

Resource Summary Report

Generated by T1D on Jul 28, 2026

HAMAP

RRID:SCR_007701

Type: Tool

Proper Citation

HAMAP (RRID:SCR_007701)

Resource Information

URL: <http://hamap.expasy.org/>

Proper Citation: HAMAP (RRID:SCR_007701)

Description: HAMAP is a system, based on manual protein annotation, that identifies and semi-automatically annotates proteins that are part of well-conserved families or subfamilies: the HAMAP families. HAMAP is based on manually created family rules and is applied to bacterial, archaeal and plastid-encoded proteins.

Abbreviations: HAMAP

Synonyms: High-quality Automated and Manual Annotation of microbial Proteomes

Resource Type: database, data or information resource

Keywords: conserved protein family, hamap family, protein annotation

Resource Name: HAMAP

Resource ID: SCR_007701

Alternate IDs: nif-0000-02939

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260725T191149+0000

Ratings and Alerts

No rating or validation information has been found for HAMAP.

No alerts have been found for HAMAP.

Data and Source Information

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Santini S, et al. (2025) Pacmanvirus isolated from the Lost City hydrothermal field extends the concept of transpoviron beyond the family Mimiviridae. *The ISME journal*, 19(1).

Asghar R, et al. (2025) Computational studies reveal structural characterization and novel families of *Puccinia striiformis* f. sp. *tritici* effectors. *PLoS computational biology*, 21(3), e1012503.

De La Forest Divonne S, et al. (2025) Diversity and functional specialization of oyster immune cells uncovered by integrative single-cell level investigations. *eLife*, 13.

Cheng L, et al. (2025) Genome assembly of *Stewartia sinensis* reveals origin and evolution of orphan genes in Theaceae. *Communications biology*, 8(1), 354.

Shuang H, et al. (2025) A High-quality chromosome-level genome assembly of *Swertia przewalskii* Pissjauk. *Scientific data*, 12(1), 2026.

Schikora-Tamarit M??, et al. (2024) Recent gene selection and drug resistance underscore clinical adaptation across *Candida* species. *Nature microbiology*, 9(1), 284.

Kaur H, et al. (2024) Genome-wide identification and characterization of flowering genes in *Citrus sinensis* (L.) Osbeck: a comparison among *C. Medica* L., *C. Reticulata* Blanco, *C. Grandis* (L.) Osbeck and *C. Clementina*. *BMC genomic data*, 25(1), 20.

Beryozkin A, et al. (2024) Best Disease: Global Mutations Review, Genotype-Phenotype Correlation, and Prevalence Analysis in the Israeli Population. *Investigative ophthalmology & visual science*, 65(2), 39.

Serra Moncadas L, et al. (2024) Freshwater genome-reduced bacteria exhibit pervasive episodes of adaptive stasis. *Nature communications*, 15(1), 3421.

Peters DL, et al. (2024) Functional domains of *Acinetobacter* bacteriophage tail fibers. *Frontiers in microbiology*, 15, 1230997.

Karavaeva V, et al. (2024) Navigating the archaeal frontier: insights and projections from bioinformatic pipelines. *Frontiers in microbiology*, 15, 1433224.

Borujeni PM, et al. (2024) Revisiting the functional annotation of TriTryp using sequence similarity tools. *Heliyon*, 10(20), e39243.

Noorani MS, et al. (2023) Whole genome characterization and diagnostics of prunus necrotic ringspot virus (PNRSV) infecting apricot in India. *Scientific reports*, 13(1), 4393.

Zhao Z, et al. (2023) Whole exome sequencing of well-differentiated liposarcoma and dedifferentiated liposarcoma in older woman: a case report. *Frontiers in medicine*, 10, 1237246.

Cerri A, et al. (2023) Identification and characterization of novel alphacoronaviruses in *Tadarida brasiliensis* (Chiroptera, Molossidae) from Argentina: insights into recombination as a mechanism favoring bat coronavirus cross-species transmission. *Microbiology spectrum*, 11(5), e0204723.

Xu Z, et al. (2023) The chromosome-scale reference genome of mirid bugs (*Adelphocoris suturalis*) genome provides insights into omnivory, insecticide resistance, and survival adaptation. *BMC biology*, 21(1), 195.

Gupta K, et al. (2023) Functional characterization of hypothetical proteins from Monkeypox virus. *Journal, genetic engineering & biotechnology*, 21(1), 46.

Zhang IH, et al. (2023) Partitioning of the denitrification pathway and other nitrite metabolisms within global oxygen deficient zones. *ISME communications*, 3(1), 76.

Wang Y, et al. (2023) Time-ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. *Plant biotechnology journal*, 21(1), 202.

Santini S, et al. (2023) The compact genome of the sponge *Oopsacas minuta* (Hexactinellida) is lacking key metazoan core genes. *BMC biology*, 21(1), 139.