

# Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 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 trimAl.

No alerts have been found for trimAl.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 673 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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 FaLRop26 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).

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.

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

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

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).

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

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).

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.

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

Gutierrez LJ, et al. (2026) Evidence for an early cadherin-catenin interaction network in ctenophores. *Molecular biology and evolution*, 43(6).

Zhang X, et al. (2026) Reappraisal of the phylogenetic relationships of hirsutella-like fungi across Ophiocordycipitaceae and Polycephalomycetaceae (Hypocreales, Sordariomycetes), and the description of seven new species. *IMA fungus*, 17, e171084.

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.

Hu S, et al. (2026) Chloroplast Genome Insights of *Gleditsia japonica* var. *velutina* and Evolutionary Implications for Variation and Phylogeny in *Gleditsia*. *Ecology and evolution*, 16(6), e73826.

Dabak T, et al. (2026) The genetic basis of mimicry in the snowy bumble bee (*Bombus niveatus*) in Anatolia with insights from a color polymorphic gynandromorph. *PLoS genetics*, 22(3), e1012060.

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