

Resource Summary Report

Generated by T1D on Jul 28, 2026

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

Funding: Wellcome Trust WT077044/Z/05/Z

Resource Name: MEROPS

Resource ID: SCR_007777

Alternate IDs: biotools:merops, r3d100012783, nif-0000-03112

Alternate URLs: <https://bio.tools/merops>, <https://doi.org/10.17616/R33225>,
<https://doi.org/10.17616/R33225>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260725T191148+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 736 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Wang ZF, et al. (2025) Chromosome-scale assemblies of three Ormosia species: repetitive sequences distribution and structural rearrangement. GigaScience, 14.

Ozhelvaci F, et al. (2025) ?? Hydrolases: Toward Unraveling Entangled Classification. Proteins, 93(4), 855.

Bickenbach K, et al. (2025) Targeted approach to determine the impact of cancer-associated protease variants. Science advances, 11(7), eadp5958.

Du Y, et al. (2025) Comparative genomics reveals the high diversity and adaptation strategies of Polaromonas from polar environments. BMC genomics, 26(1), 248.

Covarrubias-Zambrano O, et al. (2025) Few-Layer Graphene-Based Optical Nanobiosensors for the Early-Stage Detection of Ovarian Cancer Using Liquid Biopsy and an Active Learning Strategy. Cells, 14(5).

Diaz IA, et al. (2025) A haplotype-resolved chromatin landscape connects cis-regulatory variants to trait variation in Citrus. BMC genomics, 26(1), 978.

Zeng Y, et al. (2025) Prokaryotic evolution shapes specialized communities in long term engineered pit mud ecosystem. NPJ biofilms and microbiomes, 11(1), 186.

Modin O, et al. (2025) From Low-Loaded Mesophilic to High-Loaded Thermophilic Anaerobic Digestion: Changes in Reactor Performance and Microbiome. Microbial

biotechnology, 18(10), e70238.

Yang Y, et al. (2025) Alkane degradation mechanism of *Mixta calida* HXX308 isolated from sediment of the Mariana Trench. *Frontiers in microbiology*, 16, 1579612.

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

Hernández M, et al. (2025) Contrasting recovery of metagenome-assembled genomes and derived bacterial communities and functional profiles from lizard fecal and cloacal samples. *Animal microbiome*, 7(1), 15.

Yang W, et al. (2025) *Ligilactobacillus salivarius* LZZAY01 accelerated autophagy and apoptosis in colon cancer cells and improved gut microbiota in CAC mice. *Microbiology spectrum*, 13(2), e0186124.

Kaplan A, et al. (2025) N-terminomics and proteomics analysis of Calpain-2 reveal key proteolytic processing of metabolic and cell adhesion proteins. *Protein science : a publication of the Protein Society*, 34(5), e70144.

Fan Y, et al. (2025) Polypeptides synthesized by common bacteria in the human gut improve rodent metabolism. *Nature microbiology*, 10(8), 1918.

Escobar-Prieto JD, et al. (2025) Microbial diversity and functional potential of the *Halobates melleus* (Heteroptera: Gerridae) microbiome from the Red Sea coastline. *Environmental microbiome*, 20(1), 103.

Baalsrud HT, et al. (2025) Calcium starvation leads to strain-specific gene regulation of lipid and carotenoid production in *Mucor circinelloides*. *G3 (Bethesda, Md.)*, 15(11).

Bouras H, et al. (2025) Phenotypical and Genomic Characterization of the Mollusk Pathogen *Francisella halioticida*. *MicrobiologyOpen*, 14(6), e70172.

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.

Viver T, et al. (2025) Comparative metagenomics indicates metabolic niche differentiation of benthic and planktonic Woeseiaceae. *Environmental microbiome*, 20(1), 74.

Xie LQ, et al. (2025) Raptin, a sleep-induced hypothalamic hormone, suppresses appetite and obesity. *Cell research*, 35(3), 165.