

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

MUSCLE

RRID:SCR_011812

Type: Tool

Proper Citation

MUSCLE (RRID:SCR_011812)

Resource Information

URL: <http://www.ebi.ac.uk/Tools/msa/muscle/>

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Description: Multiple sequence alignment method with reduced time and space complexity. Multiple sequence alignment with high accuracy and high throughput. Data analysis service for multiple sequence comparison by log- expectation.

Abbreviations: MUSCLE

Synonyms: Multiple Sequence Comparison by Log- Expectation

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

Defining Citation: [PMID:15034147](#), [PMID:15318951](#), [DOI:10.1093/nar/gkh340](#)

Keywords: bio.tools

Resource Name: MUSCLE

Resource ID: SCR_011812

Alternate IDs: biotools:muscle, OMICS_00982

Alternate URLs: <https://bio.tools/muscle>, <http://www.drive5.com/muscle/>, <https://www.drive5.com/muscle/manual/>, <https://www.drive5.com/muscle/manual/install.html>, <http://bioconductor.org/packages/release/bioc/html/muscle.html>, <https://sources.debian.org/src/muscle/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260905T133003+0000

Ratings and Alerts

No rating or validation information has been found for MUSCLE.

No alerts have been found for MUSCLE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17169 mentions in open access literature.

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

Xiao X, et al. (2027) Highly efficient production of ??-caryophyllene in *Saccharomyces cerevisiae* using a novel synthase from *Artemisia argyi*. *Synthetic and systems biotechnology*, 15, 86.

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

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. *GigaScience*, 15.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Naing L, et al. (2026) TNFRSF13B Common Variants Enhance Antibody-Dependent Complement Activation and Susceptibility to Acute Respiratory Distress Syndrome Following Respiratory Viral Infection. *medRxiv : the preprint server for health sciences*.

Liu Q, et al. (2026) Tobacco two-pore calcium channel 1a is localised at the tonoplast, but acts on events at the plasma membrane. *Protoplasma*, 263(2), 423.

Sun G, et al. (2026) A GmNRF5a-GmCERK1-GmCAK1 module mediates chitin/chitosan-triggered immune response in soybean. *Journal of integrative plant biology*, 68(1), 257.

Liang W, et al. (2026) Evolutionary Analysis of Transcriptional Regulation Mediated by Cdx2 in Rodents. *Cell proliferation*, 59(3), e70103.

Sahoo RK, et al. (2026) Genome assembly and protein structure modeling reveal key molecular features of divergent wmk homologs in *Wolbachia*. *Microbiology spectrum*, 14(2), e0289325.

Lan MF, et al. (2026) CentriVision: An integrated platform for multiscale centromere analysis in plants. *Plant communications*, 7(2), 101689.

Spruill-Harrell B, et al. (2026) Purifying selection constrains the evolution of Juquitiba virus in wild *Oligoryzomys nigripes* communities. *PLoS pathogens*, 22(1), e1013839.

Allievi C, et al. (2026) First molecular detection and genotyping of *Enterocytozoon bieneusi* (Microsporidia) in fattening pigs from Italy. *BMC veterinary research*, 22(1).

Francette AM, et al. (2026) Evolutionary conservation and innovations of RNA polymerase II transcription elongation factors. *bioRxiv : the preprint server for biology*.

Emerling CA, et al. (2026) Pseudogenes document protracted parallel regression of oral anatomy in myrmecophagous mammals. *Molecular biology and evolution*, 43(2).

Liu S, et al. (2026) Adaptive evolution of Agaricomycetes laccases follows wood lignin diversification in plants. *Applied and environmental microbiology*, 92(2), e0197125.

Kmetiuk LB, et al. (2026) Molecular detection of hemotropic mycoplasmas (hemoplasmas) in humans and dogs living on islands and the seashore mainland of Brazil: a One Health approach. *Parasites & vectors*, 19(1), 52.

Yuan Y, et al. (2026) Phosphorothioate DNA modification by BREX type 4 systems in the human gut microbiome. *Nature communications*, 17(1), 1717.

Zhao J, et al. (2026) Identification and characterization of the class III peroxidase gene family in sea buckthorn (*Hippophae rhamnoides* subsp. *sinensis* Rousi) and its potential role in lignin biosynthesis. *BMC genomics*, 27(1), 77.

Liu X, et al. (2026) Cryo-EM structural analyses of chlorophyll b-enriched PSI-LHC and PSII-LHC supercomplexes of the siphonous green alga *Bryopsis corticulans*. *Plant communications*, 7(5), 101738.

Yue J, et al. (2026) Recreating viable YYh genotype uncovers the role of CpYYL underlying YY lethality in papaya. *Nature communications*, 17(1).