Hmmer

RRID:SCR_005305
Type: Tool

Proper Citation

Hmmer (RRID:SCR_005305)

Resource Information

URL: 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.

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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
References: PMID: 21593126

Website Status: Last checked up

Alternate IDs: nlx_144358, OMICS_00996

Abbreviations: HMMER

Mentions Count: 3199

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 3411 mentions in open access literature.

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


Barco RA, et al. (2020) A Genus Definition forandBased on a Standard Genome Relatedness Index. mBio, 11(1).


Alioto T, et al. (2020) Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. The Plant journal : for cell and molecular biology, 101(2), 455-472.


