

# Resource Summary Report

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## BioCircos

RRID:SCR\_025055

Type: Tool

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### Proper Citation

BioCircos (RRID:SCR\_025055)

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### 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

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

**Record Last Update:** 20250402T062028+0000

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### Ratings and Alerts

No rating or validation information has been found for BioCircos.

No alerts have been found for BioCircos.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 36 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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.

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  $\gamma$ -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.

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

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.

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.

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) Rubiscolome 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.

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

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.

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.