Resource Summary Report

Generated by NIF on May 25, 2025

BioCircos

RRID:SCR_025055
Type: Tool

Proper Citation

BioCircos (RRID:SCR_025055)

Resource Information

URL: https://github.com/cran/BioCircos

Proper Citation: BioCircos (RRID:SCR_025055)

Description: Software R package for generating circular multi-track plots.

Resource Type: software resource, software toolkit

Keywords: generating circular multi-track plots, generating plots,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: BioCircos

Resource ID: SCR_025055

Alternate URLs: https://github.com/lvulliard/BioCircos.R, https://cran.r-project.org/web/packages/BioCircos/vignettes/BioCircos.html

License: GNU GPL v2

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Ratings and Alerts

No rating or validation information has been found for BioCircos.

No alerts have been found for BioCircos.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Bhattacharjee A, et al. (2024) An integrated comparative genomics, subtractive proteomics and immunoinformatics framework for the rational design of a Pan-Salmonella multi-epitope vaccine. PloS one, 19(7), e0292413.

Fukuda N, et al. (2024) Cell cycle arrest combined with CDK1 inhibition suppresses genome-wide mutations by activating alternative DNA repair genes during genome editing. The Journal of biological chemistry, 300(9), 107695.

Sigova EA, et al. (2024) Complete Annotated Genome Assembly of Flax Pathogen Colletotrichum lini. Journal of fungi (Basel, Switzerland), 10(9).

Ostrem BEL, et al. (2024) Fetal brain response to maternal inflammation requires microglia. Development (Cambridge, England), 151(10).

Karlsson J, et al. (2024) Early evolutionary branching across spatial domains predisposes to clonal replacement under chemotherapy in neuroblastoma. Nature communications, 15(1), 8992.

Manaka Y, et al. (2024) Single base substitution signatures 17a, 17b, and 40 are induced by ?-ray irradiation in association with increased reactive oxidative species. Heliyon, 10(6), e28044.

Liu Y, et al. (2024) MECP2 directly interacts with RNA polymerase II to modulate transcription in human neurons. Neuron, 112(12), 1943.

Yang Z, et al. (2023) CottonMD: a multi-omics database for cotton biological study. Nucleic acids research, 51(D1), D1446.

Menzel M, et al. (2023) Accurate tumor purity determination is critical for the analysis of homologous recombination deficiency (HRD). Translational oncology, 35, 101706.

Jähne J, et al. (2023) Novel Plant-Associated Brevibacillus and Lysinibacillus Genomospecies Harbor a Rich Biosynthetic Potential of Antimicrobial Compounds.

Microorganisms, 11(1).

Jones A, et al. (2023) Cost-conscious generation of multiplexed short-read DNA libraries for whole-genome sequencing. PloS one, 18(1), e0280004.

Yang X, et al. (2023) GATA2 co-opts TGF?1/SMAD4 oncogenic signaling and inherited variants at 6q22 to modulate prostate cancer progression. Journal of experimental & clinical cancer research : CR, 42(1), 198.

Bobba S, et al. (2023) Mycobacterium tuberculosis carrying the rifampicin drug-resistance-conferring rpoB mutation H445Y is associated with suppressed immunity through type I interferons. mBio, 14(5), e0094623.

Caruana L, et al. (2022) Rubiscosome gene expression is balanced across the hexaploid wheat genome. Photosynthesis research, 152(1), 1.

Zhao X, et al. (2022) CircleBase: an integrated resource and analysis platform for human eccDNAs. Nucleic acids research, 50(D1), D72.

Ai W, et al. (2022) Deep Sequencing of HPV16 E6 Region Reveals Unique Mutation Pattern of HPV16 and Predicts Cervical Cancer. Microbiology spectrum, 10(4), e0140122.

Mould DL, et al. (2022) Metabolic basis for the evolution of a common pathogenic Pseudomonas aeruginosa variant. eLife, 11.

Gauthier CH, et al. (2022) DEPhT: a novel approach for efficient prophage discovery and precise extraction. Nucleic acids research, 50(13), e75.

Pulami D, et al. (2021) Acinetobacter stercoris sp. nov. isolated from output source of a mesophilic german biogas plant with anaerobic operating conditions. Antonie van Leeuwenhoek, 114(3), 235.

Balnis J, et al. (2021) Blood DNA methylation and COVID-19 outcomes. Clinical epigenetics, 13(1), 118.