

Resource Summary Report

Generated by T1D on Sep 5, 2026

trimAl

RRID:SCR_017334

Type: Tool

Proper Citation

trimAl (RRID:SCR_017334)

Resource Information

URL: <http://trimal.cgenomics.org/>

Proper Citation: trimAl (RRID:SCR_017334)

Description: Software tool for automated removal of spurious sequences or poorly aligned regions from multiple sequence alignment. Software package for automated alignment trimming in large scale phylogenetic analyses.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:19505945](#)

Keywords: removal, spurious, sequence, poorly, aligned, region, multiple, alignment, trimming, large, scale, phylogenetic, analysis, bio.tools

Funding: FIS ;
MEC

Availability: Free, Available for download, Freely available

Resource Name: trimAl

Resource ID: SCR_017334

Alternate IDs: biotools:trimal

Alternate URLs: <https://vicfero.github.io/trimal/>, <https://bio.tools/trimal>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260903T235423+0000

Ratings and Alerts

No rating or validation information has been found for trimAI.

No alerts have been found for trimAI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 673 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

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

Liu Y, et al. (2026) Genome-Wide Identification and Expression Analysis of the Hsp70 Gene Family in *Hylocereus undatus* Seedlings Under Heat Shock Stress. *International journal of molecular sciences*, 27(2).

Li X, et al. (2026) Genome-wide analysis of leucine-rich repeat-only proteins gene family revealed FaLRPop26 responding *Colletotrichum Siamense* infection by regulated lignin synthesis in cultivated strawberry (*Fragaria × ananassa*). *BMC plant biology*, 26(1), 328.

French RK, et al. (2026) Viral surveillance of invasive mammals in New Zealand reveals unique viral lineages reflecting their introduction history. *Journal of virology*, 100(1), e0144025.

Hägglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Xu B, et al. (2026) The Mitochondrial Genome of *Curcuma longa*: A Large and Structurally Complex Genome with Extensive Intracellular DNA Transfer. *Genes*, 17(2).

Zhao Z, et al. (2026) Evolutionary and Modification Features of Two Monkeypox Virus Strains: Insights from Integrated Genomic and Epigenomic Analyses. *Viruses*, 18(2).

Stephens TG, et al. (2026) Cosmopolitan Gene Families With Known Functions Are Hotspots for the Evolution of Novel Genes in Stony Corals. *Genome biology and evolution*, 18(4).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Zhao F, et al. (2026) Alternating High-Fat and Polysaccharide Diets Modulates Gut Phage-Bacterial Interplay. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(29), e16916.

Louboutin L, et al. (2026) Characterization of novel pesti- and astro-like viruses in hatchery-reared European seabass (*Dicentrarchus labrax*) associated with health disorders and low mortality. *Veterinary research*, 57(1).

Wang WP, et al. (2026) Biogeography and species diversity of freshwater Savoryellomycetidae (Sordariomycetes) fungi. *Mycology*, 17(2), 411.

Modolon F, et al. (2026) Resolving the evolutionary duality of marine symbionts: redefining the genus *Endozoicomonas* and proposing *Neoendozoicomonas* gen. nov. *ISME communications*, 6(1), ycag123.

Geng M, et al. (2026) Metatranscriptomic Analysis of Tick Virome Diversity in Hebei Province, China. *Viruses*, 18(4).

Oukkal S, et al. (2026) Tachinid Endoparasitoid Flies do not Rely on Domesticated Viruses, Unlike Multiple Hymenopteran Lineages. *Genome biology and evolution*, 18(3).

Hakim MS, et al. (2026) Reverse vaccinology-based design of a universal multiepitope vaccine against chikungunya virus: Phylogenetic and immunoinformatics approaches. *Scientific reports*, 16(1).

Lee YI, et al. (2026) Mycorrhizal specificity of fully mycoheterotrophic *Yoania* in Taiwan and China and novel natural abundance stable isotope patterns. *Plant biology (Stuttgart, Germany)*, 28(4), 1159.

Martínez-Alvarez L, et al. (2026) Diversity and evolution of archaeal immune strategies. *Nucleic acids research*, 54(5).

Panossian B, et al. (2026) Phage toxin variants are linked to protection specificity in a defensive symbiont. *Molecular biology and evolution*, 43(5).

Han Y, et al. (2026) Co-occurrence of diverse defense systems shapes complex microbe-virus relationships in deep-sea cold seeps. *Nature communications*, 17(1), 1427.