

Resource Summary Report

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Unicycler

RRID:SCR_024380

Type: Tool

Proper Citation

Unicycler (RRID:SCR_024380)

Resource Information

URL: <https://github.com/rwick/Unicycler>

Proper Citation: Unicycler (RRID:SCR_024380)

Description: Software assembly pipeline for bacterial genomes. Used for resolving bacterial genome assemblies from short and long sequencing reads. Can assemble Illumina only read sets where it functions as SPAdes-optimiser. Can assembly long read only sets for PacBio or Nanopore where it runs miniasm+Racon pipeline.

Synonyms: unicycler

Resource Type: software resource, software toolkit

Defining Citation: [PMID:28594827](#)

Keywords: assembly pipeline, bacterial genomes, resolving bacterial genome assemblies, short and long sequencing reads,

Availability: Free, Available for download, Freely available,

Resource Name: Unicycler

Resource ID: SCR_024380

Alternate IDs: OMICS_14591

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

License: GNU

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T190857+0000

Ratings and Alerts

No rating or validation information has been found for Unicycler.

No alerts have been found for Unicycler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 449 mentions in open access literature.

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

Mahajan S, et al. (2026) Molecular insights into the antimicrobial and cardiometabolic functions of *Lactobacillus crispatus* isolated from the reproductive tract microbiota of Indian women. *Journal of biomedical science*, 33(1), 7.

Zhou M, et al. (2026) Evaluating eravacycline's efficacy against pediatric carbapenem-resistant *Klebsiella pneumoniae* in China: a 6-year study. *Microbiology spectrum*, 14(1), e0248225.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Lopes BS, et al. (2025) Molecular epidemiology of extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* bloodstream infections from Aberdeen, Scotland, and their comparison to isolates from England. *Microbial genomics*, 11(6).

Wang Y, et al. (2025) Emergence of highly virulent *Aeromonas dhakensis* in channel catfish aquaculture: Genomic insights into pathogenicity and antimicrobial resistance. *Virulence*, 16(1), 2525933.

Martins-Gonçalves T, et al. (2025) Phylogenomic analysis of aquatic and clinical OXA-23-positive *Acinetobacter baumannii* belonging to the international clone 5 (ST79) from Southeast Brazil. *One health (Amsterdam, Netherlands)*, 21, 101140.

Hrala M, et al. (2025) Whole genome sequences of nine *Typhlocyba equigenitalis* strains isolated in the Czech Republic between 1982-2021: Molecular dating suggests a common ancestor at the time of Roman Empire. *PloS one*, 20(1), e0315946.

Zhao K, et al. (2025) IS15DIV-flanked composite transposon harboring bla NDM-5 in multidrug-resistant *Salmonella Typhimurium*. *iScience*, 28(2), 111720.

Keuleyan E, et al. (2025) Characterization of *Streptococcus pyogenes* Strains from Tonsillopharyngitis and Scarlet Fever Resurgence, 2023-FIRST Detection of M1UK in Bulgaria. *Microorganisms*, 13(1).

- Pradal I, et al. (2025) The production of esters by specific sourdough lactic acid bacteria species is limited by the precursor concentrations. *Applied and environmental microbiology*, 91(3), e0221624.
- Betim ME, et al. (2025) Influence of Sub-Inhibitory Concentrations of Sanitizers and Oxacillin on the Resistance of Methicillin-Resistant *Staphylococcus* spp. *Veterinary sciences*, 12(10).
- Zhou K, et al. (2025) Comparative genomic analysis of hypervirulent group B streptococcus of ST12/serotype Ib suggests potential virulence factors. *BMC microbiology*, 25(1), 698.
- Corretto E, et al. (2025) Evolutionary dynamics of obligate endosymbiosis in the psyllid genus *Cacopsylla*. *Communications biology*, 8(1), 1540.
- Bakkeren E, et al. (2025) Strain displacement in microbiomes via ecological competition. *Nature microbiology*, 10(12), 3122.
- Ross TA, et al. (2025) *Enterococcus lactis* is ecologically and genetically distinct from the major opportunistic pathogen *Enterococcus faecium*. *Microbial genomics*, 11(6).
- Bernaquez I, et al. (2025) Dogs fed raw meat-based diets are vectors of drug-resistant *Salmonella* infection in humans. *Communications medicine*, 5(1), 214.
- Hawkey J, et al. (2025) Genomic diversity of clinically relevant bacterial pathogens from an acute care hospital in Suva, Fiji. *JAC-antimicrobial resistance*, 7(3), dlaf058.
- Coelho JT, et al. (2025) Culture-supported ecophysiology of the SAR116 clade demonstrates metabolic and spatial niche partitioning. *The ISME journal*, 19(1).
- Adhikary R, et al. (2025) De novo assembly of seven multidrug-resistant (MDR) *Staphylococci* genomes from biofilms of hemodialysis tunneled cuffed catheter tips of patients undergoing renal failure treatment. *Microbiology resource announcements*, 14(10), e0043525.