

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

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 ;
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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: 20260803T040554+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 22450 mentions in open access literature.

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

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.

Chen Z, et al. (2026) Evaluating Probe Design for Phylogenomics Across Taxonomic Scales: First Steps for Applying Ultraconserved Elements in an Understudied Class (Mollusca: Polyplacophora). *Molecular ecology resources*, 26(1), e70076.

Huang M, et al. (2026) The application of *Rhizobium subbaroonis* TY15 increased soybean growth and disease resistance by modifying rhizosphere microbial communities. *Microbiology spectrum*, 14(1), e0115525.

Kusano K, et al. (2026) Metabolic Syndrome Develops Cardiac Cancer via Nuclear Factor- κ B-related Factor 2-Programmed Death-Ligand 1 Signaling. *Cellular and molecular gastroenterology and hepatology*, 20(1), 101629.

Li C, et al. (2026) A cell-type-specific regulon controlling monoterpene indole alkaloid biosynthesis with feedback and feedforward activation loops. *The New phytologist*, 249(2), 945.

Yanez Ortuno D, et al. (2026) Predicting bacterial-mediated entomopathogenicity through comparative genomics and statistical modeling. *Microbiology spectrum*, 14(1), e0310825.

Du Y, et al. (2026) Insect I-Type Lysozymes Function as Antiviral Proteases by Forming Biomolecular Condensates. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e14408.

Šikutová S, et al. (2026) Molecular Screening of Black Flies (Diptera: Simuliidae) for Vector-Borne Zoonotic Pathogens, South Moravia, Czech Republic. *Zoonoses and public health*, 73(1), 95.

Song W, et al. (2026) Distinct patterns of microbial association across deep-sea corals from the Western Pacific Magellan Seamounts. *Microbiology spectrum*, 14(1), e0209325.

Deng J, et al. (2026) Cats are more susceptible to the prevalent H3 subtype influenza viruses than dogs. *Virulence*, 17(1), 2605799.

Hägglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Gergonne D, et al. (2026) Genomic Evidence for Dual Introductions, Limited Gene Flow and Niche Preferences in the Invasive Wasp *Vespula germanica* in South Africa. *Molecular ecology*, 35(1), e70217.

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from *Cordia subcordata* (Boraginaceae). *Molecular biology and evolution*, 43(1).

Kulikov N, et al. (2026) The Chromosome-Scale Genome Assembly of the Redlip Blenny, *Ophioblennius macclurei* (Blenniidae). *Genome biology and evolution*, 18(1).

Zhang P, et al. (2026) Resurrection and characterization of ancestral xylose transporters enhance the capability of xylose uptake in the mixed sugar co-fermentation of Recombinant *Saccharomyces cerevisiae*. *Bioresources and bioprocessing*, 13(1), 1.

Richardson RT, et al. (2026) Sensitive Environmental DNA Methods for Low-Risk Surveillance of At-Risk Bumble Bees. *Molecular ecology resources*, 26(1), e70073.

Wang M, et al. (2026) Development and preliminary application of a multiplex qPCR assay for the detection of avian leukosis virus subgroup J, reticuloendotheliosis virus, and chicken infectious anemia virus. *Poultry science*, 105(1), 106122.

Angélica Maya M, et al. (2026) Adenovirus Genotypes Associated With Severe Acute Respiratory Infections Outbreak in Children, in Antioquia, Colombia, 2022-2023. *The Pediatric infectious disease journal*, 45(2), 112.

Jing X, et al. (2026) Phylogenetic and pathogenic analyses of circulating infectious bursal disease virus strains in China. *Poultry science*, 105(1), 106108.

Farias FM, et al. (2026) Streptocyclin BTW is a novel member of a diverse family of circular bacteriocins in the genus *Streptococcus*. *Molecular nutrition & food research*, 70(1), e70290.