

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 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: 20260912T200015+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 [SPARC SAWG](#) .

Xiao X, et al. (2027) Highly efficient production of γ -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*.

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

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.

Lu Z, et al. (2026) The *Rhus chinensis* Genome Provides Insights Into Tannin, Flavonoid Biosynthesis, and Glandular Trichome Development. *Plant biotechnology journal*, 24(3), 988.

Alharbi SA, et al. (2026) First Plastome Sequences of Two Endemic Taxa of *Orbea* Haw. from the Arabian Peninsula: Comparative Genomics and Phylogenetic Relationships Within the Tribe Ceropegieae (Asclepiadoideae, Apocynaceae). *Biology*, 15(3).

Wu CY, et al. (2026) Role of Core Microbiome Shifts in Octocoral Litophyton Under Diurnal Temperature Fluctuations. *Microbial ecology*, 89(1).

Raoelijaona F, et al. (2026) Ancestral neuronal receptors are bacterial accessory toxins. *Nature communications*, 17(1).

Harada M, et al. (2026) Four genetically distinct types of rabies virus exist in Vietnam, including the SEA1 and SEA3 subclades within the Asian clade. *Scientific reports*, 16(1).

Liao G, et al. (2026) Evolutionary repurposing of a metabolic thiolase complex enables antibiotic biosynthesis. *Nature communications*, 17(1).

Dong Z, et al. (2026) Fungal photobiont and microbiome genome composition in the *Cladonia uncialis* tripartite symbiosis. *Scientific data*, 13(1).

Bertschmann J, et al. (2026) A recently evolved domain of the human ING1 epigenetic regulator targets mitochondria and induces senescence. *Cellular and molecular life sciences : CMLS*, 83(1), 91.

Brewer TE, et al. (2026) Horizontal transfer of post-translational modifiers brings evolutionary opportunity and challenges to a conserved translation factor. *BMC biology*, 24(1).

Mu D, et al. (2026) The genome of the medicinal plant *Uncaria rhynchophylla* provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. *Molecular horticulture*, 6(1), 9.

Ramírez GA, et al. (2026) Diel transcriptional dynamics of a marine sponge and its microbiome in a natural environment. *Animal microbiome*, 8(1), 12.

Chen L, et al. (2026) Animal-associated jumbo phages as widespread and active modulators of gut microbiome ecology and metabolism. *Science advances*, 12(6), eaeb6265.

Randmäe H, et al. (2026) Yeast community associated with winter wheat leaves and its sensitivity to fungicides. *Scientific reports*, 16(1).