Hmmer
RRID:SCR_005305
Type: Tool

Proper Citation
Hmmer (RRID:SCR_005305)

Resource Information

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

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 Name: Hmmer

Proper Citation: Hmmer (RRID:SCR_005305)

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

Keywords: homolog, protein sequence, source code

Resource ID: SCR_005305

Parent Organization: Janelia Research

Funding Agency: Howard Hughes Medical Institute

Related resources: VectorBase
Usage and Citation Metrics

We found 3199 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](https://scicrunch.org).


Mughal F, et al. (2019) MANET 3.0: Hierarchy and modularity in evolving metabolic
networks. PloS one, 14(10), e0224201.


Sun D, et al. (2019) Draft genome sequence of cauliflower (L. var.) provides new insights into the C genome inspecies. Horticulture research, 6, 82.


