

Resource Summary Report

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MAFFT

RRID:SCR_011811

Type: Tool

Proper Citation

MAFFT (RRID:SCR_011811)

Resource Information

URL: <http://mafft.cbrc.jp/alignment/server/>

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Description: Software package as multiple alignment program for amino acid or nucleotide sequences. Can align up to 500 sequences or maximum file size of 1 MB. First version of MAFFT used algorithm based on progressive alignment, in which sequences were clustered with help of Fast Fourier Transform. Subsequent versions have added other algorithms and modes of operation, including options for faster alignment of large numbers of sequences, higher accuracy alignments, alignment of non-coding RNA sequences, and addition of new sequences to existing alignments.

Abbreviations: MAFFT

Synonyms: Multiple Alignment using Fast Fourier Transform, MAFFT version 5, MAFFT version 7

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

Defining Citation: [PMID:12136088](#), [PMID:17118958](#), [PMID:16362903](#), [PMID:15661851](#), [PMID:18439255](#), [PMID:23023983](#), [DOI:10.1093/bib/bbn013](#)

Keywords: alignment, amino acid, nucleotide, sequence, DNA, sequence alignment, bio.tools

Funding: EMBL ;
Ministry of Education ;
Culture ;
Sports ;
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Resource Name: MAFFT

Resource ID: SCR_011811

Alternate IDs: biotools:MAFFT, OMICS_00979

Alternate URLs: <https://www.ebi.ac.uk/Tools/msa/mafft/>, <https://www.genome.jp/tools-bin/mafft>, <https://myhits.isb-sib.ch/cgi-bin/mafft>, <https://bio.tools/MAFFT>, <https://sources.debian.org/src/mafft/>

License: BSD

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260912T195740+0000

Ratings and Alerts

No rating or validation information has been found for MAFFT.

No alerts have been found for MAFFT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24687 mentions in open access literature.

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

Campbell AS, et al. (2026) Molecular insights into electroreceptor ribbon synapses from differential gene expression in sturgeon lateral line organs. *Journal of anatomy*, 248(5), 784.

Withatanung P, et al. (2026) Genomic diversity and clade clustering of Burkholderia pseudomallei and B. thailandensis prophages with soil-derived phages. *iScience*, 29(2), 114658.

Daniel K, et al. (2026) Pre-existing neutralizing antibodies against cattle-transmitted influenza A virus H5N1 are detectable in unexposed individuals. *Immunity*, 59(2), 494.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Poulain F, et al. (2026) Clonal origin and early lineage divergence in adenosquamous carcinoma. *Cell reports*, 45(6), 117470.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Telford MS, et al. (2026) Antibacterial microcins self-assemble to promote biofilm formation in *Acinetobacter baumannii*. *Cell reports*, 45(4), 117156.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Withatanung P, et al. (2026) Phage-based diagnostic assay for melioidosis using multiplex PCR targeting *Burkholderia* phage terminase genes. *iScience*, 29(3), 114831.

Ghasemi F, et al. (2026) Expansion, functional diversification, and gene fusion events in the Ato protein family. *iScience*, 29(7), 116467.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Li SH, et al. (2026) Childhood immunological imprinting of cross-subtype antibodies targeting the hemagglutinin head domain of influenza viruses. *Cell host & microbe*, 34(5), 873.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in *Cladophorales* plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Black JJ, et al. (2026) The *Legionella pneumophila* effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. *Molecular cell*.

Grimwood RM, et al. (2026) A Novel Crustavirus as a Candidate Aetiology of Tail Fan Necrosis in New Zealand Red Rock Lobsters, *Jasus edwardsii*. *Journal of fish diseases*, 49(2), e70033.

Brown RR, et al. (2026) Phosphorylation of *Xenopus* M18BP1 governs centromeric localization and CENP-A nucleosome assembly. *EMBO reports*, 27(6), 1561.

Liu Z, et al. (2026) Chromosome-Level Genome and Organ-Specific Transcriptome of *Alnus glutinosa* Uncover Lineage-Specific Innovations in Root Nodule Symbiosis. *Plant, cell & environment*, 49(6), 3003.