

Resource Summary Report

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MSAProbs

RRID:SCR_012982

Type: Tool

Proper Citation

MSAProbs (RRID:SCR_012982)

Resource Information

URL: <http://sourceforge.net/projects/msaprobs/>

Proper Citation: MSAProbs (RRID:SCR_012982)

Description: An open-source protein multiple sequence alignment algorithm, achieving the statistically highest alignment accuracy on popular benchmarks.

Abbreviations: MSAProbs

Synonyms: MSAProbs: Multiple Sequence Alignment

Resource Type: software resource

Defining Citation: [PMID:20576627](#)

Keywords: c++

Availability: GNU General Public License, v3

Resource Name: MSAProbs

Resource ID: SCR_012982

Alternate IDs: OMICS_00980

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260919T195236+0000

Ratings and Alerts

No rating or validation information has been found for MSAProbs.

No alerts have been found for MSAProbs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Russ JE, et al. (2025) Competition between Der1 and ERAD-M substrates controls Hrd1 complex function. Proceedings of the National Academy of Sciences of the United States of America, 122(49), e2513595122.

Mendes LFS, et al. (2022) Resurrecting Golgi proteins to grasp Golgi ribbon formation and self-association under stress. International journal of biological macromolecules, 194, 264.

Matsutani M, et al. (2021) Comparative Genomics of Closely Related Tetragenococcus halophilus Strains Elucidate the Diversity and Microevolution of CRISPR Elements. Frontiers in microbiology, 12, 687985.

Jia H, et al. (2021) Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. Molecular biology and evolution, 38(11), 4765.

Ravarani CNJ, et al. (2020) Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. Nature communications, 11(1), 2384.

Garcia AK, et al. (2020) Reconstructing the evolutionary history of nitrogenases: Evidence for ancestral molybdenum-cofactor utilization. Geobiology, 18(3), 394.

Daugavet MA, et al. (2019) Features of a novel protein, rusticalin, from the ascidian Styela rustica reveal ancestral horizontal gene transfer event. Mobile DNA, 10, 4.

Zhan Q, et al. (2019) ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. BMC bioinformatics, 20(Suppl 18), 573.

Sng NJ, et al. (2019) A member of the CONSTANS-Like protein family is a putative regulator of reactive oxygen species homeostasis and spaceflight physiological adaptation. AoB PLANTS, 11(1), ply075.

Garrido-Bigotes A, et al. (2019) Evolutionary Analysis of JAZ Proteins in Plants: An Approach in Search of the Ancestral Sequence. International journal of molecular sciences, 20(20).

Catchpole RJ, et al. (2019) The Evolution of Reverse Gyrase Suggests a Nonhyperthermophilic Last Universal Common Ancestor. Molecular biology and evolution, 36(12), 2737.

Liu Q, et al. (2018) Ancient mechanisms for the evolution of the bicoid homeodomain's function in fly development. *eLife*, 7.

Catchpole R, et al. (2018) A series of new *E. coli*-*Thermococcus* shuttle vectors compatible with previously existing vectors. *Extremophiles : life under extreme conditions*, 22(4), 591.

Liu X, et al. (2018) In-depth comparative analysis of malaria parasite genomes reveals protein-coding genes linked to human disease in *Plasmodium falciparum* genome. *BMC genomics*, 19(1), 312.

Gu??rin F, et al. (2017) Flow cytometry sorting of nuclei enables the first global characterization of *Paramecium* germline DNA and transposable elements. *BMC genomics*, 18(1), 327.

Rodriguez JD, et al. (2017) Identification of a vacuolar proton channel that triggers the bioluminescent flash in dinoflagellates. *PloS one*, 12(2), e0171594.

Sechler AJ, et al. (2017) Whole genome sequence of two *Rathayibacter toxicus* strains reveals a tunicamycin biosynthetic cluster similar to *Streptomyces chartreusis*. *PloS one*, 12(8), e0183005.

Kunz S, et al. (2017) The single cyclic nucleotide-specific phosphodiesterase of the intestinal parasite *Giardia lamblia* represents a potential drug target. *PLoS neglected tropical diseases*, 11(9), e0005891.

Dias R, et al. (2017) Convergence of Domain Architecture, Structure, and Ligand Affinity in Animal and Plant RNA-Binding Proteins. *Molecular biology and evolution*, 34(6), 1429.

Li J, et al. (2015) A large-scale conformation sampling and evaluation server for protein tertiary structure prediction and its assessment in CASP11. *BMC bioinformatics*, 16, 337.