Probalign

RRID:SCR_013332
Type: Tool

Proper Citation

Probalign (RRID:SCR_013332)

Resource Information

URL: http://probalign.njit.edu/standalone.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Software that uses partition function posterior probability estimates to compute maximum expected accuracy multiple sequence alignments. Computes maximal expected accuracy multiple sequence alignments from partition function posterior probabilities. Produces accurate alignments on long and heterogeneous length datasets containing protein repeats.

Abbreviations: Probalign

Synonyms: Probalign: multiple sequence alignment using partition function posterior probabilities

Resource Type: image analysis software, data processing software, software application, alignment software, software resource

Defining Citation: PMID:16954142, DOI:10.1093/bioinformatics/btl472

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Probalign

Resource ID: SCR_013332

Alternate IDs: OMICS_00985
Alternate URLs: https://sources.debian.org/src/probalign/

Record Creation Time: 20220129T080315+0000

Record Last Update: 20240704T054008+0000

Ratings and Alerts

No rating or validation information has been found for Probalign.

No alerts have been found for Probalign.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Kinateder T, et al. (2023) Experimental and computational analysis of the ancestry of an evolutionary young enzyme from histidine biosynthesis. Protein science: a publication of the Protein Society, 32(1), e4536.


Tayengwa R, et al. (2018) Synopsis of the SOFL Plant-Specific Gene Family. G3 (Bethesda,


