

# 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

**Record Creation Time:** 20240305T200904+0000

**Record Last Update:** 20260829T183342+0000

### 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 [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.

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.

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

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).

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.

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.

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

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.

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

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