MAFFT

RRID:SCR_011811
Type: Tool

Proper Citation

MAFFT (RRID:SCR_011811)

Resource Information

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

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.

Resource Name: MAFFT

Proper Citation: MAFFT (RRID:SCR_011811)

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

Keywords: alignment, amino acid, nucleotide, sequence, DNA, sequence alignment

Resource ID: SCR_011811

Funding Agency: Culture, EMBL, Ministry of Education, Science and Technology of Japan, Sports


Availability: Free, Available for download, Freely available
Website Status: Last checked up

Alternate IDs: OMICS_00979


Abbreviations: MAFFT

Mentions Count: 6818

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 6818 mentions in open access literature.

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


Ding X, et al. (2020) Genome sequence of the agarwood tree Aquilaria sinensis (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeeae family. GigaScience, 9(3).


Adrian-Kalchhauser I, et al. (2020) The round goby genome provides insights into mechanisms that may facilitate biological invasions. BMC biology, 18(1), 11.


