

Resource Summary Report

Generated by RRID on Aug 2, 2026

Miniasm

RRID:SCR_024114

Type: Tool

Proper Citation

Miniasm (RRID:SCR_024114)

Resource Information

URL: <https://github.com/lh3/miniasm>

Proper Citation: Miniasm (RRID:SCR_024114)

Description: Software OLC-based de novo assembler for noisy long reads.

Synonyms: miniasm

Resource Type: software resource, software library, software toolkit

Keywords: de novo assembler, noisy long reads

Availability: Free, Available for download, Freely available,

Resource Name: Miniasm

Resource ID: SCR_024114

Alternate IDs: OMICS_11366

Alternate URLs: <https://sources.debian.org/src/miniasm/>

License: MIT License

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260801T190857+0000

Ratings and Alerts

No rating or validation information has been found for Miniasm.

No alerts have been found for Miniasm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Lwin HW, et al. (2025) Isolation and Whole Genome Sequence Analysis of *Alcaligenes* and *Chromobacterium* Strains with Antimicrobial Activity Against ESKAPE Pathogen Relatives. *Journal of genomics*, 13, 40.

Rivera DE, et al. (2025) Dynamics of gut colonization by commensal and pathogenic bacteria that attach to the intestinal epithelium. *NPJ biofilms and microbiomes*, 11(1), 70.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Li D, et al. (2025) Assembly and comparative analysis of the first complete mitochondrial genome of *Camellia sinensis* var. *assamica* 'Hainan Dayezhong', endemic to Hainan Province, China. *BMC plant biology*, 25(1), 1304.

Guadarrama-Orozco KD, et al. (2025) Challenging the paradigm: non-canonical exoprotease cheating in clinical *Pseudomonas aeruginosa* isolates. *FEMS microbiology ecology*, 101(11).

Delaby M, et al. (2025) Phenotypic plasticity in cell elongation among closely related bacterial species. *Nature communications*, 16(1), 5099.

Martinez-Cazorla A, et al. (2025) The early injected genomic region determines sensitivity to Type I restriction-modification defence against Autographiviridae phages. *Nucleic acids research*, 53(18).

Kumar L, et al. (2025) Strain-level differences in *Gardnerella* urinary tract persistence and pathogenesis are consistent with comparative phylogenomic analyses. *bioRxiv : the preprint server for biology*.

Menzel P, et al. (2024) Snakemake workflows for long-read bacterial genome assembly and evaluation. *GigaByte (Hong Kong, China)*, 2024, gigabyte116.

Ben Ch??hida S, et al. (2024) Increase of niche filling with increase of host richness for plant-infecting mastreviruses. *Virus evolution*, 10(1), veae107.

Lovy J, et al. (2024) Seasonal Mortality of Wild Atlantic Menhaden (*Brevoortia tyrannus*) Is Caused by a Virulent Clone of *Vibrio* (*Listonella*) *anguillarum*; Implications for Biosecurity along the Atlantic Coastal United States. *Transboundary and emerging diseases*, 2024, 8816604.

Russo A, et al. (2024) Genome of the early spider-orchid *Ophrys sphegodes* provides insights into sexual deception and pollinator adaptation. *Nature communications*, 15(1), 6308.

Ermann Lundberg L, et al. (2024) *Bifidobacterium longum* subsp. *longum* BG-L47 boosts growth and activity of *Limosilactobacillus reuteri* DSM 17938 and its extracellular membrane vesicles. *Applied and environmental microbiology*, 90(7), e0024724.

Cosma BM, et al. (2022) Evaluating long-read de novo assembly tools for eukaryotic genomes: insights and considerations. *GigaScience*, 12.

Pedersen TB, et al. (2020) Heterologous Expression of the Core Genes in the Complex Fusarubin Gene Cluster of *Fusarium Solani*. *International journal of molecular sciences*, 21(20).

Vijayakumar S, et al. (2020) Insights into the complete genomes of carbapenem-resistant *Acinetobacter baumannii* harbouring bla OXA-23, bla OXA-420 and bla NDM-1 genes using a hybrid-assembly approach. *Access microbiology*, 2(8), acmi000140.