

Resource Summary Report

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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 toolkit, software resource

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

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

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Gajigan AP, et al. (2025) A dinoflagellate-infecting giant virus with a micron-length tail. *bioRxiv : the preprint server for biology*.

Matsumoto M, et al. (2025) Role of PRC2 in the stochastic expression of Aire target genes and development of mimetic cells in the thymus. *The Journal of experimental medicine*, 222(7).

Davoodi P, et al. (2025) Multi-Genome-Wide association studies provide new insights into the genetic architecture of Varroa resistance in honeybees. *BMC genomics*, 26(1), 1156.

Wu R, et al. (2025) Reconfiguration of DNA methylation at growth resumption after winter dormancy in Kiwifruit. *Scientific reports*, 15(1), 43077.

Zhao S, et al. (2025) FuSViz-visualization and interpretation of structural variation using cancer genomics and transcriptomics data. *Nucleic acids research*, 53(4).

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.

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.

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).

Manaka Y, et al. (2024) Single base substitution signatures 17a, 17b, and 40 are induced by γ -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.

Jähne J, et al. (2023) Novel Plant-Associated *Brevibacillus* and *Lysinibacillus* Genomes Harbor a Rich Biosynthetic Potential of Antimicrobial Compounds. *Microorganisms*, 11(1).

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

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

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

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.

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

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