

# Resource Summary Report

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## Circlator

RRID:SCR\_016058

Type: Tool

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### Proper Citation

Circlator (RRID:SCR\_016058)

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### Resource Information

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

**Proper Citation:** Circlator (RRID:SCR\_016058)

**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:** image analysis software, software toolkit, alignment software, software application, data processing software, software resource

**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:** 20260801T190526+0000

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## Ratings and Alerts

No rating or validation information has been found for Circlator.

No alerts have been found for Circlator.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 321 mentions in open access literature.

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

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).

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

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.

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

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.

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.

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

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.

Krause AL, et al. (2025) Comparative and functional genomic analysis of foreign DNA defense mechanisms in *Enterococcus faecium*. *Microbiology spectrum*, 13(8), e0028925.

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).

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

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.

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.

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.

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

Yuan Z, et al. (2025) The Enzyme Glucose-1-Phosphate Thymidyltransferase RmlA Plays a Crucial Role in the Pathogenesis of *Pectobacterium actinidiae* GX1. *Molecular plant pathology*, 26(7), e70118.

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.