**MEROPS**

RRID:SCR_007777
Type: Tool

** Proper Citation**

MEROPS (RRID:SCR_007777)

**Resource Information**

**URL:** [http://merops.sanger.ac.uk/](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 database, MEROPS- the Peptidase 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

Funding Agency: Wellcome Trust

Resource Name: MEROPS

Resource ID: SCR_007777

Alternate IDs: biotools:merops

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

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 527 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Wyka SA, et al. (2021) Whole genome comparisons of ergot fungi reveals the divergence and evolution of species within the genus Claviceps are the result of varying mechanisms driving genome evolution and host range expansion. Genome biology and evolution.

Koester ST, et al. (2021) Variability in digestive and respiratory tract Ace2 expression is associated with the microbiome. PloS one, 16(3), e0248730.


Han Y, et al. (2021) Opportunistic bacteria with reduced genomes are effective competitors for organic nitrogen compounds in coastal dinoflagellate blooms. Microbiome, 9(1), 71.


Huws SA, et al. (2021) Microbiomes attached to fresh perennial ryegrass are temporally resilient and adapt to changing ecological niches. Microbiome, 9(1), 143.


