

Resource Summary Report

Generated by T1D on Aug 1, 2026

MUMmer

RRID:SCR_018171

Type: Tool

Proper Citation

MUMmer (RRID:SCR_018171)

Resource Information

URL: <http://mummer.sourceforge.net/>

Proper Citation: MUMmer (RRID:SCR_018171)

Description: Software package as system for rapidly aligning entire genomes. Alignment tool for DNA and protein sequences. Can align incomplete genomes.

Synonyms: MUMmer4, MUMmer 3.0

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

Defining Citation: [PMID:14759262](https://pubmed.ncbi.nlm.nih.gov/14759262/)

Keywords: Align, genome, DNA, protein, sequence, , bio.tools

Funding: NLM R01 LM06845;
NSF IIS 9902923;
NIAID N01 AI15447

Availability: Free, Available for download, Freely available

Resource Name: MUMmer

Resource ID: SCR_018171

Alternate IDs: OMICS_14554, biotools:mummer

Alternate URLs: <https://github.com/mummer4/mummer>, <https://bio.tools/mummer>,
<https://sources.debian.org/src/mummer/>

License: Artistic License 2.0

Record Creation Time: 20220129T080339+0000

Ratings and Alerts

No rating or validation information has been found for MUMmer.

No alerts have been found for MUMmer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 480 mentions in open access literature.

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

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Yu X, et al. (2025) Super pan-genome reveals extensive genomic variations associated with phenotypic divergence in *Actinidia*. *Molecular horticulture*, 5(1), 4.

Kim DR, et al. (2025) Functional Characterization of Polyketide Synthase Clusters in *Streptomyces anandii* J6. *The plant pathology journal*, 41(4), 539.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Hue Y, et al. (2025) Comparative Genomics Reveals Conserved Ophiobolin Biosynthetic Gene Cluster and Necrotrophic Adaptation in *Bipolaris oryzae*. *The plant pathology journal*, 41(5), 682.

Liu F, et al. (2025) Chromosome-level genome assembly of the crofton weed (*Ageratina adenophora*). *Scientific data*, 12(1), 560.

Massonnet M, et al. (2025) Evolutionary conservation of the grape sex-determining region in angiosperms and emergence of dioecy in Vitaceae. *Nature communications*, 16(1), 6047.

Guo D, et al. (2025) A pangenome reference of wild and cultivated rice. *Nature*, 642(8068), 662.

Wu J, et al. (2025) Chromosome-Level Genome Announcement of the Monokaryotic *Pleurotus ostreatus* Strain PC80. *Journal of fungi (Basel, Switzerland)*, 11(8).

Teixeira M, et al. (2025) Circling in on plasmids: benchmarking plasmid detection and reconstruction tools for short-read data from diverse species. *Briefings in bioinformatics*,

26(6).

Thiede SN, et al. (2025) Antibiotic-resistance plasmid amplified among MRSA cases in an urban jail and its connected communities. medRxiv : the preprint server for health sciences.

Zhu B, et al. (2025) A-to-I RNA editing of CYP18A1 mediates transgenerational wing dimorphism in aphids. eLife, 13.

Gutiérrez AV, et al. (2025) Population structure and gene flux of *Listeria monocytogenes* ST121 reveal prophages as a candidate driver of adaptation and persistence in food production environments. Microbial genomics, 11(4).

Ricciardi V, et al. (2025) The genome of *Vitis vinifera* cv. Mgaloblishvili reveals resistance and susceptibility factors to downy mildew in the Rpv29 and Rpv31 loci. Horticulture research, 12(6), uhaf055.

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).

Peña F, et al. (2025) In Silico Genomic Analysis of Chloroplast DNA in *Vitis Vinifera* L.: Identification of Key Regions for DNA Coding. Genes, 16(6).

Ayhan DH, et al. (2025) Host-specific adaptation in *Fusarium oxysporum* correlates with distinct accessory chromosome content in human and plant pathogenic strains. mBio, 16(8), e0095125.

Gluck-Thaler E, et al. (2025) Giant transposons promote strain heterogeneity in a major fungal pathogen. mBio, 16(6), e0109225.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. GigaByte (Hong Kong, China), 2025, gigabyte155.

Wen W, et al. (2025) Chromosome-Level Genome Assembly and Annotation of purple nutsedge (*Cyperus rotundus* Cyperaceae). Scientific data, 12(1), 1838.