Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 2025

Kalign

RRID:SCR_011810
Type: Tool

Proper Citation

Kalign (RRID:SCR_011810)

Resource Information

URL: http://www.ebi.ac.uk/Tools/msa/kalign/

Proper Citation: Kalign (RRID:SCR_011810)

Description: A fast and accurate multiple sequence alignment algorithm.

Abbreviations: Kalign

Resource Type: software resource

Defining Citation: PMID:16343337, DOI:10.1093/bioinformatics/btz795

Keywords: bio.tools

Funding:

Availability: Free

Resource Name: Kalign

Resource ID: SCR_011810

Alternate IDs: OMICS_00978, biotools:kalign

Alternate URLs: https://bio.tools/kalign, https://sources.debian.org/src/kalign/

Record Creation Time: 20220129T080306+0000

Record Last Update: 20250410T070206+0000

Ratings and Alerts

No rating or validation information has been found for Kalign.

No alerts have been found for Kalign.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

Rakesh S, et al. (2024) Reappraisal of the DNA phosphorothioate modification machinery: uncovering neglected functional modalities and identification of new counter-invader defense systems. Nucleic acids research, 52(3), 1005.

Wu Z, et al. (2024) Human pangenome analysis of sequences missing from the reference genome reveals their widespread evolutionary, phenotypic, and functional roles. Nucleic acids research, 52(5), 2212.

Marcet-Houben M, et al. (2024) Genomics of the expanding pine pathogen Lecanosticta acicola reveals patterns of ongoing genetic admixture. mSystems, 9(3), e0092823.

Tan Y, et al. (2024) Machine learning-based classification reveals distinct clusters of non-coding genomic allelic variations associated with Erm-mediated antibiotic resistance. mSystems, 9(7), e0043024.

Gao S, et al. (2024) Centromere Landscapes Resolved from Hundreds of Human Genomes. Genomics, proteomics & bioinformatics, 22(5).

Khan MF, et al. (2023) Biodegradation of Amphipathic Fluorinated Peptides Reveals a New Bacterial Defluorinating Activity and a New Source of Natural Organofluorine Compounds. Environmental science & technology, 57(26), 9762.

Scott CJR, et al. (2023) Whole genome structural predictions reveal hidden diversity in putative oxidative enzymes of the lignocellulose-degrading ascomycete Parascedosporium putredinis NO1. Microbiology spectrum, 11(6), e0103523.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. PloS one, 18(2), e0279597.

Cadena-Caballero CE, et al. (2023) APGW/AKH Precursor from Rotifer Brachionus plicatilis and the DNA Loss Model Explain Evolutionary Trends of the Neuropeptide LWamide, APGWamide, RPCH, AKH, ACP, CRZ, and GnRH Families. Journal of molecular evolution,

91(6), 882.

Crum E, et al. (2023) Coliphages of the human urinary microbiota. PloS one, 18(4), e0283930.

Jaegle B, et al. (2023) Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. Genome biology, 24(1), 44.

Mewa DB, et al. (2023) ANTHRACNOSE RESISTANCE GENE2 confers fungal resistance in sorghum. The Plant journal : for cell and molecular biology, 113(2), 308.

Kibby EM, et al. (2023) Bacterial NLR-related proteins protect against phage. Cell, 186(11), 2410.

Liu Y, et al. (2022) Housekeeping gene gyrA, a potential molecular marker for Bacillus ecology study. AMB Express, 12(1), 133.

Schneider T, et al. (2022) Photoglobin, a distinct family of non-heme binding globins, defines a potential photosensor in prokaryotic signal transduction systems. Computational and structural biotechnology journal, 20, 261.

Liedtke HC, et al. (2022) Chromosome-level assembly, annotation and phylome of Pelobates cultripes, the western spadefoot toad. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(3).

Hajieghrari B, et al. (2022) Comparative phylogeny and evolutionary analysis of Dicer-like protein family in two plant monophyletic lineages. Journal, genetic engineering & biotechnology, 20(1), 103.

Conner KN, et al. (2022) Novel internalin P homologs in Listeria. Microbial genomics, 8(7).

Foley S, et al. (2022) Evolutionary analyses of genes in Echinodermata offer insights towards the origin of metazoan phyla. Genomics, 114(4), 110431.

Tan Y, et al. (2021) Unification and extensive diversification of M/Orf3-related ion channel proteins in coronaviruses and other nidoviruses. Virus evolution, 7(1), veab014.