

Resource Summary Report

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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 processing software, data analysis software, software resource, sequence analysis software, software application

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: 20260805T044022+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 71 mentions in open access literature.

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

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.

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.

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

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.
- 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.
- Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. *GigaScience*, 12.
- 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.
- Bendixsen DP, et al. (2021) Genomic Evidence of an Ancient East Asian Divergence Event in Wild *Saccharomyces cerevisiae*. *Genome biology and evolution*, 13(2).
- Queen J, et al. (2021) Comparative Analysis of Colon Cancer-Derived *Fusobacterium nucleatum* Subspecies: Inflammation and Colon Tumorigenesis in Murine Models. *mBio*, 13(1), e0299121.
- Lin M, et al. (2021) Comparative Analysis of Genome of *Ehrlichia* sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. *BMC genomics*, 22(1), 11.
- Islam MT, et al. (2021) Population Analysis of *Vibrio cholerae* in Aquatic Reservoirs Reveals a Novel Sister Species (*Vibrio paracholerae* sp. nov.) with a History of Association with Humans. *Applied and environmental microbiology*, 87(17), e0042221.