

Resource Summary Report

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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: 20260725T190742+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 1569 mentions in open access literature.

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

Safari M, et al. (2026) Comprehensive genomic analysis of a novel *Bacillus cereus* decomposing toluene potentially applicable in bioremediation. *Microbiology spectrum*, 14(1), e0289224.

Pe??ka K, et al. (2025) Probiotic potential of *Bacillus* Isolates from Polish Bee Pollen and Bee Bread. *Probiotics and antimicrobial proteins*, 17(1), 364.

Xu L, et al. (2025) Genomic Insights into the Pathogenicity of Hypervirulent *Aeromonas hydrophila* Strain D4 Isolated from Diseased Blunt Snout Bream with the Epidemic Sequence Type 251 Clones. *Pathogens (Basel, Switzerland)*, 14(6).

Shahed K, et al. (2025) Benchmarking pangenome dynamics and horizontal gene transfer in *Mycobacterium marinum* evolution. *Frontiers in microbiology*, 16, 1537826.

Arias T, et al. (2025) Plastome phylogenomics of the diverse neotropical orchid genus *Lepanthes* with emphasis on subgenus *Marsipanthes* (Pleurothallidinae: Orchidaceae). *BMC ecology and evolution*, 25(1), 79.

Na HE, et al. (2025) Mutation of the *gidB* gene causes intrinsic streptomycin resistance in *Bacillus velezensis*. *Scientific reports*, 15(1), 5565.

Wang T, et al. (2025) Molecular phylogeny and comparative chloroplast genome analysis of the type species *Crucigenia quadrata*. *BMC plant biology*, 25(1), 64.

Meng X, et al. (2025) Identification of two new genetic loci for high-resolution genotyping of *Enterocytozoon bieneusi*. *Parasite (Paris, France)*, 32, 6.

Vera-Cabrera L, et al. (2025) *Actinomadura welshii* sp. nov., a New Mycetoma Agent in Mexico. *PLoS neglected tropical diseases*, 19(4), e0013016.

Kaplan E, et al. (2025) qPCR-Based Molecular Detection of *Trichophyton indotineae* by Targeting Divergent Sequences. *Mycopathologia*, 190(2), 32.

Jiang Y, et al. (2025) Comparative chloroplast genomes of *Incarvillea* species (Bignoniaceae) unveiled genomic diversity and shed light on phylogenetic relationships. *BMC plant biology*, 25(1), 399.

Gabor CE, et al. (2025) Characterization of *Shigella flexneri* serotype 6 strains from geographically diverse low- and middle-income countries. *mBio*, 16(1), e0221024.

Yang S, et al. (2025) Comparative Genomics Reveals Evidence of the Genome Reduction and Metabolic Potentials of *Aliineobacillus hadale* Isolated from Challenger Deep Sediment of the Mariana Trench. *Microorganisms*, 13(1).

Aminian-Dehkordi J, et al. (2025) MetaBiome: a multiscale model integrating agent-based and metabolic networks to reveal spatial regulation in gut mucosal microbial communities. *mSystems*, 10(5), e0165224.

Beebe MA, et al. (2025) Phenotypic analysis of various *Clostridioides difficile* ribotypes reveals consistency among core processes. *Applied and environmental microbiology*, 91(7), e0096425.

Ou CY, et al. (2025) Novel perspectives on plastome evolution in Onagraceae. *AoB PLANTS*, 17(3), plaf025.

Romero Picazo D, et al. (2025) Evolution of the Plant-Associated *Pantoea* was Accompanied by Plasmid Domestication Events. *Molecular biology and evolution*, 42(11).

Hidayat MT, et al. (2025) Comparative Genomic Analysis Identifies FleQ and GcbB as Virulence-Associated Factors in *Pseudomonas syringae* pv. *tabaci* Strains. *Molecular plant pathology*, 26(11), e70168.

Hou T, et al. (2025) Comparative genomic analysis of five *Eimeria* spp. in rabbits provides insights into coccidian tissue tropism. *Microbial genomics*, 11(11).

McKnight DJE, et al. (2025) Comparative genomics of '*Xanthomonas cannabis*' reveals an emerging, diverse pathogen. *Microbial genomics*, 11(11).