Resource Summary Report

Generated by NIF on Apr 29, 2025

Probalign

RRID:SCR_013332
Type: Tool

Proper Citation

Probalign (RRID:SCR_013332)

Resource Information

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

Proper Citation: Probalign (RRID:SCR_013332)

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

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

Funding:

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: 20250429T055604+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 NIF.

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.

Fernandez-Pozo N, et al. (2021) Aethionema arabicum genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. The Plant journal : for cell and molecular biology, 106(1), 275.

Root ZD, et al. (2021) Lamprey lecticans link new vertebrate genes to the origin and elaboration of vertebrate tissues. Developmental biology, 476, 282.

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.

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.

Velsko IM, et al. (2019) Resolving Phylogenetic Relationships for Streptococcus mitis and Streptococcus oralis through Core- and Pan-Genome Analyses. Genome biology and evolution, 11(4), 1077.

Tayengwa R, et al. (2018) Synopsis of the SOFL Plant-Specific Gene Family. G3 (Bethesda, Md.), 8(4), 1281.

Alves RJE, et al. (2018) Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. Nature communications, 9(1), 1517.

Marra NJ, et al. (2017) Comparative transcriptomics of elasmobranchs and teleosts highlight important processes in adaptive immunity and regional endothermy. BMC genomics, 18(1), 87.

Li N, et al. (2017) Analysis of gene gain and loss in the evolution of predatory bacteria. Gene, 598, 63.

Koga H, et al. (2016) Experimental Approach Reveals the Role of alx1 in the Evolution of the Echinoderm Larval Skeleton. PloS one, 11(2), e0149067.

Zhang Y, et al. (2016) Functional characterization of GmBZL2 (AtBZR1 like gene) reveals the conserved BR signaling regulation in Glycine max. Scientific reports, 6, 31134.

Yu X, et al. (2016) Prevalent Exon-Intron Structural Changes in the APETALA1/FRUITFULL, SEPALLATA, AGAMOUS-LIKE6, and FLOWERING LOCUS C MADS-Box Gene Subfamilies Provide New Insights into Their Evolution. Frontiers in plant science, 7, 598.

Pugh C, et al. (2016) Resurrecting ancestral structural dynamics of an antiviral immune receptor: adaptive binding pocket reorganization repeatedly shifts RNA preference. BMC evolutionary biology, 16(1), 241.

Richards VP, et al. (2015) Genome based phylogeny and comparative genomic analysis of intra-mammary pathogenic Escherichia coli. PloS one, 10(3), e0119799.

Jeong H, et al. (2015) Accurate multiple network alignment through context-sensitive random walk. BMC systems biology, 9 Suppl 1(Suppl 1), S7.