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

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 Agency: 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


**Record Creation Time:** 20220129T080306+0000

**Record Last Update:** 20240618T054012+0000

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**Ratings and Alerts**

No rating or validation information has been found for MAFFT.

No alerts have been found for MAFFT.

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**Data and Source Information**

**Source:** [SciCrunch Registry](https://www.sci crunch.org/)

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**Usage and Citation Metrics**

We found 16590 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://www.fdi-lab.org/SciCrunch).

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. Cell, 187(6), 1440.


Fatalska A, et al. (2024) Recruitment of trimeric eIF2 by phosphatase non-catalytic subunit
PPP1R15B. Molecular cell, 84(3), 506.


Lin M, et al. (2024) ?Camelliazijinica (Theaceae), a new species endemic to Danxia landscape from Guangdong Province, China. PhytoKeys, 237, 245.


Lee J, et al. (2024) Diurnal Rhythms in the Red Seaweed Gracilariopsis chorda are
Characterized by Unique Regulatory Networks of Carbon Metabolism. Molecular biology and evolution, 41(2).