

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 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: 20260821T193630+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 [dkNET](#).

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 *Schaalia* 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.

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).

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).

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.

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).

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.

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.

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.