

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

HAMAP

RRID:SCR_007701

Type: Tool

Proper Citation

HAMAP (RRID:SCR_007701)

Resource Information

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

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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: data or information resource, database

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: 20260912T200150+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 92 mentions in open access literature.

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

Rathod Y, et al. (2026) Identification of prospective PETases across prokaryotes using an in silico approach. BMC biology, 24(1).

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. Plant communications, 7(1), 101581.

Safi H, et al. (2026) Elucidating the protein interaction network of one of the largest icosahedral capsids in the virosphere. The EMBO journal, 45(10), 3514.

Stilwell PA, et al. (2026) The genome of *Istocheta aldrichi* (Diptera: Tachinidae), a parasitoid of the Japanese beetle, *Popillia japonica* (Coleoptera: Scarabaeidae). G3 (Bethesda, Md.), 16(4).

Liang M, et al. (2026) IVCDB: a comprehensive database of iridoviruses for epidemiology, genetic evolution, and disease management. Nucleic acids research, 54(D1), D790.

de Santana Nazaré PGB, et al. (2026) Metabolic Specialization and Synergy in Alkane Degradation By a Microbial Consortium: An Integrated Genomic and Geochemical Approach. Current microbiology, 83(5).

Zhao S, et al. (2026) Multi-Omics Insights Into Anthraquinone Biosynthesis in *Rheum tanguticum*. Plant biotechnology journal, 24(6), 3953.

Serra Moncadas L, et al. (2026) Deep-branching Chloroflexota lineages illuminate the eco-evolutionary foundation of cross-ecosystem colonization. Nature communications, 17(1).

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.

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.

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

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.

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

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