

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 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: software application, software resource, data analysis software, data processing software

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: 20260729T044429+0000

Ratings and Alerts

No rating or validation information has been found for trimAl.

No alerts have been found for trimAl.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 582 mentions in open access literature.

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

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

Ye H, et al. (2026) Associations between gut microbiota and personality traits: insights from a captive common marmoset (*Callithrix jacchus*) colony. *Microbiology spectrum*, 14(1), e0044325.

Qiu S, et al. (2025) Functional evolution and diversification of CYP82D subfamily members have shaped flavonoid diversification in the genus *Scutellaria*. *Plant communications*, 6(1), 101134.

Zhang Y, et al. (2025) Metabolic enhancement contributed by horizontal gene transfer is essential for dietary specialization in leaf beetles. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2415717122.

Zhang R, et al. (2025) Molecular Phylogenetic Relationships Based on Mitogenomes of Spider: Insights Into Evolution and Adaptation to Extreme Environments. *Ecology and evolution*, 15(1), e70774.

Li R, et al. (2025) Photosymbiosis shaped animal genome architecture and gene evolution as revealed in giant clams. *Communications biology*, 8(1), 7.

Shao B, et al. (2025) Versatile nitrate-respiring heterotrophs are previously concealed contributors to sulfur cycle. *Nature communications*, 16(1), 1202.

Hoile AE, et al. (2025) Gene novelty and gene family expansion in the early evolution of Lepidoptera. *BMC genomics*, 26(1), 161.

Maeda K, et al. (2025) Adaptive evolution of sesquiterpene deoxyphomenone in mycoparasitism by *Hansfordia pulvinata* associated with horizontal gene transfer from *Aspergillus* species. *mBio*, 16(4), e0400724.

Lu L, et al. (2025) ?Unveiling fungal diversity associated with coffee trees in China using a polyphasic approach and a global review of coffee saprobic fungi. *IMA fungus*, 16, e144874.

Mariano G, et al. (2025) Modularity of Zorya defense systems during phage inhibition. *Nature communications*, 16(1), 2344.

Wiredu-Boakye D, et al. (2025) Evolutionary Insights into the Length Variation of DNA Damage Response Proteins Across Eukaryotes. *Genome biology and evolution*, 17(6).

Barros KO, et al. (2025) Taxogenomic analysis of *Pichia seneci* sp. nov. and new insights into hybridization events in the *Pichia cactophila* species complex. *FEMS yeast research*, 25.

Abdallah RZ, et al. (2025) Microbial dark matter spearheading the biogeochemical cycle in the Solar Lake of Taba, Egypt. *Current research in microbial sciences*, 9, 100433.

Ament-Velásquez SL, et al. (2025) Reconstructing NOD-like receptor alleles with high internal conservation in *Podospira anserina* using long-read sequencing. *Microbial genomics*, 11(7).

Sun J, et al. (2025) Genomic and epigenomic insight into giga-chromosome architecture and adaptive evolution of royal lily (*Lilium regale*). *Nature communications*, 16(1), 5617.

Song H, et al. (2025) Plastomes provide new insights into phylogeny and evolution in Chlorellaceae (Chlorophyta, Trebouxiophyceae). *BMC plant biology*, 25(1), 1319.

Yang Z, et al. (2025) Genome-wide identification and expression patterns analysis of the DREB gene family under various abiotic stress in *Lolium perenne*. *BMC plant biology*, 25(1), 1635.

Regney M, et al. (2025) Diversity of polyomaviruses and papillomaviruses in penguins from eastern and western Antarctica. *Microbial genomics*, 11(11).

Guo T, et al. (2025) A high-quality chromosome-level genome assembly of the oligophagous fruit fly *Bactrocera tsuneonis* (Diptera: Tephritidae) and insights into its host specificity. *GigaScience*, 14.