncogenicity by CIP2A. Nature communications, 14(1), 1143.

Ramírez-Palacios C, et al. (2023) Computational prediction of ?-transaminase selectivity by deep learning analysis of molecular dynamics trajectories. QRB discovery, 4, e1.

Val-Torregrosa B, et al. (2022) Phosphate-induced resistance to pathogen infection in Arabidopsis. The Plant journal : for cell and molecular biology, 110(2), 452.

Sardar P, et al. (2022) De novo metatranscriptomic exploration of gene function in the millipede holobiont. Scientific reports, 12(1), 16173.

Nursimulu N, et al. (2022) Architect: A tool for aiding the reconstruction of high-quality metabolic models through improved enzyme annotation. PLoS computational biology, 18(9), e1010452.

Wang B, et al. (2022) MiR-630 suppresses non-small cell lung cancer by targeting vimentin. Journal of clinical laboratory analysis, 36(9), e24536.

Guo Y, et al. (2021) TMT-based quantitative proteomic analysis reveals the spleen regulatory network of dexamethasone-induced immune suppression in chicks. Journal of proteomics, 248, 104353.

Cheng H, et al. (2021) Full-Length Transcriptome of Thalassiosira weissflogii as a Reference Resource and Mining of Chitin-Related Genes. Marine drugs, 19(7).

Cattin-Ortolá J, et al. (2021) Sequences in the cytoplasmic tail of SARS-CoV-2 Spike facilitate expression at the cell surface and syncytia formation. Nature communications, 12(1), 5333.

Magalhães P, et al. (2021) Urinary fetuin-A peptides as a new marker for impaired kidney function in patients with type 2 diabetes. Clinical kidney journal, 14(1), 269.

Lin B, et al. (2021) Urinary peptidomics reveals proteases involved in idiopathic membranous nephropathy. BMC genomics, 22(1), 852.

Copoiu L, et al. (2020) ProCarbDB: a database of carbohydrate-binding proteins. Nucleic acids research, 48(D1), D368.

Brondani LA, et al. (2020) Urinary peptidomics and bioinformatics for the detection of diabetic kidney disease. Scientific reports, 10(1), 1242.

Bolleman J, et al. (2020) HAMAP as SPARQL rules-A portable annotation pipeline for genomes and proteomes. GigaScience, 9(2).