Resource Summary Report

Generated by NIF on Apr 22, 2025

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

Defining Citation: PMID:25075113

Keywords: standalone software, perl

Funding:

Availability: Artistic License, v2

Resource Name: Circleator

Resource ID: SCR_002801

Alternate IDs: OMICS_05206

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250422T055043+0000

Ratings and Alerts

No rating or validation information has been found for Circleator.

No alerts have been found for Circleator.

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 NIF.

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).