Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 26, 2025

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: data processing software, image analysis software, data access protocol, software application, software resource, service resource, alignment software, web service

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 ;

Science and Technology of Japan

Availability: Free, Available for download, Freely available

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: 20250326T060847+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 19471 mentions in open access literature.

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

Qiu S, et al. (2025) Functional evolution and diversification of CYP82D subfamily members have shaped flavonoid diversification in the genus Scutellaria. Plant communications, 6(1), 101134.

Grzech D, et al. (2025) Incorporation of nitrogen in antinutritional Solanum alkaloid biosynthesis. Nature chemical biology, 21(1), 131.

Schöneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: Ryuthela nishihirai (Liphistiidae), Uloborus plumipes (Uloboridae) and Cheiracanthium punctorium (Cheiracanthiidae). Molecular ecology resources, 25(1), e14038.

Xu T, et al. (2025) Discovery and characterization of complete genomes of 38 head-tailed proviruses in four predominant phyla of archaea. Microbiology spectrum, 13(1), e0049224.

Gauthier J, et al. (2025) Chromosome-Scale Genomes of the Flightless Caterpillar Hunter Beetles Calosoma tepidum and Calosoma wilkesii From British Columbia (Coleoptera: Carabidae). Genome biology and evolution, 17(1).

Venkatesan A, et al. (2025) Trichuriasis in Human Patients from Côte d'Ivoire Caused by Novel Trichuris incognita Species with Low Sensitivity to Albendazole/Ivermectin Combination Treatment. Emerging infectious diseases, 31(1), 104.

Polani R, et al. (2025) Cefiderocol Resistance Conferred by Plasmid-Located Ferric Citrate Transport System in KPC-Producing Klebsiella pneumoniae. Emerging infectious diseases, 31(1), 123.

Arantes I, et al. (2025) Rapid spread of the SARS-CoV-2 Omicron XDR lineage derived from recombination between XBB and BA.2.86 subvariants circulating in Brazil in late 2023. Microbiology spectrum, 13(1), e0119324.

Liu F, et al. (2025) Uneven distribution of prokaryote-derived horizontal gene transfer in fungi: a lifestyle-dependent phenomenon. mBio, 16(1), e0285524.

Li R, et al. (2025) Photosymbiosis shaped animal genome architecture and gene evolution as revealed in giant clams. Communications biology, 8(1), 7.

Hassan AM, et al. (2025) Ongoing Evolution of Middle East Respiratory Syndrome Coronavirus, Saudi Arabia, 2023-2024. Emerging infectious diseases, 31(1), 57.

Dezordi FZ, et al. (2025) Higher frequency of interstate over international transmission chains of SARS-CoV-2 virus at the Rio Grande do Sul - Brazil state borders. Virus research, 351, 199500.

Altan E, et al. (2025) Highly Pathogenic Avian Influenza (HPAI) H5N1 virus in Finland in 2021-2023 - Genetic diversity of the viruses and infection kinetics in human dendritic cells. Emerging microbes & infections, 14(1), 2447618.

Hamilton R, et al. (2025) Microbial hauberks: composition and function of surface layer proteins in gammaproteobacterial methanotrophs. Applied and environmental microbiology, 91(1), e0136424.

Shao Y, et al. (2025) Emerging antifungal resistance in Trichophyton mentagrophytes: insights from susceptibility profiling and genetic mutation analysis. Emerging microbes & infections, 14(1), 2450026.

Zhang R, et al. (2025) Molecular Phylogenetic Relationships Based on Mitogenomes of Spider: Insights Into Evolution and Adaptation to Extreme Environments. Ecology and evolution, 15(1), e70774.

Robinson LR, et al. (2025) In vitro evolution of ciprofloxacin resistance in Neisseria commensals and derived mutation population dynamics in natural Neisseria populations. FEMS microbiology letters, 372.

Shi C, et al. (2025) Development of a mitochondrial mini-barcode and its application in metabarcoding for identification of leech in traditional Chinese medicine. Scientific reports, 15(1), 1698.

Loria SF, et al. (2025) The world's most venomous spider is a species complex: systematics of the Sydney funnel-web spider (Atracidae: Atrax robustus). BMC ecology and evolution, 25(1), 7.

Yehia FAA, et al. (2025) From Isolation to Application: Utilising Phage-Antibiotic Synergy in Murine Bacteremia Model to Combat Multidrug-Resistant Enterococcus faecalis. Microbial biotechnology, 18(1), e70075.