Resource Summary Report

Generated by NIF on Apr 20, 2025

MEROPS

RRID:SCR_007777
Type: Tool

Proper Citation

MEROPS (RRID:SCR_007777)

Resource Information

URL: http://merops.sanger.ac.uk/

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Description: An information resource for peptidases (also termed proteases, proteinases and proteolytic enzymes) and the proteins that inhibit them. The MEROPS database uses an hierarchical, structure-based classification of the peptidases. In this, each peptidase is assigned to a Family on the basis of statistically significant similarities in amino acid sequence, and families that are thought to be homologous are grouped together in a Clan. There is a Summary page for each family and clan, and these have indexes. Each of the Summary pages offers links to supplementary pages. About 3000 individual peptidases and inhibitors are included in the database, and there is a Summary page describing each one. You can navigate to this by any of several routes. There are indexes of Name, MEROPS Identifier and source Organism on the menu bar. Each Summary page describes the classification and nomenclature of the peptidase or inhibitor, and provides links to supplementary pages showing sequence identifiers, the structure if known, literature references and more.

Abbreviations: MEROPS, MEROPS fam

Synonyms: MEROPS- the Peptidase Database, MEROPS - the Peptidase Database, MEROPS database, MEROPS fam

Resource Type: database, data or information resource

Defining Citation: PMID:19892822

Keywords: peptidase, protease, proteinase, proteolytic enzyme, protein, inhibitor, bio.tools, FASEB list

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Resource Name: MEROPS

Resource ID: SCR_007777

Alternate IDs: biotools:merops, nif-0000-03112

Alternate URLs: https://bio.tools/merops

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250420T015559+0000

Ratings and Alerts

No rating or validation information has been found for MEROPS.

No alerts have been found for MEROPS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 691 mentions in open access literature.

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

McReynolds E, et al. (2025) An ecological-evolutionary perspective on the genomic diversity and habitat preferences of the Acidobacteriota. Microbial genomics, 11(1).

James M, et al. (2025) Multi-scale phenotyping of senescence-related changes in roots of rapeseed in response to nitrate limitation. Journal of experimental botany, 76(2), 312.

Spínola MP, et al. (2025) Improving protein hydrolysis and digestibility in Arthrospira platensis biomass through recombinant peptidases (EC 3.4): Opportunities for monogastric animal diets. Heliyon, 11(1), e41460.

Kim MW, et al. (2025) Endogenous self-peptides guard immune privilege of the central nervous system. Nature, 637(8044), 176.

Li Z, et al. (2025) Structure and metabolic function of spatiotemporal pit mud microbiome. Environmental microbiome, 20(1), 10.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in Colletotrichum fungi. GigaScience, 13.

Kalogeropoulos K, et al. (2024) CLIPPER 2.0: Peptide-Level Annotation and Data Analysis for Positional Proteomics. Molecular & cellular proteomics : MCP, 23(6), 100781.

Gomez-Cardona E, et al. (2024) Application of N-Terminal Labeling Methods Provide Novel Insights into Endoproteolysis of the Prion Protein in Vivo. ACS chemical neuroscience, 15(1), 134.

Dang YR, et al. (2024) Phytoplankton-derived polysaccharides and microbial peptidoglycans are key nutrients for deep-sea microbes in the Mariana Trench. Microbiome, 12(1), 77.

Ugrani S, et al. (2024) Inhibitor design for TMPRSS2: insights from computational analysis of its backbone hydrogen bonds using a simple descriptor. European biophysics journal : EBJ, 53(1-2), 27.

McReynolds E, et al. (2024) An ecological-evolutionary perspective on the genomic diversity and habitat preferences of the Acidobacteriota. bioRxiv : the preprint server for biology.

Matveev EV, et al. (2024) Genome-wide bioinformatics analysis of human protease capacity for proteolytic cleavage of the SARS-CoV-2 spike glycoprotein. Microbiology spectrum, 12(2), e0353023.

Zhang Y, et al. (2024) Viral afterlife: SARS-CoV-2 as a reservoir of immunomimetic peptides that reassemble into proinflammatory supramolecular complexes. Proceedings of the National Academy of Sciences of the United States of America, 121(6), e2300644120.

Glendinning L, et al. (2024) Infectious bronchitis virus vaccination, but not the presence of XCR1, is correlated with large differences in chicken caecal microbiota. Microbial genomics, 10(9).

Varona NS, et al. (2024) Host-specific viral predation network on coral reefs. The ISME journal, 18(1).

Ghaly TM, et al. (2024) Exploring virus-host-environment interactions in a chemotrophic-based underground estuary. Environmental microbiome, 19(1), 9.

Allison SD, et al. (2024) Molecular Cloning, Characterization, and Application of Organic Solvent-Stable and Detergent-Compatible Thermostable Alkaline Protease from Geobacillus thermoglucosidasius SKF4. Journal of microbiology and biotechnology, 34(2), 436.

Qin X, et al. (2024) Characterization of psychrotrophic and thermoduric bacteria in raw milk using a multi-omics approach. Microbial genomics, 10(11).

Aylward J, et al. (2024) IMA Genome - F19 : A genome assembly and annotation guide to empower mycologists, including annotated draft genome sequences of Ceratocystis pirilliformis, Diaporthe australafricana, Fusarium ophioides, Paecilomyces lecythidis, and Sporothrix stenoceras. IMA fungus, 15(1), 12.

Wasmund K, et al. (2024) The predicted secreted proteome of activated sludge microorganisms indicates distinct nutrient niches. mSystems, 9(10), e0030124.