

Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

Mauve

RRID:SCR_012852

Type: Tool

Proper Citation

Mauve (RRID:SCR_012852)

Resource Information

URL: <https://darlinglab.org/mauve/mauve.html>

Proper Citation: Mauve (RRID:SCR_012852)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Software as system for efficiently constructing multiple genome alignments in the presence of large-scale evolutionary events such as rearrangement and inversion.

Abbreviations: Mauve

Resource Type: software resource

Defining Citation: [DOI:10.1101/gr.2289704](https://doi.org/10.1101/gr.2289704)

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Mauve

Resource ID: SCR_012852

Alternate IDs: OMICS_00940, biotools:mauve

Alternate URLs: <https://bio.tools/mauve>

Old URLs: <http://gel.ahabs.wisc.edu/mauve/>

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260905T132728+0000

Ratings and Alerts

No rating or validation information has been found for Mauve.

No alerts have been found for Mauve.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1675 mentions in open access literature.

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

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of *Mycoplasma ovipneumoniae* strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. *Veterinary research*, 57(1).

Rahim N, et al. (2026) A case of yogurt central line-associated bloodstream infection in a child with intestinal failure. *Nutrition in clinical practice : official publication of the American Society for Parenteral and Enteral Nutrition*, 41(3), 968.

Abdullah , et al. (2026) Evolutionary dynamics of the chloroplast genome in *Daphne* (Thymelaeaceae): comparative analysis with related genera and insights into phylogenetics. *FEBS open bio*, 16(3), 503.

Ricci ML, et al. (2026) Genomic characterization of *Legionella pneumophila* serogroup 1 ST901 isolates responsible for recurrent travel-associated Legionnaires' disease cases and clusters. *Pathogens and global health*, 120(3), 178.

Saldamando CI, et al. (2026) Genomic and phylogenetic insights for three species of thrips (Thysanoptera: Terebrantia) associated with Colombian avocado. *Journal of insect science (Online)*, 26(1).

Feng L, et al. (2026) Comprehensive analysis of the complete chloroplast genome of white pomegranate and phylogenetic relationships within Myrtales. *BMC genomics*, 27(1), 220.

Kovács ÁB, et al. (2026) Genome-wide association study of *Mycoplasma anserisalpiginidis* strains for antibiotic susceptibility. *Scientific reports*, 16(1).

Jiang J, et al. (2026) Genomic analysis of a clinical *Streptococcus suis* ST1 isolate from CSF reveals antimicrobial resistance, virulence, and an evolutionary link to ST7. *Scientific reports*, 16(1).

Long W, et al. (2026) Comprehensive Analysis of Wild Rice Mitochondrial Genomes Reveals Structural Variation, Repeat Dynamics, and the Evolution of orf182. *Plants (Basel, Switzerland)*, 15(7).

Baasanmunkh S, et al. (2026) Integrative study of the rare *Incarvillea potaninii* (Bignoniaceae) in Mongolia: conservation, comparative plastome, distribution modelling,

phylogeny, and taxonomic insights. *Scientific reports*, 16(1).

Senavirathna I, et al. (2026) Genomic analysis of human-infecting *Leptospira borgpetersenii* isolates in Sri Lanka: Expanded PF07598 gene family repertoire and less genome reduction than bovine isolates. *PLoS neglected tropical diseases*, 20(3), e0012540.

Shin GY, et al. (2026) Comparative genomics of *Pantoea allii* lineages and distribution of ecologically relevant traits. *Microbial genomics*, 12(2).

Mohammadi T, et al. (2026) New Species of Kronosvirus Bacteriophages That Infect *Caulobacter* Strain CBR1. *Viruses*, 18(4).

Yu S, et al. (2026) Mitochondrial genome of *Iodes seguinii* reveals repeat-mediated recombination and phylogenetic insights in Icacinaceae. *BMC genomics*, 27(1).

Yu R, et al. (2026) Linking oxidative stress defense to biofilm architecture: Ohr mediates strain-dependent persistence in *Acinetobacter baumannii*. *Virulence*, 17(1), 2664989.

Liu S, et al. (2026) Complete chloroplast genome features and phylogenetic analysis of *Clematis cadmia*. *Scientific reports*, 16(1).

Shahid I, et al. (2026) Comparative genome analysis of *Pseudomonas chlororaphis* strains reveals biosynthetic diversity underlying plant growth promotion and soil health improvement. *BMC genomics*, 27(1).

Hwang H, et al. (2026) Organelle genome evolution in the early-diverging brown algal lineage, *Ishigeales*. *Journal of phycology*, 62(3), 1090.

Xiang N, et al. (2026) Decoding coral resistance to eutrophication through the association of hyper-efficient denitrifiers as key microbial allies. *Nature communications*, 17(1).

Segura A, et al. (2026) *Novosphingobium aeonii* sp. nov., isolated from leaves of *Aeonium decorum*, is able to grow with polycyclic aromatic hydrocarbons. *International journal of systematic and evolutionary microbiology*, 76(6).