**Hmmer**

**RRID:** SCR_005305  
**Type:** Tool

**Proper Citation**

Hmmer (RRID:SCR_005305)

**Resource Information**

**URL:** [http://hmmer.janelia.org/](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.

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

**References:** PMID:21593126

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

**Parent Organization:** Janelia Research

**Funding Agency:** Howard Hughes Medical Institute

**Related resources:** VectorBase

**Website Status:** Last checked up
Abbreviations: HMMER

Resource Name: Hmmer

Resource ID: SCR_005305

Alternate IDs: nlx_144358, OMICS_00996

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 4160 mentions in open access literature.

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


Zhao H, et al. (2020) Mycoparasitism illuminated by genome and transcriptome sequencing of, an important biocontrol fungus of the plant pathogen. Microbial genomics.


Tanaka M, et al. (2020) Group A Streptococcus establishes pharynx infection by degrading the deoxyribonucleic acid of neutrophil extracellular traps. Scientific reports, 10(1), 3251.

Ishaque NM, et al. (2020) Isolation, Genomic and Metabolomic Characterization of Vitakn with Quorum Sensing Inhibitory Activity from Southern India. Microorganisms, 8(1).


