

Resource Summary Report

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Hmmer

RRID:SCR_005305

Type: Tool

Proper Citation

Hmmer (RRID:SCR_005305)

Resource Information

URL: <http://hmmer.janelia.org/>

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Description: Tool for searching sequence databases for homologs of protein sequences, and for making protein sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs). Compared to BLAST, FASTA, and other sequence alignment and database search tools based on older scoring methodology, HMMER aims to be significantly more accurate and more able to detect remote homologs because of the strength of its underlying mathematical models. In the past, this strength came at significant computational expense, but in the new HMMER3 project, HMMER is now essentially as fast as BLAST.

Abbreviations: HMMER

Synonyms: HMMER - biosequence analysis using profile hidden Markov models

Resource Type: production service resource, data analysis service, software application, data processing software, data analysis software, analysis service resource, service resource, software resource

Defining Citation: [PMID:21593126](#), [DOI:10.1093/bioinformatics/14.9.755](#)

Keywords: homolog, protein sequence, source code, FASEB list

Funding: Howard Hughes Medical Institute

Resource Name: Hmmer

Resource ID: SCR_005305

Alternate IDs: OMICS_00996, nlx_144358

Alternate URLs: <https://sources.debian.org/src/hmmer/>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260804T043249+0000

Ratings and Alerts

No rating or validation information has been found for Hmmer.

No alerts have been found for Hmmer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8774 mentions in open access literature.

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

Medvedeva S, et al. (2026) Widespread and intron-rich mirusviruses are predicted to reproduce in nuclei of unicellular eukaryotes. *Nature microbiology*, 11(1), 228.

García JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3* (Bethesda, Md.), 16(1).

Häggglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Lima Cunha W, et al. (2026) Molecular mechanisms associated with rootstock-scion interactions in rubber trees. *The plant genome*, 19(1), e70147.

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Richardson RT, et al. (2026) Sensitive Environmental DNA Methods for Low-Risk Surveillance of At-Risk Bumble Bees. *Molecular ecology resources*, 26(1), e70073.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Mendel HC, et al. (2025) PeptideMiner-neuropeptide discovery across the animal kingdom. *GigaScience*, 14.

Záhonová K, et al. (2025) Diplonemid protists possess exotic endomembrane machinery, impacting models of membrane trafficking in modern and ancient eukaryotes. *Current biology : CB*, 35(7), 1508.

Kim CW, et al. (2025) Gut dysbiosis from high-salt diet promotes glioma via propionate-mediated TGF- β activation. *The Journal of experimental medicine*, 222(8).

Kariyayama H, et al. (2025) Hagfish olfactory repertoire illuminates lineage-specific diversification of olfaction in basal vertebrates. *iScience*, 28(12), 114118.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.

Han B, et al. (2025) Evolutionarily diverse caveolins share a common structural framework built around amphipathic disks. *The Journal of cell biology*, 224(9).

Xue HC, et al. (2025) A unified cell atlas of vascular plants reveals cell-type foundational genes and accelerates gene discovery. *Cell*.

Zhao Q, et al. (2025) The unique architecture of umbrella toxins permits a two-tiered molecular bet-hedging strategy for interbacterial antagonism. *Cell*.

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in *Dictyostelium*. *Molecular biology of the cell*, 36(8), ar98.

Penot-Raquin M, et al. (2025) Prevalence and environmental abundance of the TSET complex in cosmopolitan algal groups. *iScience*, 28(6), 112679.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.