

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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

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: 20260808T190028+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 363 mentions in open access literature.

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

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in Mycobacterium tuberculosis constitutively generates subpopulations with distinct clinical phenotypes. iScience, 29(5), 115045.

Mulaudzi S, et al. (2026) Benchmarking within-sample minority variant detection with short-read sequencing in M. tuberculosis. bioRxiv : the preprint server for biology.

Wang D, et al. (2026) Seroprevalence, isolation, comprehensive characterization, and pathogenicity of Clostridium perfringens strain from yak in Xizang, China. Scientific reports, 16(1).

Senavirathna I, et al. (2026) Genomic analysis of human-infecting Leptospira borgpetersenii isolates in Sri Lanka: Expanded PF07598 gene family repertoire and less genome reduction than bovine isolates. PLoS neglected tropical diseases, 20(3), e0012540.

Zhang H, et al. (2026) Integrated metatranscriptomics identifies Lachnospiraceae as keystone taxa regulating rumen biohydrogenation and milk ω -6/ ω -3 polyunsaturated fatty acids ratio in dairy cows. Microbiome, 14(1).

Flatau R, et al. (2026) Metabolic potential structures gill symbiont communities in two common shipworm species. The ISME journal, 20(1).

He G, et al. (2026) A novel Schinkia sp. respire nitrous oxide over a broad pH range. Applied and environmental microbiology, 92(6), e0006926.

Xiang N, et al. (2026) Decoding coral resistance to eutrophication through the association of hyper-efficient denitrifiers as key microbial allies. Nature communications, 17(1).

Yabe S, et al. (2026) Chromid-like secondary replicons as predicted key sites of biosynthetic gene clusters in Ktedonobacteria. mSystems, 11(6), e0019726.

González-Navarro MP, et al. (2026) Phenotypic and whole genome characterization of multidrug-resistant Campylobacter coli from chicken liver. Poultry science, 105(10),

107271.

Yue M, et al. (2026) Natural Pigment Production by *Bacillus velezensis* YM-3 Isolated from Traditional Pixian Douban Condiment: Biosynthesis Pathway, Structural Characterization, and Bioactivities. *Foods* (Basel, Switzerland), 15(12).

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.

Lee S, et al. (2026) Peptidoglycan from *Bifidobacterium adolescentis* enhances IL-10 production in regulatory B cells to alleviate gut inflammation. *Gut microbes*, 18(1), 2611603.

Rondinelli M, et al. (2026) Variations in carbapenem resistance associated with the VIM-1 metallo- β -lactamase across the Enterobacterales. *Microbiology* (Reading, England), 172(1).

Latrofa MS, et al. (2026) Nuclear, mitochondrial, and *Wolbachia* endosymbiont genomes of *Onchocerca lupi*, Portugal. *mSphere*, 11(2), e0062525.

Nibbering B, et al. (2026) Characterization of the clade 4 non-toxigenic *C. difficile* isolate L-NTCD03 carrying the cfr(B) gene. *FEMS microbes*, 7, xtag010.

Xu T, et al. (2026) Genophenotypic insights into biocontrol and growth-promoting mechanisms of *Bacillus velezensis* BV25 against tomato *Fusarium* wilt. *BMC microbiology*, 26(1).

Taheri N, et al. (2026) Genomic characterization of Enterotoxigenic *Escherichia coli* lineage 2 (CS2 + CS3) by long-read sequencing reveals distinct lineage-specific genome organization. *Scientific reports*, 16(1).

Jordi SBU, et al. (2026) StrainCascade: An automated, modular workflow for high-throughput long-read bacterial genome reconstruction and characterization. *iScience*, 29(6), 116189.

Tao J, et al. (2026) Identification of a novel SXT/R391 integrative and conjugative element harboring bla NDM-1 in a clinical *Providencia huaxiensis* isolate. *Frontiers in microbiology*, 17, 1818759.