

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

Mugsy

RRID:SCR_001414

Type: Tool

Proper Citation

Mugsy (RRID:SCR_001414)

Resource Information

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

Proper Citation: Mugsy (RRID:SCR_001414)

Description: Software resource for multiple whole genome alignment. It uses Nucmer, a custom graph-based segmentation procedure, for pairwise alignment, and the Seqan:TCoffee's multiple alignment strategy.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:21148543](#), [DOI:10.1093/bioinformatics/btq665](#)

Keywords: software, genome, genome alignment, segmentation, pairwise alignment, sequence analysis software

Availability: Free, Available for download, Freely available

Resource Name: Mugsy

Resource ID: SCR_001414

Alternate IDs: OMICS_03606

Old URLs: <https://sources.debian.org/src/mugsy/>

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260912T195525+0000

Ratings and Alerts

No rating or validation information has been found for Mugsy.

No alerts have been found for Mugsy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 75 mentions in open access literature.

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

Hu J, et al. (2026) Population Ecology of Glacier Bacteria from the View of Gene Flow in Cryobacterium. Microorganisms, 14(2).

Yu XA, et al. (2026) Genome-wide sweeps create ecological units in the human gut microbiome. Nature, 655(8121), 202.

Hariharan J, et al. (2026) Biogeographical and phylogenetic constraints on horizontal gene transfer and genome evolution in Streptomyces. Microbiology spectrum, 14(2), e0295825.

Ahearn CP, et al. (2026) Identification of interbacterial adhesion between oral Schaalaa species and streptococcal serine-rich repeat glycoproteins. FEMS microbiology letters, 373.

Kilian M, et al. (2025) Re-evaluation of boundaries of Streptococcus mitis and Streptococcus oralis and demonstration of multiple later synonyms of Streptococcus mitis, Streptococcus oralis and Streptococcus thalassemae: description of Streptococcus mitis subsp. carlssonii subsp. nov. and emended description of Streptococcus mitis. International journal of systematic and evolutionary microbiology, 75(3).

Xavier KVM, et al. (2025) Diversity and Role of Prophages in Pseudomonas aeruginosa: Resistance Genes and Bacterial Interactions. Genes, 16(6).

Steensen K, et al. (2024) Tailless and filamentous prophages are predominant in marine Vibrio. The ISME journal, 18(1).

Papudeshi B, et al. (2023) Host Association and Spatial Proximity Shape but Do Not Constrain Population Structure in the Mutualistic Symbiont Xenorhabdus bovienii. mBio, 14(3), e0043423.

Shallom SJ, et al. (2023) Evolution of Mycobacterium abscessus in the human lung: Cumulative mutations and genomic rearrangement of porin genes in patient isolates. Virulence, 14(1), 2215602.

Shi ZJ, et al. (2023) Maast: genotyping thousands of microbial strains efficiently. Genome biology, 24(1), 186.

Xu T, et al. (2023) A Global Survey of Hypervirulent Aeromonas hydrophila (vAh) Identified vAh Strains in the Lower Mekong River Basin and Diverse Opportunistic Pathogens from Farmed Fish and Other Environmental Sources. Microbiology spectrum,

11(2), e0370522.

Drewes JL, et al. (2022) Human Colon Cancer-Derived *Clostridioides difficile* Strains Drive Colonic Tumorigenesis in Mice. *Cancer discovery*, 12(8), 1873.

Gundappa MK, et al. (2022) Genome-Wide Reconstruction of Rediploidization Following Autopolyploidization across One Hundred Million Years of Salmonid Evolution. *Molecular biology and evolution*, 39(1).

Allué-Guardia A, et al. (2022) Pathogenomes and variations in Shiga toxin production among geographically distinct clones of *Escherichia coli* O113:H21. *Microbial genomics*, 8(4).

Hénault M, et al. (2022) Hybridization drives mitochondrial DNA degeneration and metabolic shift in a species with biparental mitochondrial inheritance. *Genome research*, 32(11-12), 2043.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. *GigaScience*, 12.

Wade KJ, et al. (2022) Phylodynamics of a regional SARS-CoV-2 rapid spreading event in Colorado in late 2020. *PloS one*, 17(10), e0274050.

Udaondo Z, et al. (2022) Insertion sequences and other mobile elements associated with antibiotic resistance genes in *Enterococcus* isolates from an inpatient with prolonged bacteraemia. *Microbial genomics*, 8(8).

Uengwetwanit T, et al. (2021) A chromosome-level assembly of the black tiger shrimp (*Penaeus monodon*) genome facilitates the identification of growth-associated genes. *Molecular ecology resources*, 21(5), 1620.

Dienstbier A, et al. (2021) Comparative Omics Analysis of Historic and Recent Isolates of *Bordetella pertussis* and Effects of Genome Rearrangements on Evolution. *Emerging infectious diseases*, 27(1), 57.