Hmmer

RRID:SCR_005305
Type: Tool

Proper Citation

Hmmer (RRID:SCR_005305)

Resource Information

**URL:** [http://hmmer.janelia.org/](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:** service resource, production service resource, data analysis service, data processing software, data analysis software, analysis service resource, software resource, software application

**Defining Citation:** PMID:21593126, DOI:10.1093/bioinformatics/14.9.755

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

**Funding Agency:** Howard Hughes Medical Institute

**Resource Name:** Hmmer
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 6954 mentions in open access literature.

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


Berry MA, et al. (2024) Diverse domain architectures of CheA histidine kinase, a central component of bacterial and archaeal chemosensory systems. Microbiology spectrum, 12(1), e0346423.
Reji L, et al. (2024) A genomic view of environmental and life history controls on microbial nitrogen acquisition strategies. Environmental microbiology reports, 16(1), e13220.


Hoepner CM, et al. (2024) Proteotranscriptomics of the Most Popular Host Sea Anemone Entacmaea quadricolor Reveals Not All Toxin Genes Expressed by Tentacles Are Recruited into Its Venom Arsenal. Toxins, 16(2).

