

Resource Summary Report

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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: data or information resource, database

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, 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: 20260912T200152+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 762 mentions in open access literature.

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

Niu M, et al. (2026) 35 metagenomic datasets from the northern and southern parts??of the??Yap trench sediments. Scientific data, 13(1).

Sokolov VV, et al. (2026) Whole Genome Sequencing, Comparative Genome Analysis, and Biotechnological Potential of *Emericellopsis alkalina* and *E. fimetaria* (Bionectriaceae, Ascomycota) from the Sediment of Alkaline, Saline Lakes. Journal of fungi (Basel, Switzerland), 12(5).

Chang SC, et al. (2026) Phenotypic and Genomic Characterization of Bacterial Strain TAM1, a Potential Biocontrol Agent Against *Tetranychus urticae*. Microorganisms, 14(6).

Iizuka R, et al. (2026) First high-quality genome assembly of *Umbelopsis nana* isolated from forest soil. G3 (Bethesda, Md.), 16(4).

Wang H, et al. (2026) Isolation and Identification of Pathogens Associated with Fruit Rot of *Tamarindus indica* L. and Screening for Their Biocontrol Agents. Microorganisms, 14(6).

Leal K, et al. (2026) Exploration of inactive metabolic pathways in Antarctic *Pseudogymnoascus australis* through elicitation: a genomic and metabolomic approach to investigate its biotechnological potential. IMA fungus, 17, e156018.

Rocha VD, et al. (2026) Evolutionary History and Diversification of M35 Metalloproteases in Dothideomycetes: A Phylogenomic Overview and Case Study in *Corynespora*

cassiicola. *Current microbiology*, 83(4).

Aizpurua O, et al. (2026) Grass supplementation to a pellet-based diet fails to enrich gut microbiomes with wild-like functions in captive-bred hares. *Microbiology spectrum*, 14(4), e0369125.

Tamang A, et al. (2026) Unravelling the fungal endomicrobiome of *Picrorhiza kurroa* for increasing in-planta picroside biosynthesis using endophytic *Trichoderma harzianum* PKRF1. *Environmental microbiome*, 21(1).

Chedraoui C, et al. (2026) Integrated Genomic and Phenotypic Analyses Reveal Convergent Resistance Patterns in Clinical *Candida tropicalis* Isolates. *Mycoses*, 69(5), e70181.

Vu DQ, et al. (2026) A chromosome-scale genome assembly of *Tigridiopalma magnifica*. *Scientific data*, 13(1).

Akresi JE, et al. (2026) *Limousia* bacteria encode mucinolysome for mucin utilization in animal gut microbiomes. *Gut microbes*, 18(1), 2645267.

Lai Y, et al. (2026) Transposable Element-Driven Genomic Plasticity: Unveiling the Evolutionary Mechanisms of Lifestyle Transition and Ecological Adaptation in Endophytic Fungi. *Journal of fungi (Basel, Switzerland)*, 12(4).

Cheng X, et al. (2026) Comparative Genomics Analysis Reveals the Genomic Basis of S8 Proteases, CAZymes, and Secondary Metabolism Associated with Nematode Biocontrol in *Purpureocillium lilacinum*. *International journal of molecular sciences*, 27(11).

Azamar KMM, et al. (2026) Comparative Genomic and Functional Profiling of ECM-Targeting Enzymes in *Bacteroides*, a Key Genus of the Human Gut Microbiome. *bioRxiv* : the preprint server for biology.

Huang YT, et al. (2026) Genome diversification of symbiotic fungi in beetle-fungus mutualistic symbioses. *The ISME journal*, 20(1).

Cifuentes P, et al. (2026) Predicting enzymatic cleavage sites in cyclic peptides with non-canonical amino acids using a Graphormer model trained on MetID user data. *Scientific reports*, 16(1).

Osorio-Navarro Y, et al. (2026) Whole Genome Sequence of *Xylaria chamelensis* (Xylariales, Ascomycota), A New Species Associated with Fabaceae Pods. *Mycobiology*, 54(3), 384.

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

Kapilan 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.