

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

Circleator

RRID:SCR_002801

Type: Tool

Proper Citation

Circleator (RRID:SCR_002801)

Resource Information

URL: <http://jonathancrabtree.github.io/Circleator/>

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Description: A Perl-based visualization software tool that generates circular figures of genome-associated data. Common uses of the tool include: * Displaying the sequence and/or genes in a GenBank flat file. * Highlighting differences and/or similarities in gene content between related organisms. * Comparing SNPs and indels between closely-related strains or serovars. * Comparing gene expression values across multiple samples or timepoints. * Visualizing coverage plots of RNA-Seq read alignments.

Synonyms: Charm City Circleator

Resource Type: data visualization software, software resource, software application, data processing software

Defining Citation: [PMID:25075113](#)

Keywords: standalone software, perl

Availability: Free, Freely available, Available for download

Resource Name: Circleator

Resource ID: SCR_002801

Alternate IDs: OMICS_05206

Alternate URLs: <https://github.com/jonathancrabtree/Circleator/>

License: Artistic License, v2

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260729T044040+0000

Ratings and Alerts

No rating or validation information has been found for Circlearator.

No alerts have been found for Circlearator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Salamzade R, et al. (2023) Comparative Genomic and Metagenomic Investigations of the *Corynebacterium tuberculostearicum* Species Complex Reveals Potential Mechanisms Underlying Associations To Skin Health and Disease. *Microbiology spectrum*, 11(1), e0357822.

Trevisan B, et al. (2021) Comparative Characterization of Mitogenomes From Five Orders of Cestodes (Eucestoda: Tapeworms). *Frontiers in genetics*, 12, 788871.

Majander K, et al. (2020) Ancient Bacterial Genomes Reveal a High Diversity of *Treponema pallidum* Strains in Early Modern Europe. *Current biology : CB*, 30(19), 3788.

Larriba E, et al. (2018) The landscape of mitochondrial small non-coding RNAs in the PGCs of male mice, spermatogonia, gametes and in zygotes. *BMC genomics*, 19(1), 634.

Schiettekatte O, et al. (2018) Characterization of LE3 and LE4, the only lytic phages known to infect the spirochete *Leptospira*. *Scientific reports*, 8(1), 11781.

Chen R, et al. (2017) Whole genome sequences of three Clade 3 *Clostridium difficile* strains carrying binary toxin genes in China. *Scientific reports*, 7, 43555.

Florea M, et al. (2016) Genome sequence and plasmid transformation of the model high-yield bacterial cellulose producer *Gluconacetobacter hansenii* ATCC 53582. *Scientific reports*, 6, 23635.

Eloe-Fadrosh EA, et al. (2015) Functional dynamics of the gut microbiome in elderly people during probiotic consumption. *mBio*, 6(2).