

Resource Summary Report

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Circlator

RRID:SCR_016058

Type: Tool

Proper Citation

Circlator (RRID:SCR_016058)

Resource Information

URL: <http://sanger-pathogens.github.io/circlator/>

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Description: Software that automates assembly circularization and produces accurate linear representations of circular sequences. It is used for assembling of DNA sequence data of complete bacterial and small eukaryotic genomes.

Resource Type: data processing software, software toolkit, software resource, image analysis software, alignment software, software application

Defining Citation: [PMID:26714481](#), [DOI:10.1186/s13059-015-0849-0](#)

Keywords: assembly, sequence, genome, DNA, circularization, accurate, bacteria, eukaryote, tool

Funding: Wellcome Trust grant 098051

Availability: Free, Available for download

Resource Name: Circlator

Resource ID: SCR_016058

Alternate IDs: OMICS_09488

Alternate URLs: <https://github.com/sanger-pathogens/circlator>,
<https://sources.debian.org/src/circlator/>

License: GPL 3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260731T042951+0000

Ratings and Alerts

No rating or validation information has been found for Circlator.

No alerts have been found for Circlator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 321 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Qi J, et al. (2026) Integrated genomic and metabolomic analysis reveals the biocontrol potential of endophytic *Bacillus velezensis* NS13 against *Fusarium* species in *Lonicera macranthoides*. *BMC microbiology*, 26(1), 5.

Tizabi D, et al. (2025) Nanopore Sequencing of *Amoebophrya* Species Reveals Novel Collection of Bacteria Putatively Associated With *Karodinium veneficum*. *Genome biology and evolution*, 17(3).

Jaakkola K, et al. (2025) Understanding *Serratia bockelmannii* transmission during a neonatal intensive care unit outbreak: a combined genotyping and case-control study. *Antimicrobial resistance and infection control*, 14(1), 128.

Lu Y, et al. (2025) Comparative genomics of *Nocardia tsunamensis* IFM 10818, a new source of the antibacterial macrolide nargenicin A1. *Microbiology spectrum*, 13(12), e0122025.

Peng F, et al. (2025) Biocontrol potential and comparative genomic analysis of two *Bacillus velezensis* strains against sclerotinosis in mulberry fruit. *Frontiers in microbiology*, 16, 1587301.

Coluzzi C, et al. (2025) Comparative genomics of *Salmonella enterica* serovars Paratyphi A, Typhi and Typhimurium reveals distinct profiles of their pangenome, mobile genetic elements, antimicrobial resistance and defense systems repertoire. *Virulence*, 16(1), 2504658.

Maron B, et al. (2025) Uncovering the genetic basis of *Staphylococcus aureus* resistance to single antimicrobial peptides and their combinations. *iScience*, 28(6), 112671.

Lee Y, et al. (2025) Therapeutic potential of *Bacillus sonorensis* PMC204 membrane vesicles against drug-resistant *Mycobacterium tuberculosis*. *Medical microbiology and immunology*, 214(1), 43.

Stritt C, et al. (2025) Gene conversion and duplication contribute to genetic variation in an outbreak of *Mycobacterium tuberculosis*. *Microbial genomics*, 11(5).

Bae J, et al. (2025) Multi-omics analysis reveals the genetic basis for rapid CO₂ utilization in the acetogenic bacterium *Sporomusa sphaeroides* KIAC. *mSystems*, 10(9), e0045125.

Bae J, et al. (2025) Determination of the transcription unit landscape and associated regulatory elements in *Methylosinus sporium* 5. *Microbiology spectrum*, 13(9), e0128125.

Lee S, et al. (2025) Functional characterization of a novel plant growth-promoting rhizobacterium enhancing root growth and salt stress tolerance. *Scientific reports*, 15(1), 30405.

Arredondo-Alonso S, et al. (2025) Plasmid-driven strategies for clone success in *Escherichia coli*. *Nature communications*, 16(1), 2921.

Gasser MT, et al. (2025) Complete genome sequences of two shipworm endosymbiont strains, *Teredinibacter turnerae* SR01903 and SR02026. *Microbiology resource announcements*, 14(6), e0026525.

Liu Z, et al. (2025) Functional genomic analysis of *Bacillus cereus* BC4 strain for chromium remediation in contaminated soil. *Current research in microbial sciences*, 8, 100388.

Xu L, et al. (2025) Mobilome-mediated transcriptional activation of biosynthetic gene clusters and its impact on strain competitiveness in food fermentation microbiomes. *Microbiome*, 13(1), 191.

Liu Z, et al. (2025) C15-bacillomycin D produced by *Bacillus amyloliquefaciens* 4-9-2 suppress *Fusarium graminearum* infection and mycotoxin biosynthesis. *Frontiers in microbiology*, 16, 1599452.

Duan G, et al. (2025) An Emerging Bacterial Leaf Disease in Rice Caused by *Pantoea ananatis* and *Pantoea eucalypti* in Northeast China. *Microorganisms*, 13(6).

Charles H, et al. (2025) Epidemiologic and Genomic Investigation of Sexually Transmitted *Shigella sonnei*, England. *Emerging infectious diseases*, 31(7), 1394.

Manzanares-Pedrosa A, et al. (2025) Phenotypic and whole genome-based characterization of antibiotic resistance of *Campylobacter jejuni* isolates from chicken livers. *Poultry science*, 104(8), 105302.