

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 resource, software toolkit

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 44 mentions in open access literature.

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

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

Kusumoto-Matsuo R, et al. (2026) Genome instability is increased during DNA replication in the presence of the CPD UV photoproduct in transcriptionally active genes. *iScience*, 29(7), 116322.

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.

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).

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

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

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

Carrasco-Martin M, et al. (2025) Insights on genomic profiles of drug resistance and virulence in a cohort of *Leishmania infantum* isolates from the Mediterranean area. *Parasites & vectors*, 19(1), 28.

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.

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

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

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).

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.

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 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.