

Resource Summary Report

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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

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: 20260815T182423+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 123 mentions in open access literature.

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

Palmer D, et al. (2026) pH-dependent allosteric remodeling of a bacterial riboswitch couples alkaline activation to metal sensing. *bioRxiv : the preprint server for biology*.

Rakesh S, et al. (2026) Expanding the landscape of BREX diversity: uncovering multi-layered functional frameworks and identification of novel BREX-related defense systems. *Nucleic acids research*, 54(3).

Manzano-Morales S, et al. (2026) Phylogenomics of Asgard archaea reveals a unique blend of prokaryotic-like horizontal transfer and eukaryotic-like gene duplication. *Nature communications*, 17(1).

So-In C, et al. (2026) Gene expression in immune cells infected with *Orientia tsutsugamushi* and the antigenic variability of 56-kDa type-specific antigen. *Scientific reports*, 16(1).

Chen Z, et al. (2025) Overlooked role of heterotrophic prokaryotes in sulfur oxidation makes the sediment of the Bohai Sea a sufficient sink of hydrogen sulfide. *mBio*, 16(8), e0172225.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Zhang H, et al. (2025) Genomic Characterization and Pathogenicity of a Novel Birnavirus Strain Isolated from Mandarin Fish (*Siniperca chuatsi*). *Genes*, 16(6).

Hu GA, et al. (2025) Exploring the Biosynthetic Potential of Microorganisms from the South China Sea Cold Seep Using Culture-Dependent and Culture-Independent Approaches. *Marine drugs*, 23(8).

Kosovsky GY, et al. (2025) *Bos taurus* and *Bison bison* conservative retrotransposon recombination products. *Frontiers in veterinary science*, 12, 1516731.

Marquardt A, et al. (2025) Disruption of SETD3-mediated histidine-73 methylation by the BWCFF-associated ??-actin G74S mutation. *FEBS letters*, 599(17), 2449.

Zhao Q, et al. (2025) The unique architecture of umbrella toxins permits a two-tiered molecular bet-hedging strategy for interbacterial antagonism. *Cell*.

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.