

Resource Summary Report

Generated by [NIF](#) on Aug 28, 2026

Hmmer

RRID:SCR_005305

Type: Tool

Proper Citation

Hmmer (RRID:SCR_005305)

Resource Information

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

Proper Citation: Hmmer (RRID:SCR_005305)

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: analysis service resource, data analysis service, data analysis software, data processing software, production service resource, service resource, software application, 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: 20260821T193737+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 9520 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Yan L, et al. (2026) A NACHT domain-containing protein Ncp is required for appendage-associated unconventional protein secretion in the fungus *Penicillium herquei*. *iScience*, 29(7), 116464.

Ghasemi F, et al. (2026) Expansion, functional diversification, and gene fusion events in the Ato protein family. *iScience*, 29(7), 116467.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. *Microbial genomics*, 12(4).

Black JJ, et al. (2026) The *Legionella pneumophila* effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. *Molecular cell*.

Chasapi MN, et al. (2026) metagRoot: a comprehensive database of protein families associated with plant root microbiomes. *Nucleic acids research*, 54(D1), D1733.

Kannan S, et al. (2026) Evolution-guided protein design of IscB for persistent epigenome editing in vivo. *Nature biotechnology*, 44(5), 759.

Baek JH, et al. (2026) Genome-resolved insights into the ecology, metabolic potential, salt-stress adaptation, and safety of *Staphylococcus* in traditional Korean soybean fermentation. *NPJ science of food*, 10(1).

Guan K, et al. (2026) Comparative characterization of Cas12f orthologs reveals mechanistic features underlying enhanced genome editing efficiency. *Nature structural & molecular biology*, 33(5), 756.

Zhang X, et al. (2026) Genome-wide identification and characterization of the RPA gene family in maize. *BMC plant biology*, 26(1).

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the *Gerbera* (*Gerbera hybrida*) using HiFi long-read and Hi-C technologies. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Xu Y, et al. (2026) Phosphate deprivation restricts bacterial degradation of the marine polysaccharide fucoidan. *Nature microbiology*, 11(2), 391.

Sleutel M, et al. (2026) Auto-crosslinking sporesilk fibers promote endospore and Cry toxin clustering. *Nature communications*, 17(1).

Xue T, et al. (2026) Pan-genomic analysis and abiotic stress expression of eight TPS gene families in *Brassica napus*. *BMC plant biology*, 26(1).

Zhou P, et al. (2026) Chromosome-Level Genome Assembly of the Allotetraploid *Gynostemma pentaphyllum* Provides Novel Insights Into the Biosynthesis of Ginsenoside and Gypenoside LVI. *Plant biotechnology journal*, 24(6), 4204.

Duarte SA, et al. (2026) ET-Pfam: ensemble transfer learning for protein family prediction. *Bioinformatics (Oxford, England)*, 42(4).